Contract No. HHSN272201200010C

Immune Epitope Database and Analysis Program

2017 Annual IEDB Compendium

La Jolla Institute for Allergy and Immunology
9420 Athena Circle
La Jolla, CA 92037

858-752-6647
858-752-6987 (fax)
smartini@lji.org

2 November 2018

Table of Contents

Table of Figures

Introduction

The Immune Epitope Database and Analysis Resource (IEDB) is a public repository of immune epitope data and is sponsored by the National Institute for Allergy and Infectious Diseases (NIAID). The IEDB development started in December 2003 and it became available to the public in a beta test phase on 15 February 2006. The IEDB primarily contains data related to antibody and T cell epitopes for humans, non-human primates, rodents, and other animal species. The IEDB also makes available a variety of analytical and epitope prediction tools and resources within its Analysis Resource.

This thirteenth Annual Compendium of the Immune Epitope Database and Analysis Resource, and consists of three sections. The first section contains a list of the antibody and T cell epitope information in the database as of 9 January 2018. The second section describes the features of the IEDB 3.8 website and the Analysis Resource 2.18. The third section lists the scientific publications in 2017 for which the IEDB played a contributory role.

Since the publication of last year's 2016 Annual Compendium, the quantity of data available in the IEDB has increased significantly with the addition of 796 fully curated references and 11 data submissions. The curation of peptidic and non-peptidic epitope data relating to all infectious diseases (excluding HIV), allergens, autoimmune diseases, and transplant/alloantigens, has been kept current throughout the year.

1 Antibody and T Cell Epitopes

Many new references and many new species were added to the IEDB in 2017, as demonstrated in Table 1.1. The table lists the number of distinct B cell and T cell epitopes in the database by source species at the end of 2016 and 2017. Of the 3,502 species/strains listed, 76 were added in 2017. It should be noted that the source organism is the species/strain from which the epitopes originate, and may not be from an infecting organism or vaccine target. The curation of MHC binding peptides, cross-reactive epitopes, and autoimmune epitopes has resulted in the appearance of human (Homo sapiens) and mouse (Mus musculus) epitopes on the list.

In the table below, the leftmost column labeled "New" indicates with an "X" if epitopes for the species/strain was added to the IEDB in 2017. A font color of red is used to highlight the information in the row. The Organism ID matches the NCBI taxonomy ID if it exists. Otherwise it represents an IEDB-assigned identifier, which are eight digit numbers starting with "1000". These are easily distinguishable from the NCBI identifiers which are six digits or less. The columns labeled "B-15", "T-15", "B-16", and "T-16" indicate the cumulative number of distinct B cell and T cell epitopes in the database at the end of 2016 and 2017, respectively. The two rightmost columns display the differences in the B and T cell epitope counts from 2016 to 2017. The changes in B and T cell epitope counts are shown in red. In 2017, the number of B cell epitopes increased by 3,842 from 40,904 to 44,746, and the number of T cell epitopes increased by 154,555 from 233,724 to 388,279.

Table 1.1 Summary of B and T cell epitopes contained in the IEDB

ID	NEW	ORGANISM_ID	SPECIES_STRAIN	B_16	T_16	B_17	T_17	D_B	D_T
237		3816	Abrus precatorius	1		1			
317		5755	Acanthamoeba castellanii	14	3	14	3		
1325		57068	Acanthisitta chloris		1		1		
247		4026	Acer pseudoplatanus	1		1			
1530		104102	Acetobacter tropicalis		1		1		
1510		97477	Acetomicrobium mobile		1		1		
202		2147	Acholeplasma	1		1			
1929		264635	Acholeplasma granularum	1		1			
203		2148	Acholeplasma laidlawii		2		2		
2989		1003200	Achromobacter insuavis AXX-A	1		1			
1409		72556	Achromobacter piechaudii	1		1			
2223		349163	Acidiphilium cryptum JF-5		1		1		
101		920	Acidithiobacillus ferrooxidans		1		1		
3038		1214225	Acidocella sp. MX-AZ02	1		1			
2239		351607	Acidothermus cellulolyticus 11B		2		2		
36		470	Acinetobacter baumannii		1		1		
2502		400667	Acinetobacter baumannii ATCC 17978	10	13	10	13		
2747		509173	Acinetobacter baumannii AYE		1		1		
37		471	Acinetobacter calcoaceticus		1		1		
1057		29430	Acinetobacter haemolyticus	1		1			
3512		10001530	Acinetobacter haemolyticus strain 57	1		1			
3513		10001531	Acinetobacter haemolyticus strain 61	1		1			
1239		40214	Acinetobacter johnsonii		1		1		
3501		10001503	Acinetobacter lwoffii F78	1		1			
1369		62977	Acinetobacter sp. ADP1		2		2		
437		7902	Acipenser gueldenstaedtii	1		1			
82		715	Actinobacillus pleuropneumoniae		1		1		
1852		228399	Actinobacillus pleuropneumoniae serovar 1 str. 4074	2	1	2	1		
2577		416269	Actinobacillus pleuropneumoniae serovar 5b str. L20		1		1		
1789		209841	Actinobacillus pleuropneumoniae serovar 7	1		1			
1971		272636	Adeno-associated virus		18		18		
1462		85106	Adeno-associated virus - 1		11		11		
660		10804	Adeno-associated virus - 2	42	81	42	81		
1439		82300	Adeno-associated virus - 5	9		9			
1759		202812	Adeno-associated virus - 7		2		2		
1760		202813	Adeno-associated virus - 8	17	14	17	14		
1870		235455	Adeno-associated virus 9	9		9			
419		7160	Aedes albopictus	7		7			
263		4494	Aegilops markgrafii		1		1		
262		4487	Aegilops searsii	1		1			
1216		37682	Aegilops tauschii		1		1		
360		6100	Aequorea victoria	3	5	3	5		
1531		105751	Aeromonas bestiarum		1		1		
71		644	Aeromonas hydrophila	4	1	7	2	3	1
72		645	Aeromonas salmonicida	59		59			
1063		29491	Aeromonas salmonicida subsp. salmonicida		1		1		
1324		56636	Aeropyrum pernix	3		3			
1959		272557	Aeropyrum pernix K1		2		2		

1549		117204	African horse sickness virus 3	21		21			
1187		36421	African horse sickness virus 4	28	4	42	4	14	
608		10497	African swine fever virus	1		1			
609		10498	African swine fever virus BA71V	46		46			
1468		85777	Agelas mauritiana		1		1		
81		714	Aggregatibacter actinomycetemcomitans	1	4	1	4		
3536		10001628	Aggregatibacter actinomycetemcomitans serotype b str. Y4	1		1			
32		358	Agrobacterium tumefaciens	1	1	1	1		
927		11966	Aids-associated retrovirus		2		2		
3362		10000828	Ajellomyces dermatitidis ATCC 60636		2		2		
1384		65690	AK7 murine leukemia virus		1		1		
910		11791	AKR (endogenous) murine leukemia virus		12		12		
909		11790	AKT8 murine leukemia virus	1		1			
42		511	Alcaligenes faecalis	3	1	3	1		
43		512	Alcaligenes sp.		1		1		
652		10783	Aleutian mink disease parvovirus (STRAIN G)	3		3			
1037		28314	Aleutian mink disease virus	3		9		6	
3046		1263035	Alistipes finegoldii CAG:68		1		1		
1687		172148	Alkhumra hemorrhagic fever virus		4		4		
220		3517	Alnus glutinosa		17		17		
488		9502	Alouatta caraya	1		1			
2149		333754	Alphapapillomavirus 10	4		4			
2155		333766	Alphapapillomavirus 13		1		1		
2178		337043	Alphapapillomavirus 4		1		1		
2177		337042	Alphapapillomavirus 7	9		9			
300		5599	Alternaria alternata	5	36	5	36		
1026		28108	Alteromonas macleodii		1		1		
2088		314275	Alteromonas mediterranea		1		1		
1915		261202	Alto Paraguay hantavirus		3		3		
1271		45218	Amapari mammarenavirus		3		3		
3065		1338344	Ambigolimax valentianus	1		1			
3095		1581419	Amblyomma sculptum	1		1			
257		4212	Ambrosia artemisiifolia	4	215	4	215		
259		4215	Ambrosia artemisiifolia var. elatior	9	12	9	12		
1069		29715	Ambrosia psilostachya		10		10		
258		4214	Ambrosia trifida		10		10		
2754	X	515817	Amphioctopus fangsiao			1		1	
1474		86782	Amur virus		35		35		
1682		170955	Amur virus Solovey/AP63/1999		2		2		
1686		171929	Anacardium occidentale	64		64	10		10
280		4615	Ananas comosus	3		3			
87		769	Anaplasma centrale		2		2		
2822	X	574556	Anaplasma centrale str. Israel				2		2
88		770	Anaplasma marginale	17	14	17	14		
3313		10000760	Anaplasma marginale South Idaho		2		2		
2115		320483	Anaplasma marginale str. Florida	19	61	19	61		
1868		234826	Anaplasma marginale str. St. Maries	16	22	16	28		6
104		948	Anaplasma phagocytophilum	29		29			
1798		212042	Anaplasma phagocytophilum str. HZ	21		21			
3519		10001573	Anatid herpesvirus 1 Clone-03	1		1			
1310		53326	Ancylostoma ceylanicum		1		1		

3112		1980456	Andes orthohantavirus	2	77	2	77		
3280		10000553	Andes virus CHI-7913	53		53			
400		6858	Androctonus australis	9		9			
1400		70175	Androctonus australis hector	24		24			
401		6860	Androctonus mauritanicus mauritanicus	1		1			
2160		334426	Angiostrongylus costaricensis	1	1	1	1		
1346		59799	Angomonas deanei		2		2		
377		6269	Anisakis simplex	38	28	38	28		
1629		155017	Anogeissus	1		1			
420		7165	Anopheles gambiae	8	2	8	2		
1699		180454	Anopheles gambiae str. PEST	6	2	6	2		
1074	X	30069	Anopheles stephensi			1		1	
1149		33934	Anoxybacillus flavithermus		1		1		
470		8845	Anser cygnoides	2		2			
1067		29661	Anthoxanthum odoratum		3		3		
489		9505	Aotus trivirgatus	1		1			
428		7460	Apis mellifera	14	106	15	106	1	
429		7469	Apis mellifera ligustica		1		1		
249		4045	Apium graveolens		14		14		
1373		63363	Aquifex aeolicus	2		2			
1837		224324	Aquifex aeolicus VF5	1	4	1	4		
227		3702	Arabidopsis thaliana	2	10	2	10		
1758		201444	Aracatuba virus		5		5		
238		3818	Arachis hypogaea	445	193	455	193	10	
2076		308159	Araucaria virus		6		6		
3401		10000980	Arcanobacterium pyogenes Strain 42	4		4			
204	X	2234	Archaeoglobus fulgidus			1		1	
1838		224325	Archaeoglobus fulgidus DSM 4304		1		1		
832		11618	Arenavirus		2		2		
228		3704	Armoracia rusticana	5		5			
393		6661	Artemia franciscana	2		2			
260		4220	Artemisia vulgaris	1	70	1	70		
2015		290399	Arthrobacter sp. FB24		2		2		
3052	X	1285902	Artificial vector pGEX-2T			1		1	
375		6253	Ascaris suum	1	1	1	1		
2949		746128	Aspergillus fumigatus	126	86	126	86		
2656		451804	Aspergillus fumigatus A1163		13		13		
2134		330879	Aspergillus fumigatus Af293		18		18		
286		5061	Aspergillus niger		1		1		
288		5067	Aspergillus parasiticus		1		1		
287		5064	Aspergillus restrictus	1		1			
1134		33178	Aspergillus terreus	2		2			
2190		341663	Aspergillus terreus NIH2624	2		2			
490		9509	Ateles geoffroyi		1		1		
491		9510	Ateles paniscus	1		1			
492		9511	Ateles sp.	1		1			
2010		287752	Aurantimonas manganoxydans SI85-9A1		1		1		
1283		46015	Autographa californica nucleopolyhedrovirus		1		1		
264		4497	Avena nuda		1		1		
265		4498	Avena sativa		15		15		
761		11176	Avian avulavirus 1	14	5	14	5		
916		11861	Avian erythroblastosis virus	1		1			

1689		172851	Avian hepatitis E virus	20		20			
3654		10002165	Avian infectious bronchitis virus (strain CHINA/Sczy3/09)	2		2			
3655		10002169	Avian infectious bronchitis virus (strain Holte)		2		2		
749		11127	Avian infectious bronchitis virus (strain M41)	4	3	4	3		
1860		231428	Avian infectious bronchitis virus (strain Vic S)	11	8	11	8		
917		11864	Avian leukosis virus	1		2		1	
3076		1401444	Avian leukosis virus ev/J	5		5			
2300		363020	Avian leukosis virus HPRS103	1		1			
3615		10001967	Avian leukosis virus isolate CAUHM01	1		1			
3614		10001965	Avian leukosis virus strain NX0101	1		1			
1220		38171	Avian reovirus strain S1133	5		5			
1740		195700	Avian rotavirus PO-13	6		6			
31		354	Azotobacter vinelandii		2		2		
2120		322710	Azotobacter vinelandii DJ		2		2		
353		5866	Babesia bigemina		3		3		
352		5865	Babesia bovis	3	8	3	8		
3488		10001459	Babesia bovis Argentina R1A	4		4			
3185		10000382	Babesia bovis Mexico	1	4	1	4		
3186		10000383	Babesia bovis Mexico Mo7	1	33	1	33		
354		5868	Babesia microti	2		2			
1556		120505	Baboon cytomegalovirus		1		1		
1742		196403	Baboon endogenous virus	1	1	1	1		
905		11764	Baboon endogenous virus strain M7	1		1			
142		1390	Bacillus amyloliquefaciens	18	3	18	3		
143		1392	Bacillus anthracis	399	203	399	203		
2699		486619	Bacillus anthracis str. A0193		3		3		
2835		592021	Bacillus anthracis str. A0248		1		1		
2702		486623	Bacillus anthracis str. A0389		5		5		
2701		486621	Bacillus anthracis str. A0442		1		1		
2700		486620	Bacillus anthracis str. A0465		5		5		
2703		486624	Bacillus anthracis str. A0488		91		91		
1729		191218	Bacillus anthracis str. A2012		29		29		
1753		198094	Bacillus anthracis str. Ames		2		2		
1917		261594	Bacillus anthracis str. 'Ames Ancestor'		1		1		
2814		568206	Bacillus anthracis str. CDC 684		3		3		
1912		260799	Bacillus anthracis str. Sterne	5	4	5	4		
3131		10000291	Bacillus anthracis str. Sterne 34F2	1		1			
2532		405536	Bacillus anthracis str. Tsiankovskii-I		1		1		
1799		212045	Bacillus anthracis str. Western North America USA6153		1		1		
144		1396	Bacillus cereus	1	5	1	5		
2818		572264	Bacillus cereus 03BB102		2		2		
2655		451709	Bacillus cereus 03BB108		8		8		
2531		405533	Bacillus cereus AH1134		3		3		
1825		222523	Bacillus cereus ATCC 10987		1		1		
1847		226900	Bacillus cereus ATCC 14579		2		2		
2773		526977	Bacillus cereus ATCC 4342		1		1		
2530		405532	Bacillus cereus B4264		1		1		
2772		526974	Bacillus cereus BDRD-ST24		1		1		
2219		347495	Bacillus cereus F837/76		1		1		
1949		269801	Bacillus cereus G9241		41		41		

2529		405531	Bacillus cereus G9842		3		3		
2654		451708	Bacillus cereus H3081.97		12		12		
2653		451707	Bacillus cereus NVH0597-99		7		7		
2533		405917	Bacillus cereus W		1		1		
1387		66692	Bacillus clausii KSM-K16		1		1		
2633		441769	Bacillus coahuilensis m4-4		1		1		
2098		315749	Bacillus cytotoxicus NVH 391-98		3		3		
152		1467	Bacillus lentus		1		1		
145		1402	Bacillus licheniformis		10		10		
146		1404	Bacillus megaterium		1		1		
2097		315730	Bacillus mycoides KBAB4		5		5		
147		1408	Bacillus pumilus		1		1		
2086		313627	Bacillus sp. NRRL B-14911		2		2		
149		1423	Bacillus subtilis	2	4	2	4		
1836		224308	Bacillus subtilis subsp. subtilis str. 168		1		1		
2785		535026	Bacillus subtilis subsp. subtilis str. NCIB 3610		1		1		
150		1428	Bacillus thuringiensis	7	1	7	1		
2775		527019	Bacillus thuringiensis IBL 200		1		1		
2183		339854	Bacillus thuringiensis serovar israelensis ATCC 35646		7		7		
1053		29339	Bacillus thuringiensis serovar kurstaki	3		3			
2778		527029	Bacillus thuringiensis serovar pondicheriensis BGSC 4BA1		1		1		
151		1435	Bacillus thuringiensis serovar san diego		2		2		
2777		527026	Bacillus thuringiensis serovar sotto str. T04001		1		1		
2776		527024	Bacillus thuringiensis serovar tochigiensis BGSC 4Y1		1		1		
2564		412694	Bacillus thuringiensis str. Al Hakam		8		8		
1		2	Bacteria	45		45			
2696		483215	Bacteroides finegoldii DSM 17565		1		1		
99		817	Bacteroides fragilis		3		3		
2133		329854	Bacteroides intestinalis		1		1		
2882		667015	Bacteroides salanitronis DSM 18170		1		1		
2830	X	585544	Bacteroides sp. D22			1		1	
1846		226186	Bacteroides thetaiotaomicron VPI-5482		1		1		
2823	X	575590	Bacteroidetes oral taxon 274 str. F0058			1		1	
2996	X	1016852	Banana streak CA virus			5		5	
2128	X	328670	Banana streak GF virus			4		4	
2997	X	1016853	Banana streak IM virus			10		10	
3090	X	1476909	Banana streak MY virus			39		39	
2129	X	328671	Banana streak OL virus			4		4	
935		12040	Barley yellow dwarf virus-PAV	1		1			
2288		360095	Bartonella bacilliformis KC583		1		1		
1995		283166	Bartonella henselae str. Houston-1	1	1	1	1		
2224		349344	Bat SARS CoV Rp3/2004		1		1		
3113		1980459	Bayou orthohantavirus	1		1			
989		12260	Bean pod mottle virus	2		2			
1116		31715	Bean-pod mottle virus (strain Kentucky G7)	9	1	9	1		
1117		31721	Beet necrotic yellow vein virus	10		10			
978		12161	Beet yellows virus	5		5			
106		1022	Beggiatoa alba	1		1			
224		3645	Bertholletia excelsa	7	24	7	24		

1657		161934	Beta vulgaris	5		5			
3048		1263720	Betacoronavirus England 1	4		5		1	
218		3505	Betula pendula	75	331	76	335	1	4
167		1681	Bifidobacterium bifidum		1		1		
1774		205913	Bifidobacterium longum DJO10A		2		2		
1896	X	246618	Bifidobacterium thermacidophilum			1		1	
3572		10001761	BK polyomavirus strain Dunlop		1		1		
642	X	10631	BK virus strain AS				1		1
1386		65743	Blackcurrant reversion virus	2		2			
3019		1146883	Blastococcus saxobsidens DD2		1		1		
285		5039	Blastomyces dermatitidis		1		1		
2646		447095	Blastomyces dermatitidis ATCC 26199		1		1		
412		6973	Blattella germanica	23	501	23	501		
1242		40697	Blomia tropicalis	19		19	6		6
1238		40051	Bluetongue virus	9		9			
670		10904	Bluetongue virus (serotype 1 / isolate Australia)	7		7			
668		10900	Bluetongue virus (serotype 10 / American isolate)	3		3			
1138		33717	Bluetongue virus (serotype 13 / isolate USA)	2		2			
1139		33718	Bluetongue virus (serotype 17 / isolate USA)	4		4			
1164		35327	Bluetongue virus 1	4		4			
671		10906	Bluetongue virus 10	3		3			
1165		35329	Bluetongue virus 11	6		6			
1500		94966	Bluetongue virus 12	15		15			
1166		35330	Bluetongue virus 13	1		1			
1167		35331	Bluetongue virus 15	7		7			
1269		45029	Bluetongue virus 16	3		3			
3634		10002028	Bluetongue virus 16 Beatrice Hill/1987	2		2			
3622		10002006	Bluetongue virus 16 BN96/16	2		2			
3633		10002027	Bluetongue virus 16 Kumamoto/1985	2		2			
669		10903	Bluetongue virus 17	4		4			
1501		94967	Bluetongue virus 4	7		7			
1751		197780	Bluetongue virus 8	2	21	2	21		
2462		388634	Bombyx mandarina nuclear polyhedrosis virus		1		1		
1957		271108	Bombyx mori nucleopolyhedrovirus	2		2			
2296		360910	Bordetella avium 197N		1		1		
44		518	Bordetella bronchiseptica		1		1		
45		520	Bordetella pertussis	336	218	338	218	2	
3638		10002069	Bordetella pertussis 509		7		7		
1910		257313	Bordetella pertussis Tohama I		11		11		
993		12455	Borna disease virus	8	4	8	4		
3260		10000518	Borna disease virus Giessen strain He/80	6		6			
2465		390236	Borrelia afzelii PKo	2		2			
2723		498740	Borrelia burgdorferi 64b		2		2		
1839		224326	Borrelia burgdorferi B31	103	10	104	10	1	
3440		10001091	Borrelia burgdorferi BEP4	1		1			
3291		10000675	Borrelia burgdorferi CA12		6		6		
2765		521007	Borrelia burgdorferi N40	4	3	4	3		
2643		445985	Borrelia burgdorferi ZS7	2	45	2	45		
2561		412419	Borrelia duttonii Ly	7		7			
3270		10000530	Borrelia garinii IP90	3		3			
1065		29518	Borreliella afzelii	2	1	5	1	3	

2017		290434	Borreliella bavariensis PBi	1		1			
4		139	Borreliella burgdorferi	64	41	65	41	1	
1066		29519	Borreliella garinii	5	29	5	29		
1406	X	72004	Bos mutus				1		1
527		9913	Bos taurus	1258	806	1300	821	42	15
462		8722	Bothrops asper	1		1			
463		8725	Bothrops atrox	5		5			
464		8726	Bothrops jararacussu	13		13			
570		10320	Bovine alphaherpesvirus 1	5	40	5	40		
750		11128	Bovine coronavirus	7		7			
3629		10002018	Bovine coronavirus Kakegawa	1		1			
1863		233262	Bovine enteric coronavirus (strain 98TXSF-110-ENT)		1		1		
939		12065	Bovine enterovirus strain VG-5-27	6		6			
3232		10000472	Bovine ephemeral fever virus BB7721	2		2			
3195		10000404	Bovine herpesvirus 1 Lam	1		1			
1925		263683	Bovine herpesvirus 5 strain TX89	2		2			
1432		79889	Bovine herpesvirus type 1.1	2		2			
571		10323	Bovine herpesvirus type 1.1 (strain Cooper)	9	17	9	17		
572		10324	Bovine herpesvirus type 1.1 (strain P8-2)	1		1			
919		11901	Bovine leukemia virus	108	40	108	40		
782		11246	Bovine orthopneumovirus	3	2	3	2		
617		10560	Bovine papillomavirus type 2	15		15			
618		10562	Bovine papillomavirus type 4	10	3	10	3		
1583		129727	Bovine papular stomatitis virus		2		2		
1091		31611	Bovine respiratory syncytial virus (strain 391-2)	3		3			
783		11249	Bovine respiratory syncytial virus (strain RB94)	4		4			
1444		82823	Bovine respiratory syncytial virus strain lelystad	1		1			
1445		82824	Bovine respiratory syncytial virus strain snook	1	75	1	75		
772		11215	Bovine respirovirus 3	3	1	3	1		
676		10927	Bovine rotavirus	9	1	9	1		
1188		36439	Bovine rotavirus strain NCDV/G6	1		1			
677		10933	Bovine rotavirus strain RF	12	7	12	7		
678		10934	Bovine rotavirus strain UK/G6		1		1		
738		11099	Bovine viral diarrhea virus 1	1	12	1	12		
739		11100	Bovine viral diarrhea virus 1-NADL	4	3	4	3		
1313		54315	Bovine viral diarrhea virus 2	1		1			
1441		82470	Bovine viral diarrhea virus strain Oregon C24V	5	3	5	3		
1646		158474	Bovine viral diarrhea virus strain Trangie Y546	1		1			
1823		221918	Bovine viral diarrhea virus VEDEVAC	6		6			
1020		15368	Brachypodium distachyon	1		1			
2011		288000	Bradyrhizobium sp. BTAi1		1		1		
229		3707	Brassica juncea	9		9			
12		234	Brucella		28		28		
13		235	Brucella abortus	6	36	7	36	1	
2286		359391	Brucella abortus 2308		31		31		
1921		262698	Brucella abortus bv. 1 str. 9-941		1		1		
2759		520450	Brucella abortus bv. 2 str. 86/8/59		1		1		
2824		575591	Brucella abortus NCTC 8038		1		1		

2611		430066	Brucella abortus S19		15		15		
2850		641140	Brucella abortus str. 2308 A		1		1		
3484		10001424	Brucella abortus W99	1		1			
2695		483179	Brucella canis ATCC 23365		9		9		
1060		29459	Brucella melitensis	15	93	17	93	2	
1841		224914	Brucella melitensis bv. 1 str. 16M	6	16	6	16		
2760		520464	Brucella melitensis bv. 1 str. Rev.1	1		1			
2938		703352	Brucella melitensis M5-90		26	5	26	5	
14		236	Brucella ovis		1		1		
3597		10001886	Brucella ovis 020	2		2			
3599		10001888	Brucella ovis 63/290	1		1			
2636		444178	Brucella ovis ATCC 25840		10		10		
3598		10001887	Brucella ovis Reo 198	1		1			
1061		29461	Brucella suis	1	7	1	7		
1771		204722	Brucella suis 1330	1	29	1	29		
2677		470137	Brucella suis ATCC 23445	1	6	1	6		
378		6279	Brugia malayi	3	5	10	5	7	
379		6280	Brugia pahangi	1		1			
1487		89462	Bubalus bubalis	7	1	7	1		
1129		32605	Buffalopox virus		1		1		
2809		565995	Bundibugyo ebolavirus	7		7			
451		8613	Bungarus fasciatus	1		1			
452		8616	Bungarus multicinctus	17	3	17	3		
1120		32008	Burkholderia	1		1			
2182		339670	Burkholderia ambifaria AMMD		4		4		
1503		95486	Burkholderia cenocepacia		1	1	1	1	
2137		331271	Burkholderia cenocepacia AU 1054		8		8		
2138		331272	Burkholderia cenocepacia HI2424		1		1		
2232		350702	Burkholderia cenocepacia PC184		1		1		
22		292	Burkholderia cepacia	3	2	3	2		
2694		482957	Burkholderia lata		2		2		
1011		13373	Burkholderia mallei		45	1	45	1	
1881		243160	Burkholderia mallei ATCC 23344		40		40		
2163		334802	Burkholderia mallei FMH		1		1		
2114		320390	Burkholderia mallei GB8 horse 4		1		1		
2164		334803	Burkholderia mallei JHU		2		2		
2560		412022	Burkholderia mallei NCTC 10229		10		10		
2113		320388	Burkholderia mallei SAVP1		31		31		
1476		87883	Burkholderia multivorans		2		2		
2490		395019	Burkholderia multivorans ATCC 17616	1		1			
1042		28450	Burkholderia pseudomallei	13	6	14	6	1	
2279		357348	Burkholderia pseudomallei 1106a		2		2		
2632		441160	Burkholderia pseudomallei 14		1		1		
2110		320372	Burkholderia pseudomallei 1710b		4		4		
2601		425067	Burkholderia pseudomallei 305		3		3		
2294		360118	Burkholderia pseudomallei 406e		2		2		
2111		320373	Burkholderia pseudomallei 668		12		12		
2630		441158	Burkholderia pseudomallei 9		1		1		
2631		441159	Burkholderia pseudomallei 91		2		2		
1960		272560	Burkholderia pseudomallei K96243	3	735	3	735		
2140		331978	Burkholderia pseudomallei Pasteur 52237		1		1		
2112		320374	Burkholderia pseudomallei S13		2		2		

1958		271848	Burkholderia thailandensis E264		2		2		
1945		269482	Burkholderia vietnamiensis G4		9		9		
1350		60879	Cabassou virus		1		1		
372		6238	Caenorhabditis briggsae	1		1			
373		6239	Caenorhabditis elegans	2	10	2	10		
471	X	8855	Cairina moschata			2	1	2	1
2240		351627	Caldicellulosiruptor saccharolyticus DSM 8903		1		1		
1163		35305	California encephalitis virus		1		1		
485		9483	Callithrix jacchus		4		4		
1046		28873	Camelpox virus		2		2		
1765		203172	Camelpox virus CMS		28		28		
1767		203174	Camelpox virus CP1		1		1		
1766		203173	Camelpox virus M-96		133		133		
9		195	Campylobacter coli		1		1		
2069		306254	Campylobacter coli RM2228		3		3		
1121		32019	Campylobacter fetus subsp. fetus	3		3			
10		197	Campylobacter jejuni	102	22	103	22	1	
1738		195099	Campylobacter jejuni RM1221		13		13		
1122		32022	Campylobacter jejuni subsp. jejuni	2		2			
3292		10000679	Campylobacter jejuni subsp. jejuni 16971.94GSH (O:41)	2		2			
2538		407148	Campylobacter jejuni subsp. jejuni 81116		14		14		
2258		354242	Campylobacter jejuni subsp. jejuni 81-176		4		4		
2693		482628	Campylobacter jejuni subsp. jejuni BH-01-0142		1		1		
2290		360112	Campylobacter jejuni subsp. jejuni HB93-13		2		2		
2813		567106	Campylobacter jejuni subsp. jejuni IA3902		1		1		
1731		192222	Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819	10	23	10	23		
3621		10002003	Campylobacter jejuni subsp. jejuni serotype HS:15	1		1			
2070		306263	Campylobacter lari RM2100		1		1		
1025		28080	Campylobacter upsaliensis	3		3			
2071		306264	Campylobacter upsaliensis RM3195		1		1		
1261		44088	Canarypox virus		8		8		
294		5476	Candida albicans	107	79	107	80		1
3158		10000335	Candida albicans A-9 (serotype B)	1		1			
3159		10000337	Candida albicans KIT 1113	1		1			
3549		10001652	Candida albicans NIH B-792 (serotype B)	1		1			
1872		237561	Candida albicans SC5314		3		3		
3160		10000339	Candida albicans serotype A	1		1			
2045		300021	Candida albicans var. stellatoidea	2		2			
3570		10001740	Candida glabrata IFO 0622	1		1			
295		5480	Candida parapsilosis	1		1			
3571		10001747	Candida parapsilosis M1015	1		1			
1278		45582	Candida saitoana	1		1			
1866		234267	Candidatus Solibacter usitatus Ellin6076		2		2		
1677		170325	Canid alphaherpesvirus 1		1		1		
2022		292348	Canine calicivirus (strain 48)	2		2			
776		11233	Canine distemper virus strain Onderstepoort	6	19	6	19		
775		11232	Canine morbillivirus	5	8	10	9	5	1
654		10788	Canine parvovirus	23	20	23	20		
1897		246878	Canine parvovirus 2	3		3			

655		10790	Canine parvovirus strain CPV-D CORNELL 320	1		1			
656		10791	Canine parvovirus strain N	47		47			
511		9615	Canis lupus familiaris	8	199	12	1539	4	1340
3114		1980463	Cano Delgadito orthohantavirus		1		1		
2766		521097	Capnocytophaga ochracea DSM 7271		1		1		
2939		712212	Capnocytophaga sp. oral taxon 326		1		1		
528		9925	Capra hircus	11		11			
847		11660	Caprine arthritis encephalitis virus	14	1	14	1		
849		11662	Caprine arthritis encephalitis virus G63	6		6			
848		11661	Caprine arthritis encephalitis virus strain Cork	9		9			
439		7957	Carassius auratus	3	1	3	1		
1379		64289	Carey Island virus		2		2		
1125		32201	Carya illinoinensis	19		19			
541		10185	Castor fiber		1		1		
1581		129052	Catelliglobosispora koreensis		1		1		
2066		304895	Catenulispora acidiphila		1		1		
1918		261658	Cavenderia fasciculata		1		1		
540		10141	Cavia porcellus	36	75	37	75	1	
1136		33706	Caviid betaherpesvirus 2	3	3	3	3		
402		6878	Centruroides noxius	10		10			
2101		316287	Ceratogyrus marshalli	1		1			
569		10317	Cercopithecine alphaherpesvirus 2		1		1		
1914		260965	Cercopithecine herpesvirus 1 (strain E2490)	18		18			
525		9864	Cervus canadensis nelsoni	5		5			
524		9860	Cervus elaphus	2		2			
515		9721	Cetacea	1		1			
1219		38033	Chaetomium globosum	1		1			
2955		759272	Chaetomium thermophilum var. thermophilum DSM 1495	1		1			
1012		13415	Chamaecyparis obtusa	5	68	5	68		
1938		266779	Chelativorans sp. BNC1		4		4		
998		12618	Chicken anemia virus	3		3			
1205		37124	Chikungunya virus	53	3	53	3		
3661		10002197	Chikungunya virus MY/08/065	15		15			
3608		10001934	Chikungunya virus Singapore/11/2008	3		3			
3618		10001997	Chikungunya virus strain LR2006_OPY1 IMT/Reunion Island/2006	1		1			
2324		371094	Chikungunya virus strain S27-African prototype	24		24			
2077		310542	Chimpanzee adenovirus	2		2			
417		7154	Chironomus thummi	2	3	2	3		
418		7155	Chironomus thummi thummi	58	27	58	27		
482		9397	Chiroptera	1		1			
1458		83555	Chlamydia abortus	3		3			
1460		83560	Chlamydia muridarum		3		3		
1882		243161	Chlamydia muridarum str. Nigg		42		42		
1459		83558	Chlamydia pneumoniae	67	23	67	23		
1457		83554	Chlamydia psittaci	78	2	78	2		
2139		331636	Chlamydia psittaci 6BC	1		1			
98		813	Chlamydia trachomatis	128	67	128	69		2
2095		315277	Chlamydia trachomatis A/HAR-13	6	1	6	1		
3382		10000858	Chlamydia trachomatis B/Jali-20/OT	2		2			

1961		272561	Chlamydia trachomatis D/UW-3/CX		26		26		
3453		10001141	Chlamydia trachomatis Serovar A	22	8	22	8		
3349		10000804	Chlamydia trachomatis Serovar B	47	5	47	5		
3315		10000763	Chlamydia trachomatis Serovar C	16	1	16	1		
3439		10001085	Chlamydia trachomatis Serovar D	3		3			
3447		10001121	Chlamydia trachomatis Serovar Da	1		1			
3316		10000764	Chlamydia trachomatis Serovar E	19	2	19	2		
3371		10000845	Chlamydia trachomatis Serovar F	3		3			
3317		10000765	Chlamydia trachomatis Serovar H	7		7			
3318		10000766	Chlamydia trachomatis Serovar I	10		10			
3415		10001008	Chlamydia trachomatis Serovar J	6		6			
3319		10000767	Chlamydia trachomatis serovar K	14		14			
3378		10000853	Chlamydia trachomatis Serovar L1	21	3	21	3		
3320		10000768	Chlamydia trachomatis Serovar L2	15	12	15	12		
3321		10000769	Chlamydia trachomatis Serovar L3	2		2			
1769		204428	Chlamydiae	16		16			
3284		10000559	Chlamydophila abortus B-577	11		11			
1546		115713	Chlamydophila pneumoniae CWL029		49		49		
3377		10000852	Chlamydophila pneumoniae Kajaani 6		7		7		
1701		182082	Chlamydophila pneumoniae TW-183	7		7			
2180		337090	Chlorobium chlorochromatii		1		1		
2184		340177	Chlorobium chlorochromatii CaD3		1		1		
496		9534	Chlorocebus aethiops		5		5		
1672		169173	Choclo virus		3		3		
434		7777	Chondrichthyes	1		1			
431	X	7719	Ciona intestinalis			2		2	
47		544	Citrobacter	1		1			
48		546	Citrobacter freundii	1		1			
979		12162	Citrus tristeza virus	8		8			
1072		29918	Cladosporium herbarum		18		18		
736		11096	Classical swine fever virus	14	4	14	4		
2283		358769	Classical swine fever virus - Alfort/187	70		70			
2284		358805	Classical swine fever virus - Alfort/Tuebingen	5		5			
737		11098	Classical swine fever virus - Brescia	4		4			
2285		358812	Classical swine fever virus - C	2		2			
1984		279150	Classical swine fever virus 96TD	2		2			
3419		10001025	Classical swine fever virus Glentorf		26		26		
3520		10001578	Classical swine fever virus LPC/AHRI	4		4			
3575		10001764	Classical swine fever virus Margarita (AJ704817)	4	1	4	1		
3219		10000451	Classical swine fever virus Shimen	16		16			
1388		68621	Classical swine fever virus strain Riems		5		5		
1197		36911	Clavispora lusitaniae	1		1			
1433	X	79923	Clonorchis sinensis			2	1	2	1
154		1496	Clostridioides difficile	53		57		4	
3022		1169127	Clostridioides difficile genomovar ribotype_087	1		1			
1962		272562	Clostridium acetobutylicum ATCC 824		1		1		
3017		1137848	Clostridium arbusti		1		1		
2146		333367	Clostridium asparagiforme		1		1		
153		1491	Clostridium botulinum	194	99	194	99		
1192		36826	Clostridium botulinum A	46		46			
3132		10000293	Clostridium botulinum A 1	1		1			

3133		10000294	Clostridium botulinum A 2	2		2			
3139		10000302	Clostridium botulinum A Kyoto-F	1		1			
2568		413999	Clostridium botulinum A str. ATCC 3502		3		3		
2634		441771	Clostridium botulinum A str. Hall	44		44			
3138		10000301	Clostridium botulinum A str. Hall hyper	3		3			
1193		36827	Clostridium botulinum B	29		29			
3134		10000295	Clostridium botulinum B 111	2		2			
3140		10000303	Clostridium botulinum B Lammana	1		1			
3142		10000305	Clostridium botulinum B Okra	3		3			
2981		935198	Clostridium botulinum B str. Eklund 17B (NRP)		1		1		
3136		10000297	Clostridium botulinum C 92-13	5		5			
3143		10000306	Clostridium botulinum C Stockholm	2		2			
1194		36829	Clostridium botulinum D	2		2			
3135		10000296	Clostridium botulinum D 1873	2		2			
1195		36830	Clostridium botulinum E	3	3	3	3		
3137		10000299	Clostridium botulinum E Beluga	2		2			
2744		508767	Clostridium botulinum E3 str. Alaska E43		1		1		
1196		36831	Clostridium botulinum F	3		3			
3141		10000304	Clostridium botulinum F NCTC 10281	1		1			
2640		445335	Clostridium botulinum NCTC 2916		2		2		
2641		445338	Clostridium botulinum str. Iwanei E	6		6			
3144		10000307	Clostridium difficile BART'S W1	1		1			
3590		10001847	Clostridium difficile BI / NAP1/ 027	1		1			
3639		10002079	Clostridium difficile VPI 10463	2		2			
2444		386415	Clostridium novyi NT		2		2		
1054		29362	Clostridium papyrosolvens	1	1	1	1		
155		1502	Clostridium perfringens	10	1	41	1	31	
1538		107819	Clostridium perfringens D	1		44		43	
1739		195102	Clostridium perfringens str. 13		1		1		
1055		29371	Clostridium termitidis	1		1			
156		1513	Clostridium tetani	77	245	78	272	1	27
1800		212717	Clostridium tetani E88		16		16		
296		5501	Coccidioides immitis		1		1		
1756		199306	Coccidioides posadasii		9		9		
474		9014	Colinus virginianus	1	3	1	3		
2992		1005048	Collimonas fungivorans Ter331		2		2		
472		8932	Columba livia		10		10		
2091		314285	Congregibacter litoralis KT71		1		1		
388		6491	Conus geographus	30		30			
389		6492	Conus magus	2		2			
390		6493	Conus striatus	11		11			
1131		32614	Convict Creek 107 virus	1	3	1	3		
2554		410072	Coprococcus comes	1		1			
1013		13451	Corylus avellana	27	53	27	57		4
1258		43765	Corynebacterium amycolatum		1		1		
168		1717	Corynebacterium diphtheriae	15	52	15	52		
1626		152794	Corynebacterium efficiens		5		5		
1741		196164	Corynebacterium efficiens YS-314		4		4		
169		1718	Corynebacterium glutamicum		26		26		
1746		196627	Corynebacterium glutamicum ATCC 13032		14		14		
2072		306537	Corynebacterium jeikeium K411		1		1		
990		12264	Cowpea mosaic virus		1		1		

542		10243	Cowpox virus		25		25		
1935		265872	Cowpox virus (Brighton Red)		1		1		
3289		10000571	Cowpox virus (Brighton Red) White-pock		1		1		
89		777	Coxiella burnetii	2	199	2	199		
2621		434923	Coxiella burnetii CbuG_Q212		1		1		
2622		434924	Coxiella burnetii CbuK_Q154		1		1		
2620		434922	Coxiella burnetii Dugway 5J108-111		8		8		
2292		360116	Coxiella burnetii 'MSU Goat Q177'		8		8		
2293		360117	Coxiella burnetii Q321		14		14		
2291		360115	Coxiella burnetii RSA 331		9		9		
1848		227377	Coxiella burnetii RSA 493		14		14		
940		12066	Coxsackievirus	1		1			
1114		31704	Coxsackievirus A16	2		4		2	
1253		42782	Coxsackievirus A20	1		1			
1472	X	86107	Coxsackievirus A6			1		1	
941		12067	Coxsackievirus A9	30		30			
942		12071	Coxsackievirus B1	12		12			
1442		82639	Coxsackievirus B2	2		2			
943		12072	Coxsackievirus B3	7	15	7	15		
1524		103903	Coxsackievirus B3 (strain Nancy)	13	30	13	30		
944		12073	Coxsackievirus B4	17	51	17	51		
1525		103905	Coxsackievirus B4 (strain E2)	7	41	7	41		
1526		103906	Coxsackievirus B4 (strain JVB / Benschoten / New York/51)		76		76		
532		10029	Cricetulus griseus	1		1			
3127		1980519	Crimean-Congo hemorrhagic fever orthonairovirus	20	2	20	2		
2314		368445	Crocodilepox virus		2		2		
465		8732	Crotalus durissus terrificus	4		4			
292		5207	Cryptococcus neoformans	2	2	2	2		
1698		178876	Cryptococcus neoformans var. grubii	1		1			
1996		283643	Cryptococcus neoformans var. neoformans B-3501A	1	3	1	3		
3449		10001132	Cryptococcus neoformans var. neoformans Serotype A	1		1			
3446		10001120	Cryptococcus neoformans var. neoformans Serotype D	1		1			
216		3369	Cryptomeria japonica	44	182	44	299		117
1875		237895	Cryptosporidium hominis		3		3		
321		5807	Cryptosporidium parvum	3	30	3	30		
2251		353152	Cryptosporidium parvum Iowa II	1	84	1	84		
1820		220837	Cryptosporidium sp. MNJ-1		1		1		
430		7515	Ctenocephalides felis		2		2		
991		12305	Cucumber mosaic virus	1		1			
1548		117125	Cucumber mosaic virus (strain Pepo)	1		1			
225		3656	Cucumis melo	13		13			
1785		208899	Cupixi mammarenavirus		1		1		
1014		13469	Cupressus sempervirens		8		8		
1937		266264	Cupriavidus metallidurans CH34		3		3		
297		5503	Curvularia lunata	20	10	20	10		
299		5554	Cutaneotrichosporon cutaneum	1		1			
170		1747	Cutibacterium acnes		1		1		
2062		301964	CY1014 virus		1		1		

283		4903	Cyberlindnera jadinii	12		12			
2991		1004253	Cyberlindnera mrakii	1	1	1	1		
1288		46457	Cycloclasticus oligotrophus		1		1		
1049		28909	Cynodon dactylon	27	48	27	48		
440	X	7962	Cyprinus carpio			4	1	4	1
1947		269798	Cytophaga hutchinsonii ATCC 33406		1		1		
266		4509	Dactylis glomerata		12		12		
438		7955	Danio rerio	1	3	1	3		
1051		29271	Dasheen mosaic virus	1		1			
248		4039	Daucus carota		1		46		45
2067		305674	Deerpox virus W-848-83		2		2		
1883		243164	Dehalococcoides mccartyi 195		1		1		
1390		68909	Deinococcus geothermalis	1		1			
120		1299	Deinococcus radiodurans	3		3			
1884	X	243230	Deinococcus radiodurans R1			1		1	
2179		337052	Deltapapillomavirus 4	24		24			
999		12637	Dengue virus	38	546	39	553	1	7
708		11053	Dengue virus 1	32	482	40	507	8	25
2541		408685	Dengue virus 1 Brazil/97-11/1997		1058		1058		
3522		10001582	Dengue virus 1 Mochizuki	4		4			
710		11059	Dengue virus 1 Nauru/West Pac/1974	4	50	4	50		
3611		10001945	Dengue virus 1 PVP159	2		2			
1143		33741	Dengue virus 1 Singapore/S275/1990		245		245		
709		11057	Dengue virus 1 Thailand/AHF 82-80/1980		1		1		
711		11060	Dengue virus 2	159	620	178	641	19	21
1097		31635	Dengue virus 2 16681-PDK53	4	32	4	32		
3626		10002010	Dengue virus 2 D2/SG/05K4155DK1/2005		49		49		
713		11064	Dengue virus 2 Jamaica/1409/1983	264	1254	264	1254		
712		11062	Dengue virus 2 Malaysia M2	1		1			
3523		10001583	Dengue virus 2 New Guinea C	1	4	1	4		
2550		408694	Dengue virus 2 Peru/IQT2913/1996		87		87		
3538		10001635	Dengue virus 2 PL046		7		7		
715		11066	Dengue virus 2 Puerto Rico/PR159-S1/1969	32	21	32	21		
3576		10001768	Dengue virus 2 S-16803	1		1			
3539		10001636	Dengue virus 2 S221		42		42		
3564		10001705	Dengue virus 2 strain 43	1		1			
1096		31634	Dengue virus 2 Thailand/16681/84	32	62	32	62		
714		11065	Dengue virus 2 Thailand/NGS-C/1944	17	37	18	37	1	
716		11067	Dengue virus 2 Tonga/EKB194/1974		3		3		
717		11069	Dengue virus 3	54	554	58	578	4	24
2546		408690	Dengue virus 3 China/80-2/1980		84		84		
2547		408691	Dengue virus 3 Martinique/1243/1999		889		889		
2551		408870	Dengue virus 3 Philippines/H87/1956	8	13	8	13		
2549		408693	Dengue virus 3 Singapore/8120/1995		69		69		
2548		408692	Dengue virus 3 Sri Lanka/1266/2000		66		66		
3534		10001619	Dengue virus 3 strain 16652	16		16			
3610		10001944	Dengue virus 3 Thailand/PaH881/1988	2		2			
718		11070	Dengue virus 4	47	367	50	374	3	7
3644		10002112	Dengue virus 4 1036	1		1			
3609		10001943	Dengue virus 4 Burma/63632/1976	3		3			
2552		408871	Dengue virus 4 Dominica/814669/1981	1	256	1	256		
3651		10002148	Dengue virus 4 Mexico/BC287/1997	1		1			

2542		408686	Dengue virus 4 Philippines/H241/1956	4	947	4	947		
2543		408687	Dengue virus 4 Singapore/8976/1995		5		5		
2544		408688	Dengue virus 4 Thailand/0348/1991		15		15		
2545		408689	Dengue virus 4 Thailand/0476/1997		3		3		
3643		10002111	Dengue virus 4 TVP-376	1		1			
3395		10000965	Dengue virus type 1 FGA/89	4		4			
3213		10000440	Dengue virus type 1 Hawaii	29	22	29	22		
3393		10000961	Dengue virus type 1 strain 16007	15		15			
3214		10000442	Dengue virus type 3 CH53489		7		7		
408		6953	Dermatophagoides		578		578		
409		6954	Dermatophagoides farinae	33	111	33	111		
410		6956	Dermatophagoides pteronyssinus	81	298	83	301	2	3
2626		439235	Desulfatibacillum alkenivorans AK-01		1		1		
1963		272564	Desulfitobacterium hafniense DCB-2		3		3		
1351		60893	Desulfobacca acetoxidans		1		1		
3054		1286635	Desulfotignum phosphitoxidans DSM 13687		1		1		
1992		281689	Desulfuromonas acetoxidans DSM 684		1		1		
810		11319	Dhori virus (strain Indian/1313/61)	1		1			
1267		44689	Dictyostelium discoideum	1	1	1	1		
255		4163	Digitalis	1		1			
1473		86600	Discosoma sp.		1		1		
3115		1980467	Dobrava-Belgrade orthohantavirus		25		25		
424		7441	Dolichovespula maculata	11	20	11	20		
2025		292633	Dragon grouper nervous necrosis virus	20		20			
421		7227	Drosophila melanogaster	9	17	9	17		
422		7234	Drosophila persimilis	1		1			
1286		46245	Drosophila pseudoobscura pseudoobscura	1		1			
3650		10002132	Duck hepatitis A virus 1 HP-1	1		2		1	
3652		10002151	Duck hepatitis A virus 1 LY0801	1		1			
3653		10002152	Duck hepatitis A virus 3 SD1201	1		1			
1000		12639	Duck hepatitis B virus	262	20	262	20		
3075		1399582	Duck Tembusu virus	2		3		1	
1222		38767	Duvenhage lyssavirus		2		2		
1861		231455	Dyella japonica	1		1			
691		11021	Eastern equine encephalitis virus	42	2	42	2		
692		11022	Eastern equine encephalitis virus (STRAIN VA33[TEN BROECK])		1		1		
3212		10000439	Eastern equine encephalitis virus SV	8		8			
1579		129000	Ebola virus - Eckron (Zaire, 1976)		12		12		
1571		128947	Ebola virus - Gabon (1994-1997)		18		18		
1575		128952	Ebola virus - Mayinga, Zaire, 1976	36	13	36	13		
1574		128951	Ebola virus - Zaire (1995)		1		1		
1773		205488	Ebola virus sp.		10		10		
1311		53751	Echinacea purpurea	1		1			
370		6210	Echinococcus granulosus	39		39			
371		6211	Echinococcus multilocularis	6		6			
1513		99586	Echis ocellatus	5		5			
1147		33758	Echovirus		1		1		
948		12078	Echovirus E11	1		1			
936		12060	Echovirus E9	1		1			
1001		12643	Ectromelia virus		6		6		
102		944	Ehrlichia canis	7	1	7	1		

1946		269484	Ehrlichia canis str. Jake	16		16			
103		945	Ehrlichia chaffeensis	14	1	14	1		
1776		205920	Ehrlichia chaffeensis str. Arkansas	23		23			
1174		35795	Ehrlichia muris	2	3	2	3		
90		779	Ehrlichia ruminantium	3		3			
319		5801	Eimeria acervulina	1		1			
320		5802	Eimeria tenella	6		6			
3116		1980468	El Moro Canyon orthohantavirus		2		2		
441		8005	Electrophorus electricus	3		3			
211		2903	Emiliania huxleyi		1		1		
1990		280463	Emiliania huxleyi CCMP1516		1		1		
359		6035	Encephalitozoon cuniculi		5		5		
2004		284813	Encephalitozoon cuniculi GB-M1		28		28		
3026		1178016	Encephalitozoon romaleae SJ-2008		1		1		
956		12104	Encephalomyocarditis virus		1		1		
2317		370354	Entamoeba dispar SAW760		20		20		
318		5759	Entamoeba histolytica	30	13	30	13		
2031		294381	Entamoeba histolytica HM-1:IMSS		103		103		
2970		885311	Entamoeba histolytica KU27		1		1		
3165		10000352	Entamoeba histolytica YS-27	1		1			
49		550	Enterobacter cloacae		9		9		
992		12340	Enterobacteria phage 933J	1		1			
649		10730	Enterobacteria phage 933W	1		1			
662		10863	Enterobacteria phage f1	1	1	1	1		
663		10864	Enterobacteria phage fd	7	1	7	1		
2936		697227	Enterobacteria phage IME08		1		1		
651		10760	Enterobacteria phage T7	1		1			
1507		97081	Enterobacteria phage VT2-Sakai		1		1		
46		543	Enterobacteriaceae	3		3			
934		12022	Enterobacterio phage MS2	1		1			
139		1351	Enterococcus faecalis	2		2			
140		1352	Enterococcus faecium	6		6			
2156		333849	Enterococcus faecium DO		1		1		
1623		150846	Enterovirus 5865/sin/000009	2		2			
1607		138948	Enterovirus A	1		1			
1228		39054	Enterovirus A71	90	1	91	1	1	
3637		10002056	Enterovirus A71 TW/2086/98	1		1			
1608		138950	Enterovirus C	6	3	6	3		
938		12064	Enterovirus E	13		13			
1081		31330	Ephydatia fluviatilis		1		1		
1446		82830	Epstein-barr virus strain ag876	1	1	1	1		
574		10326	Equid alphaherpesvirus 1	7	218	7	218		
575		10331	Equid alphaherpesvirus 4	6		6			
3265		10000525	Equid herpesvirus 2 16V	1		1			
3266		10000526	Equid herpesvirus 2 5FN	1		1			
3264		10000524	Equid herpesvirus 2 691	1		1			
3191		10000391	Equid herpesvirus 2 ER32	1		1			
3267		10000527	Equid herpesvirus 2 FIN60	1		1			
3196		10000405	Equid herpesvirus 4 TH20	2		2			
1447		82831	Equid herpesvirus type 2 strain 86/87	1		1			
705		11047	Equine arteritis virus	3		3			
2039		299386	Equine arteritis virus Bucyrus	2		2			

850		11665	Equine infectious anemia virus	93	111	93	112		1
851		11670	Equine infectious anemia virus (CLONE 1369)		1		1		
852		11671	Equine infectious anemia virus (STRAIN WSU5)		19		19		
3247		10000499	Equine infectious anemia virus PV		2		2		
3366		10000835	Equine rhinitis A virus 393/76	4		4			
2871		650131	Equine rhinitis B virus 1 strain P1436/71	6		6			
3606		10001929	Equine rhinitis B virus 2 strain 313/75	5		5			
3607		10001930	Equine rhinitis B virus 3 isolate 2225AS	5		5			
519		9796	Equus caballus	48	45	48	45		
520		9798	Equus przewalskii		1		1		
1504		95602	Eriocheir sinensis	10		10			
497		9538	Erythrocebus patas		1		1		
52		562	Escherichia coli	241	143	243	143	2	
1809	X	216592	Escherichia coli 042			2		2	
3537		10001633	Escherichia coli 055:B5	3		3			
2282		358709	Escherichia coli 101-1		5		5		
3454		10001145	Escherichia coli 1471	2		2			
3297		10000727	Escherichia coli 180/C3	1		1			
2299		362663	Escherichia coli 536		66		66		
2212		344610	Escherichia coli 53638		1		1		
2769		525281	Escherichia coli 83972		4		4		
2534		405955	Escherichia coli APEC O1		8		8		
2691		481805	Escherichia coli ATCC 8739		1		1		
1217		37762	Escherichia coli B	1	1	1	1		
3298		10000728	Escherichia coli B B/r CM6		1		1		
2210		344601	Escherichia coli B171		25		25		
2793		550676	Escherichia coli B185		1		1		
2185		340184	Escherichia coli B7A		5		5		
1757		199310	Escherichia coli CFT073	1	2	1	2		
2187		340186	Escherichia coli E110019		2		2		
2186		340185	Escherichia coli E22		13		13		
2103		316401	Escherichia coli ETEC H10407	64	31	64	31		
2188		340197	Escherichia coli F11		12		12		
3511		10001528	Escherichia coli F515	1		1			
3030		1197131	Escherichia coli F576	1		1			
2136		331112	Escherichia coli HS		14		14		
2829		585034	Escherichia coli IAI1	3		3			
3084		1432555	Escherichia coli ISC7		1		1		
3500		10001502	Escherichia coli J-5	1		1			
3074		1392869	Escherichia coli K1		1		1		
1454		83333	Escherichia coli K-12	21	19	23	19	2	
2885		679206	Escherichia coli MS 119-7		1		1		
2884		679205	Escherichia coli MS 124-1		1		1		
3550		10001659	Escherichia coli O125	1		1			
1669		168807	Escherichia coli O127:H6	1		1			
2135		331111	Escherichia coli O139:H28 str. E24377A		36		36		
1455		83334	Escherichia coli O157:H7		123		123		
2686		478005	Escherichia coli O157:H7 str. EC4486		1		1		
2687		478006	Escherichia coli O157:H7 str. EC4501		2		2		
2688		478008	Escherichia coli O157:H7 str. EC869		14		14		
1637		155864	Escherichia coli O157:H7 str. EDL933	3	32	3	32		

2445		386585	Escherichia coli O157:H7 str. Sakai		17		17		
3299		10000733	Escherichia coli O5:K4:H4	1		1			
1890		244320	Escherichia coli O55:H7		1		1		
1816		217992	Escherichia coli O6		7		7		
3631		10002022	Escherichia coli O6 O6:K15:H31		1		1		
3300		10000734	Escherichia coli O65:K-:H-	1		1			
3648		10002127	Escherichia coli O86:B7	1		1			
2102		316385	Escherichia coli str. K-12 substr. DH10B		3		3		
2749		511145	Escherichia coli str. K-12 substr. MG1655	1	31	1	31		
2104		316407	Escherichia coli str. K-12 substr. W3110		1		1		
2301		364106	Escherichia coli UTI89		2		2		
648		10710	Escherichia virus Lambda		6		6		
661		10847	Escherichia virus phiX174	1		1			
1236	X	39803	Escherichia virus Qbeta				2		2
1547		115991	Escherichia virus RB43		1		1		
647		10665	Escherichia virus T4	10	20	10	20		
212		3039	Euglena gracilis	1		1			
210		2759	Eukaryota	1		1			
1154		34828	Eulemur mongoz	1		1			
411		6958	Euroglyphus maynei		10		10		
2592	X	420521	Expression vector pNIC-NHT-CF			1		1	
134		1323	Faecalicoccus pleomorphus		1		1		
223		3617	Fagopyrum esculentum	40		40			
1355		62330	Fagopyrum tataricum	5		5			
396		6690	Farfantepenaeus aztecus	51	31	51	31		
1290		46835	Fasciola gigantica	2		2			
365		6192	Fasciola hepatica	270	28	272	28	2	
929		11978	Feline calicivirus	4		4			
2023		292349	Feline calicivirus (strain Urbana)	1		1			
931		11981	Feline calicivirus strain F9	2		2			
930		11980	Feline calicivirus strain Japanese F4	6		6			
1002		12663	Feline coronavirus		1		1		
1308	X	53182	Feline foamy virus			7		7	
853		11673	Feline immunodeficiency virus		28		28		
854		11674	Feline immunodeficiency virus (isolate Petaluma)	2	3	2	3		
1275		45409	Feline immunodeficiency virus (isolate wo)	3		3			
1178		36372	Feline immunodeficiency virus (strain UK8)		1		1		
1142		33734	Feline infectious peritonitis virus (strain 79-1146)	15	14	15	14		
3535		10001624	Feline infectious peritonitis virus (strain KU-2)	22	43	22	43		
906		11769	Feline leukemia virus strain A/Glasgow-1	6		6			
3448		10001130	Feline leukemia virus subtype A	2		2			
653		10786	Feline panleukopenia virus		4		4		
514		9685	Felis catus	40	99	40	99		
1073		29960	Fenneropenaeus indicus	2		2			
279		4606	Festuca arundinacea	1		1			
113		1260	Finegoldia magna		1		1		
3635		10002034	Fish	4		4			
1640		156586	Flavobacteria bacterium BBFL7		2		2		
2706		487797	Flavobacteria bacterium MS024-3C		1		1		
958		12110	Foot-and-mouth disease virus	24	5	24	5		
959		12111	Foot-and-mouth disease virus - type A	1	5	3	5	2	

3405		10000991	Foot-and-mouth disease virus - type A (strain A22 Iraq)	5	1	5	1		
3404		10000989	Foot-and-mouth disease virus - type A (strain A22)	8	6	8	6		
1540		110195	Foot-and-mouth disease virus - type Asia 1	10	3	10	3		
3630		10002020	Foot-and-mouth disease virus - type Asia 1 Nepal 29/97	4		4			
3409		10000995	Foot-and-mouth disease virus - type Asia 1 Pakistan	1		1			
3612		10001946	Foot-and-mouth disease virus - type Asia 1 YS/CHA/05	4		4			
964		12116	Foot-and-mouth disease virus - type C	6	26	6	26		
966		12118	Foot-and-mouth disease virus - type O	36	5	43	5	7	
3347		10000801	Foot-and-mouth disease virus - type O (O/SKR/2002)	1		1			
3445		10001118	Foot-and-mouth disease virus - type O (strain HKN/14/82)	2		2			
3380		10000856	Foot-and-mouth disease virus - type O isolate O/UKG/35/2001		14		14		
3542		10001642	Foot-and-mouth disease virus - type O Wuppertal/FRG/82		1		1		
3406		10000992	Foot-and-mouth disease virus - type SAT 1 (Strain Bot 1/68)	1		1			
1161		35292	Foot-and-mouth disease virus - type SAT 2	1	1	1	1		
3407		10000993	Foot-and-mouth disease virus - type SAT 2 (Strain Ken 3/57)	1		1			
3410		10001000	Foot-and-mouth disease virus - type SAT 2 (strain Rho 1/48)	4		4			
969		12123	Foot-and-mouth disease virus - type SAT 3		1		1		
3408		10000994	Foot-and-mouth disease virus - type SAT 3 (Strain Bec 1/65)	1		1			
960		12112	Foot-and-mouth disease virus (strain A10-61)	8		8			
962		12114	Foot-and-mouth disease virus (strain A12)	21	1	21	1		
963		12115	Foot-and-mouth disease virus (strain A24 Cruzeiro)	17	27	17	32		5
961		12113	Foot-and-mouth disease virus (strain A5)	3		3			
967		12120	Foot-and-mouth disease virus (strain C1-Santa Pau)	1		1			
965		12117	Foot-and-mouth disease virus (strain C3 Indaial)	2		2			
1413		73482	Foot-and-mouth disease virus (strain O1)	18	1	18	1		
3358		10000820	Foot-and-mouth disease virus (strain O1) (O/Taiwan/1/97)	1		1			
3394		10000964	Foot-and-mouth disease virus (strain O1) (O1 Brugge)	2		2			
3259		10000516	Foot-and-mouth disease virus (strain O1) (O1 Campos)	18	18	18	19		1
3256		10000513	Foot-and-mouth disease virus (strain O1) (O1 Kaufbeuren)	43	8	43	8		
3350		10000806	Foot-and-mouth disease virus (strain O1) (O1 Manisa)	5		5			
3257		10000514	Foot-and-mouth disease virus (strain O1) (O1BFS 1860)	9		9			
3258		10000515	Foot-and-mouth disease virus (strain O1) (O1BFS)	5		5			
3283		10000556	Foot-and-mouth disease virus (strain O1) Kaufbeuren	43	12	43	12		

3443		10001102	Foot-and-mouth disease virus (strain O1) O/UKG/11/2001	1	1	1	1		
1656		161727	Foot-and-mouth disease virus A10/Holland	11	14	11	14		
968		12121	Foot-and-mouth disease virus C1	1	4	1	4		
3368		10000840	Foot-and-mouth disease virus C1 Brescia It/64	2		2			
3402		10000986	Foot-and-mouth disease virus C1 CS30	1		1			
3367		10000836	Foot-and-mouth disease virus C1 CS8	22	24	22	24		
1287		46290	Foot-and-mouth disease virus C3	4	1	4	1		
3423		10001039	Foot-and-mouth disease virus C3 (strain Resendne-Br/55)	1		1			
1891		244367	Foot-and-mouth disease virus C-S8c1	15	17	15	17		
1094		31621	Four Corners hantavirus	2	8	2	8		
552		10261	Fowlpox virus		7		7		
553		10263	Fowlpox virus isolate HP-438/Munich		1		1		
2977		928301	Fowlpox virus strain NVSL		3		3		
15		263	Francisella tularensis	4	13	4	13		
2238		351581	Francisella tularensis subsp. holarctica FSC200		1		1		
2664		458234	Francisella tularensis subsp. holarctica FTNF002-00		1		1		
2340		376619	Francisella tularensis subsp. holarctica LVS	10	291	10	291		
2475		393011	Francisella tularensis subsp. holarctica OSU18		6		6		
2508		401614	Francisella tularensis subsp. novicida U112		1		1		
1554		119856	Francisella tularensis subsp. tularensis		5		5		
2614		430557	Francisella tularensis subsp. tularensis FSC033		27		27		
2476		393115	Francisella tularensis subsp. tularensis FSC198		85		85		
1697		177416	Francisella tularensis subsp. tularensis SCHU S4		92		92		
2585		418136	Francisella tularensis subsp. tularensis WY96-3418		2		2		
2036		298653	Frankia sp. EAN1pec		2		2		
1437		81475	Frateuria aurantia	1		1			
1224		38873	Fraxinus excelsior		3		3		
911		11795	Friend murine leukemia virus	6	53	6	53		
1790		209882	Fusobacterium nucleatum subsp. vincentii ATCC 49256		2		2		
445		8049	Gadus morhua	43		43			
446		8053	Gadus morhua callarias	10		10			
416		7137	Galleria mellonella	1		1			
2492		395494	Gallionella capsiferriformans ES-2		1		1		
475		9031	Gallus gallus	321	337	331	337	10	
2326		373098	Gambierdiscus toxicus	6		6			
2812		566466	gamma proteobacterium NOR5-3		1		1		
914		11824	Gardner-Arnstein feline leukemia oncovirus B	13		13			
1312		54290	GB virus C	16		16			
2679		471223	Geobacillus sp. WCH70		2		2		
148		1422	Geobacillus stearothermophilus	2	1	2	1		
2591		420246	Geobacillus thermodenitrificans NG80-2	1		1			
316		5741	Giardia intestinalis		10		10		
2837		598745	Giardia intestinalis ATCC 50581		7		7		
1709		184922	Giardia lamblia ATCC 50803	1	249	1	249		

2879		658858	Giardia lamblia P15		1		1		
1215		37546	Glossina morsitans morsitans	2		2			
239		3847	Glycine max	179	2	193	2	14	
1352		61466	Gnathostoma binucleatum	10		10			
1221		38251	Goose parvovirus	9		9			
504		9593	Gorilla gorilla		2		2		
505		9595	Gorilla gorilla gorilla		6		6		
2983		940614	Granulicella mallensis		1		1		
1323		55951	Grapevine leafroll-associated virus 3	1		1			
1160		35288	Grapevine virus A	12		12			
1577		128987	Grass carp reovirus		1		1		
2875		655863	Grosmannia clavigera kw1407		1		1		
1272		45219	Guanarito mammarenavirus		842		842		
3531		10001616	Guanarito virus strain INH-95551		1		1		
1527		103920	Guinea pig cytomegalovirus (strain 22122 / ATCC VR682) (GPCMV)	1		1			
1543		114727	H1N1 subtype	12	44	12	44		
3234		10000477	H1N1 subtype Influenza A virus (A/Netherlands/306/00 (H1N1))		1		1		
3470		10001225	H1N1 subtype Influenza A/Oklahoma/7485/01		5		5		
1186		36420	H1N1 swine influenza virus		13		13		
3476		10001315	H1N1 swine influenza virus (A/swine/Korea/S10/2004(H1N1))		3		3		
3477		10001316	H1N1 swine influenza virus (A/swine/Korea/S175/2004(H1N1))		1		1		
1679		170500	H1N9 subtype	1		1			
1544		114729	H2N2 subtype		1		1		
1550		119210	H3N2 subtype	4	23	4	23		
3460		10001157	H3N2 subtype Influenza A virus (A/Hong Kong(H3N2))		15		15		
1551		119211	H3N8 subtype	1		1			
1520		102793	H5N1 subtype	21	36	21	36		
1552		119218	H7N7 subtype		1		1		
2144		333278	H7N9 subtype	1	26	1	26		
1521		102796	H9N2 subtype	1		1			
3478		10001317	H9N2 subtype Influenza A virus (A/swine/Korea/S81/2004(H9N2))		1		1		
3479		10001318	H9N2 subtype Influenza A virus (A/swine/Korea/S83/2004(H9N2))		2		2		
381		6289	Haemonchus contortus	3		3			
1747		197575	Haemophilus aegyptius	1		1			
84		730	Haemophilus ducreyi	3	2	3	2		
1864		233412	Haemophilus ducreyi 35000HP	1		1			
83		727	Haemophilus influenzae	30	66	30	66		
2332		374927	Haemophilus influenzae 22.1-21		3		3		
2337		375177	Haemophilus influenzae 3655		1		1		
2763		521004	Haemophilus influenzae 6P18H1		1		1		
3432		10001055	Haemophilus influenzae 6U	2		2			
2764		521005	Haemophilus influenzae 7P49H1		2		2		
1991		281310	Haemophilus influenzae 86-028NP	13		13			
3433		10001056	Haemophilus influenzae ATCC 9795	2		2			
3431		10001053	Haemophilus influenzae MinnA	9		9			
3365		10000833	Haemophilus influenzae NTHi 1128	6		6			

3425		10001042	Haemophilus influenzae NTHi 1479	12	4	12	4		
3351		10000807	Haemophilus influenzae NTHi UC19	2	2	2	2		
2333		374928	Haemophilus influenzae PittAA		2		2		
2334		374931	Haemophilus influenzae PittGG		1		1		
2335		374932	Haemophilus influenzae PittHH	1		1			
2336		374933	Haemophilus influenzae PittII		3		3		
1923		262727	Haemophilus influenzae R2846		6		6		
1924		262728	Haemophilus influenzae R2866		2		2		
2338		375432	Haemophilus influenzae R3021		3		3		
1404		71421	Haemophilus influenzae Rd KW20		3		3		
3384		10000860	Haemophilus influenzae Serotype B	17	9	18	9	1	
3458		10001155	Haemophilus influenzae strain 1479	2		2			
3456		10001150	Haemophilus influenzae Strain Eagan	58		58			
3508		10001523	Haemophilus influenzae strain I-69 Rd-/b+	4		4			
3507		10001520	Haemophilus influenzae strain RM7004	1		1			
3455		10001149	Haemophilus influenzae Subtype 1H	23		23			
3385		10000861	Haemophilus influenzae Variant d1	18		18			
85		738	Haemophilus parasuis	1		1			
3012	X	1117322	Haemophilus parasuis str. Nagasaki			1		1	
1775		205914	Haemophilus somnus 129PT		2		2		
1853		228400	Haemophilus somnus 2336	1		1			
387		6454	Haliotis rufescens	1		1			
205		2242	Halobacterium salinarum	1		1			
1354		62319	Halococcus saccharolyticus		1		1		
3117		1980471	Hantaan orthohantavirus	2	51	2	51		
828		11602	Hantaan virus 76-118	13	53	14	68	1	15
2322		370830	Hantaan virus Q32		4		4		
2678		470918	Hantaanvirus CGHu1		1		1		
2665		458678	Hantaanvirus CGRn93P8		2		2		
1420		74942	Hantavirus CRF355		1		1		
2075		308061	Hantavirus HPR/02-73		1		1		
1251		42358	Hantavirus Monongahela-3		5		5		
1985		279233	Hantavirus Z37		2		2		
1015		13557	Hapalemur griseus		1		1		
2710		489455	HBV genotype A	1		1			
2711		489460	HBV genotype B	1		1			
2712		489466	HBV genotype C	4		10		6	
2714		489483	HBV genotype D	1	3	1	3		
261		4232	Helianthus annuus	18		18			
1123		32025	Helicobacter hepaticus		1		1		
1869		235279	Helicobacter hepaticus ATCC 51449	2		2			
11		210	Helicobacter pylori	46	16	47	53	1	37
1469		85962	Helicobacter pylori 26695	13	11	13	11		
3553		10001667	Helicobacter pylori 487	1		1			
3580		10001794	Helicobacter pylori B128 Gerbil-adapted variant 7.13	1		1			
2807		563041	Helicobacter pylori G27	2		2			
2987		992121	Helicobacter pylori Hp M5	1		1			
3293		10000718	Helicobacter pylori J223	2		2			
1470		85963	Helicobacter pylori J99		53		53		
2848		637383	Helicobacter pylori NCTC 11639		2		2		
2816		570508	Helicobacter pylori P12		2		2		
3064		1337393	Helicobacter pylori PZ5056	1		1			

3070		1352357	Helicobacter pylori SouthAfrica50	1		1			
1519		102617	Helicobacter pylori SS1	3	3	3	3		
3294		10000720	Helicobacter pylori UA948	2		2			
3295		10000721	Helicobacter pylori UA955	1		1			
1617		148363	Helicoverpa armigera nucleopolyhedrovirus G4	2		2			
385		6339	Heligmosomoides polygyrus	3		3			
392		6536	Helix pomatia	1		1			
1372		63330	Hendra henipavirus	9	2	9	2		
740		11103	Hepacivirus C	666	1113	683	1127	17	14
595		10407	Hepatitis B virus	265	639	265	643		4
1082		31512	Hepatitis B virus adr/mutant		1		1		
597		10409	Hepatitis B virus adr4		13		13		
598		10410	Hepatitis B virus adw/991	2	2	2	2		
600		10412	Hepatitis B virus adw/Indonesia/PIDW420		3		3		
2692		482134	Hepatitis B virus adw/Japan/Nishioka/1983		1		1		
602		10415	Hepatitis B virus adw/Okinawa/PODW282		5		5		
1276		45410	Hepatitis B virus adw4/Brazil/isolate w4b		12		12		
599		10411	Hepatitis B virus alpha1		24		24		
2713		489469	Hepatitis B virus ayw/China/Tibet127/2002	1		1			
2718		490133	Hepatitis B virus ayw/France/Tiollais/1979		4		4		
2467		391647	Hepatitis B virus ayw2	8		8			
2466		391646	Hepatitis B virus ayw3	1		1			
2468		391650	Hepatitis B virus ayw4	1		1			
3208		10000435	Hepatitis B virus genotype D		6		6		
601		10414	Hepatitis B virus LSH/chimpanzee		2		2		
3459		10001156	Hepatitis B virus subtype AD	3	2	3	2		
1532		106820	Hepatitis B virus subtype adr	23	25	23	25		
1533		106821	Hepatitis B virus subtype adw	17	75	17	75		
596		10408	Hepatitis B virus subtype adw2	82	61	82	61		
604		10419	Hepatitis B virus subtype adyw	2	45	2	45		
3209		10000436	Hepatitis B virus subtype AY	7		7			
3210		10000437	Hepatitis B virus subtype AYR		1		1		
603		10418	Hepatitis B virus subtype ayw	57	184	57	184		
741		11104	Hepatitis C virus (isolate 1)	37	256	37	256		
2263		356391	Hepatitis C virus (isolate 6a33)		11		11		
2266		356413	Hepatitis C virus (isolate BEBE1)		14		14		
742		11105	Hepatitis C virus (isolate BK)	3	84	3	90		6
2145		333284	Hepatitis C virus (isolate Con1)	4	3	4	3		
2271		356419	Hepatitis C virus (isolate EUH1480)		5		5		
2131		329389	Hepatitis C virus (isolate Glasgow)	3	4	3	4		
743		11108	Hepatitis C virus (isolate H)	145	84	145	84		
1377		63746	Hepatitis C virus (isolate H77)	106	208	137	208	31	
2264		356410	Hepatitis C virus (isolate HC-G9)	2	1	2	1		
2268		356416	Hepatitis C virus (isolate HCV-K3a/650)		21		21		
2262		356386	Hepatitis C virus (isolate India)		1		1		
747		11116	Hepatitis C virus (isolate Japanese)	6	19	6	19		
2269		356417	Hepatitis C virus (isolate JK049)		6		6		
2267		356415	Hepatitis C virus (isolate NZL1)	1	3	1	3		
1100		31645	Hepatitis C virus (isolate Taiwan)	3	15	3	15		
2272		356421	Hepatitis C virus (isolate Th580)		7		7		
2280		357355	Hepatitis C virus (isolate Tr Kj)		3		3		
2273		356424	Hepatitis C virus (isolate VN004)		1		1		

2270		356418	Hepatitis C virus ED43		1		1		
1244		41856	Hepatitis C virus genotype 1	2	158	2	163		5
1240		40271	Hepatitis C virus genotype 2	41	6	41	6		
2261		356114	Hepatitis C virus genotype 3	121	17	121	17		
1144		33745	Hepatitis C virus genotype 4		2		2		
1145		33746	Hepatitis C virus genotype 5		2		2		
1248		42182	Hepatitis C virus genotype 6		7		7		
744		11110	Hepatitis C virus HCT18	1		1			
1099		31644	Hepatitis C virus HCV-KF	1	1	1	1		
2595		421877	Hepatitis C virus isolate HC-J1	3	26	3	26		
2589		420174	Hepatitis C virus isolate HC-J4		143	1	143	1	
745		11113	Hepatitis C virus isolate HC-J6	8	3	8	3		
746		11115	Hepatitis C virus isolate HC-J8	1	1	1	1		
2265		356411	Hepatitis C virus JFH-1	7	1	8	1	1	
1101		31646	Hepatitis C virus subtype 1a	201	396	201	399		3
3220		10000453	Hepatitis C virus subtype 1a (isolate Gla)	5		5			
3221		10000455	Hepatitis C virus subtype 1a 1/910		18		18		
3223		10000457	Hepatitis C virus subtype 1a Chiron Corp.	1	1	1	1		
1102		31647	Hepatitis C virus subtype 1b	608	253	608	293		40
3222		10000456	Hepatitis C virus subtype 1b AD78	71		71			
3396		10000968	Hepatitis C virus subtype 1b isolate BE-11	3		3			
3225		10000460	Hepatitis C virus subtype 1b JK1	13		13			
1103		31649	Hepatitis C virus subtype 2a	80	22	80	22		
1104		31650	Hepatitis C virus subtype 2b	103	4	103	4		
2274		356426	Hepatitis C virus subtype 3a	12	105	12	105		
1254		42792	Hepatitis C virus subtype 3g	1		1			
1105		31653	Hepatitis C virus subtype 4a	1	1	1	1		
1106		31654	Hepatitis C virus subtype 5a	1	1	1	1		
1107		31655	Hepatitis C virus subtype 6a		1		1		
995		12475	Hepatitis delta virus	56	7	56	7		
3263		10000523	Hepatitis delta virus TW2667		5		5		
994		12461	Hepatitis E virus	151	27	151	76		49
1118		31767	Hepatitis E virus (strain Burma)	160		160			
1119		31768	Hepatitis E virus (strain Mexico)	31		31			
3261		10000519	Hepatitis E virus China Xinjiang	1		1			
3262		10000520	Hepatitis E virus SAR-55	2	6	2	6		
1711		185579	Hepatitis E virus type 1	3		3			
1712		185580	Hepatitis E virus type 4	1		1			
3660		10002196	Hepatitis E virus type 4 JAK-Sai	1		1			
1230		39113	Hepatitis GB virus B		4		4		
954		12092	Hepatovirus A	25	22	26	22	1	
1036		28300	Heron hepatitis B virus		1		1		
558		10299	Herpes simplex virus (type 1 / strain 17)	44	46	44	46		
559		10301	Herpes simplex virus (type 1 / strain Angelotti)		4		4		
561		10304	Herpes simplex virus (type 1 / strain F)	17	5	17	5		
560		10303	Herpes simplex virus (type 1 / strain HFEM)	2		2			
563		10308	Herpes simplex virus (type 1 / strain Patton)	3		3			
564		10309	Herpes simplex virus (type 1 / strain SC16)	6	2	6	2		
1566		126283	Herpes simplex virus unknown type		1		1		
556		10292	Herpesviridae		1		1		
1300		49011	Hesperocyparis arizonica	2	6	2	6		
1496		93621	Heteropneustes fossilis		1		1		

244		3981	Hevea brasiliensis	170	43	170	43		
386	X	6421	Hirudo medicinalis				3		3
2680		471721	HIV-1 CRF01_AE	1		1			
2463		388799	HIV-1 group O	1		1			
2736		505184	HIV-1 M:A	8	1	9	1	1	
2737		505185	HIV-1 M:B	8	1	8	1		
2510		401671	HIV-1 M:B_89.6		1		1		
862		11685	HIV-1 M:B_ARV2/SF2	1	44	1	44		
879		11706	HIV-1 M:B_HXB2R	13	12	13	14		2
871		11696	HIV-1 M:B_MN	9	23	10	23	1	
2738		505186	HIV-1 M:C	9		10		1	
3068	X	1345266	HIV-1 M:CRF01_AE			1		1	
2739		505228	HIV-1 M:G	3		4		1	
2124		327105	HIV-1 O_ANT70	1		1			
825		11583	HoJo virus		1		1		
1068		29679	Holcus lanatus	14	3	14	3		
510		9606	Homo sapiens	7867	140199	8503	246326	636	106127
1371		63221	Homo sapiens neanderthalensis		1		1		
267		4513	Hordeum vulgare		26		26		
1428		77009	Hordeum vulgare subsp. spontaneum		2		2		
1541		112509	Hordeum vulgare subsp. vulgare		18		18		
2495		397342	Horsepox virus		6		6		
615		10533	Human adenovirus 1		1		1		
616		10541	Human adenovirus 11		12		12		
2208		343463	Human adenovirus 11a	1		1			
2207		343462	Human adenovirus 11p	7		7			
1032		28282	Human adenovirus 12	11	3	11	3		
612		10521	Human adenovirus 14	4		4			
1031		28276	Human adenovirus 15	1		1			
610		10515	Human adenovirus 2	28	8	28	8		
613		10529	Human adenovirus 31		7		7		
1033		28284	Human adenovirus 40	2	1	2	1		
1294		46941	Human adenovirus 46	1		1			
1034		28285	Human adenovirus 5	25	184	25	184		
2940		714978	Human adenovirus 55	4		4			
611		10519	Human adenovirus 7	4		4			
3481		10001392	Human adenovirus B strain Harbin04B	5		5			
1280		45659	Human adenovirus B3	29	1	29	2		1
1293		46921	Human adenovirus D13	1		1			
1085		31545	Human adenovirus D8	1	1	1	1		
557		10298	Human alphaherpesvirus 1	151	175	153	178	2	3
565		10310	Human alphaherpesvirus 2	223	226	224	226	1	
576		10335	Human alphaherpesvirus 3	10	127	10	127		
1003	X	12701	Human astrovirus 2			1		1	
3042		1235996	Human betacoronavirus 2c EMC/2012	7		7			
580		10359	Human betaherpesvirus 5	88	532	118	536	30	4
1127		32603	Human betaherpesvirus 6A	2	7	2	7		
1128		32604	Human betaherpesvirus 6B	2	42	2	42		
588		10372	Human betaherpesvirus 7	2	4	2	4		
2931		689403	Human bocavirus 1	8		8			
2821		573977	Human bocavirus 2	4		4			
2849		638313	Human bocavirus 3	6		6			

1645		158465	Human calicivirus Hu/NLV/GII/MD145-12/1987/US	1		1			
751		11137	Human coronavirus 229E		2		2		
1095		31631	Human coronavirus OC43		1		1		
3628		10002015	Human coxsackievirus A16 shzh05-1	92		92			
3466		10001213	Human coxsackievirus B3 (strain RK)	1		1			
915		11827	Human endogenous retrovirus	1	1	1	1		
1382		64382	Human Endogenous Retrovirus IDDMK1,2-22	3		3			
1279		45617	Human endogenous retrovirus K	14		14			
1392		69153	Human enterovirus 71 (strain BRCR)	1		1			
3603		10001902	Human enterovirus 71 NUH0083/SIN/08	4		4			
3276	X	10000547	Human enterovirus 71 Subgenogroup B5			12		12	
3277		10000548	Human enterovirus 71 Subgenogroup C2	19		19			
3278		10000549	Human enterovirus 71 Subgenogroup C4	3		11		8	
590		10376	Human gammaherpesvirus 4	179	560	2316	609	2137	49
1210		37296	Human gammaherpesvirus 8	26	488	26	488		
1782		208726	Human hepatitis A virus	4		4			
955		12098	Human hepatitis A virus Hu/Australia/HM175/1976	86	83	86	83		
3192		10000394	Human herpesvirus 1 103/65	1		1			
3193		10000396	Human herpesvirus 1 McIntyre		1		1		
3194		10000398	Human herpesvirus 1 NS	1		1			
562		10306	Human herpesvirus 1 strain KOS	17	4	17	4		
566		10312	Human herpesvirus 2 strain 186	1	1	1	1		
567		10313	Human herpesvirus 2 strain 333	2	5	2	5		
568		10315	Human herpesvirus 2 strain HG52		31		31		
3197		10000406	Human herpesvirus 3 H-551	26	15	26	15		
577		10338	Human herpesvirus 3 strain Dumas		29		29		
2192		341980	Human herpesvirus 3 strain Oka vaccine	3	34	3	34		
3203		10000420	Human herpesvirus 4 BL74		1		1		
3204		10000421	Human herpesvirus 4 CKL		10		10		
3205		10000424	Human herpesvirus 4 GD1		1		1		
591		10377	Human herpesvirus 4 strain B95-8	170	353	171	354	1	1
1083		31525	Human herpesvirus 4 strain CAO		1		1		
592		10378	Human herpesvirus 4 strain RAJI	1		1			
1177		36352	Human herpesvirus 4 type 1	4	14	4	14		
996		12509	Human herpesvirus 4 type 2	2	10	2	10		
3206		10000427	Human herpesvirus 4 type A		5		5		
581		10360	Human herpesvirus 5 strain AD169	231	416	233	417	2	1
2032		295027	Human herpesvirus 5 strain Merlin	1	3	2	3	1	
2079		311339	Human herpesvirus 5 strain Toledo	9		9			
582		10363	Human herpesvirus 5 strain Towne	5	26	5	26		
3198		10000408	Human herpesvirus 5 TB40		1		1		
586		10369	Human herpesvirus 6 (strain GS)	2		2			
587		10370	Human herpesvirus 6 (strain Uganda-1102)	1	2	1	2		
1176		36351	Human herpesvirus 6 strain Z29	1	96	1	96		
3271		10000535	Human herpesvirus 6B HST	1		1			
1328		57278	Human herpesvirus 7 strain JI		1		1		
855		11676	Human immunodeficiency virus 1	163	463	196	481	33	18
3248		10000500	Human immunodeficiency virus 1 IIIB	1	2	1	2		
881		11709	Human immunodeficiency virus 2	1	7	1	7		
859		11682	Human immunodeficiency virus type 1 (BH5 ISOLATE)		1		1		

863		11686	Human immunodeficiency virus type 1 (BRU ISOLATE)	1	4	1	4		
864		11687	Human immunodeficiency virus type 1 (CDC-451 ISOLATE)		3		3		
857		11679	Human immunodeficiency virus type 1 (CLONE 12)		7		7		
866		11689	Human immunodeficiency virus type 1 (ELI ISOLATE)		7		7		
2298		362651	Human immunodeficiency virus type 1 (isolate YU2)	15	21	15	21		
869		11694	Human immunodeficiency virus type 1 (JH3 ISOLATE)		4		4		
865		11688	Human immunodeficiency virus type 1 (JRCSF ISOLATE)	3	37	3	37		
1180		36375	Human immunodeficiency virus type 1 (KB-1 isolate)		2		2		
872		11697	Human immunodeficiency virus type 1 (MAL ISOLATE)		8		8		
877		11704	Human immunodeficiency virus type 1 (MFA ISOLATE)		2		2		
870		11695	Human immunodeficiency virus type 1 (NDK ISOLATE)		8		8		
873		11698	Human immunodeficiency virus type 1 (NEW YORK-5 ISOLATE)	1	2	1	2		
874		11699	Human immunodeficiency virus type 1 (OYI ISOLATE)		3		3		
875		11701	Human immunodeficiency virus type 1 (RF/HAT ISOLATE)	1	19	1	19		
868		11691	Human immunodeficiency virus type 1 (SF162 ISOLATE)	2	1	2	1		
867		11690	Human immunodeficiency virus type 1 (SF33 ISOLATE)		3		3		
876		11703	Human immunodeficiency virus type 1 (STRAIN UGANDAN / ISOLATE U455)		15		15		
1108		31678	Human immunodeficiency virus type 1 (WMJ1 isolate)		16		16		
878		11705	Human immunodeficiency virus type 1 (WMJ2 ISOLATE)		1		1		
860		11683	Human immunodeficiency virus type 1 (Z2/CDC-Z34 ISOLATE)		1		1		
880		11708	Human immunodeficiency virus type 1 (ZAIRE 6 ISOLATE)		1		1		
856		11678	Human immunodeficiency virus type 1 BH10	2	25	2	26		1
884		11714	Human immunodeficiency virus type 2 (ISOLATE BEN)		12		12		
885		11715	Human immunodeficiency virus type 2 (ISOLATE CAM2)		2		2		
883		11713	Human immunodeficiency virus type 2 (ISOLATE D194)		1		1		
886		11716	Human immunodeficiency virus type 2 (ISOLATE D205,7)		2		2		
887		11717	Human immunodeficiency virus type 2 (ISOLATE GHANA-1)		7		7		
1414		73484	Human immunodeficiency virus type 2 (isolate KR)		3		3		
889		11720	Human immunodeficiency virus type 2 (ISOLATE ROD)		2		2		
888		11718	Human immunodeficiency virus type 2 (ISOLATE SBLISY)		2		2		

1584		129875	Human mastadenovirus A		1		1		
1539		108098	Human mastadenovirus B	1		1			
1585		129951	Human mastadenovirus C	1	3	1	3		
1586		130309	Human mastadenovirus F	1		1			
1658		162145	Human metapneumovirus	8	130	8	130		
784		11250	Human orthopneumovirus	29	205	32	205	3	
619		10566	Human papillomavirus	1	1	3	1	2	
622		10580	Human papillomavirus type 11	9	43	9	43		
620		10573	Human papillomavirus type 13	1	1	1	1		
2150		333760	Human papillomavirus type 16	334	421	335	429	1	8
2151		333761	Human papillomavirus type 18	26	85	26	85		
623		10583	Human papillomavirus type 1a	8	14	8	14		
2148		333751	Human papillomavirus type 2		7		7		
2152		333762	Human papillomavirus type 26		1		1		
1200		37111	Human papillomavirus type 28		1		1		
1201		37112	Human papillomavirus type 29		1		1		
636		10614	Human papillomavirus type 3		3		3		
635		10611	Human papillomavirus type 30	1		1			
624		10585	Human papillomavirus type 31	10	7	13	7	3	
2153		333763	Human papillomavirus type 32	1	1	1	1		
625		10586	Human papillomavirus type 33	6	9	6	9		
626		10587	Human papillomavirus type 35	1	1	1	1		
627		10588	Human papillomavirus type 39	1	1	1	1		
638		10617	Human papillomavirus type 4		4		4		
637		10615	Human papillomavirus type 40	1	1	1	1		
628		10589	Human papillomavirus type 41		1		1		
629		10592	Human papillomavirus type 44		1		1		
630		10593	Human papillomavirus type 45	2	9	2	9		
2157		333923	Human papillomavirus type 5	1		1			
631		10595	Human papillomavirus type 51	1	1	1	1		
639		10618	Human papillomavirus type 52	1	36	1	36		
2154		333765	Human papillomavirus type 53		1		1		
632		10596	Human papillomavirus type 56	1	5	1	5		
633		10598	Human papillomavirus type 58	48	32	49	32	1	
1202		37115	Human papillomavirus type 59	1	1	2	1	1	
1086		31552	Human papillomavirus type 6	12	4	12	4		
1203		37120	Human papillomavirus type 67	2		2			
1274		45240	Human papillomavirus type 68		1		1		
1204		37121	Human papillomavirus type 69		1		1		
634		10600	Human papillomavirus type 6b	11	29	11	29		
640		10620	Human papillomavirus type 7	1	3	1	3		
1234		39457	Human papillomavirus type 70		1		1		
1305		51033	Human papillomavirus type 73		1		1		
1184		36412	Human parainfluenza 1 virus (strains A1426 / 86-315 / 62M-753)		1		1		
774		11217	Human parainfluenza 3 virus (strain NIH 47885)	8		8			
771		11214	Human parainfluenza virus 2 (strain Toshiba)	3		3			
937		12063	Human parechovirus 1	7		7			
2014		289365	Human parvovirus 4		3		3		
659		10798	Human parvovirus B19	93	44	93	44		
3211		10000438	Human parvovirus B19 genotype 1	1		1			
949		12080	Human poliovirus 1	6	1	6	1		

950		12081	Human poliovirus 1 Mahoney	58	31	62	31	4	
951		12082	Human poliovirus 1 strain Sabin	7		7			
3421		10001028	Human poliovirus 2 (strain MEF-1)	1		1			
3424		10001040	Human poliovirus 2 (strain Sabin)	2	7	2	7		
952		12086	Human poliovirus 3	5	2	5	2		
1950		270338	Human poliovirus 3 strain Sabin	80	1	80	1		
3105		1891762	Human polyomavirus 1	1	52	3	52	2	
788		11255	Human respiratory syncytial virus (strain RSB6190)	6		6			
789		11256	Human respiratory syncytial virus (strain RSB6256)	10		10			
786		11252	Human respiratory syncytial virus (strain RSB642)	1		1			
785		11251	Human respiratory syncytial virus (subgroup B / strain 18537)	2	1	2	1		
1900	X	253182	Human Respiratory syncytial virus 9320			1		1	
1783		208893	Human respiratory syncytial virus A	1	3	1	3		
3392		10000960	Human respiratory syncytial virus A Mon/3/88	6		6			
791		11260	Human respiratory syncytial virus A strain Long	124	31	128	31	4	
3487		10001456	Human respiratory syncytial virus A strain RGH	1		1			
790		11259	Human respiratory syncytial virus A2	62	127	80	127	18	
1430		79692	Human respiratory syncytial virus B1	1	25	1	25		
2555		410078	Human respiratory syncytial virus S2	1		1			
773		11216	Human respirovirus 3	2		2			
976		12134	Human rhinovirus 1A		19		19		
3403		10000987	Human rhinovirus 2 Vienna	5		5			
1115	X	31708	Human rhinovirus A16				30		30
973		12130	Human rhinovirus A2	11		11			
1714		185905	Human rhinovirus A34		54		54		
1715	X	185907	Human rhinovirus A39				1		1
975		12132	Human rhinovirus A89	3		3			
3040		1219377	Human rhinovirus C3		52		52		
680		10950	Human rotavirus (SEROTYPE 2 / STRAIN DS1)	1		1			
1088		31569	Human rotavirus (serotype 2 / strain RV-5)	1		1			
679		10941	Human rotavirus A	13	84	14	84	1	
684		10960	Human rotavirus G4 strain St. Thomas 3	6	1	6	1		
2331		374507	Human rotavirus G9 isolate F45	7		7			
3467		10001215	Human rotavirus G9 WI61	1		1			
2540		408599	Human rotavirus G9P[8]	1		1			
1499		94432	Human rotavirus MP409	1	1	1	1		
681		10952	Human rotavirus strain KU	9		9			
682		10957	Human rotavirus strain P	1	4	1	4		
683		10958	Human rotavirus strain RRV	1		1			
685		10962	Human rotavirus strain WA	10	7	10	7		
3108		1979160	Human rubulavirus 2	10		10			
924		11927	Human T-cell lymphotrophic virus type 1 (Caribbean isolate)		6		6		
3413		10001004	Human T-cell lymphotrophic virus type 1 (Caribbean isolate) (Strain HS35)	1		1			
925		11928	Human T-cell lymphotrophic virus type 1 (isolate MT-2)	1		1			

923		11926	Human T-cell lymphotrophic virus type 1 (strain ATK)	30	118	30	118		
1227		39015	Human T-cell lymphotropic virus type 1 (african isolate)		2		2		
921		11908	Human T-lymphotropic virus 1	234	280	234	280		
922		11909	Human T-lymphotropic virus 2	63	2	63	2		
503		9580	Hylobates lar		1		1		
748		11120	Infectious bronchitis virus	7	4	7	4		
3361		10000825	Infectious bronchitis virus Avian strain D207	11		11			
3485		10001431	Infectious bronchitis virus CK/CH/LDL/97I	1		1			
2847		633557	Infectious bronchitis virus CK/CH/LHLJ/04V	1		1			
687		10995	Infectious bursal disease virus	12		12			
689		10997	Infectious bursal disease virus 002-73/AUS	1		1			
688		10996	Infectious bursal disease virus 52/70		10		10		
1087		31560	Infectious bursal disease virus E	1		1			
802		11290	Infectious hematopoietic necrosis virus	8		8			
690		11002	Infectious pancreatic necrosis virus	1		1			
811		11320	Influenza A virus	68	512	69	518	1	6
1858		229051	Influenza A virus (A/81/HO)		6		6		
2603		425551	Influenza A virus (A/AA/Huston/1945(H1N1))	1		1			
2448		387139	Influenza A virus (A/Aichi/2/1968(H3N2))	10	11	10	11		
1764		203129	Influenza A virus (A/Aichi/2/1994(H3N2))		1		1		
3073		1391655	Influenza A virus (A/Aichi/2-1/1968(H3N2))	1		1			
2795		553345	Influenza A virus (A/Aichi/72/2007(H3N2))	1		1			
2425		385576	Influenza A virus (A/Alaska/6/1977(H3N2))		2		2		
2407		383602	Influenza A virus (A/Anas acuta/Primorje/695/1976(H2N3))		17		17		
2319		370810	Influenza A virus (A/Anhui/1/2005(H5N1))	6		6			
3091		1481964	Influenza A virus (A/Anhui/1-DEWH730/2013(H7N9))	1	26	1	35		9
3099		1663996	Influenza A virus (A/Anhui/1-YK_RG01/2013(H7N9))	1		1			
3097	X	1663864	Influenza A virus (A/Anhui/1-YK_RG134/2013(H7N9))				1		1
3098	X	1663934	Influenza A virus (A/Anhui/1-YK_RG64/2013(H7N9))				2		2
2320		370811	Influenza A virus (A/Anhui/2/2005(H5N1))	1		1			
3080		1413188	Influenza A virus (A/Anhui/PA-1/2013(H7N9))	1	3	1	3		
2670		464314	Influenza A virus (A/Anhui/T2/2006(H5N1))	1		1			
2415		384498	Influenza A virus (A/Ann Arbor/6/1960(H2N2))	1	270	1	270		
2984		947939	Influenza A virus (A/aquatic bird/Korea/w44/2005(H7N3))		1		1		
1356		62446	Influenza A virus (A/Argentina/3779/94(H3N2))		1		1		
2855		642794	Influenza A virus (A/Auckland/1/2009(H1N1))		1		1		
2639		444793	Influenza A virus (A/Auckland/590/2000(H1N1))		1		1		
2287		359921	Influenza A virus (A/Australian shelduck/Western Australia/1756/1983(H15N2))	1		1			
2437		385630	Influenza A virus (A/Bangkok/1/1979(H3N2))	1	7	1	7		
1829		223931	Influenza A virus (A/Bangkok/10/1983(H1N1))		1		1		
2460		388041	Influenza A virus (A/bar-headed goose/Qinghai/1A/2005(H5N1))	1		1			

2958		762378	Influenza A virus (A/bar-headed goose/Qinghai/3/2005(H5N1))		1		1		
2172		336238	Influenza A virus (A/Bar-headed Goose/Qinghai/61/05(H5N1))		8		8		
2862		647096	Influenza A virus (A/Beijing/01/2009(H1N1))		24		24		
2417		384500	Influenza A virus (A/Beijing/11/1956(H1N1))		30		30		
2755		518922	Influenza A virus (A/Beijing/262/1995(H1N1))	1		1			
2368		380950	Influenza A virus (A/Beijing/32/1992(H3N2))		54		54		
2870		648856	Influenza A virus (A/Beijing/501/2009(H1N1))	1		1			
2065		304883	Influenza A virus (A/Belfast/53582/2004(H3N?))		2		2		
3008		1086859	Influenza A virus (A/Bilthoven/4791/1981(H3N2))		3		3		
2169		336092	Influenza A virus (A/black-headed goose/Qinghai/1/2005(H5N1))	2		2			
1483		88776	Influenza A virus (A/Brevig Mission/1/1918(H1N1))		1		1		
2684		476294	Influenza A virus (A/Brisbane/10/2007(H3N2))	5		5			
2734		504904	Influenza A virus (A/Brisbane/59/2007(H1N1))	26	13	26	13		
2430		385587	Influenza A virus (A/budgerigar/Hokkaido/1/1977(H4N6))		10		10		
2685	X	476303	Influenza A virus (A/California/04/2007(H1N1))				1		1
2851		641501	Influenza A virus (A/California/04/2009(H1N1))	62	96	65	103	3	7
2786		535852	Influenza A virus (A/California/06/2008(H1N1))		1		1		
2852		641809	Influenza A virus (A/California/07/2009(H1N1))	25	10	25	13		3
2854		642261	Influenza A virus (A/California/08/2009(H1N1))	8		8			
2604		425557	Influenza A virus (A/California/10/1978(H1N1))		1		1		
2250		352963	Influenza A virus (A/California/7/2004(H3N2))		1		1		
2452		387191	Influenza A virus (A/camel/Mongolia/1982(H1N1))		8		8		
2422		384527	Influenza A virus (A/Cameron/1946(H1N1))		1		1		
2514		402518	Influenza A virus (A/Canada/rv504/2004(H7N3))	1		1			
2255		353466	Influenza A virus (A/Canterbury/236/2005(H3N2))		1		1		
2840		616922	Influenza A virus (A/chicken/Anhui/1/1998(H9N2))		1		1		
1777		205946	Influenza A virus (A/Chicken/Beijing/1/95(H9N2))		1		1		
2517		404137	Influenza A virus (A/chicken/Beijing/nl/2002(H9N2))		1		1		
1185		36418	Influenza A virus (A/chicken/Brescia/1902(H7N7))		1		1		
2194		342137	Influenza A virus (A/chicken/CA/375TR/2002(H6N2))		1		1		
1743		196462	Influenza A virus (A/chicken/California/1002a/00(H6N2))	1	1	1	1		
813		11384	Influenza A virus (A/chicken/FPV/Weybridge(H7N7))		2		2		
2132		329593	Influenza A virus (A/chicken/Fujian/25/00(H9N2))		6		6		
1748		197579	Influenza A virus (A/Chicken/Guangdong/11/97(H9N2))		1		1		

2539		407418	Influenza A virus (A/chicken/Guiyang/2147/2005(H5N1))		1		1		
2624		435359	Influenza A virus (A/chicken/Hebei/706/2005(H5N1))		1		2		1
2244		352348	Influenza A virus (A/chicken/Hong Kong/17/1977(H6N1))		1		1		
1517		100835	Influenza A virus (A/Chicken/Hong Kong/258/97 (H5N1))	1		1			
2275		357205	Influenza A virus (A/chicken/Hong Kong/3123.1/2002(H5N1))		1		1		
1509		97353	Influenza A virus (A/Chicken/Hong Kong/739/94(H9N2))		1		1		
1508		97348	Influenza A virus (A/Chicken/Hong Kong/G23/97(H9N2))		1		1		
3066		1342397	Influenza A virus (A/chicken/Hong Kong/TP38/2003(H9N2))		3		3		
2020		292039	Influenza A virus (A/chicken/HongKong/SF1/03(H9N2))	1		1			
2021		292045	Influenza A virus (A/chicken/HongKong/YU427/03(H9N2))	1		1			
2980		932622	Influenza A virus (A/chicken/Huadong/4/2008(H5N1))	1		1			
2519		404150	Influenza A virus (A/chicken/Hubei/wk/1997(H5N1))		2		2		
2521		404155	Influenza A virus (A/chicken/Hunan/fg/2004(H5N1))		2		2		
2891		680729	Influenza A virus (A/chicken/Italy/1067/1999(H7N1))		17		17		
2647		447133	Influenza A virus (A/chicken/Japan/1925(H7N7))	1		1			
3078		1403514	Influenza A virus (A/chicken/Jiangsu/x1/2004(H9N2))	7		7			
2522		404163	Influenza A virus (A/chicken/Jilin/hg/2002(H5N1))		1		1		
2054		300750	Influenza A virus (A/chicken/Korea/S1/2003(H9N2))		1		1		
2198		342221	Influenza A virus (A/chicken/Korea/S4/2003(H9N2))		1		1		
2037		298713	Influenza A virus (A/chicken/Korea/SNU0091/00(H9N2))		1		1		
2038		298716	Influenza A virus (A/chicken/Korea/SNU1035C/00(H9N2))		1		1		
2341		376721	Influenza A virus (A/chicken/Kurgan/05/2005(H5N1))	1		1			
2892		680739	Influenza A virus (A/chicken/Mexico/37821-771/1996(H5N2))		1		1		
1954		270490	Influenza A virus (A/chicken/Nakorn-Patom/Thailand/CU-K3/2004(H5N1))		1		1		
1805		215862	Influenza A virus (A/Chicken/Nanchang/2-220/2001(H3N6))		1		1		
2526		404573	Influenza A virus (A/chicken/Netherlands/03010132/03(H7N7))	1		1			
2846		632134	Influenza A virus (A/chicken/Pakistan/UDL-01/2008(H9N2))	7		7			
2429		385586	Influenza A virus (A/chicken/Pennsylvania/1/1983(H5N2))		1		1		
1484		89169	Influenza A virus (A/Chicken/Pennsylvania/13552-1/98 (H7N2NSB))	1		1			

2435		385617	Influenza A virus (A/chicken/Pennsylvania/1370/1983(H5N2))	1		1			
2473		392810	Influenza A virus (A/chicken/Rostock/8/1934(H7N1))	2	4	2	4		
2515		402527	Influenza A virus (A/chicken/Scotland/1959(H5N1))		1		1		
1749		197585	Influenza A virus (A/chicken/Shandong/6/96(H9N2))	1		1			
1704		183741	Influenza A virus (A/Chicken/Shanghai/F/98(H9N2))	5		5			
2988		996581	Influenza A virus (A/chicken/Shanghai/Q0808-1/2008(H9N2))		1		1		
2525		404408	Influenza A virus (A/chicken/Shanxi/2/2006(H5N1))	1		1			
2325		371214	Influenza A virus (A/chicken/Taiwan/0329/01(H6N1))	5		5			
2651		449656	Influenza A virus (A/chicken/Taiwan/2838V/00(H6N1))	15		15			
3007		1082519	Influenza A virus (A/chicken/Taixing/10/2010(H9N2))	2		2			
1927		264510	Influenza A virus (A/chicken/Thailand/LV1NF/2004(H5N1))		1		1		
2486		393548	Influenza A virus (A/chicken/Tula/Russia/Oct-5/2005(H5N1))		1		1		
2963		768647	Influenza A virus (A/chicken/Uchal/8286/2006(H9N2))		1		1		
2962		768646	Influenza A virus (A/chicken/Uchal/8293/2006(H9N2))		1		1		
2041		299730	Influenza A virus (A/chicken/Viet Nam/AG-010/2004(H5N1))		1		1		
2365		380836	Influenza A virus (A/chicken/Vietnam/5/2003(H5N1))		1		1		
2307		365129	Influenza A virus (A/chicken/Vietnam/DT171/2004(H5N1))		1		1		
1955	X	270510	Influenza A virus (A/chicken/Vietnam/HD1/2004(H5N1))				3		3
3057		1310532	Influenza A virus (A/chicken/West Java/Sbg-29/2007(H5N1))	7		7			
1936	X	266093	Influenza A virus (A/chicken/Yamaguchi/7/2004(H5N1))			3		3	
2374		380985	Influenza A virus (A/Chile/1/1983(H1N1))		4		4		
1362		62541	Influenza A virus (A/Christchurch/2/1988(H3N2))		1		1		
2751		514193	Influenza A virus (A/CHU/2-524/2005(H3N2))		2		2		
1997		284168	Influenza A virus (A/Ck/HK/2133.1/2003(H5N1))		1		1		
2257		354235	Influenza A virus (A/Ck/HK/CSW161/2003(H9N2))		1		1		
1998		284177	Influenza A virus (A/Ck/HK/YU22/2002(H5N1))	1		1			
1999		284190	Influenza A virus (A/Ck/Viet Nam/36/2004(H5N1))	1		1			
2000		284195	Influenza A virus (A/Ck/YN/115/2004(H5N1))		1		1		
1536		107493	Influenza A virus (A/Cordoba/3278/96(H3N2))		1		1		
2109		320306	Influenza A virus (A/crested eagle/Belgium/01/2004(H5N1))	2		2			
2019		291592	Influenza A virus (A/crow/Kyoto/53/2004(H5N1))	1		1			

2733		504697	Influenza A virus (A/Cygnus olor/Czech Republic/10732/07(H5N1))		1		1		
2427		385583	Influenza A virus (A/Denver/1957(H1N1))		2		2		
2001		284202	Influenza A virus (A/Dk/ST/5048/2001(H3N8))	1		1			
2246	X	352561	Influenza A virus (A/duck/Australia/341/1983(H15N8))				1		1
3101		1727172	Influenza A virus (A/duck/Bavaria/1/1977(H1N1))		2		2		
2453		387203	Influenza A virus (A/duck/Bavaria/2/1977(H1N1))		1		1		
2877		658578	Influenza A virus (A/duck/Beijing/MG0617/2005(H9N2))		1		1		
2397		383550	Influenza A virus (A/duck/England/1/1956(H11N6))		2		2		
1981		274828	Influenza A virus (A/duck/Fujian/13/2002(H5N1))		1		1		
1982		274829	Influenza A virus (A/duck/Fujian/17/2001(H5N1))		1		1		
2305		365078	Influenza A virus (A/duck/Guangxi/1586/2004(H5N1))		1		1		
2306		365080	Influenza A virus (A/duck/Guangxi/1793/2004(H5N1))		1		1		
2493		395841	Influenza A virus (A/duck/Hokkaido/1130/01(H1N1))		1		1		
1898		249372	Influenza A virus (A/duck/Hokkaido/13/00(H9N2))	2		2			
2454		387207	Influenza A virus (A/duck/Hokkaido/8/1980(H3N8))		6		6		
2893		680767	Influenza A virus (A/duck/Hong Kong/140/1998(H5N1))		1		1		
1707		183783	Influenza A virus (A/duck/Hong Kong/3096/99(H6N2))		2		2		
1692		176672	Influenza A virus (A/Duck/Hong Kong/ww461/2000(H5N1))		1		1		
2424		384946	Influenza A virus (A/duck/Hungary/1/1970(H6N2))		1		1		
2321		370813	Influenza A virus (A/duck/IT/701/2005(H10N7))		1		1		
2078		311169	Influenza A virus (A/duck/Korea/S10/03(H3N2))		1		1		
2635		441962	Influenza A virus (A/duck/Mongolia/47/2001(H7N1))		3		3		
2254		353253	Influenza A virus (A/duck/Novosibirsk/56/2005(H5N1))	6	2	6	2		
2243		352034	Influenza A virus (A/duck/Potsdam/1402-6/1986(H5N2))	1		1			
1792		210656	Influenza A virus (A/Duck/Shantou/1881/00(H9N2))		1		1		
1793		210659	Influenza A virus (A/Duck/Shantou/2088/01(H9N2))		1		1		
1794		210663	Influenza A virus (A/Duck/Shantou/2134/00(H9N2))		1		1		
1791		210655	Influenza A virus (A/Duck/Shantou/2144/00(H9N2))		1		1		
2648		447188	Influenza A virus (A/duck/Tasmania/277/2007(H7N2))	1		1			
2426		385580	Influenza A virus (A/duck/Ukraine/1/1963(H3N8))	3		3			
2366		380842	Influenza A virus (A/duck/Vietnam/15/2003(H5N1))		1		3		2
2720		496036	Influenza A virus (A/duck/Vietnam/37/2007(H5N1))		1		1		

2748		510222	Influenza A virus (A/duck/Vietnam/NCVD-9/2007(H5N1))	1		1			
1986		279797	Influenza A virus (A/egret/Hong Kong/757.3/2002(H5N1))		3		3		
2596		421901	Influenza A virus (A/Egypt/0636-NAMRU3/2007(H5N1))	2	1	2	1		
2586		418868	Influenza A virus (A/Egypt/14724-NAMRU3/2006(H5N1))	1		1			
2805		562988	Influenza A virus (A/Egypt/2289-NAMRU3/2008(H5N1))	1		1			
2806		562992	Influenza A virus (A/Egypt/3300-NAMRU3/2008(H5N1))	1		1			
1733		192549	Influenza A virus (A/Egypt/96/2002(H1N2))		1		1		
1821		220977	Influenza A virus (A/England/10/67(H2N2))		1		1		
2352		380284	Influenza A virus (A/England/268/1996(H7N7))	1	1	1	1		
2348		380210	Influenza A virus (A/England/333/1980(H1N1))	1	1	1	1		
1752		198059	Influenza A virus (A/England/627/01(H1N2))		2		2		
2820		573797	Influenza A virus (A/England/654/2007(H1N1))		1		1		
2449		387147	Influenza A virus (A/England/878/1969(H3N2))	1	2	1	2		
1604		137578	Influenza A virus (A/England/939/69 x A/PR/8/34)		2		2		
2887		680689	Influenza A virus (A/England/AV877/1996(H7N7))		1		1		
2894		680785	Influenza A virus (A/environment/Hong Kong/156/1997(H5N1))	1		1			
1599		135661	Influenza A virus (A/environment/Hong Kong/437-10/99 (H5N1))		1		1		
2895		680789	Influenza A virus (A/environment/Viet Nam/1203/2004(H5N1))	1		1			
1649		159471	Influenza A virus (A/eq/Sussex/89/(H3N8))	4		4			
2456		387213	Influenza A virus (A/equine/Alaska/1/1991(H3N8))		1		1		
2683		475493	Influenza A virus (A/equine/California/8560/2002(H3N8))		2		2		
3013		1122279	Influenza A virus (A/equine/Guangxi/3/2011(H9N2))		1		1		
2428		385585	Influenza A virus (A/equine/Jilin/1/1989(H3N8))	1		1			
2433		385605	Influenza A virus (A/equine/Kentucky/2/1986(H3N8))		3		3		
2360		380340	Influenza A virus (A/equine/London/1416/1973(H7N7))	1	1	1	1		
2174		336794	Influenza A virus (A/equine/Massachussetts/213/2003(H3N8))		1		1		
2457		387223	Influenza A virus (A/equine/Miami/1963(H3N8))	5		5			
2682		475478	Influenza A virus (A/equine/New Market/1/1979(H3N8))	1		1			
2175		336800	Influenza A virus (A/equine/New York/1/1999(H3N8))		3		3		
1845		225089	Influenza A virus (A/equine/NewMarket/D64/79(H3N8))		1		1		
2358		380337	Influenza A virus (A/equine/Prague/1/1956(H7N7))		1		1		

2359		380339	Influenza A virus (A/equine/Tennessee/5/1986(H3N8))		1		1		
2828		578079	Influenza A virus (A/ferret/Maryland/P10-UMD/2008(H9N2))		1		1		
1780		207401	Influenza A virus (A/finch/Canada/NS1301/2001(H3N8))		1		1		
2311		367120	Influenza A virus (A/Fort Monmouth/1/1947(H1N1))	1		1			
2351		380282	Influenza A virus (A/Fort Monmouth/1/1947-mouse adapted(H1N1))		47		47		
3069		1346336	Influenza A virus (A/Fort Monmouth/1-JY2/1947(H1N1))		1		1		
1913		260806	Influenza A virus (A/FPV/Dutch/1927(H7N7))	1		1			
1537		107558	Influenza A virus (A/France/75/97(H3N2))		1		1		
2029		293090	Influenza A virus (A/Fujian/411/2002(H3N2))		1		1		
1363		62549	Influenza A virus (A/Fukuoka/C29/1985(H3N2))	5		5			
2256		354228	Influenza A virus (A/Gf/HK/SSP607/2003(H9N2))		1		1		
1498		93838	Influenza A virus (A/goose/Guangdong/1/1996(H5N1))	1	6	1	9		3
1665		165512	Influenza A virus (A/goose/Guangdong/3/1997(H5N1))	3	1	3	1		
1702		182781	Influenza A virus (A/Goose/Hong Kong/385.3/2000(H5N1))		1		1		
2896		680799	Influenza A virus (A/goose/Hong Kong/437-6/1999(H5N1))		1		1		
2897		680803	Influenza A virus (A/goose/Hong Kong/739.2/2002(H5N1))		1		1		
2356		380330	Influenza A virus (A/goose/Hong Kong/8/1976(H1N1))		2		2		
2512		402464	Influenza A virus (A/gray teal/Australia/2/1979(H4N4))		1		1		
3002		1041990	Influenza A virus (A/Guangdong/15/2007(H3N2))	3		3			
2458		387239	Influenza A virus (A/gull/Delaware/475/1986(H2N2))		1		1		
2416		384499	Influenza A virus (A/gull/Maryland/704/1977(H13N6))		1		1		
2559		411662	Influenza A virus (A/Hanoi/TN405/2005(H3N2))		1		1		
2450		387156	Influenza A virus (A/Harbin/1/1988(H1N2))		17		17		
2064		303316	Influenza A virus (A/Hatay/2004/(H5N1))	3		3			
2369		380951	Influenza A virus (A/Hebei/19/1995(H3N2))	1		1			
2459		387243	Influenza A virus (A/herring gull/DE/677/1988(H2N8))		1		1		
2668		462695	Influenza A virus (A/Hiroshima/52/2005(H3))	2		2			
1832		223947	Influenza A virus (A/Hokkaido/20/89(H3N2))		3		3		
2861		645724	Influenza A virus (A/Hong Kong/01/2009(H1N1))	3		3			
2741		506350	Influenza A virus (A/Hong Kong/1/1968(H3N2))	13	2	18	2	5	
1587		130760	Influenza A virus (A/Hong Kong/1073/99(H9N2))	1	25	1	25		
2888		680690	Influenza A virus (A/Hong Kong/1074/1999(H9N2))	2	1	2	1		
1661		164326	Influenza A virus (A/Hong Kong/1131/1998(H1N1))	1	1	1	1		
1659		162326	Influenza A virus (A/Hong Kong/1143/99(H3N2))	1		1			

1588		130763	Influenza A virus (A/Hong Kong/156/97(H5N1))	2	26	2	26		
1862		231851	Influenza A virus (A/Hong Kong/1774/99(H3N2))		1		1		
2105		317652	Influenza A virus (A/Hong Kong/2/68(H3N2))		4		4		
2876		657165	Influenza A virus (A/Hong Kong/213/03)	2	2	2	2		
2617		432070	Influenza A virus (A/Hong Kong/213/2003(H5N1))	1	4	1	4		
2942		715494	Influenza A virus (A/Hong Kong/33982/2009(H9N2))		3		3		
1631		155218	Influenza A virus (A/Hong Kong/482/97(H5N1))	7	1	7	1		
1482		88104	Influenza A virus (A/Hong Kong/483/1997(H5N1))	3	10	3	10		
2889		680692	Influenza A virus (A/Hong Kong/485/1997(H5N1))	1	1	1	1		
1633		155222	Influenza A virus (A/Hong Kong/488/97(H5N1))		1		1		
1627		153969	Influenza A virus (A/Hong Kong/497/97(H3N2))		1		1		
1634		155225	Influenza A virus (A/Hong Kong/507/97(H5N1))		5		5		
1635		155226	Influenza A virus (A/Hong Kong/514/97(H5N1))		1		1		
1636		155227	Influenza A virus (A/Hong Kong/516/97(H5N1))		2		2		
1481		88103	Influenza A virus (A/Hong Kong/532/1997(H5N1))		1		1		
1632		155220	Influenza A virus (A/Hong Kong/542/97(H5N1))	1		1			
2644		446023	Influenza A virus (A/Hong Kong/68(H3N2))	1		1			
2725		499286	Influenza A virus (A/Hong Kong/CUHK13527/2003(H3N2))		2		2		
2937		697610	Influenza A virus (A/India/GWMH05/2009(H1N1))		1		1		
3006		1081253	Influenza A virus (A/Indiana/08/2011(H3N2))		6		6		
2503		400788	Influenza A virus (A/Indonesia/5/2005(H5N1))	1	3	1	3		
2676		468968	Influenza A virus (A/Indonesia/560H/2006(H5N1))	1		1			
2594		421472	Influenza A virus (A/Indonesia/CDC1032N/2007(H5N1))	1		1			
2660		453057	Influenza A virus (A/Indonesia/CDC540/2006(H5N1))	1		1			
2504		400810	Influenza A virus (A/Indonesia/CDC594/2006(H5N1))	1		1			
2505		400828	Influenza A virus (A/Indonesia/CDC669/2006(H5N1))	4		4			
2506		400830	Influenza A virus (A/Indonesia/CDC699/2006(H5N1))	2		2			
2681		472511	Influenza A virus (A/Indonesia/TLL007/2006(H5N1))	1		1			
2708		488233	Influenza A virus (A/Iran/1/1957(H2N2))		1		1		
2511		402194	Influenza A virus (A/Istanbul/CTF/10/2004(H3N2))		1		1		
2451		387161	Influenza A virus (A/Japan/305/1957(H2N2))	4	29	4	29		
2382		382813	Influenza A virus (A/Japan/305+/1957(H2N2))	2		2			
2074		307819	Influenza A virus (A/Jiangsu/38/2004(H3N2))		1		1		
1763		203126	Influenza A virus (A/Kamata/14/91(H3N2))	1		1			
1628		154540	Influenza A virus (A/Kayano/57(H2N2))		1		1		
2414		384495	Influenza A virus (A/Kiev/59/1979(H1N1))		5		5		

2126		327310	Influenza A virus (A/Kinmen/645/04(H3N2))		1		1		
1844		225088	Influenza A virus (A/Kitakyushu/159/93(H3N2))		1		1		
1357		62478	Influenza A virus (A/Kitakyushu/93(H3N2))		1		1		
2858		644289	Influenza A virus (A/Korea/01/2009(H1N1))	3		3			
2709		488241	Influenza A virus (A/Korea/426/1968(H2N2))		2		2		
2625		436004	Influenza A virus (A/kunke/1/71(H3N2))		1		1		
2487		393557	Influenza A virus (A/Leningrad/1954/1(H1N1))		8		8		
2488		393697	Influenza A virus (A/Liaoning/25/2000(H1N1))		1		1		
1364		62559	Influenza A virus (A/Los Angeles/1987(H3N2))	5		5			
3082	X	1420840	Influenza A virus (A/Luxembourg/46/2009(H1N1))				1		1
1505		95888	Influenza A virus (A/mallard duck/PA/10218/84(H5N2))	8		8			
1993		282124	Influenza A virus (A/mallard/Alberta/127/00(H3N8))		1		1		
2248		352764	Influenza A virus (A/mallard/Alberta/202/1996(H2N5))	1		1			
2245		352520	Influenza A virus (A/mallard/Alberta/35/1976(H1N1))		6		6		
2247		352564	Influenza A virus (A/mallard/Astrakhan/263/1982(H14N5))	1		1			
2800	X	558177	Influenza A virus (A/mallard/Bavaria/10/2007(H5N1))				1		1
1713		185794	Influenza A virus (A/mallard/NZ/1/97(H5N2))		1		1		
2028		293055	Influenza A virus (A/mallard/Ohio/556/1987(H5N9))		1		1		
2874		655288	Influenza A virus (A/mallard/Quebec/10969/2006(H2N3))		1		1		
2779		527221	Influenza A virus (A/mallard/Sweden/S90391/2005(H3N8))		1		1		
2406		383586	Influenza A virus (A/Memphis/1/1971(H3N2))	19	11	19	11		
2344		378139	Influenza A virus (A/Memphis/1/1978(H1N1))		7		7		
2404		383577	Influenza A virus (A/Memphis/1/1990(H3N2))		1		1		
1431		79695	Influenza A virus (A/Memphis/1/71H-A/Bellamy/42N)		1		1		
2580		416730	Influenza A virus (A/Memphis/10/1996(H1N1))		1		1		
2438		385640	Influenza A virus (A/Memphis/102/1972(H3N2))		8		8		
2343		378131	Influenza A virus (A/Memphis/13/1978(H1N1))		1		1		
2403		383574	Influenza A virus (A/Memphis/2/1985(H3N2))	1		1			
1856		228928	Influenza A virus (A/Memphis/31/98(H3N2))	6		6			
1225		38973	Influenza A virus (A/Memphis/4/1973(H3N2))		1		1		
2405		383578	Influenza A virus (A/Memphis/4/1980(H3N2))		1		1		
2402		383571	Influenza A virus (A/Memphis/6/1986(H3N2))	4		4			
2957		761251	Influenza A virus (A/Mexico City/WR1704T/2009(H1N1))		1		1		
2971		887118	Influenza A virus (A/Mexico/UASLP-012/2008(H3N2))		1		1		
2516		402938	Influenza A virus (A/Michigan/2/2003(H1N2))	1		1			
3093	X	1507381	Influenza A virus (A/Minnesota/11/2010(H3N2))			10		10	
2689		480019	Influenza A virus (A/Moscow/10/1999(H3N2))		2		2		

2162		334590	Influenza A virus (A/Moscow/343/2003(H3N2))		1		1		
1840		224819	Influenza A virus (A/Nagasaki/76/98(H3N2))		1		1		
2464		389259	Influenza A virus (A/Nagasaki/N03/2005(H3N2))		1		1		
2237		351277	Influenza A virus (A/Nanchang/0058/1994(H3N2))		1		1		
1358		62488	Influenza A virus (A/Nanchang/58/1993(H3N2))		1		1		
1899		251297	Influenza A virus (A/Netherlands/127/03(H7N7))		1		1		
2982		936115	Influenza A virus (A/Netherlands/18/1994(H3N2))		1		1		
2890		680693	Influenza A virus (A/Netherlands/219/2003(H7N7))	1		1			
1595		132884	Influenza A virus (A/Netherlands/458/98 (H3N2))		1		1		
2856		643212	Influenza A virus (A/Netherlands/602/2009(H1N1))	2	14	2	14		
1593		132783	Influenza A virus (A/Netherlands/626/89 (H3N2))		1		1		
1594		132841	Influenza A virus (A/Netherlands/785e/90 (H3N2))		1		1		
2375		381512	Influenza A virus (A/New Caledonia/20/1999(H1N1))	39	228	39	228		
2501		400331	Influenza A virus (A/New South Wales/15/1999(H3N2))		1		1		
2080		311695	Influenza A virus (A/New York/124/2001(H3N2))		1		1		
2082		311775	Influenza A virus (A/New York/205/2001(H1N1))		12		12		
2167		335358	Influenza A virus (A/New York/232/2004(H3N2))		110		110		
2125		327205	Influenza A virus (A/New York/348/2003(H1N1))		146		146		
2165		335333	Influenza A virus (A/New York/384/2005(H3N2))		62		64		2
2166		335337	Influenza A virus (A/New York/388/2005(H3N2))		14		14		
2200		342508	Influenza A virus (A/New York/444/2001(H1N1))		24		24		
2302		364132	Influenza A virus (A/New York/504/1998(H3N2))		1		1		
2389		383028	Influenza A virus (A/New York/687/1995(H3N2))	1		1			
1365		62564	Influenza A virus (A/New_York/15/94(H3N2))		1		1		
1359		62496	Influenza A virus (A/New_York/17/94(H3N2))		1		1		
2316		370128	Influenza A virus (A/Northern Territory/60/1968(H3N2))		3		3		
2419		384505	Influenza A virus (A/nt/60/1968(H3N2))		69		69		
1638		155917	Influenza A virus (A/NWS/33HA-A/tern/Australia/G70C/75NA(H1N9))	1		1			
1360		62503	Influenza A virus (A/Ohio/3/95(H3N2))		1		1		
3021		1163697	Influenza A virus (A/Oklahoma/309/2006(H3N2))	4	3	4	3		
1831		223935	Influenza A virus (A/Okuda/1957(H2N2))	1	9	1	9		
2953		754366	Influenza A virus (A/Ontario/309862/2009(H1N1))	1		1			
2393		383281	Influenza A virus (A/Otago/5/2005(H1N1))		1		1		
2376		381513	Influenza A virus (A/Panama/2007/1999(H3N2))	10	14	10	14		
1605		137885	Influenza A virus (A/parakeet/Chiba/1/97(H9N2))		4		4		

1606		137886	Influenza A virus (A/parakeet/Narita/92A/98(H9N2))		2		2		
815		11448	Influenza A virus (A/parrot/Ulster/73(H7N1))		1		1		
2873		654811	Influenza A virus (A/Perth/16/2009(H3N2))	1		1			
2383		382825	Influenza A virus (A/Philippines/2/1982(H3N2))	1	1	1	1		
2436		385624	Influenza A virus (A/Port Chalmers/1/1973(H3N2))	7	1	7	1		
2432		385600	Influenza A virus (A/Puerto Rico/8/1934(Cambridge)(H1N1))	1		1			
1795		211044	Influenza A virus (A/Puerto Rico/8/1934(H1N1))	31	468	31	478		10
1705		183764	Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))	7	100	7	100		
1485		89172	Influenza A virus (A/quail/Arkansas/16309-7/94 (H7N3NSA))	1		1			
1813		216877	Influenza A virus (A/quail/Hong Kong/FY298/00(H9N2))		4		4		
1706		183778	Influenza A virus (A/quail/Hong Kong/SF550/00(H6N1))		2		2		
1750		197589	Influenza A virus (A/Quail/Shanghai/8/96(H9N2))		1		1		
2584		417758	Influenza A virus (A/quail/Shantou/1475/2004(H9N2))	1		1			
2899		682728	Influenza A virus (A/Quebec/144147/2009(H1N1))	10		10			
2558		411167	Influenza A virus (A/Queensland/11/2001(H3N2))		1		1		
2868		647923	Influenza A virus (A/reassortant/NYMC X-179A(California/07/2009 x NYMC X-157)(H1N1))	7		7			
2883	X	673446	Influenza A virus (A/reassortant/NYMC X-181(California/07/2009 x NYMC X-157)(H1N1))			1		1	
2006		286239	Influenza A virus (A/red knot/Delaware/2561/1987(H10N5))		1		1		
2384		382828	Influenza A virus (A/RI/5-/1957(H2N2))		1		1		
1822		221012	Influenza A virus (A/Rio/6/69(H3N2))		1		1		
2941		715091	Influenza A virus (A/Roma/ISS1941/2009(H1N1))		1		1		
1610		142948	Influenza A virus (A/ruddy turnstone/Delaware/67/1998(H12N4))		1		1		
2362		380343	Influenza A virus (A/ruddy turnstone/New Jersey/47/1985(H4N6))		2		2		
2434		385616	Influenza A virus (A/ruddy turnstone/NJ/60/1985(N9))		1		1		
1734		192720	Influenza A virus (A/Saudi Arabia/2581/2001(H1N2))		1		1		
1732		192535	Influenza A virus (A/Saudi Arabia/7971/2000(H1N1))		1		1		
2413		384493	Influenza A virus (A/seal/Mass/1/1980(H7N7))	1	1	1	1		
3018		1144025	Influenza A virus (A/Shandong/9/1993(H3N2))	13		13			
1361		62512	Influenza A virus (A/Shangdong/5/94(H3N2))		1		1		
3061		1332244	Influenza A virus (A/Shanghai/02/2013(H7N9))	6		7		1	
2401		383568	Influenza A virus (A/Shanghai/11/1987(H3N2))		1		1		
3010		1093545	Influenza A virus (A/shorebird/Delaware Bay/277/2000(H9N7))		1		1		

2196		342207	Influenza A virus (A/shorebird/Delaware/141/2002(H9N9))		1		1		
2197		342210	Influenza A virus (A/shorebird/Delaware/275/2001(H9N7))		1		1		
1366		62575	Influenza A virus (A/Sichuan/2/1987(H3N2))		5		5		
2381		382781	Influenza A virus (A/Singapore/1/1957(H2N2))	1	31	1	31		
3060		1331560	Influenza A virus (A/Singapore/H2011.447/2011(H3N2))	1		1			
2944		742305	Influenza A virus (A/slaty-backed gull/Japan/6KS0185/2006(H4N8))		1		1		
2672		464622	Influenza A virus (A/Solomon Islands/3/2006 (Egg passage)(H1N1))	1		1			
2673		464623	Influenza A virus (A/Solomon Islands/3/2006(H1N1))	7		9		2	
1343		59375	Influenza A virus (A/South Carolina/1/1918(H1N1))	8	1	8	1		
1695		177131	Influenza A virus (A/SW/KS/13481-T/00(H1N2))		1		1		
1694		177128	Influenza A virus (A/SW/MN/12883/00(H1N2))		2		2		
1696		177188	Influenza A virus (A/SW/MN/3227/00(H1N2))		1		1		
3663	X	10002238	Influenza A virus (A/swan/Poland/305-135V08/2006(H5N1))			1		1	
2387		382842	Influenza A virus (A/swine/29/1937(H1N1))		2		2		
2171		336207	Influenza A virus (A/swine/Bakum/1832/2000(H1N2))		3		3		
2170		336205	Influenza A virus (A/swine/Bakum/5/95(H1N1))		2		2		
2839		614035	Influenza A virus (A/swine/Belgium/1/1998(H1N1))	1		1			
1908		256045	Influenza A virus (A/swine/Chiai/77-10/2001(H3N1))		1		1		
1602		136474	Influenza A virus (A/Swine/Colorado/23619/99(H3N2))		1		1		
1671		169169	Influenza A virus (A/swine/Cotes d'Armor/1482/1999(H1N1))		1		1		
1644		158306	Influenza A virus (A/swine/Cotes d'Armor/800/00(H1N2))		1		1		
3642	X	10002090	Influenza A virus (A/swine/Denmark/101310-1/2011(H1N1))				7		7
1668		168278	Influenza A virus (A/swine/Finistere/127/99(H3N2))		4		4		
2649		448058	Influenza A virus (A/swine/Guangdong/01/2005(H3N2))		1		1		
3004		1068705	Influenza A virus (A/swine/Guangdong/221/2009(H1N1))		1		1		
2767		522740	Influenza A virus (A/swine/Hannover/1/1981(H1N1))		12		12		
2976		915014	Influenza A virus (A/swine/Heilongjiang/44/2009(H1N1))	1		1			
1612		145306	Influenza A virus (A/swine/Hong Kong/10/98(H9N2))	5		5			
2388		382848	Influenza A virus (A/swine/Hong Kong/126/1982(H3N2))		1		1		
2410		384483	Influenza A virus (A/swine/Hong Kong/127/1982(H3N2))		1		1		
1690		173473	Influenza A virus (A/swine/Hong Kong/2106/98(H9N2))		2		2		

2357		380332	Influenza A virus (A/swine/Hong Kong/273/1994(H1N1))		1		1		
1691		173477	Influenza A virus (A/swine/Hong Kong/3297/98(H9N2))		3		3		
2350		380217	Influenza A virus (A/swine/Hong Kong/4/1976(H3N2))		1		1		
1901		253682	Influenza A virus (A/swine/Hong Kong/5190/99(H3N2))		3		3		
2986		991335	Influenza A virus (A/swine/Hong Kong/71/2009(H1N1))		1		1		
1902		253686	Influenza A virus (A/swine/Hong Kong/74/02(H3N2))		1		1		
2411		384484	Influenza A virus (A/swine/Hong Kong/81/1978(H3N2))		12		12		
1613		145307	Influenza A virus (A/swine/Hong Kong/9/98(H9N2))	2		2			
2068		306061	Influenza A virus (A/swine/IDT/Bakum1832/2000(H1N2))		1		1		
2412		384487	Influenza A virus (A/Swine/Indiana/1726/1988(H1N1))		2		2		
1576		128982	Influenza A virus (A/Swine/Indiana/9K035/99 (H1N2))		2		2		
2361		380342	Influenza A virus (A/swine/Iowa/15/1930(H1N1))	1		1			
2396		383537	Influenza A virus (A/swine/Iowa/1946(H1N1))		1		1		
1654		161502	Influenza A virus (A/swine/Italy/1509-6/97(H1N1))		15		15		
3025		1176042	Influenza A virus (A/swine/Italy/1513-1/1998(H1N1))		1		1		
1670		169166	Influenza A virus (A/swine/Italy/1521/98(H1N2))		4		4		
1678		170342	Influenza A virus (A/swine/Italy/1654-1/99(H1N2))		1		1		
2399		383561	Influenza A virus (A/swine/Italy/1850/1977(H3N2))		1		1		
2395		383531	Influenza A virus (A/swine/Italy/2/1979(H1N1))		4		4		
1614		147095	Influenza A virus (A/Swine/Italy/25823/94(H3N2))		2		2		
2400		383566	Influenza A virus (A/swine/Italy/425/1976(H1N1))		1		1		
2985		986174	Influenza A virus (A/swine/Korea/4382/2009(H1N2))		1		1		
2787		538555	Influenza A virus (A/swine/Korea/Hongsong2/2004(H1N2))		2		2		
2052		300748	Influenza A virus (A/swine/Korea/S190/2004(H9N2))		3		3		
2053		300749	Influenza A virus (A/swine/Korea/S452/2004(H9N2))		1		1		
1722		187164	Influenza A virus (A/Swine/Minnesota/55551/2000(H1N2))		1		1		
2606		426738	Influenza A virus (A/swine/Miyagi/5/2003(H1N2))		2		2		
3023		1171336	Influenza A virus (A/swine/Nebraska/A01116984/2011(H3N2))		1		1		
1717		186460	Influenza A virus (A/swine/New Jersey/11/1976(H1N1))	1		1			
2752		515581	Influenza A virus (A/swine/Ohio/24366/2007(H1N1))		1		1		
2024		292590	Influenza A virus (A/swine/Ontario/42729A/01(H3N3))	1		1			

1320		55532	Influenza A virus (A/swine/Quebec/1192/1986(H1))		1		1		
1688		172149	Influenza A virus (A/swine/Quebec/192/81(H1N1))	1		1			
1450		83206	Influenza A virus (A/swine/Scotland/410440/94(H1N2))		5		5		
3056	X	1289562	Influenza A virus (A/swine/Spain/SF11131/2007(H1N1))				3		3
2143		332747	Influenza A virus (A/swine/Tennessee/25/1977(H1N1))	1		1			
3089		1470614	Influenza A virus (A/swine/Thailand/CU-S3673N/2012(H3N2))		1		1		
2439		385644	Influenza A virus (A/swine/Ukkel/1/1984(H3N2))		1		1		
1440		82372	Influenza A virus (A/Sydney/05/97-like(H3N2))		1		1		
2832		587884	Influenza A virus (A/Sydney/5/1997(H3N2))	7		7			
2349		380213	Influenza A virus (A/Taiwan/1/1986(H1N1))		1		1		
2323		371082	Influenza A virus (A/Taiwan/2/2006(H1N1))		7		7		
2802		560463	Influenza A virus (A/Taiwan/VGHYM0325-06/2002(H3N2))		1		1		
2494		395842	Influenza A virus (A/tern/Australia/1/04(H2N5))		1		1		
2528		405050	Influenza A virus (A/tern/Australia/1402/2004(H2N5))		1		1		
2420		384509	Influenza A virus (A/tern/Australia/G70C/1975(H11N9))	9		9			
2421		384510	Influenza A virus (A/tern/South Africa/1961(H5N3))	1		1			
2853		641812	Influenza A virus (A/Texas/05/2009(H1N1))	1		1			
2638		444318	Influenza A virus (A/Texas/1/1977(H3N2))	1	15	1	15		
2371		380964	Influenza A virus (A/Texas/36/1991(H1N1))		1		1		
1939		266827	Influenza A virus (A/Thailand/1(KAN-1)/2004(H5N1))	3		3			
2569		414044	Influenza A virus (A/Thailand/1(KAN-1A)/2004(H5N1))	1		1			
2557		411157	Influenza A virus (A/Thailand/271/2005(H1N1))	1		1			
1956		270945	Influenza A virus (A/Thailand/4(SP-528)/2004(H5N1))		21		21		
2972		908203	Influenza A virus (A/Thailand/CU-H126/2009(H1N1))		1		1		
2607		427773	Influenza A virus (A/Thailand/SP83/2004(H5N1))	1		1			
1953		270484	Influenza A virus (A/tiger/Thailand/CU-LV/2004(H5N1))		2		2		
2118		322564	Influenza A virus (A/tiger/Thailand/CU-T4/04(H5N1))		5		5		
2119		322566	Influenza A virus (A/tiger/Thailand/CU-T6/04(H5N1))		1		1		
1843		225071	Influenza A virus (A/Tokyo/1566/98(H3N2))		1		1		
2370		380960	Influenza A virus (A/Tokyo/3/1967(H2N2))	2		2			
2199		342396	Influenza A virus (A/turkey/Canada-Ontario/NS-01839-1/05(H3))		1		1		
2750		511839	Influenza A virus (A/turkey/England/N28/1973(H5N2))	1		1			
2353		380285	Influenza A virus (A/turkey/Ireland/1378/1983(H5N8))		1		1		
1932		265120	Influenza A virus (A/turkey/Italy/214845/2002(H7N3))	1		1			

2513		402489	Influenza A virus (A/turkey/Minnesota/1200/1980(H7N3))		1		1		
3067		1342434	Influenza A virus (A/turkey/Minnesota/511/1978(H9N2))		1		1		
2408		383603	Influenza A virus (A/turkey/Minnesota/833/1980(H4N2))		1		1		
2195		342145	Influenza A virus (A/turkey/MN/735/79(H6N2))		2		2		
1664		165420	Influenza A virus (A/Turkey/MO/24093/99(H1N2))		4		4		
2784		533026	Influenza A virus (A/turkey/Ohio/313053/2004(H3N2))	1	2	1	2		
2027		293054	Influenza A virus (A/turkey/Ontario/6213/66(H5N?))	1		1			
2355		380301	Influenza A virus (A/turkey/Ontario/7732/1966(H5N9))	5	8	5	8		
2354		380299	Influenza A virus (A/turkey/Wisconsin/1968(H5N9))		1		1		
2431		385599	Influenza A virus (A/udorn/1972(H3N2))		1		1		
2378		381517	Influenza A virus (A/Udorn/307/1972(H3N2))		5		5		
2474		392811	Influenza A virus (A/Udorn/8/1972(H3N2))	1		1			
2740		506282	Influenza A virus (A/unknown/New York/11646-5/2005(H7N2))	1		1			
2782		529058	Influenza A virus (A/Uruguay/716/2007(H3N2))	1		1			
1367		62596	Influenza A virus (A/USSR/26/1985(H3N2))		1		1		
2377		381516	Influenza A virus (A/USSR/90/1977(H1N1))	11		11			
2315		370127	Influenza A virus (A/Victoria/1968(H3N2))		1		1		
2472		392809	Influenza A virus (A/Victoria/3/1975(H3N2))	45	9	45	9		
2002		284218	Influenza A virus (A/Viet Nam/1203/2004(H5N1))	71	123	71	133		10
2040		299390	Influenza A virus (A/Viet Nam/HN/2004(H5N1))		6		6		
2609		427890	Influenza A virus (A/Viet Nam/JP4207/2005(H5N1))	1		1			
2859		644788	Influenza A virus (A/Vietnam/1194/2004(H5N1))	12	4	13	4	1	
2277		357210	Influenza A virus (A/Vietnam/CL100/2004(H5N1))	1		1			
2276		357208	Influenza A virus (A/Vietnam/CL26/2004(H5N1))		79		79		
2385		382832	Influenza A virus (A/VM113-V1(H1N1))	1		1			
2390		383121	Influenza A virus (A/Waikato/7/2000(H3N2))		2		2		
3058	X	1318439	Influenza A virus (A/Washington/05/2011(H1N1))			1		1	
1728		191090	Influenza A virus (A/Weiss/1943(H1N1))		1		1		
2391		383152	Influenza A virus (A/Wellington/22/2001(H3N2))		1		1		
2735		504910	Influenza A virus (A/Wellington/75/2006(H1N1))		1		1		
2392		383231	Influenza A virus (A/Wellington/8/2004(H3N2))		2		2		
816		11484	Influenza A virus (A/whale/Maine/1/84(H13N9))	3		3			
2209		344598	Influenza A virus (A/whooper swan/Mongolia/6/05(H5N1))		1		1		
2379		381518	Influenza A virus (A/Wilson-Smith/1933(H1N1))		148	1	148	1	
2363		380346	Influenza A virus (A/Wisconsin/3523/1988(H1N1))	2		2			

2667		461772	Influenza A virus (A/Wisconsin/43/2006(H3N2))	1		1			
2373		380979	Influenza A virus (A/Wisconsin/4754/1994(H1N1))		1		1		
2372		380978	Influenza A virus (A/Wisconsin/4755/1994(H1N1))		5		5		
2489		393902	Influenza A virus (A/Wisconsin/67/2005(H3N2))	1	5	1	5		
2386		382835	Influenza A virus (A/WSN/1933(H1N1))	6	3	6	3		
1370		63106	Influenza A virus (A/Wuhan/359/1995(H3N2))	5		5			
2690		480024	Influenza A virus (A/Wyoming/03/2003(H3N2))		8		8		
2618		432094	Influenza A virus (A/Wyoming/3/2003-X-147(H3N2))		1		1		
2612		430417	Influenza A virus (A/Wyoming/3e5/2003(H3))	1		1			
1591		132504	Influenza A virus (A/X-31(H3N2))	77	189	77	189		
2756		518968	Influenza A virus (A/X-31B(Puerto Rico/8/1934-Aichi/2/1968)(H3N2))	1		1			
2367		380905	Influenza A virus (A/X-47(H3N2))	3	2	3	2		
2827		577543	Influenza A virus (A/Xinjiang/1/2006(H5N1))	4		4			
2127		327311	Influenza A virus (A/Yilan/515/03(H3N2))		1		1		
1906		255681	Influenza A virus (A/Yokohama/22/2002(H1N2))		2		2		
1907		255682	Influenza A virus (A/Yokohama/47/2002(H1N2))		1		1		
814		11408	Influenza A virus (STRAIN A/EQUINE/NEW MARKET/76)		1		1		
1245		41857	Influenza A virus H3N2	1	48	2	49	1	1
3389		10000865	Influenza A virus H3N2 (A/Kiev/301/94)	3		3			
3279		10000550	Influenza A virus H3N2 (A/Netherlands/9/03 (H3N2))		1		1		
3233		10000474	Influenza A virus H3N2 (A/Resvir-9 (H3N2))		10		10		
2570		415166	Influenza A virus(A/swine/Henan/2/2004(H9N2))		1		1		
2571		415167	Influenza A virus(A/swine/Henan/3/2004(H9N2))		1		1		
2572		415169	Influenza A virus(A/swine/Henan/5/2004(H9N2))		1		1		
2573		415172	Influenza A virus(A/swine/Henan/8/2004(H9N2))		2		2		
2574		415176	Influenza A virus(A/swine/Shandong/fNY/2003(H9N2))		3		3		
2575		415177	Influenza A virus(A/swine/Shandong/fZC/2003(H9N2))		7		7		
817		11520	Influenza B virus	3	6	3	6		
818		11521	Influenza B virus (B/Ann Arbor/1/1986)		3		3		
1534		107404	Influenza B virus (B/Beijing/184/93)		1		1		
2838		604436	Influenza B virus (B/Brisbane/60/2008)	2		2			
1535		107406	Influenza B virus (B/Chiba/447/98)		1		1		
2666		461739	Influenza B virus (B/Florida/4/2006)	1		1			
1779		206203	Influenza B virus (B/Hong Kong/330/2001)		23		23		
2608		427826	Influenza B virus (B/Hong Kong/8/1973)		1		1		
1842		224964	Influenza B virus (B/Johannesburg/5/99)	1		1			
1708		184816	Influenza B virus (B/Kadoma/122/99)	2		2			
1909		256080	Influenza B virus (B/Kobe/1/2003)	1		1			
2731		504664	Influenza B virus (B/Kobe/113/2005)	1		1			
2732		504666	Influenza B virus (B/Kobe/115/2005-T1)	1		1			

2728		503386	Influenza B virus (B/Kobe/3/2004)	1		1			
2730		504662	Influenza B virus (B/Kobe/39/2005)	1		1			
2729		504660	Influenza B virus (B/Kobe/67/2005)	1		1			
1685		171425	Influenza B virus (B/Kobe/87/2001)	1		1			
2757		518987	Influenza B virus (B/Lee/1940)	5	3	5	3		
2671		464417	Influenza B virus (B/Malaysia/2506/2004)	1		1			
2013		289338	Influenza B virus (B/Nanchang/12/98)		1		1		
820		11541	Influenza B virus (B/Oregon/5/80)	16		16			
1620		150127	Influenza B virus (B/Osaka/983/97-V3)	1		1			
2168		335812	Influenza B virus (B/Shanghai/361/2002)	1		1			
3005		1077587	Influenza B virus (B/Victoria/2/1987)	2	1	2	1		
2579	X	416674	Influenza B virus (B/Yamagata/16/1988)			4		4	
819		11532	Influenza B virus (STRAIN B/HT/84)		1		1		
821		11552	Influenza C virus		1		1		
822		11553	Influenza C virus (C/Ann Arbor/1/50)	9		9			
1834		224197	Influenza C virus (C/Nara/1/85)		1		1		
516		9725	Inia geoffrensis		1		1		
1303		50557	Insecta	7		7			
1322		55635	Inula helenium		1		1		
1247		42097	Isla Vista hantavirus	1	2	1	2		
1916		261204	Itapua hantavirus		10		10		
407		6945	Ixodes scapularis	11		11			
903	X	11746	Jaagsiekte sheep retrovirus			1		1	
2083		313589	Janibacter sp. HTCC2649		1		1		
719		11072	Japanese encephalitis virus	40	122	40	143		21
3215		10000444	Japanese encephalitis virus CH2195LA	1		1			
3216		10000445	Japanese encephalitis virus JaOH0566	1		1			
721		11075	Japanese encephalitis virus strain JAOARS982	4	4	4	4		
722		11076	Japanese encephalitis virus strain Nakayama	2	2	2	2		
720		11073	Japanese encephalitis virus strain SA-14	6	1	6	1		
3546		10001648	Japanese encephalitis virus strain SA-14 - 14-2	2		2			
3480		10001335	Japanese encephalitis virus Vellore P20778	1	1	1	1		
1700		180498	Jatropha curcas	6		6			
643		10632	JC polyomavirus	7	39	7	78		39
3573		10001762	JC polyomavirus strain MAD1		1		1		
1022		16719	Juglans nigra	1		1			
1306		51240	Juglans regia	34	19	34	19		
833		11619	Junin mammarenavirus	4	873	5	873	1	
3529		10001614	Junin virus strain MC2		1		1		
1008		13101	Juniperus ashei	13		13			
2661		453927	Juniperus formosana	1		1			
1391		69008	Juniperus oxycedrus		3		3		
2613		430511	Juquitiba virus		2		2		
1624		151250	Kali turgidum		22		22		
1561		122291	Kappapapillomavirus 1	2		2			
641		10623	Kappapapillomavirus 2	5	7	5	7		
1639		156230	Karenia brevis	1		1			
3118		1980475	Khabarovsk orthohantavirus		1		1		
645		10638	Kilham polyomavirus		1		1		
1941		266940	Kineococcus radiotolerans SRS30216 = ATCC BAA-149		2		2		

2658		452652	Kitasatospora setae KM-6054		1		1		
1905		255431	Klebsiella phage phiKO2		1		1		
53		573	Klebsiella pneumoniae	23	8	29	8	6	
1964		272620	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	28		28			
2697		484021	Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044		1		1		
2951		749535	Klebsiella sp. MS 92-3		1		1		
1041		28448	Komagataeibacter xylinus		1		1		
2117		322053	Konjac mosaic virus	1		1			
735		11092	Kumlinge virus	26		26			
723		11077	Kunjin virus	12	1	12	1		
724		11078	Kunjin virus (STRAIN MRM61C)		4		4		
823		11577	La Crosse virus	2	1	2	1		
824		11578	La Crosse virus L74		2		2		
466		8753	Lachesis muta muta	21		45		24	
2878		658655	Lachnospiraceae bacterium 1_4_56FAA		1		1		
2043		300015	Lactate dehydrogenase elevating virus C	1		1			
2044		300016	Lactate dehydrogenase elevating virus Plagemann	1		1			
706		11048	Lactate dehydrogenase-elevating virus	14		14			
159		1604	Lactobacillus amylovorus		1		1		
1818		219334	Lactobacillus casei subsp. casei ATCC 393	2		2			
1024		28038	Lactobacillus curvatus		1		1		
157		1585	Lactobacillus delbrueckii subsp. bulgaricus	1		1			
3604		10001913	Lactobacillus johnsonii JCM 1022	3		3			
2798		557433	Lactobacillus reuteri JCM 1112	3		3			
158		1599	Lactobacillus sakei		1		1		
141		1358	Lactococcus lactis		2		2		
1168		35345	Lactococcus phage TP901-1	3		3			
1156		35241	Lactococcus phage Tuc2009	1		1			
1903		254252	Lactococcus virus P2	2		2			
494		9519	Lagothrix lagotricha	1		1			
3119		1980476	Laguna Negra orthohantavirus		12		12		
2346		378830	Lake Victoria marburgvirus - Angola2005	6	18	6	18		
1141		33728	Lake Victoria marburgvirus - Popp	2	15	2	15		
523	X	9844	Lama glama			1		1	
1157		35258	Lambdapapillomavirus 2		25		25		
1434		80365	Laminaria digitata	2		2			
731		11085	Langat virus		1		1		
834		11620	Lassa mammarenavirus	13	670	13	670		
835		11621	Lassa virus GA391		54		54		
836		11622	Lassa virus Josiah	9	409	10	409	1	
404		6925	Latrodectus tredecimguttatus		1		1		
1463		85223	Laurus nobilis		1		1		
2100		316068	Leadbetterella byssophila		1		1		
1394		69245	Lechiguanas virus		9		9		
2880		661367	Legionella longbeachae NSW150		1		1		
3092		1498499	Legionella norrlandica		1		1		
35		446	Legionella pneumophila		1		1		
2035		297245	Legionella pneumophila str. Lens	1		1			
1966		272624	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	1		1			

301		5658	Leishmania	2		4		2	
307		5667	Leishmania aethiopica	16		16			
302		5659	Leishmania amazonensis		15		15		
303		5660	Leishmania braziliensis	6		6			
2590		420245	Leishmania braziliensis MHOM/BR/75/M2904	14	8	14	8		
1263		44271	Leishmania chagasi	3		3			
304		5661	Leishmania donovani	15	41	16	55	1	14
1514		99875	Leishmania donovani donovani	1		1			
3161		10000341	Leishmania donovani donovani 1S2D	1		1			
308		5671	Leishmania infantum	99	4	99	9		5
2623		435258	Leishmania infantum JPCM5	28	5	28	5		
3162		10000345	Leishmania infantum LEM 75	14		14			
305		5664	Leishmania major	17	184	17	184		
2220		347515	Leishmania major strain Friedlin	30	38	30	38		
306		5665	Leishmania mexicana	2	3	2	3		
2979		929439	Leishmania mexicana MHOM/GT/2001/U1103		1		1		
309		5679	Leishmania panamensis	3	7	3	7		
310		5682	Leishmania pifanoi		20		20		
707		11049	Lelystad virus	66	12	66	12		
483		9447	Lemur catta	1		1			
240		3864	Lens culinaris	19		19			
1198		36936	Lepidoglyphus destructor	5	10	5	10		
8		173	Leptospira interrogans	4	4	4	4		
1797		211882	Leptospira interrogans serovar Australis	2		2			
1264		44275	Leptospira interrogans serovar Copenhageni	2		2			
1944		267671	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	12		12			
1333		57678	Leptospira interrogans serovar Lai	10	10	10	10		
1726		189518	Leptospira interrogans serovar Lai str. 56601	1		1			
3353		10000814	Leptospira interrogans serovar Lai str. HY-1	1		1			
1265		44276	Leptospira interrogans serovar Pomona		3	2	3	2	
1064		29507	Leptospira kirschneri	1		1			
3372		10000847	Leptospira sp. Akiyami A AUT10	1		1			
111		1245	Leuconostoc mesenteroides	1		1			
398		6850	Limulus polyphemus		1		1		
163		1641	Listeria grayi		1		1		
164		1642	Listeria innocua	2	3	2	3		
161		1638	Listeria ivanovii	1	1	1	1		
162		1639	Listeria monocytogenes	21	99	21	99		
2483		393133	Listeria monocytogenes 10403S		4		4		
3145		10000308	Listeria monocytogenes ATCC 35967		1		1		
3146		10000309	Listeria monocytogenes ATCC 43251		3		3		
1674		169963	Listeria monocytogenes EGD-e	5	64	5	64		
2481		393128	Listeria monocytogenes F6900		1		1		
2477		393117	Listeria monocytogenes FSL J1-194		2		2		
2478		393124	Listeria monocytogenes FSL N3-165		2		2		
2479		393125	Listeria monocytogenes FSL R2-503		1		1		
2480		393126	Listeria monocytogenes FSL R2-561		1		1		
2794		552536	Listeria monocytogenes HCC23		2		2		
2509		401650	Listeria monocytogenes HPB2262		3		3		
2482		393130	Listeria monocytogenes J0161		6		6		

1942		267409	Listeria monocytogenes serotype 1/2a str. F6854		3		3		
2815		568819	Listeria monocytogenes serotype 4b str. CLIP 80459		6		6		
1934		265669	Listeria monocytogenes serotype 4b str. F2365		7		7		
1943		267410	Listeria monocytogenes serotype 4b str. H7858		25		25		
2442		386043	Listeria welshimeri serovar 6b str. SLCC5334		3		3		
383		6299	Litomosoides carinii	3		3			
395		6689	Litopenaeus vannamei	140		140			
1815		217686	Little cherry virus 1		1		1		
268		4522	Lolium perenne	36	122	44	122	8	
1182		36386	Louping ill virus (strain 31)	1		1			
1335		58216	Loxosceles gaucho	1		1			
1337		58218	Loxosceles intermedia	83		83			
1336		58217	Loxosceles laeta	2		2			
837		11623	Lymphocytic choriomeningitis mammarenavirus	5	653	5	654		1
838		11624	Lymphocytic choriomeningitis virus (strain Armstrong)		1158		1158		
3245		10000496	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 3)		1		1		
3239		10000487	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 4)	1		1			
3246		10000497	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 5)	1		1			
3240		10000488	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 53b)		61		61		
839		11625	Lymphocytic choriomeningitis virus (strain Pasteur)		5		5		
840		11626	Lymphocytic choriomeningitis virus (strain Traub)		3		3		
841		11627	Lymphocytic choriomeningitis virus (strain WE)		69		69		
3243		10000494	Lymphocytic choriomeningitis virus (strain WE) variant 8.7		1		1		
3244		10000495	Lymphocytic choriomeningitis virus (strain WE) WE CL1.2		1		1		
3241		10000490	Lymphocytic choriomeningitis virus A22.2b		1		1		
3242		10000491	Lymphocytic choriomeningitis virus Docile		2		2		
498		9541	Macaca fascicularis	3	3	3	3		
499		9544	Macaca mulatta	2	5	2	5		
589		10373	Macaca mulatta cytomegalovirus		76		76		
3106		1891767	Macaca mulatta polyomavirus 1	16	42	16	42		
500		9548	Macaca radiata	14	1	14	1		
573		10325	Macacine alphaherpesvirus 1	1		1			
1296		47929	Macacine betaherpesvirus 3		99		99		
1277		45455	Macacine gammaherpesvirus 4		24		24		
842		11628	Machupo mammarenavirus		800		800		
3530		10001615	Machupo virus strain Carvallo		1		1		
1170		35725	Macrophomina phaseolina		1		1		
3015		1126212	Macrophomina phaseolina MS6		1		1		
480		9322	Macropus sp.	1		1			
2615		431944	Magnetospirillum gryphiswaldense MSR-1		1		1		
1967		272627	Magnetospirillum magnetotacticum MS-1		5		5		

1424		76777	Malassezia sympodialis	1		1			
233		3750	Malus domestica	27	48	27	48		
3044		1239567	Mamastrovirus 3	2		2			
1241		40674	Mammalia	6		6			
2236		351073	Mammalian orthoreovirus		1		1		
665	X	10884	Mammalian orthoreovirus 1 Lang			1		1	
666	X	10886	Mammalian orthoreovirus 3 Dearing			1		1	
3109		1979162	Mammalian rubulavirus 5	1	1	1	1		
415		7130	Manduca sexta		3		3		
1071		29780	Mangifera indica	1		1			
1270		45201	Mannheimia haemolytica serotype 1	82		82			
1824		221988	Mannheimia succiniciproducens MBEL55E		2		2		
793		11269	Marburg marburgvirus	1	95	4	95	3	
1140		33727	Marburg virus - Musoke, Kenya, 1980	3	84	3	84		
594		10388	Marek's disease herpesvirus strain GA		1		1		
105		1006	Marivirga tractuosa		1		1		
1218		38020	marmosets	3		3			
777		11234	Measles morbillivirus	63	39	64	39	1	
3226		10000462	Measles virus CAM/RB		1		1		
1919		262307	Measles virus genotype A	4		4			
1684		171264	Measles virus genotype D3	1		1			
1680	X	170525	Measles virus genotype D4			1		1	
1681	X	170529	Measles virus genotype D7			1		1	
778		11235	Measles virus strain Edmonston	167	210	167	210		
1398		70146	Measles virus strain Edmonston-B	2	78	2	78		
1399		70149	Measles virus strain Edmonston-Zagreb	1		1			
779		11236	Measles virus strain Halle		34		34		
1590		132487	Measles virus strain Schwarz	1	1	1	1		
1318		55429	Megathura crenulata	1		1			
478		9103	Meleagris gallopavo	5		5			
1625		152219	Menangle virus	2		2			
957		12107	Mengo virus	5	13	5	13		
2719		493803	Merkel cell polyomavirus	2	2	2	2		
533		10036	Mesocricetus auratus	56		56			
3103		1891729	Mesocricetus auratus polyomavirus 1	11		11			
1126		32278	Metapenaeus ensis		6	1	6	1	
1885		243232	Methanocaldococcus jannaschii DSM 2661	3	2	3	2		
1231		39152	Methanococcus maripaludis	1		1			
1724		187420	Methanothermobacter thermautotrophicus str. Delta H		2		2		
2593		420662	Methylibium petroleiphilum PM1		1		1		
115		1270	Micrococcus luteus	2		2			
1223		38832	Micromonas		1		1		
3088		1464048	Micromonospora parva		1		1		
2085		313606	Microscilla marina ATCC 23134		1		1		
1315		54390	Micrurus corallinus	123		123			
3062		1335626	Middle East respiratory syndrome-related coronavirus	4		4	12		12
657		10793	Mink enteritis virus strain Abashiri	1		1			
1316		55097	Mobala mammarenavirus	1		1			
2675		467144	Modified Vaccinia Ankara virus		22		22		
912		11801	Moloney murine leukemia virus		5		5		
543		10244	Monkeypox virus	5	2	5	2		

3188		10000386	Monkeypox virus USA_2003_039		1		1		
1016		13616	Monodelphis domestica	1	4	1	4		
3120		1980481	Montano orthohantavirus	3		3			
1931		264732	Moorella thermoacetica ATCC 39073		1		1		
2046		300180	Mopeia Lassa virus reassortant 29		4		4		
843		11629	Mopeia mammarenavirus		14		14		
38		480	Moraxella catarrhalis	10		10			
3514		10001556	Moraxella catarrhalis 26404	1		1			
2965		857571	Moraxella catarrhalis O35E	3		3			
3591		10001849	Moraxella catarrhalis serotype A	3		3			
3586		10001831	Moraxella catarrhalis serotype B	1		1			
3592		10001851	Moraxella catarrhalis serotype C	1		1			
54		582	Morganella morganii	1		1			
904		11757	Mouse mammary tumor virus		12		12		
3110		1979165	Mumps rubulavirus	3		3			
759		11169	Mumps virus strain Kilham	1		1			
760		11173	Mumps virus strain SBL-1	6		6			
2158		334203	Mupapillomavirus 1	1	39	1	39		
583		10366	Murid betaherpesvirus 1	2	54	2	64		10
1137		33708	Murid gammaherpesvirus 4	1	53	1	53		
3199		10000411	Murid herpesvirus 1 deltaMS94.5		2		2		
3200		10000412	Murid herpesvirus 1 Isolate G4		1		1		
3201		10000413	Murid herpesvirus 1 Isolate K6		1		1		
3272		10000536	Murid herpesvirus 4 G2.4		3		3		
3273		10000537	Murid herpesvirus 4 WUMS		19		19		
3085		1440122	Murid herpesvirus 68		2		2		
614		10530	Murine adenovirus 1	1	2	1	2		
1393		69156	Murine cytomegalovirus (strain K181)	2	14	2	14		
584		10367	Murine cytomegalovirus (strain Smith)		32		32		
3482		10001396	Murine cytomegalovirus (strain Smith) MW97.01		5		5		
1159		35275	Murine endogenous retrovirus		13		13		
752		11138	Murine hepatitis virus	3	31	3	31		
1005		12760	Murine hepatitis virus strain 4		5		5		
753		11142	Murine hepatitis virus strain A59	26	4	26	4		
754		11144	Murine hepatitis virus strain JHM	25	16	25	16		
908		11786	Murine leukemia virus	1	23	1	23		
3463		10001207	Murine leukemia virus LP-BM5		1		1		
1833		223997	Murine norovirus 1	4	1	4	1		
3632		10002026	Murine norovirus 1 Mu/NoV/GV/MNV1/2002/USA		1		1		
2669		463722	Murine norovirus GV/CR6/2005/USA		1		1		
792		11263	Murine orthopneumovirus		14		14		
644		10636	Murine polyomavirus strain A2		3		3		
766		11191	Murine respirovirus	63	10	63	10		
1038		28327	Murine rotavirus		3		3		
1402		70865	Murine rotavirus EDIM		27		27		
913		11812	Murine sarcoma virus 3611	4		4			
1266		44561	Murine type C retrovirus		1		1		
725		11079	Murray Valley encephalitis virus	21	9	21	9		
2061		301478	Murray valley encephalitis virus (strain MVE-1-51)	11	14	11	14		
534		10090	Mus musculus	648	16478	670	16885	22	407
3416		10001019	Mus musculus B10.D2		1		1		

3128		10000000	Mus musculus BALB/c		3		3		
3129		10000055	Mus musculus DBA/2	1		1			
535		10092	Mus musculus domesticus		12		12		
1331		57486	Mus musculus molossinus		1		1		
1233		39442	Mus musculus musculus		1		1		
2960		763552	Mus musculus papillomavirus type 1		4		4		
3104		1891730	Mus musculus polyomavirus 1	4	30	4	30		
281		4641	Musa acuminata	50	1	50	1		
1803		214697	Musa acuminata AAA Group	1		1			
1211		37325	Muscovy duck parvovirus	11		11			
3605		10001918	Muscovy duck reovirus S12	2		2			
513		9666	Mustela lutreola	1		1			
172		1763	Mycobacterium	3	15	3	19		4
1191		36809	Mycobacterium abscessus		19		19		
3031		1198627	Mycobacterium abscessus subsp. massiliense str. GO 06		1		1		
173		1764	Mycobacterium avium	6	14	6	14		
1886		243243	Mycobacterium avium 104		43		43		
3147		10000313	Mycobacterium avium serovar 1	1		1			
3148		10000314	Mycobacterium avium serovar 2	1		1			
3149		10000316	Mycobacterium avium serovar 25	1		1			
3150		10000317	Mycobacterium avium serovar 26	1		1			
3151		10000318	Mycobacterium avium serovar 4	2		2			
3152		10000319	Mycobacterium avium serovar 8	1	1	1	1		
3153		10000320	Mycobacterium avium serovar 9	1		1			
179		1770	Mycobacterium avium subsp. paratuberculosis	105	15	105	15		
1920		262316	Mycobacterium avium subsp. paratuberculosis K-10	4	58	4	58		
3155		10000328	Mycobacterium avium subsp. paratuberculosis Strain Ben		1		1		
174		1765	Mycobacterium bovis	48	147	48	326		179
1865		233413	Mycobacterium bovis AF2122/97		50		50		
3072		1389959	Mycobacterium bovis AN5	9	28	9	28		
1148		33892	Mycobacterium bovis BCG	12	146	12	146		
2556		410289	Mycobacterium bovis BCG str. Pasteur 1173P2	1	229	1	229		
3154		10000323	Mycobacterium bovis T/91/1378		6		6		
183		1774	Mycobacterium chelonae	1		1			
3001		1041522	Mycobacterium colombiense CECT 3035		20		20		
175		1766	Mycobacterium fortuitum		1		1		
1611		144549	Mycobacterium fortuitum subsp. fortuitum		1		1		
3157		10000331	Mycobacterium gastri W471	1		1			
188		1804	Mycobacterium gilvum		1		1		
2230		350054	Mycobacterium gilvum PYR-GCK		64		64		
1983		278137	Mycobacterium gilvum Spyr1		53		53		
184		1778	Mycobacterium gordonae	1		1			
1451	X	83262	Mycobacterium immunogenum				5		5
176		1767	Mycobacterium intracellulare		1		1		
2705		487521	Mycobacterium intracellulare ATCC 13950	1		1			
2974		912594	Mycobacterium iranicum		1		1		
177		1768	Mycobacterium kansasii	9	13	9	13		
2799		557599	Mycobacterium kansasii ATCC 12478	1		1			
178		1769	Mycobacterium leprae	119	409	119	409		

1968		272631	Mycobacterium leprae TN		30		30		
185		1781	Mycobacterium marinum		1		1		
1810		216594	Mycobacterium marinum M		29		29		
187		1795	Mycobacterium neoaurum		1		1		
2770		525368	Mycobacterium parascrofulaceum ATCC BAA-614		35		35		
1257		43304	Mycobacterium peregrinum	2		2			
2788		543153	Mycobacterium phage Predator		1		1		
180		1771	Mycobacterium phlei		1		1		
186		1783	Mycobacterium scrofulaceum	4		4			
2968		875328	Mycobacterium sinense		10		10		
181		1772	Mycobacterium smegmatis		2		24		22
1892		246196	Mycobacterium smegmatis str. MC2 155		61		61		
1663		164757	Mycobacterium sp. JLS		77		77		
1727		189918	Mycobacterium sp. KMS		69		69		
1662		164756	Mycobacterium sp. MCS		73		73		
3071		1380386	Mycobacterium sp. URHB0044		1		1		
182		1773	Mycobacterium tuberculosis	530	2349	622	2469	92	120
3156		10000329	Mycobacterium tuberculosis 103	1		1			
2221		348776	Mycobacterium tuberculosis C		176		176		
1452		83331	Mycobacterium tuberculosis CDC1551		42		42		
2176		336982	Mycobacterium tuberculosis F11		24		24		
2588		419947	Mycobacterium tuberculosis H37Ra		130		130		
1453		83332	Mycobacterium tuberculosis H37Rv	61	860	61	876		16
2872		652616	Mycobacterium tuberculosis str. Erdman = ATCC 35801	15	19	15	19		
2491		395095	Mycobacterium tuberculosis str. Haarlem		127		127		
1703		182785	Mycobacterium tuberculosis subsp. tuberculosis		1		1		
1422		75922	Mycobacterium tusciae		2		2		
189		1809	Mycobacterium ulcerans		8		10		2
2297		362242	Mycobacterium ulcerans Agy99		16		16		
2231		350058	Mycobacterium vanbaalenii PYR-1		55		55		
2218		347257	Mycoplasma agalactiae PG2	3		3			
1048		28903	Mycoplasma bovis	21		21			
2994		1006581	Mycoplasma gallisepticum S6	1		1			
197		2097	Mycoplasma genitalium		1		1		
1887		243273	Mycoplasma genitalium G37	8	1	8	1		
198		2099	Mycoplasma hyopneumoniae	2		2			
2034		295358	Mycoplasma hyopneumoniae 232	21		21			
2954		754503	Mycoplasma hyopneumoniae 7422	1		1			
1922		262722	Mycoplasma hyopneumoniae 7448	1		1			
1030		28227	Mycoplasma penetrans	39		39			
1969		272633	Mycoplasma penetrans HF-2	1		1			
199		2104	Mycoplasma pneumoniae	12	2	12	2		
2943		722438	Mycoplasma pneumoniae FH	3		3			
1970		272634	Mycoplasma pneumoniae M129	9		9			
1330		57372	Mycoplasma suis	3		3			
1017		13618	Myrmecia pilosula	2		2			
1425		76832	Myroides odoratimimus		1		1		
1456		83455	Myxococcus stipitatus		1		1		
3050		1278073	Myxococcus stipitatus DSM 14675		1		1		
1893		246197	Myxococcus xanthus DK 1622		1		1		

554		10273	Myxoma virus		4		4		
2948		744533	Naegleria gruberi strain NEG-M	1		1			
455		8656	Naja atra	8		8			
1169		35670	Naja naja	3		3			
453		8654	Naja nigricollis	3	2	3	2		
456		8657	Naja oxiana	4		4			
457		8658	Naja pallida	1	1	1	1		
1304		51031	Necator americanus	17		17			
2312		367400	Neembucu hantavirus		5		5		
39		485	Neisseria gonorrhoeae	25	15	76	15	51	
3515		10001558	Neisseria gonorrhoeae 15253	1		1			
3387		10000863	Neisseria gonorrhoeae 4505	1		1			
2781		528354	Neisseria gonorrhoeae MS11	8		8			
3436		10001077	Neisseria gonorrhoeae SU89	1		1			
3437		10001078	Neisseria gonorrhoeae SU96	3		3			
40		487	Neisseria meningitidis	85	23	86	23	1	
1972		272831	Neisseria meningitidis FAM18	1		1			
2973		909420	Neisseria meningitidis H44/76	1		1			
3516		10001560	Neisseria meningitidis M982B	2		2			
1563		122586	Neisseria meningitidis MC58	17		17			
3024		1172206	Neisseria meningitidis NMB	1		1			
1385		65699	Neisseria meningitidis serogroup A	5		5			
3430		10001051	Neisseria meningitidis serogroup A Strain 8659	1		1			
41		491	Neisseria meningitidis serogroup B	40	1	40	1		
3370		10000843	Neisseria meningitidis serogroup B H44/76	74	22	74	22		
3412		10001003	Neisseria meningitidis serogroup B CU385	2		2			
3461		10001161	Neisseria meningitidis serogroup B Strain 2996	1		1			
3429		10001050	Neisseria meningitidis serogroup B Strain 7967	1		1			
3400		10000979	Neisseria meningitidis serogroup B Strain 8047	4		4			
3399		10000972	Neisseria meningitidis serogroup B Strain B16.B6	1		1			
3462		10001162	Neisseria meningitidis serogroup B Strain M1239	2		2			
3428		10001049	Neisseria meningitidis serogroup B Strain S3446	1		1			
1600		135720	Neisseria meningitidis serogroup C	3		3			
3426		10001044	Neisseria meningitidis serogroup C MC51	1		1			
3578		10001783	Neisseria meningitidis serogroup C strain C11	1	1	1	1		
3582		10001797	Neisseria meningitidis serogroup C strain MC19	1		1			
3565		10001713	Neisseria meningitidis serogroup W-135	1		1			
3593		10001860	Neisseria meningitidis serogroup X	3		3			
2869		648194	Neisseria meningitidis serogroup Y	3		3			
3509		10001524	Neisseria meningitidis strain 3006	1		1			
1050		29176	Neospora caninum	2	17	2	17		
2819		572307	Neospora caninum Liverpool		1		1		
2657		452646	Neovison vison		1		1		
291		5141	Neurospora crassa	6	3	6	3		
1268		44755	New York hantavirus		2		2		
762		11177	Newcastle disease virus (STRAIN AUSTRALIA-VICTORIA/32)	4		4			

3451		10001138	Newcastle disease virus (strain Eaves)	1		1			
3422		10001032	Newcastle disease virus (strain La Sota)	1		1			
3452		10001140	Newcastle disease virus (strain WA2116)	1		1			
2235		351071	Newcastle disease virus AF2240	1		1			
763		11178	Newcastle disease virus strain Beaudette C/45	12		12			
764		11180	Newcastle disease virus strain D26/76	4		4			
765		11186	Newcastle disease virus strain Queensland/66	4		4			
252		4100	Nicotiana benthamiana	5		5			
251		4097	Nicotiana tabacum	5		5			
3051		1285600	Nile crocodilepox virus		2		2		
1560		121791	Nipah henipavirus	5		5			
2089		314278	Nitrococcus mobilis Nb-231		1		1		
1212		37329	Nocardia farcinica		1		1		
1213		37333	Nocardia transvalensis		1		1		
1989		280240	Nocardiopsis baichengensis	1		1			
1877		239984	Nocardiopsis ganjiahuensis		1		1		
3489		10001484	Norovirus genogroup 1 GI.12	1		1			
3444		10001116	Norovirus genogroup 1 isolates 96-908	4		4			
3364		10000832	Norovirus genogroup 2 Camberwell 1890	1		1			
3528		10001606	Norovirus genogroup 2 Hu/NoV/Farmington Hills/2002/USA	1	2	1	2		
3363		10000829	Norovirus genogroup 2 Mexico type strain 36	3		3			
3285		10000560	Norovirus genogroup 3 Bo/Jena/1980/DE	1		1			
3490		10001485	Norovirus genogroup 3 GIII.1	1		1			
1564		122928	Norovirus GI	2		2			
2863		647514	Norovirus GI.1	1		1			
2864		647515	Norovirus GI.2	1		1			
2865		647516	Norovirus GI.3		1		1		
2866		647519	Norovirus GI.5	1		1			
2867		647521	Norovirus GI.7	1		1			
3100		1665645	Norovirus GI/Hu/NL/2012/GI.6/Groningen		1		1		
1565		122929	Norovirus GII	2		2			
2724		499191	Norovirus GII.1	1		1			
2950		747305	Norovirus GII.10	1		1			
2761		520963	Norovirus GII.11	1		1			
2762		520964	Norovirus GII.18	1		1			
2717		490039	Norovirus GII.2	1		1			
2715		489821	Norovirus GII.4	1	10	1	10		
2746		508775	Norovirus GII.9	1	1	1	1		
2768		524364	Norovirus Hu/1968/US	2	1	3	1	1	
3053		1286616	Norovirus Hu/GII.3/693/425/2008/AU	6		6			
2576		416035	Norovirus Hu/GII.4/DenHaag89/2006/NL	1		1			
3027		1182144	Norovirus Hu/GII.4/Minerva/2006/USA	2		2			
3020		1156983	Norovirus Hu/GII.4/Minerva/CS1258/2006/USA	1		1			
3045		1241973	Norovirus Hu/GII.4/Sydney/NSW0514/2012/AU	1		1			
2833		588533	Norovirus Hu/GII/GZ-1/2008/CHN	1		1			
2790		546980	Norovirus Hu/GII-4/Saga1/2006/JP	1		1			
2716		489822	Norovirus Hu/Houston/TCH186/2002/US	2		2			
1619		150080	Norovirus isolates	1		1			
932		11983	Norwalk virus	4	1	4	1		

1376		63737	Nostoc punctiforme PCC 73102		2		2		
458		8663	Notechis scutatus	2		2			
1299		48935	Novosphingobium aromaticivorans		1		1		
473		8996	Numida meleagris	1		1			
530		9978	Ochotona princeps		1		1		
526		9874	Odocoileus virginianus	1		2		1	
2993		1005962	Ogataea parapolymorpha		1		1		
2967		871575	Ogataea parapolymorpha DL-1		1		1		
254		4146	Olea europaea	70	19	70	19		
1252		42764	Oliveros mammarenavirus		2		2		
380		6282	Onchocerca volvulus	3	39	3	39		
442		8018	Oncorhynchus keta		6		6		
443		8022	Oncorhynchus mykiss	1		1			
1396		69247	Oran virus		2		2		
517		9733	Orcinus orca		1		1		
94		784	Orientia tsutsugamushi	87		87			
3314		10000761	Orientia tsutsugamushi Karp	1		1			
2278		357244	Orientia tsutsugamushi str. Boryong	2	2	2	2		
2159		334380	Orientia tsutsugamushi str. Ikeda		1		1		
1933		265619	Ornithodoros erraticus	22		22			
405		6938	Ornithodoros moubata	20		20			
479		9258	Ornithorhynchus anatinus		1		1		
3111		1980442	Orthohantavirus		15		15		
531		9986	Oryctolagus cuniculus	55	10	59	10	4	
269		4530	Oryza sativa	2		2			
1237		39947	Oryza sativa Japonica Group	5	1	5	1		
447		8090	Oryzias latipes	1	1	2	1	1	
1155		34862	Otospermophilus beecheyi		1		1		
1044		28869	Ovine respiratory syncytial virus	1		1			
529		9940	Ovis aries	91	17	92	17	1	
459		8667	Oxyuranus scutellatus scutellatus	4		4			
1052		29320	Paenarthrobacter nicotinovorans	1		1			
2121		324057	Paenibacillus sp. JDR-2	1		1			
506		9597	Pan paniscus		1		1		
507		9598	Pan troglodytes	7	25	7	25		
1725		188763	Panine betaherpesvirus 2		4		4		
1344		59538	Pantholops hodgsonii		1		1		
217		3469	Papaver somniferum	1		1			
501		9555	Papio anubis	1		1			
502		9556	Papio cynocephalus	1		1			
2443		386056	Paraburkholderia ferrariae		1		1		
1597		134537	Paraburkholderia fungorum	1		1			
1559		121759	Paracoccidioides brasiliensis	4	16	4	16		
3286		10000566	Paracoccidioides brasiliensis B339		8		8		
2727		502780	Paracoccidioides brasiliensis Pb18	1	1	1	1		
16		266	Paracoccus denitrificans	3		3			
2107		318586	Paracoccus denitrificans PD1222		2		2		
448		8255	Paralichthys olivaceus	1		1			
1273		45222	Parana mammarenavirus		1		1		
1133		33127	Parietaria judaica	65	2	65	2		
1009		13187	Parietaria officinalis	2		2			
1615		147272	Paspalum notatum		16		16		

86		747	Pasteurella multocida	1	10	1	10		
1973		272843	Pasteurella multocida subsp. multocida str. Pm70		5		5		
3312		10000759	Pasteurella multocida X-73	2		2			
50		554	Pectobacterium carotovorum	2		2			
1557	X	121224	Pediculus humanus corporis			1		1	
112		1254	Pediococcus acidilactici	1		1			
2181		338966	Pelobacter propionicus DSM 2379		3		3		
394		6687	Penaeus monodon	10	23	10	23		
289		5076	Penicillium chrysogenum	45	19	45	19		
290		5077	Penicillium citrinum	13		13			
1397		69248	Pergamino virus		1		1		
413		6978	Periplaneta americana	13	3	16	6	3	3
1078		31276	Perkinsus marinus		1		1		
3417		10001020	Peste-des-petits-ruminants virus (strain Nigeria 75/1)		1		1		
3647		10002123	Peste-des-petits-ruminants virus China/Tibet/Geg/07-30	31		53		22	
1043		28479	Phalaris aquatica		12		12		
241		3885	Phaseolus vulgaris	5	1	5	1		
476		9057	Phasianus colchicus colchicus	1		1			
1021		15957	Phleum pratense	63	1129	63	1129		
3227		10000463	Phocine distemper virus 2558/Han 88	5		5			
1250		42345	Phoenix dactylifera		3		3		
2094		314292	Photobacterium angustum S14		1		1		
73		659	Photobacterium phosphoreum		1		1		
1558		121723	Photobacterium sp. SKA34		1		1		
1408		72539	Physalis mottle virus	2		2			
518		9755	Physeter catodon	1	32	1	32		
844		11630	Pichinde mammarenavirus		11		11		
3533		10001618	Pichinde virus strain Munchique		1		1		
214		3318	Pinaceae	2		2			
215		3352	Pinus taeda	4		4			
1319	X	55513	Pistacia vera				6		6
1349		60876	Pixuna virus		1		1		
1232		39414	Plantago lanceolata		2		2		
207		2439	Plasmid ColB2	1		1			
208		2465	Plasmid F	1		1			
323		5820	Plasmodium	4	5	4	5		
324		5821	Plasmodium berghei	14	49	14	49		
325		5823	Plasmodium berghei ANKA	7	16	7	65		49
3169		10000356	Plasmodium berghei NK65	2	2	2	2		
326		5824	Plasmodium brasilianum	2		2			
327		5825	Plasmodium chabaudi	4	4	4	4		
3170		10000357	Plasmodium chabaudi adami DS	2	37	2	37		
1076		31271	Plasmodium chabaudi chabaudi		3		3		
328		5827	Plasmodium cynomolgi	2		2			
330		5833	Plasmodium falciparum	756	810	762	813	6	3
3171		10000358	Plasmodium falciparum 366		1		1		
1175		36329	Plasmodium falciparum 3D7	172	270	181	270	9	
1326		57266	Plasmodium falciparum 7G8	42	52	42	52		
3175		10000363	Plasmodium falciparum Brazil-608	1	1	1	1		
332		5835	Plasmodium falciparum CAMP/Malaysia	36	3	36	3		

333		5836	Plasmodium falciparum CDC/Honduras	18		18			
334		5837	Plasmodium falciparum FC27/Papua New Guinea	47	60	47	60		
3176		10000366	Plasmodium falciparum FCB-2	1		1			
335		5838	Plasmodium falciparum FCR-3/Gambia	94		94			
3177		10000369	Plasmodium falciparum FVO		5		5		
3178		10000370	Plasmodium falciparum GAM5		1		1		
3179		10000371	Plasmodium falciparum Indochina I/CDC	32		32			
3623		10002007	Plasmodium falciparum isolate UAS22	4		4			
3625		10002009	Plasmodium falciparum isolate UAS29	2		2			
3624		10002008	Plasmodium falciparum isolate UAS31	1		1			
342		5848	Plasmodium falciparum isolate WELLCOME	25	51	25	51		
3180		10000373	Plasmodium falciparum ItG2G1		1		1		
336		5839	Plasmodium falciparum K1	18	19	18	19		
337		5840	Plasmodium falciparum LE5		2		2		
338		5841	Plasmodium falciparum Mad20/Papua New Guinea	8	47	8	47		
340		5843	Plasmodium falciparum NF54	13	31	13	31		
339		5842	Plasmodium falciparum NF7/Ghana	5		5			
1327		57270	Plasmodium falciparum Palo Alto/Uganda	38		38			
3627		10002011	Plasmodium falciparum R29/IT4	1		1			
331		5834	Plasmodium falciparum RO-33	8	1	8	1		
3181		10000375	Plasmodium falciparum RO71	1	1	1	1		
341		5846	Plasmodium falciparum T4/Thailand	25	1	25	1		
3355		10000816	Plasmodium falciparum T9/96	1	1	1	1		
3182		10000376	Plasmodium falciparum UF-5	2		2			
348		5857	Plasmodium fragile		5		5		
343		5850	Plasmodium knowlesi	2	17	2	17		
344		5851	Plasmodium knowlesi strain H	41	10	41	10		
345		5852	Plasmodium knowlesi strain Nuri		10		10		
349		5858	Plasmodium malariae	1		1			
346		5854	Plasmodium reichenowi		2		2		
350		5859	Plasmodium simium	2		2			
347		5855	Plasmodium vivax	99	147	125	149	26	2
3183		10000378	Plasmodium vivax NK		2		2		
3000		1035514	Plasmodium vivax North Korean	1		1			
1567		126793	Plasmodium vivax Sal-1	17	1	17	1		
1077		31273	Plasmodium vivax strain Belem	6	34	6	34		
3386		10000862	Plasmodium vivax VK247	1		1			
1023		27990	Plasmodium vivax-like sp.	3		3	1		1
351		5861	Plasmodium yoelii	17	39	17	39		
1412		73239	Plasmodium yoelii yoelii	22	42	22	42		
2249		352914	Plasmodium yoelii yoelii 17XNL	6	3	6	3		
3282		10000555	Plasmodium yoelii yoelii 265BY		1		1		
3184		10000381	Plasmodium yoelii yoelii YM	1	5	1	5		
484		9479	Platyrrhini	1		1			
1523		103448	Pleistophora sp. LS		1		1		
80		703	Plesiomonas shigelloides		2		2		
980		12211	Plum pox virus	1		1			
3442		10001100	Plum pox virus (strain W)	6		6			
981		12213	Plum pox virus isolate NAT		1		1		
282		4754	Pneumocystis carinii	2	1	2	1		
1926		263815	Pneumocystis murina	3		3			

1951		270473	Pneumonia virus of mice J3666		6		10		4
270		4545	Poa pratensis	34	35	34	35		
2303		365044	Polaromonas naphthalenivorans CJ2		2		2		
953		12088	Poliovirus type 3 (strains P3/LEON/37 AND P3/LEON 12A[1]B)	4	15	4	15		
1436		80956	Pomacentrus moluccensis		1		1		
509		9601	Pongo abelii		2		2		
508		9600	Pongo pygmaeus		2		2		
1284		46221	Porcine circovirus	1	49	1	49		
1596		133704	Porcine circovirus 1	5		5			
3613		10001964	Porcine circovirus 1 strain 1/G	7		7			
1466		85708	Porcine circovirus 2	27		31		4	
3595		10001881	Porcine circovirus 2 -A	3		3			
3472		10001239	Porcine circovirus strain ISU31	7		7			
1467		85709	Porcine circovirus type 2-B	2		2			
1353		61673	Porcine endogenous retrovirus	2	11	2	11		
1736		194958	Porcine endogenous retrovirus A	2		2			
1737		194959	Porcine endogenous retrovirus B	1		1			
1035		28295	Porcine epidemic diarrhea virus	1		2		1	
3620		10002000	Porcine epidemic diarrhea virus CH/SHH/06	1		1			
1857		229032	Porcine epidemic diarrhea virus CV777	5		5			
658		10796	Porcine parvovirus	40		40			
1039		28344	Porcine reproductive and respiratory syndrome virus	85	53	87	53	2	
3524		10001586	Porcine reproductive and respiratory syndrome virus 07V063	3		3			
3525		10001587	Porcine reproductive and respiratory syndrome virus 08V204	2		2			
3584		10001800	Porcine reproductive and respiratory syndrome virus HuN4	1	4	1	4		
3577		10001771	Porcine reproductive and respiratory syndrome virus HuN4-F112	4	1	4	1		
3641		10002089	Porcine reproductive and respiratory syndrome virus SY0608	17		17			
3397		10000969	Porcine respiratory and reproductive syndrome virus 111/92	9		9			
3268	X	10000528	Porcine respiratory and reproductive syndrome virus BJ-4			1		1	
3269		10000529	Porcine respiratory and reproductive syndrome virus CH-1a	7	1	7	1		
3383		10000859	Porcine respiratory and reproductive syndrome virus JA142	1		1			
3388		10000864	Porcine respiratory and reproductive syndrome virus MD-001	2		2			
3390		10000888	Porcine respiratory and reproductive syndrome virus Olot/91	3	5	3	5		
3391		10000890	Porcine respiratory and reproductive syndrome virus SD92-23983		33		33		
672		10915	Porcine rotavirus (SEROTYPE 5 / STRAIN OSU)	1		1			
674		10919	Porcine rotavirus (STRAIN YM)	2	1	2	1		
1518		101350	Porcine rotavirus strain A253	2		2			
673		10917	Porcine rotavirus strain Gottfried	2		2			
1307		53179	Porcine rubulavirus	3		3			

3041		1225860	Porcine torque teno virus 1	2		2			
756		11150	Porcine transmissible gastroenteritis coronavirus strain FS772/70	2		2			
3583		10001798	Porcine transmissible gastroenteritis coronavirus strain Pur46-MAD	4		4			
757		11151	Porcine transmissible gastroenteritis coronavirus strain Purdue	14		14			
100		837	Porphyromonas gingivalis	91	21	91	21		
3077		1403335	Porphyromonas gingivalis 381	71	55	71	55		
2616		431947	Porphyromonas gingivalis ATCC 33277	1	4	1	4		
3438		10001081	Porphyromonas gingivalis HG66	2		2			
3469		10001223	Porphyromonas gingivalis OMZ 409	23		23			
3014		1125722	Porphyromonas gingivalis W50		36		36		
1880		242619	Porphyromonas gingivalis W83	4		4			
1206		37128	Potato mop-top virus	8		8			
982		12216	Potato virus Y	2		2			
983		12219	Potato virus Y strain N	1		1			
984		12220	Potato virus Y strain O	7		7			
729		11083	Powassan virus		3		3		
3047	X	1263102	Prevotella copri CAG:164				1		1
1027		28130	Prevotella disiens		1		1		
2842	X	619693	Prevotella sp. oral taxon 472 str. F0295			1		1	
397	X	6728	Procambarus clarkii			3		3	
1493		93058	Prochlorococcus marinus str. MIT 9202	1		1			
2642		445700	Prochlorococcus phage P-HM1		1		1		
2961		765103	Propionibacterium acnes HL030PA1		1		1		
3009	X	1091045	Propionibacterium acnes subsp. defendens ATCC 11828			5		5	
171		1752	Propionibacterium freudenreichii subsp. shermanii		1		1		
3121		1980485	Prospect Hill orthohantavirus	1	2	1	2		
2018		290512	Prosthecochloris aestuarii DSM 271		1		1		
110		1224	Proteobacteria	3		3			
55		583	Proteus	2		2			
56		584	Proteus mirabilis	6		7		1	
3414		10001006	Proteus mirabilis CFT322	1		1			
2783		529507	Proteus mirabilis HI4320	1		1			
3496		10001498	Proteus mirabilis O23	1		1			
3492		10001490	Proteus mirabilis O24	1		1			
3493		10001491	Proteus mirabilis O29	1		1			
3498		10001500	Proteus mirabilis O43	1		1			
3497		10001499	Proteus mirabilis O6	1		1			
1522		102862	Proteus penneri	1		1			
3588		10001836	Proteus penneri 14 (O59)	2		2			
3589		10001837	Proteus penneri 15 (O52)	2		2			
3587		10001835	Proteus penneri 7 (O61)	2		2			
3521		10001581	Proteus penneri 8 (O67)	1		1			
3499		10001501	Proteus penneri ATCC 33519	1		1			
3491		10001489	Proteus vulgaris Strain 5/43	1		1			
1479		88086	Protobothrops elegans	7		7			
1480		88087	Protobothrops flavoviridis	3		3			
3505		10001514	Providencia stuartii O33	1		1			
3526		10001588	Providencia stuartii O4	1		1			

2050		300559	PRRSV VR2332	21		21			
1190		36596	Prunus armeniaca	4		4			
1249		42229	Prunus avium	3	1	3	1		
235		3758	Prunus domestica	4		4			
234		3755	Prunus dulcis	19		19			
236		3760	Prunus persica	18	51	18	51		
460		8671	Pseudechis porphyriacus	3		3			
2202		342610	Pseudoalteromonas atlantica T6c		1		1		
2792		549169	Pseudogulbenkiania ferrooxidans		1		1		
20		286	Pseudomonas	1		1			
21		287	Pseudomonas aeruginosa	77	122	78	162	1	40
2233		350703	Pseudomonas aeruginosa 2192		2		2		
2234		350704	Pseudomonas aeruginosa C3719		2		2		
3434		10001057	Pseudomonas aeruginosa CD4	1		1			
3359		10000822	Pseudomonas aeruginosa Immunotype 3	1		1			
3296		10000723	Pseudomonas aeruginosa Immunotype 4	4		4			
3435		10001058	Pseudomonas aeruginosa K122-4	1		1			
3356		10000817	Pseudomonas aeruginosa KB7	2		2			
3357		10000818	Pseudomonas aeruginosa P1	1		1			
2461		388272	Pseudomonas aeruginosa PACS2		12		12		
2995		1009714	Pseudomonas aeruginosa PAK	7	3	7	3		
3354		10000815	Pseudomonas aeruginosa PAO	2	2	2	2		
1787		208964	Pseudomonas aeruginosa PAO1	1	5	1	5		
3506		10001519	Pseudomonas aeruginosa serotype O11	1		1			
1786		208963	Pseudomonas aeruginosa UCBPP-PA14		23		23		
1873		237609	Pseudomonas alkylphenolica		1		1		
1582		129138	Pseudomonas amygdali pv. morsprunorum	2		2			
2423		384676	Pseudomonas entomophila L48		1		1		
23		294	Pseudomonas fluorescens		4		4		
25		300	Pseudomonas mendocina		1		1		
1562		122355	Pseudomonas psychrophila	1		1			
26		303	Pseudomonas putida	1	8	1	8		
2242		351746	Pseudomonas putida F1		6		6		
1426		76869	Pseudomonas putida GB-1		1		1		
30		319	Pseudomonas savastanoi pv. phaseolicola	1		1			
1930		264730	Pseudomonas savastanoi pv. phaseolicola 1448A		1		1		
27		306	Pseudomonas sp.		1		1		
1415		74138	Pseudomonas sp. DJ-12		1		1		
1403		71238	Pseudomonas sp. G-179		1		1		
1648		159091	Pseudomonas sp. KIE171		1		1		
1491		91465	Pseudomonas sp. MIS38		1		1		
1622		150396	Pseudomonas sp. MT-1		1		1		
28		312	Pseudomonas sp. RS-16	1		1			
1730		192087	Pseudomonas syringae pv. atrofaciens	4		4			
3559		10001690	Pseudomonas syringae pv. atrofaciens str. IMV 4394	1		1			
3557		10001688	Pseudomonas syringae pv. atrofaciens str. IMV 7836	1		1			
3558		10001689	Pseudomonas syringae pv. atrofaciens str. IMV K-1025	1		1			
3563		10001700	Pseudomonas syringae pv. morsprunorum str. CFBP 1650	1		1			

3562		10001698	Pseudomonas syringae pv. morsprunorum str. GSPB 883	1		1			
3561		10001697	Pseudomonas syringae pv. phaseolicola str. IMV 120a	1		1			
3560		10001693	Pseudomonas syringae pv. tagetis str. ICMP 6370	1		1			
1058		29442	Pseudomonas tolaasii		1		1		
664		10879	Pseudomonas virus phi6	7		7			
1246	X	41953	Pseudo-nitzschia			1		1	
2817		571800	Psychrobacter sp. G	1		1			
3122		1980486	Puumala orthohantavirus	32	20	32	20		
3238		10000485	Puumala virus (STRAIN HALLNAS B1) Vranica/Hallnas	4		4			
3471		10001238	Puumala virus (strain Umea/hu)	1		1			
3063		1337063	Puumala virus bank vole/CG1820/Russia/1984		1		1		
3236		10000483	Puumala virus CG18-20	4		4			
829		11605	Puumala virus Hallnas B1		1		1		
3237		10000484	Puumala virus Kazan	26	7	26	7		
1226		39002	Puumala virus sotkamo/v-2969/81	196		196			
1974		272844	Pyrococcus abyssi GE5		1		1		
1545		114742	Pythium insidiosum	2		2			
219		3513	Quercus alba		5		5		
928		11976	Rabbit hemorrhagic disease virus	4		4			
3255		10000507	Rabbit hemorrhagic disease virus Olot/89	1		1			
1130		32606	Rabbitpox virus		2		2		
803		11292	Rabies lyssavirus	13	26	13	26		
804		11293	Rabies virus AVO1		3		3		
3229		10000467	Rabies virus CVS	14		14			
805		11294	Rabies virus CVS-11	2		2			
806		11295	Rabies virus ERA	10	27	10	27		
3230		10000470	Rabies virus Flury LEP		1		1		
807		11296	Rabies virus HEP-FLURY	7	1	7	1		
808		11298	Rabies virus Nishigahara RCEH	1		1			
1207		37132	Rabies virus Ontario fox	3		3			
3231		10000471	Rabies virus RC-HL	4		4			
1528		103929	Rabies virus strain Pasteur vaccin	2	1	2	1		
2380		381666	Ralstonia eutropha H16		1		1		
231		3726	Raphanus sativus	1		1			
536		10114	Rattus	11		11			
537		10116	Rattus norvegicus	236	577	242	30446	6	29869
3450		10001133	Rattus norvegicus DA		3		3		
3290		10000662	Rattus norvegicus Lewis		1		1		
3483		10001412	Rattus norvegicus Wistar-Furth		11		11		
538		10117	Rattus rattus		1		1		
539	X	10118	Rattus sp.				1		1
2345		378809	Ravn virus - Ravn, Kenya, 1987	1	32	1	32		
1298		48483	Reclinomonas americana		1		1		
3003	X	1053141	Recombinant Hepatitis C virus J6/JFH1-J6			2		2	
2090		314283	Reinekea blandensis MED297		1		1		
165		1646	Renibacterium salmoninarum	12		12			
667		10891	Reovirus sp.		2		2		
1006		12814	Respiratory syncytial virus	3	13	4	13	1	
1719		186539	Reston ebolavirus	1	11	1	11		

1580		129003	Reston ebolavirus - Reston	2	27	2	27		
2440		386032	Reston ebolavirus - Reston (1989)		4		4		
846		11636	Reticuloendotheliosis virus		5	2	5	2	
3619		10001999	Reticuloendotheliosis virus strain HLJ07I	1		1			
1529		103930	Rhesus cytomegalovirus strain 68-1		18		18		
686		10969	Rhesus rotavirus	10	1	10	1		
3640		10002082	Rhesus rotavirus MMU 18006		3		3		
974		12131	Rhinovirus B14	14	1	15	1	1	
1152		34631	Rhipicephalus appendiculatus	1		1			
1347		60189	Rhipicephalus decoloratus	5		5			
406		6941	Rhipicephalus microplus	1		1			
1153		34632	Rhipicephalus sanguineus	1		1			
34		384	Rhizobium leguminosarum		1		1		
2999		1035271	Rhizobium nepotum		1		1		
1383		64495	Rhizopus oryzae	4	1	4	1		
107		1063	Rhodobacter sphaeroides		1		1		
1975		272943	Rhodobacter sphaeroides 2.4.1		1		1		
2222		349101	Rhodobacter sphaeroides ATCC 17029		1		1		
193		1833	Rhodococcus erythropolis		2		2		
191		1828	Rhodococcus fascians		2		2		
1259		43767	Rhodococcus hoagii	18	2	18	2		
192		1830	Rhodococcus ruber		1		1		
3049		1268303	Rhodococcus sp. AW25M09	1	1	1	1		
108		1076	Rhodopseudomonas palustris		2		2		
2099		316056	Rhodopseudomonas palustris BisB18		1		1		
246		4012	Rhus		1		1		
245		3988	Ricinus communis	48	4	52	4	4	
1171		35788	Rickettsia africae		1		1		
2030		293614	Rickettsia akari str. Hartford		1		1		
96		787	Rickettsia australis		1		1		
2469		391896	Rickettsia bellii OSU 85-389		3		3		
2173		336407	Rickettsia bellii RML369-C	1	7	1	7		
97		788	Rickettsia canadensis		1		1		
91		781	Rickettsia conorii		13		13		
1976		272944	Rickettsia conorii str. Malish 7		5		5		
1255		42862	Rickettsia felis		1		1		
2096		315456	Rickettsia felis URRWXCal2		7		7		
1172		35791	Rickettsia massiliae		1		1		
2578		416276	Rickettsia massiliae MTU5		2		2		
92		782	Rickettsia prowazekii		21		21		
1977		272947	Rickettsia prowazekii str. Madrid E		10		10		
93		783	Rickettsia rickettsii		1		1		
2659		452659	Rickettsia rickettsii str. Iowa		1		1		
2470		392021	Rickettsia rickettsii str. 'Sheila Smith'		3		3		
1173		35793	Rickettsia sibirica		4		4		
1978		272951	Rickettsia sibirica 246		27		27		
95		785	Rickettsia typhi		3		3		
1911		257363	Rickettsia typhi str. Wilmington		6		6		
826		11588	Rift Valley fever virus	5	27	5	27		
827		11589	Rift valley fever virus (STRAIN ZH-548 M12)		2		2		
3235		10000482	Rift Valley fever virus ZH501	2		2			
780		11241	Rinderpest morbillivirus	2	3	2	3		

781		11243	Rinderpest virus (strain L)	6		6			
1183		36409	Rinderpest virus (strain RBOK)	33	5	33	5		
3228		10000465	Rinderpest virus LATC	2		2			
1292		46920	Rio Mamore hantavirus	1	1	1	1		
1209		37207	Rio Segundo hantavirus	1		1			
2084		313596	Robiginitalea biformata HTCC2501		1		1		
2087		314262	Roseobacter sp. MED193		1		1		
693		11029	Ross River virus		1		1		
694		11032	Ross river virus (STRAIN T48)	3		3			
3102		1835656	Rotavirus A RVA/Cow-tc/USA/B223/1983/G10P[11]	2		2			
1407		72132	Rotavirus G1	1	1	1	1		
1411		73036	Rotavirus G3		1		1		
3468		10001216	Rotavirus G3 strain RV-3	1		1			
918		11886	Rous sarcoma virus	4	4	4	4		
701		11041	Rubella virus	81	96	81	96		
702		11043	Rubella virus strain M33	3	11	3	11		
704		11045	Rubella virus strain Therien	20	35	20	35		
703		11044	Rubella virus vaccine strain RA27/3	2	6	2	6		
1761		203119	Ruminiclostridium thermocellum ATCC 27405		1		1		
114		1265	Ruminococcus flavefaciens		1		1		
2		106	Runella slithyformis		1		1		
2956		761193	Runella slithyformis DSM 19594		1		1		
1650		159479	Saaremaa hantavirus		21		21		
1281		45709	Sabia mammarenavirus		879		879		
1378		64284	Saboya virus		1		1		
284		4932	Saccharomyces cerevisiae	28	11	28	11		
2789		545124	Saccharomyces cerevisiae AWRI1631		2		2		
2857		643680	Saccharomyces cerevisiae EC1118		1		1		
2005		285006	Saccharomyces cerevisiae RM11-1a		3		3		
2801		559292	Saccharomyces cerevisiae S288C	6		8		2	
3011		1095631	Saccharomyces cerevisiae x Saccharomyces kudriavzevii VIN7		1		1		
487		9491	Saguinus imperator	1		1			
486		9488	Saguinus mystax	1		1			
495		9521	Saimiri sciureus	1		1			
593		10381	Saimiriine gammaherpesvirus 2		3		3		
444		8030	Salmo salar	31		31			
58		590	Salmonella	3		3			
1047		28901	Salmonella enterica		54		55		1
1341		59203	Salmonella enterica subsp. arizonae		1		1		
1243		41514	Salmonella enterica subsp. arizonae serovar 62:z4,z23:-		4		4		
1339		59201	Salmonella enterica subsp. enterica		18		18		
2629		440534	Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701		1		1		
1555		119912	Salmonella enterica subsp. enterica serovar Choleraesuis		3		3		
2116		321314	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67		5		5		
1511		98360	Salmonella enterica subsp. enterica serovar Dublin		2		2		

1618		149539	Salmonella enterica subsp. enterica serovar Enteritidis		2		2		
3494		10001492	Salmonella enterica subsp. enterica serovar Enteritidis SH1262	3		3			
1062		29477	Salmonella enterica subsp. enterica serovar Essen	1		1			
3517		10001569	Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 11	1		1			
3518		10001570	Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 77	1		1			
2009		286783	Salmonella enterica subsp. enterica serovar Indiana		1		1		
3281		10000554	Salmonella enterica subsp. enterica serovar Minnesota R595	2		2			
59		596	Salmonella enterica subsp. enterica serovar Muenchen	1		1			
2597		423368	Salmonella enterica subsp. enterica serovar Newport str. SL254		1		1		
1314		54388	Salmonella enterica subsp. enterica serovar Paratyphi A		1		1		
2797		554290	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601		3		3		
2033		295319	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150		3		3		
2998		1016998	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7		11		11		
61		605	Salmonella enterica subsp. enterica serovar Pullorum		1		1		
2628		439847	Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29		1		1		
2627		439843	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633		1		1		
1489		90370	Salmonella enterica subsp. enterica serovar Typhi	13	111	15	111	2	
2722		497977	Salmonella enterica subsp. enterica serovar Typhi str. 404ty		1		1		
1819		220341	Salmonella enterica subsp. enterica serovar Typhi str. CT18		92		92		
2721		497976	Salmonella enterica subsp. enterica serovar Typhi str. E00-7866		1		1		
1788		209261	Salmonella enterica subsp. enterica serovar Typhi str. Ty2		5		5		
1490		90371	Salmonella enterica subsp. enterica serovar Typhimurium	15	75	15	75		
1465		85569	Salmonella enterica subsp. enterica serovar Typhimurium str. DT104	1	1	1	1		
1512		99287	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2		79		79		
1811		216597	Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344		2		2		
1297		48409	Salmonella enterica subsp. enterica serovar Virchow		1		1		
1342		59205	Salmonella enterica subsp. houtenae		1		1		
1340		59202	Salmonella enterica subsp. salamae		1		1		
3504		10001511	Salmonella 'group A'	2		2			
3566		10001722	Salmonella 'group D'	3		3			

60		599	Salmonella sp.	1		1			
1410		72590	Salmonella sp. 'group B'	6		6			
3510		10001526	Salmonella thompson C1 strain IS40	1		1			
3302		10000739	Salmonella typhi 620Ty	1		1			
3303		10000740	Salmonella typhi Ty21a		6		6		
3301		10000738	Salmonella typhimurium PL5 (O9,12)	1		1			
3304		10000742	Salmonella typhimurium SH 4809	4		4			
3305		10000743	Salmonella typhimurium SL3261		4		4		
650		10754	Salmonella virus P22	5		5			
646		10658	Salmonella virus PRD1	2		2			
3123		1980489	Sangassou orthohantavirus		6		6		
493		9515	Sapajus apella	1		1			
1867		234603	Sapovirus Mc114		1		1		
830		11607	Sapporo rat virus	1	4	1	4		
1443		82659	Sapporo virus-Manchester		1		1		
423		7386	Sarcophaga peregrina		1		1		
1849		227859	SARS coronavirus	170	501	170	501		
1855		228407	SARS coronavirus BJ01	64	28	64	28		
1859		229992	SARS coronavirus Frankfurt 1	5	26	5	26		
2843		627442	SARS coronavirus P2	1		1			
2003		284672	SARS coronavirus TJF		14		14		
1850		227984	SARS coronavirus Tor2	171	2205	171	2205		
1851		228330	SARS coronavirus Urbani	24	52	24	52		
361		6181	Schistosoma	3		3			
364		6184	Schistosoma bovis	2		2			
362		6182	Schistosoma japonicum	43	53	43	53		
363		6183	Schistosoma mansoni	78	48	82	50	4	2
3187		10000385	Schistosoma mansoni Puerto Rico	20	7	20	7		
293		5334	Schizophyllum commune		1		1		
3016		1133363	Schmallenberg virus	1		6		5	
1464		85552	Scylla paramamosain	7		7			
271		4550	Secale cereale	51	42	51	42		
1630		155091	Secale cereale subsp. afghanicum		2		2		
1301		49318	Secale cereale x Triticum aestivum		1		1		
1338		58866	Secale strictum		1		1		
1477		88036	Selaginella moellendorffii		1		1		
695		11033	Semliki Forest virus	36	5	36	5		
1603		136966	SEN virus		7		7		
767		11194	Sendai virus (strain Enders)	7	11	7	11		
768		11195	Sendai virus (strain Fushimi)		1		1		
769		11196	Sendai virus (strain Harris)	2		2			
2063		302272	Sendai virus (strain Ohita)	1		1			
770		11198	Sendai virus (Z)		1		1		
3124		1980490	Seoul orthohantavirus		5		5		
997		12557	Seoul virus 80-39		3		3		
831		11610	Seoul virus SR11	1		1			
1260		44026	Sepik virus		1		1		
62		615	Serratia marcescens	1	3	1	3		
2500		399741	Serratia proteamaculans 568		1		1		
256		4182	Sesamum indicum	11		11			
2934		694009	Severe acute respiratory syndrome-related coronavirus		1		1		

2990	X	1003835	Severe fever with thrombocytopenia virus			1		1	
2123		325240	Shewanella baltica OS155		2		2		
2108		319224	Shewanella putrefaciens CN-32		1		1		
2241		351745	Shewanella sp. W3-18-1		1		1		
63		621	Shigella boydii		2		2		
2211		344609	Shigella boydii CDC 3083-94		20		20		
2048		300268	Shigella boydii Sb227		5		5		
64		622	Shigella dysenteriae	6	2	6	2		
2281		358708	Shigella dysenteriae 1012		1		1		
2047		300267	Shigella dysenteriae Sd197		5		5		
3306		10000748	Shigella dysenteriae serotype 1	3		3			
3307		10000749	Shigella dysenteriae serotype 1 114Sd	1		1			
65		623	Shigella flexneri	77	11	77	11		
2834		591020	Shigella flexneri 2002017		1		1		
1256		42897	Shigella flexneri 2a	35		35			
1755		198215	Shigella flexneri 2a str. 2457T		2		2		
1754		198214	Shigella flexneri 2a str. 301		4		4		
3055		1288825	Shigella flexneri 2b	2		2			
2598		424717	Shigella flexneri 3a	4		4			
2329		373384	Shigella flexneri 5 str. 8401		23		23		
2599		424718	Shigella flexneri 5a	2		2			
3308		10000752	Shigella flexneri 5b	1		1			
3309		10000754	Shigella flexneri X	1		1			
2600		424720	Shigella flexneri Y	8		8			
66		624	Shigella sonnei		1		1		
2049		300269	Shigella sonnei Ss046		9		9		
1492		92652	Shrimp white spot syndrome virus	3		3			
890		11723	Simian immunodeficiency virus		221		221		
882		11711	Simian immunodeficiency virus - mac		1		1		
3249		10000501	Simian immunodeficiency virus - mac - mac 239		474		474		
3250		10000502	Simian immunodeficiency virus - mac - mac 32H		9		9		
3251		10000503	Simian immunodeficiency virus - mac - mac BK28		4		4		
3252		10000504	Simian immunodeficiency virus - mac - mac F965		2		2		
896		11735	Simian immunodeficiency virus - mac K6W		125		125		
1110		31682	Simian immunodeficiency virus - mac1A11		18		18		
1835		224206	Simian immunodeficiency virus - mon		1		1		
3254		10000506	Simian immunodeficiency virus - sm - sm PT573		3		3		
1111		31683	Simian immunodeficiency virus - stm		7		7		
891		11730	Simian immunodeficiency virus (AGM3 ISOLATE)		1		1		
898		11737	Simian immunodeficiency virus (F236/SMH4 ISOLATE) (SOOTY MANGABEY)		17		17		
1112		31684	Simian immunodeficiency virus (isolate AGM / clone GRI-1)		2		2		
897		11736	Simian immunodeficiency virus (K78 ISOLATE)		29		29		
894		11733	Simian immunodeficiency virus (MM142-83 ISOLATE)		102		102		
895		11734	Simian immunodeficiency virus (MM251 ISOLATE)		1		1		

899		11738	Simian immunodeficiency virus (PBJ/BC13 ISOLATE) (SOOTY MANGABEY)		2		2		
1653		160753	Simian immunodeficiency virus 17E-Fr		2		2		
926		11942	Simian retrovirus 1	1		1			
2637		444186	Simian rotavirus A strain TUCH		5		5		
675		10923	Simian rotavirus A/SA11	8	5	8	5		
1208		37137	Simian rotavirus A/SA11-both	20	2	20	2		
1146		33747	Simian T-lymphotropic virus 1		14		14		
1289		46771	Simian virus 12	1		1			
3574		10001763	Simian virus 40 strain 776		1		1		
1090		31608	Simian virus 5 (isolate canine/CPI+)	1		1			
1332	X	57667	Simian-Human immunodeficiency virus			1		1	
3125		1980491	Sin Nombre orthohantavirus	1	35	1	35		
3275		10000544	Sin Nombre virus NM H10	4		4			
232		3728	Sinapis alba	2		2			
696		11034	Sindbis virus	26		26			
1416	X	74368	Sinonatrix annularis			1		1	
2309		366394	Sinorhizobium medicae WSM419		1		1		
33		382	Sinorhizobium meliloti		1		1		
1940		266834	Sinorhizobium meliloti 1021		3		3		
1904		254355	Small ruminant lentivirus	1		1			
3474		10001307	Small ruminant lentivirus strain It-561	1		1			
3475		10001308	Small ruminant lentivirus strain It-Pi1	1		1			
1089		31604	Small ruminant morbillivirus	13	1	13	31		30
907		11780	Snyder-Theilen feline sarcoma virus	1		1			
1040		28375	Soil-borne wheat mosaic virus	1		1			
250		4081	Solanum lycopersicum	3		3			
809		11307	Sonchus yellow net nucleorhabdovirus		1		1		
2007		286542	Soochong virus-2		1		1		
933		11984	Southampton virus	1		1			
1334		58024	Spermatophyta	3	1	3	1		
2946		743722	Sphingobacterium sp. 21	1		1			
1018		13687	Sphingomonas	1	4	1	4		
1716		185949	Sphingomonas aurantiaca		1		1		
2106		317655	Sphingopyxis alaskensis RB2256		1		1		
221		3562	Spinacia oleracea	4		4			
201		2133	Spiroplasma citri		1		1		
3		108	Spirosoma linguale	1		1			
414		7108	Spodoptera frugiperda		3		3		
1542		113370	Spodoptera frugiperda ascovirus 1a		1		1		
1285		46242	Spodoptera litura nucleopolyhedrovirus		1		1		
2811		566270	Spodoptera litura nucleopolyhedrovirus II		1		1		
1878		240426	Squirrelpox virus		1		1		
726		11080	St. Louis encephalitis virus	9	1	9	1		
727		11081	St. Louis encephalitis virus (strain MS1-7)	7		7			
1419		74722	Stachybotrys chartarum	11		11			
116		1279	Staphylococcus	1		1			
117		1280	Staphylococcus aureus	109	43	131	46	22	3
2796		553583	Staphylococcus aureus A9635	1		1			
3646		10002122	Staphylococcus aureus Becker	2		2			
3551		10001662	Staphylococcus aureus Cowan 1	2		2			
3645		10002121	Staphylococcus aureus Reynolds	2		2			

3649		10002129	Staphylococcus aureus RN4850	1		1			
1495		93062	Staphylococcus aureus subsp. aureus COL	17	1	17	1		
2791		548470	Staphylococcus aureus subsp. aureus MN8	11		11			
1994		282458	Staphylococcus aureus subsp. aureus MRSA252	87		87			
1745		196620	Staphylococcus aureus subsp. aureus MW2		7		7		
1647		158879	Staphylococcus aureus subsp. aureus N315		5		5		
1494		93061	Staphylococcus aureus subsp. aureus NCTC 8325	5	1	5	1		
2605		426430	Staphylococcus aureus subsp. aureus str. Newman	1		2		1	
2313		367830	Staphylococcus aureus subsp. aureus USA300	1		1			
3086	X	1458279	Staphylococcus aureus USA300-ISMMS1			1		1	
1056		29388	Staphylococcus capitis	1		1			
2771		525374	Staphylococcus epidermidis BCM-HMP0060		1		1		
3043		1236978	Staphylococcus epidermidis JCM 2414	1		1			
119	X	1292	Staphylococcus warneri			1		1	
2966	X	868597	Stenotrophomonas maltophilia JV3			1		1	
121		1301	Streptococcus	5		5			
128		1311	Streptococcus agalactiae	5		5			
2203		342613	Streptococcus agalactiae 18RS21	2		2			
1781		208435	Streptococcus agalactiae 2603V/R	1	2	1	2		
2204		342614	Streptococcus agalactiae 515	1		1			
2206		342617	Streptococcus agalactiae CJB111	2		2			
2205		342615	Streptococcus agalactiae H36B	1		1			
1796		211110	Streptococcus agalactiae NEM316		1		1		
2259		355315	Streptococcus agalactiae serogroup Ia	1		1			
1808		216495	Streptococcus agalactiae serogroup III	12		12			
3602		10001900	Streptococcus agalactiae serogroup III M781	1	1	1	1		
1807		216466	Streptococcus agalactiae serogroup V	1		1			
3552		10001663	Streptococcus anginosus K214-2K	4		4			
131		1317	Streptococcus downei	2	1	2	1		
136		1334	Streptococcus dysgalactiae	3	6	3	6		
1553		119602	Streptococcus dysgalactiae subsp. equisimilis	21		21			
3554		10001676	Streptococcus dysgalactiae subsp. equisimilis ATCC 12388	2		2			
3541		10001641	Streptococcus dysgalactiae subsp. equisimilis D181	1		1			
137		1336	Streptococcus equi	22	14	22	14		
126		1309	Streptococcus mutans	146	89	146	89		
3032		1198676	Streptococcus mutans GS-5		14		14		
3322		10000773	Streptococcus mutans MT 8148	40	12	40	12		
2964		857099	Streptococcus mutans OMZ175	2	1	2	1		
122		1303	Streptococcus oralis	12		12			
129		1313	Streptococcus pneumoniae	87	8	87	8		
1812		216600	Streptococcus pneumoniae 23F	6		6			
3543		10001644	Streptococcus pneumoniae CCUG 1378	1		1			
3544		10001645	Streptococcus pneumoniae CSR-SCS-2	1		1			
2328		373153	Streptococcus pneumoniae D39		52		52		
1683		171101	Streptococcus pneumoniae R6		12		12		
1676		170187	Streptococcus pneumoniae TIGR4		2		2		
3548		10001651	Streptococcus pneumoniae type 14	18		19		1	
3568		10001731	Streptococcus pneumoniae type 2	1		8		7	

3540		10001638	Streptococcus pneumoniae type 27	2		2			
3579		10001792	Streptococcus pneumoniae type 3	1		6		5	
3545		10001646	Streptococcus pneumoniae type 37	2		2			
3555		10001686	Streptococcus pneumoniae type 6A	2		2			
3556		10001687	Streptococcus pneumoniae type 6B	5		5			
3567		10001730	Streptococcus pneumoniae type 6C	1		1			
130		1314	Streptococcus pyogenes	357	115	376	115	19	
3323		10000775	Streptococcus pyogenes 156	1		1			
3324		10000776	Streptococcus pyogenes 88/25	1		1			
3325		10000777	Streptococcus pyogenes 88/30	1		1			
3326		10000778	Streptococcus pyogenes 88/544	1		1			
3327		10000779	Streptococcus pyogenes 90/85	1		1			
3329		10000781	Streptococcus pyogenes BSA10	3		3			
3033	X	1207470	Streptococcus pyogenes M1 476			1		1	
1651		160490	Streptococcus pyogenes M1 GAS	13	2	13	2		
2008		286636	Streptococcus pyogenes MGAS10394		1		1		
3330		10000782	Streptococcus pyogenes NS1	1		1			
3331		10000783	Streptococcus pyogenes NS14	1		1			
3332		10000784	Streptococcus pyogenes NS27	1		1			
3333		10000785	Streptococcus pyogenes NS5	1		1			
3334		10000786	Streptococcus pyogenes serotype M11	2		2			
2193		342023	Streptococcus pyogenes serotype M12	3	1	3	1		
3328		10000780	Streptococcus pyogenes serotype M12 A374	1		1			
3335		10000787	Streptococcus pyogenes serotype M13	1		1			
2059		301451	Streptococcus pyogenes serotype M18	1		1			
2523		404330	Streptococcus pyogenes serotype M2	2		2			
3336		10000788	Streptococcus pyogenes serotype M22	1		1			
3337		10000789	Streptococcus pyogenes serotype M24	6	2	6	2		
2056		301448	Streptococcus pyogenes serotype M3	1		1			
3274		10000542	Streptococcus pyogenes serotype M3 D58	4		4			
3338		10000790	Streptococcus pyogenes serotype M30	1		1			
2524		404331	Streptococcus pyogenes serotype M4	2		2			
3339		10000791	Streptococcus pyogenes serotype M41	1		1			
2060		301452	Streptococcus pyogenes serotype M49	1		1			
2057		301449	Streptococcus pyogenes serotype M5	56	57	56	57		
3340		10000792	Streptococcus pyogenes serotype M52	1		1			
3341		10000793	Streptococcus pyogenes serotype M54	1		1			
3342		10000794	Streptococcus pyogenes serotype M55	1		1			
3343		10000795	Streptococcus pyogenes serotype M57	1		1			
2058		301450	Streptococcus pyogenes serotype M6	9	7	9	7		
3360		10000824	Streptococcus pyogenes serotype M6 strain D471	4		4			
3344		10000796	Streptococcus pyogenes serotype M60	1		1			
3345		10000797	Streptococcus pyogenes serotype M75	1		1			
3346		10000798	Streptococcus pyogenes serotype M8	1		1			
2553		410069	Streptococcus pyogenes serotype M80	1		1			
1652		160491	Streptococcus pyogenes str. Manfredo	3	35	3	35		
3617		10001975	Streptococcus salivarius JCM 5707	1		1			
124		1305	Streptococcus sanguinis		1		1		
3486		10001439	Streptococcus sanguinis strain BD113-20		6		6		
127		1310	Streptococcus sobrinus	1		1			
1894		246202	Streptococcus sobrinus 6715	4	4	4	4		
135		1324	Streptococcus sp. G148	14	5	14	5		

1189		36470	Streptococcus sp. 'group A'	21		21			
132		1319	Streptococcus sp. 'group B'	1		1			
125		1307	Streptococcus suis	1		1			
3658		10002192	Streptococcus suis 1178027	2		2			
3037		1214159	Streptococcus suis 13730	2		2			
3036		1214154	Streptococcus suis 2651	1		1			
3028		1184252	Streptococcus suis S735	2		2			
138		1349	Streptococcus uberis	8		8			
194		1902	Streptomyces coelicolor		2		2		
1516		100226	Streptomyces coelicolor A3(2)		1		1		
196		1946	Streptomyces kasugaensis		1		1		
195		1916	Streptomyces lividans	10		10			
2318		370623	Streptomyces phage mu1/6		1		1		
1435		80859	Streptomyces ribosidificus		1		1		
2674		465541	Streptomyces sp. Mg1		1		1		
3087		1463841	Streptomyces sp. NRRL F-2580		1		1		
1162		35297	Striped Jack nervous necrosis virus	1		1			
468		8801	Struthio camelus	2		2			
432		7726	Styela plicata	6		6			
1720		186540	Sudan ebolavirus	2	280	2	280		
1573		128949	Sudan ebolavirus - Maleo (1979)		30		30		
2441		386033	Sudan ebolavirus - Uganda (2000)	1	6	1	6		
1572		128948	Sudan virus - Boniface, Sudan,1976	2	1	2	1		
578		10345	Suid alphaherpesvirus 1	6	2	6	2		
579		10349	Suid herpesvirus 1 (strain NIA-3)	4		4			
1135		33703	Suid herpesvirus 1 strain Kaplan	4		4			
206	X	2287	Sulfolobus solfataricus			1		1	
2447		387093	Sulfurovum sp. NBC37-1		1		1		
521		9823	Sus scrofa	105	53	113	53	8	
522		9825	Sus scrofa domesticus		5		5		
3130		10000187	Sus scrofa Landrace X Large White	1		1			
3441		10001097	Sus scrofa Yorkshire	1		1			
1374		63421	Swine hepatitis E virus	3		7		4	
945		12075	Swine vesicular disease virus	1		1			
946		12076	Swine vesicular disease virus (STRAIN H/3 '76)	5		5			
947		12077	Swine vesicular disease virus (STRAIN UKG/27/72)	3		3			
3352		10000809	Swine vesicular disease virus ITL/1/66	1		1			
3369		10000842	Swine vesicular disease virus NET/1/92	1		1			
3411		10001002	Swine vesicular disease virus SPA/1/93	16		16			
555		10276	Swinepox virus		2		2		
1124		32049	Synechococcus sp. PCC 7002		1		1		
109		1148	Synechocystis sp. PCC 6803		2		2		
845		11631	Tacaribe mammarenavirus		106		106		
2978		928313	Tacaribe virus strain Franze-Fernandez		6		6		
1092		31615	Tacaribe virus strain V5		1		1		
1093		31616	Tacaribe virus strain V7		1		1		
399		6853	Tachypleus tridentatus	1		1			
369		6207	Taenia crassiceps	11	1	11	1		
3348		10000802	Taenia crassiceps Strain ORF	3	3	3	3		
366		6203	Taenia ovis	8		8			
368		6206	Taenia saginata	7		7			

367		6204	Taenia solium	28	4	28	4		
1345		59729	Taeniopygia guttata		1		1		
1721		186541	Tai Forest ebolavirus		1		1		
1578		128999	Tai Forest virus - Cote d'Ivoire, Cote d'Ivoire, 1994	1	3	1	3		
1570		127999	Tanacetum parthenium		1		1		
2602		425088	Tanganya virus		1		1		
2845		630277	Tarsius lariang		1		1		
1045		28871	Taterapox virus		4		4		
3079		1408475	Taylorella asinigenitalis ATCC 700933	1		1			
2947		743973	Taylorella equigenitalis ATCC 35865	1		1			
1380	X	64293	Tembusu virus			2		2	
2471		392734	Terriglobus roseus		1		1		
1515		99883	Tetraodon nigroviridis		2		2		
435		7787	Tetronarce californica	149	75	149	75		
2498		398812	TGEV virulent Purdue	4		4			
356		5874	Theileria annulata	1		1			
2253		353154	Theileria annulata strain Ankara		4		4		
355		5872	Theileria equi	8		8			
357		5875	Theileria parva	28	20	28	20		
3473		10001243	Theileria parva strain Marikebuni		1		1		
2147		333668	Theileria parva strain Muguga	14	18	14	18		
3373		10000848	Theileria sergenti Type B1		1		1		
3374		10000849	Theileria sergenti Type B2		2		2		
3375		10000850	Theileria sergenti Type C		5		5		
3376		10000851	Theileria sergenti Type I		1		1		
970		12124	Theiler's encephalomyelitis virus		18		18		
971		12125	Theiler's encephalomyelitis virus (STRAIN BEAN 8386)	16	52	16	52		
972		12126	Theiler's encephalomyelitis virus (STRAIN DA)	3	2	3	2		
3379		10000855	Theiler's murine encephalomyelitis virus (strain BeAn 8386) (variant M2)		1		1		
1770		204711	Theilovirus		10		10		
2295		360549	Themiste hennahi	1		1			
607		10479	Thermoproteus tenax virus 1	1		1			
17		271	Thermus aquaticus	1		1			
18		274	Thermus thermophilus	1	1	1	1		
2055		300852	Thermus thermophilus HB8		1		1		
1010		13286	Theromyzon tessulatum	1		1			
278		4601	Thinopyrum bessarabicum		1		1		
1826		222994	Thinopyrum ponticum x Triticum aestivum		7		7		
1461		83810	Thosea asigna virus		1		1		
730		11084	Tick-borne encephalitis virus	14	137	14	137		
732		11087	Tick-borne encephalitis virus (STRAIN SOFJIN)	6		6			
3218		10000449	Tick-borne encephalitis virus (WESTERN SUBTYPE) - Neudoerfl	10		10			
403		6887	Tityus serrulatus	92		92			
1827		223337	Tobacco leaf curl Zimbabwe virus		1		1		
986		12242	Tobacco mosaic virus	36	13	36	13		
3465		10001210	Tobacco mosaic virus (strain Ni568)	1		1			
3464		10001209	Tobacco mosaic virus (strain PM5)	1		1			
987		12243	Tobacco mosaic virus (vulgare)	1		1			

988		12246	Tobacco mosaic virus strain Dahlemense	2		2			
2945		742503	Tokudaia muenninki		1		1		
977		12146	Tomato bushy stunt virus (STRAIN BS-3)	3		3			
1449		83192	Topografov hantavirus	1		1			
436		7788	Torpedo marmorata	3	3	3	3		
2929		687385	Torque teno canis virus		1		1		
2927		687383	Torque teno douroucouli virus		5		5		
2928		687384	Torque teno felis virus		1		1		
2922		687369	Torque teno mini virus 1		1		1		
2923		687371	Torque teno mini virus 3		2		2		
2924		687375	Torque teno mini virus 7		2		2		
2925		687376	Torque teno mini virus 8		2		2		
2930		687386	Torque teno sus virus 1a	12	1	12	1		
3039		1218488	Torque teno sus virus k2	11		11			
2926		687382	Torque teno tamarin virus		2		2		
1389		68887	Torque teno virus	5	94	5	94		
2900		687340	Torque teno virus 1		3		3		
2907		687350	Torque teno virus 11		1		1		
2908		687351	Torque teno virus 12		1		1		
2909		687353	Torque teno virus 14		5		5		
2910		687354	Torque teno virus 15		3		3		
2911		687355	Torque teno virus 16		4		4		
2912		687358	Torque teno virus 19		5		5		
2901		687341	Torque teno virus 2		4		4		
2913		687359	Torque teno virus 20		2		2		
2914		687360	Torque teno virus 21		2		2		
2915		687362	Torque teno virus 23		2		2		
2916		687363	Torque teno virus 24		3		3		
2917		687364	Torque teno virus 25		3		3		
2918		687365	Torque teno virus 26		5		5		
2919		687366	Torque teno virus 27		5		5		
2920		687367	Torque teno virus 28		3		3		
2921		687368	Torque teno virus 29		4		4		
2902		687342	Torque teno virus 3		4		4		
2903		687343	Torque teno virus 4		6		6		
2904		687345	Torque teno virus 6		2		2		
2905		687346	Torque teno virus 7		3		3		
2906		687347	Torque teno virus 8		6		6		
2704		487067	Torque teno virus Human/Ghana/GH1/1996		3		3		
2698		486280	Torque teno virus VT416		3		3		
376		6265	Toxocara canis	3		3			
322		5811	Toxoplasma gondii	77	95	78	99	1	4
3166		10000353	Toxoplasma gondii 76K	5	5	5	5		
3167		10000354	Toxoplasma gondii BK	1	1	1	1		
3636		10002052	Toxoplasma gondii Gansu Jingtai	27		27			
2743		507601	Toxoplasma gondii GT1		203		205		2
2745		508771	Toxoplasma gondii ME49	21	88	21	88		
3168		10000355	Toxoplasma gondii Prugniaud		1		1		
2394		383379	Toxoplasma gondii RH	27	23	27	23		
3035		1209525	Toxoplasma gondii type I		2		2		
3034		1209523	Toxoplasma gondii type II		2		2		
2497		398031	Toxoplasma gondii type III		1		1		

2619		432359	Toxoplasma gondii VEG	14		14			
755		11149	Transmissible gastroenteritis virus	13	1	15	1	2	
3457		10001154	Transmissible gastroenteritis virus MAD88	8	1	8	1		
6		158	Treponema denticola		1		1		
7		160	Treponema pallidum	6	2	6	2		
3418		10001021	Treponema pallidum subsp. pallidum (strain Chicago)	19		19			
2662		455434	Treponema pallidum subsp. pallidum SS14	1		1			
1888		243276	Treponema pallidum subsp. pallidum str. Nichols	277	9	277	9		
2952		754027	Treponema phagedenis F0421		1		1		
384		6334	Trichinella spiralis	15	2	16	7	1	5
1762		203124	Trichodesmium erythraeum IMS101		2		2		
315		5722	Trichomonas vaginalis	75	1	75	1		
1438		81847	Trichophyton quinckeanum	1		1			
298		5551	Trichophyton rubrum	2	27	2	27		
226		3677	Trichosanthes kirilowii	1		3		2	
3029		1186058	Trichosporon asahii var. asahii CBS 2479		1		1		
481		9337	Trichosurus vulpecula	45		45			
272		4565	Triticum aestivum	647	537	647	564		27
2707		488177	Triticum aestivum x Thinopyrum elongatum		1		1		
274		4568	Triticum monococcum		1		1		
1988		279889	Triticum spelta var. arduini		3		3		
273		4567	Triticum turgidum subsp. durum		1		1		
275		4572	Triticum urartu	1	1	1	1		
1817		218496	Tropheryma whipplei TW08/27	1		1			
166	X	1661	Trueperella pyogenes			7		7	
311		5691	Trypanosoma brucei	13	6	13	6		
314		5702	Trypanosoma brucei brucei	5		5			
1710		185431	Trypanosoma brucei brucei TREU927		1		1		
1079		31285	Trypanosoma brucei gambiense	2		2			
2886		679716	Trypanosoma brucei gambiense DAL972		1		1		
1080		31286	Trypanosoma brucei rhodesiense		9		9		
312	X	5692	Trypanosoma congolense			1		1	
313		5693	Trypanosoma cruzi	159	435	159	454		19
3081		1416333	Trypanosoma cruzi Dm28c	2		2			
3163		10000348	Trypanosoma cruzi G	1		1			
2252		353153	Trypanosoma cruzi strain CL Brener	2053	10	2058	10	5	
3164		10000351	Trypanosoma cruzi Y	1		1			
1497		93678	TTV-like mini virus		1		1		
1667		167758	TTV-like virus DXL1		10		10		
3126		1980494	Tula orthohantavirus	1	14	1	14		
1214		37347	Tupaia belangeri		1		1		
1895		246437	Tupaia chinensis	1		1			
1375		63673	Turbo cornutus	2		2			
758		11152	Turkey coronavirus	1		1			
1601		136371	Umbilicaria papulosa	1		1			
1132		32644	unidentified		1309		16362		15053
1874		237631	Ustilago maydis 521		2		2		
544		10245	Vaccinia virus	9	494	11	494	2	
3616		10001973	Vaccinia virus Acambis 2000	8		8			
2141		332193	Vaccinia Virus Acambis 3000 MVA		20		20		
1568		126794	Vaccinia virus Ankara		127		127		

3420		10001027	Vaccinia virus Connaught	1		1			
547		10249	Vaccinia virus Copenhagen	31	829	31	829		
2726		502057	Vaccinia virus GLV-1h68		2		2		
548		10251	Vaccinia virus IHD-J	1		1			
546		10248	Vaccinia virus LC16M8		5		5		
1084		31531	Vaccinia virus L-IPV		8		8		
3189		10000388	Vaccinia virus NYCBH - Dryvax		29		29		
549		10253	Vaccinia virus Tian Tan		21		21		
2935		696871	Vaccinia virus Western Reserve		4		4		
550		10254	Vaccinia virus WR	31	6688	31	6689		1
545		10247	Vaccinia virus WR 65-16		4		4		
1007		12870	Variola major virus		17		17		
3190		10000390	Variola major virus India-1967		1		1		
1309		53258	Variola minor virus		93		93		
551		10255	Variola virus		248		248		
2831		587200	Variola virus human/India/Ind3/1967		4		4		
697		11036	Venezuelan equine encephalitis virus	2	1	2	1		
1181		36382	Venezuelan equine encephalitis virus (strain 3880)		1		1		
698		11037	Venezuelan equine encephalitis virus (strain TC-83)	24		24			
699		11038	Venezuelan equine encephalitis virus (strain Trinidad donkey)	15		15			
433		7742	Vertebrata	4		4			
795		11277	Vesicular stomatitis Indiana virus	6	7	9	7	3	
796		11278	Vesicular stomatitis Indiana virus strain Glasgow		1		1		
797		11279	Vesicular stomatitis Indiana virus strain Mudd-Summers	1		1			
800		11285	Vesicular stomatitis Indiana virus strain San Juan		1		1		
798		11280	Vesicular stomatitis New Jersey virus		1		1		
794		11276	Vesicular stomatitis virus		10		10		
425		7444	Vespa basalis	1		1			
426		7453	Vespula maculifrons	1		1			
427		7454	Vespula vulgaris	2	95	2	95		
2092		314288	Vibrio alginolyticus 12G01		3		3		
1321		55601	Vibrio anguillarum	1		1			
1621		150340	Vibrio antiquarius		15		15		
74		666	Vibrio cholerae	38	90	38	90		
2836		592313	Vibrio cholerae 12129(1)		1		1		
2566		412966	Vibrio cholerae 1587		3		3		
2563		412614	Vibrio cholerae 2740-80		44		44		
1262		44104	Vibrio cholerae 569B	37		37			
2527		404974	Vibrio cholerae AM-19226		1		1		
2583		417400	Vibrio cholerae B33		5		5		
2567		412967	Vibrio cholerae MAK 757		9		9		
2213		345072	Vibrio cholerae MO10		1		1		
2581		417398	Vibrio cholerae MZO-2		2		2		
2565		412883	Vibrio cholerae MZO-3		1		1		
2582		417399	Vibrio cholerae NCTC 8457		1		1		
1569		127906	Vibrio cholerae O1	9		9			
79		686	Vibrio cholerae O1 biovar El Tor	3	1	3	1		
1889		243277	Vibrio cholerae O1 biovar El Tor str. N16961	1	3	4	3	3	

3287		10000567	Vibrio cholerae O1 serotype Inaba	1		1			
3288		10000568	Vibrio cholerae O1 serotype Ogawa	6		6			
2214		345073	Vibrio cholerae O395		4		4		
2215		345074	Vibrio cholerae RC385		2		2		
2216		345075	Vibrio cholerae V51		3		3		
2217		345076	Vibrio cholerae V52		32		32		
78		674	Vibrio mimicus	2		2			
75		670	Vibrio parahaemolyticus		57		57		
2808		563773	Vibrio parahaemolyticus AN-5034		4		4		
2587		419109	Vibrio parahaemolyticus AQ3810		38		38		
2844		627611	Vibrio parahaemolyticus K5030		22		22		
1828		223926	Vibrio parahaemolyticus RIMD 2210633	2	17	2	17		
76		671	Vibrio proteolyticus	1		1			
2093		314291	Vibrio splendidus 12B01		2		2		
2825		575788	Vibrio tasmaniensis LGP32		1		1		
1401		70203	Vibrio virus fs1		1		1		
77		672	Vibrio vulnificus	1	66	1	66		
1814		216895	Vibrio vulnificus CMCP6		53		53		
1744		196600	Vibrio vulnificus YJ016		75		75		
461		8704	Vipera ammodytes	1		1			
1735		194601	Vipera aspis aspis	3		3			
801		11288	Viral hemorrhagic septicemia virus 07-71	12	1	12	1		
243		3972	Viscum album	17		17			
902		11743	Visna lentivirus (strain 1514 / clone LV1-1KS1)	4		4			
901		11742	Visna lentivirus (strain 1514)	1		1			
900		11741	Visna/maedi virus	5	7	5	7		
1004		12750	Visna/maedi virus EV1	1		1			
1179		36374	Visna/maedi virus EV1 KV1772	2		2			
1070		29760	Vitis vinifera	1		1			
1417		74537	Vladivostok virus	1		1			
213		3068	Volvox carteri f. nagariensis		1		1		
512		9627	Vulpes vulpes	1		1			
1616		148360	Watermelon mosaic virus 2 (isolate USA)	2		2			
3107		1933300	Watermelon silver mottle orthotospovirus	3		3			
728		11082	West Nile virus	50	439	51	440	1	1
3217		10000447	West Nile virus 3000.0259	2		2			
3398		10000971	West Nile virus NY-99	15	21	15	21		
2650		449278	West Nile virus SPU116/89		1		1		
3427		10001047	West Nile virus strain 2741	32		32			
2073		307044	West Nile virus strain 385-99	22	12	22	12		
3594		10001879	West Nile virus strain 68856	2		2			
3547		10001649	West Nile virus strain 956	1		1			
2535		406269	West Nile virus strain PTRoxo		12		12		
700		11039	Western equine encephalitis virus		1		1		
1291		46919	Whitewater Arroyo mammarenavirus		349		349		
3532		10001617	Whitewater Arroyo virus strain AV9310135		1		1		
1660		163164	Wolbachia endosymbiont of Drosophila melanogaster		1		1		
2026		292805	Wolbachia endosymbiont strain TRS of Brugia malayi	1		1			
1158		35269	Woodchuck hepatitis virus	4	6	4	6		
605		10430	Woodchuck hepatitis virus 1	3		3			
2191		341946	Woodchuck hepatitis virus 2	4		4			

606		10433	Woodchuck hepatitis virus 8		34		34		
382		6293	Wuchereria bancrofti	13	8	13	8		
19		280	Xanthobacter autotrophicus		1		1		
1429		78245	Xanthobacter autotrophicus Py2		1		1		
1059		29447	Xanthomonas albilineans		1		1		
449		8355	Xenopus laevis	3	3	4	3	1	
450		8364	Xenopus tropicalis	2	2	2	2		
1589		132475	Yaba-like disease virus		3		3		
733		11089	Yellow fever virus		1333		1333		
734		11090	Yellow fever virus 17D		281		364		83
2841		617102	Yellow fever virus 17D/Tiantan	4	5	4	5		
1098		31641	Yellow fever virus 1899/81		36		36		
2537		407141	Yellow fever virus isolate Ethiopia/Couma/1961		2		2		
2536		407134	Yellow fever virus strain Ghana/Asibi/1927		5		5		
1655		161600	Yellow grouper nervous necrosis virus	1		1			
2229		349968	Yersinia bercovieri ATCC 43970		5		5		
67		630	Yersinia enterocolitica	6	26	6	26		
1150		34054	Yersinia enterocolitica (type O:8)		1		1		
2484		393305	Yersinia enterocolitica subsp. enterocolitica 8081		16		16		
2975		913028	Yersinia enterocolitica W22703		1		1		
2227		349966	Yersinia frederiksenii ATCC 33641		2		2		
1029		28152	Yersinia kristensenii		1		1		
2228		349967	Yersinia mollaretii ATCC 43969		3		3		
68		632	Yersinia pestis	23	145	24	324	1	179
3311		10000757	Yersinia pestis 195/P	5		5			
2225		349746	Yersinia pestis Angola		3		3		
2289		360102	Yersinia pestis Antiqua		36		36		
2330		373665	Yersinia pestis biovar Orientalis str. IP275		1		1		
2562		412420	Yersinia pestis CA88-4125		21		21		
1801		214092	Yersinia pestis CO92	4	22	4	22		
2339		375450	Yersinia pestis FV-1		2		2		
3310		10000756	Yersinia pestis KIM 5	21		21			
1723		187410	Yersinia pestis KIM10+		11		11		
2342		377628	Yersinia pestis Nepal516		135		135		
2446		386656	Yersinia pestis Pestoides F		2		2		
69		633	Yersinia pseudotuberculosis		2		2		
2226		349747	Yersinia pseudotuberculosis IP 31758		9		9		
1979		273123	Yersinia pseudotuberculosis IP 32953		1		1		
3601		10001895	Yersinia pseudotuberculosis str. 32777		1		1		
3502		10001504	Yokenella regensburgei PCM 2476	1		1			
3503		10001505	Yokenella regensburgei PCM 2477	1		1			
1718		186538	Zaire ebolavirus	16	867	20	867	4	
1952		270478	Zantedeschia mild mosaic virus	1		1			
277		4577	Zea mays	3	1	3	1		
1381		64320	Zika virus	3		15	131	12	131
3657		10002183	ZIKV/H. sapiens/French Polynesia/PF13/2013	4		4			
1151		34245	Zinnia violacea		1		1		
1643		157914	Ziziphus mauritiana	4		4			
985		12232	Zucchini yellow mosaic virus	1		1			

2 Website Features

There were two major releases (Releases 3.7 and 3.8) of the IEDB external website since the 2016 Annual Compendium was produced plus numerous smaller updates made throughout the year. Changes of note include:

- Revised home page to include Finders and autocomplete boxes
- Revised Receptor export on Database Export page
- Revised all assay and epitope CSV exports
- Added Browse-by-3D structure to V3 interface
- Removed legacy v2 (IEDB 2.x) code
- Updated Learn More page to use new Zendesk API to refresh news properly
- Added new 3D exports to Database Export page
- Revised Epitope Details page to include Reference Epitope information
- Added new linkouts for Europe PMC, Wikidata and GlyTouCan
- Added new receptor tabs on search results pages

In addition, there were two major releases (Releases 2.17 and 2.18) of the Analysis Resource since the 2016 Annual Compendium was produced plus numerous smaller updates made throughout the year. Changes of note include:

- Completed migration away from Java and Tomcat into Python and Django
- Added functionality to email prediction results for class I and II binding
- Completed migration of the processing tool to the cluster
- Integrated performance enhancements to the Deimmunization and TepiTool applications
- Replaced PIGS tool with Lyra
- Synchronized 3D viewer code across the main and Analysis Resource sites

The IEDB website functionality can be divided into five categories– Home Page (Section 2.1), Specialized Searches (Section 2.2.2), Analysis Resource (Section 2.3), Help (Section 2.4), and More IEDB (Section 2.5), which largely correspond to the pull-down menus at the top of the home page. The subsections that follow describe the website features within these categories.

The reader will find it helpful to keep in mind how data are stored in the IEDB. Each item contained in the IEDB consists of a reference (article or submission) containing information about one or more epitopes and associated binding or response information. The same epitope can exist in multiple references.

2.1 Home Page

The IEDB Home Page (www.iedb.org) is the default screen displayed when users enter the IEDB system. Besides providing a general description of the IEDB project, the home page displays system level status and notification of scheduled updates or maintenance. As one can see in Figure 2.1, the page is divided into three columns that contain introductory information, Summary Metrics of the data, a basic data search capability, and links to the epitope prediction and analysis tools in the Analysis Resource. As users browse the IEDB system, they can return to the home page anytime by clicking *Home* on the far left of the main menu bar or by clicking on the IEDB logo in the upper left-hand corner of the page.

The top box in the left column contains a welcome statement that briefly describes the content of the database. It also has a "Learn More" link that brings the user to a web page containing more information about the support and user help features available, about the data itself, and about the IEDB program. This page is described in detail in Section 2.6. The Summary Metrics are displayed in the bottom box of this column. These numbers are intended to be a gauge of the volume of data available in the system. The Summary Metrics provide the number of epitopes (peptidic and non-peptidic), assays (T cell, B cell, and MHC ligand assays), epitope source organisms, restricting MHC alleles, and references. A middle box may appear when there are special messages to convey to users. The text will appear in red. The middle column contains the initial search interface that is described in detail in Section 2.2.1. This section was updated at the end of March 2017 to include several finders on the search interface, thus enabling more complete queries without the need for further filtering of the results. The rightmost column has links to the most frequently used tools in the Analysis Resource.

Welcome

The IEDB is a free resource, funded by a contract from the National Institute of Allergy and Infectious Diseases. It offers easy searching of experimental data characterizing antibody and T cell epitopes studied in humans, non-human primates, and other animal species. Epitopes involved in infectious disease, allergy, autoimmunity, and transplant are included.

The IEDB also hosts tools to assist in the prediction and analysis of B cell and T cell epitopes.

Learn More

Summary Metrics

Peptidic Epitopes	424,182
Non-Peptidic Epitopes	2,561
T Cell Assays	325,676
B Cell Assays	404,397
MHC Ligand Assays	684,053
Epitope Source Organisms	3,635
Restricting MHC Alleles	755
References	18,955

Epitope Analysis Resource

T Cell Epitope Prediction

Scan an antigen sequence for amino acid patterns indicative of:

- MHC I Binding
- MHC II Binding
- MHC I Processing (Proteasome,TAP)
- MHC I Immunogenicity

B Cell Epitope Prediction

Predict linear B cell epitopes using:

- Antigen Sequence Properties

Predict discontinuous B cell epitopes using antigen structure via:

- Discotope
- ElliPro

Epitope Analysis Tools

Analyze epitope sets of:

- Population Coverage
- Conservation Across Antigens
- Clusters with Similar Sequences

Figure 2.1 IEDB 3.7 Home page

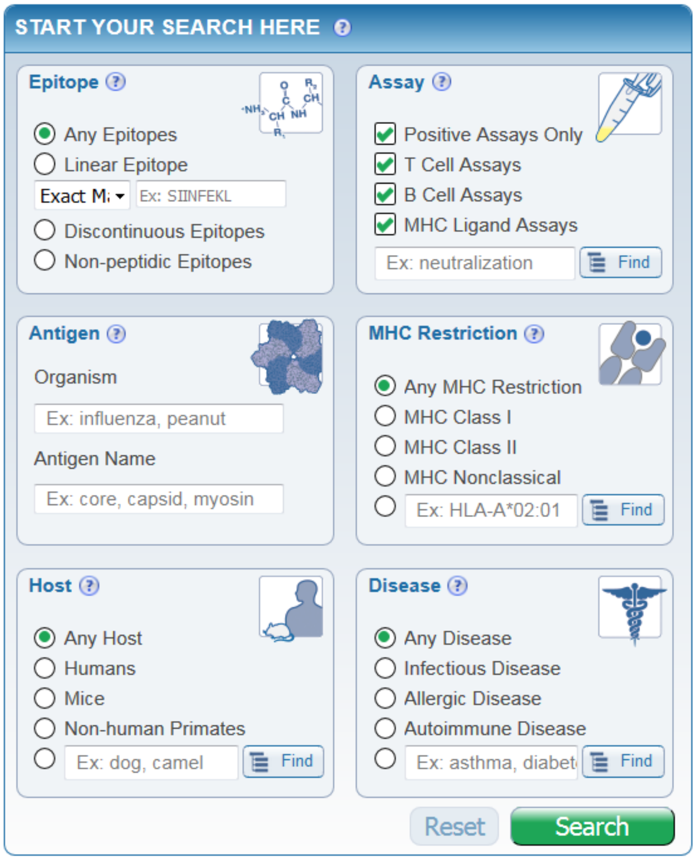
2.2 Query

There are several ways users can find information in the IEDB. A family of advanced query-by-example searches can be accessed on the Search pull-down menu and consist of “B Cell Search”, “T Cell Search”, “MHC Ligand Search”, “Epitope Search”, and “Identifier Search”. This group of queries are referred to as Specialized Searches. A simplified search that is especially designed for the needs of most immunologists appears on the home page. This document will refer to this particular query as the Simple Search or Home Page Search. All of these methods return results in a common format, as described in Section 2.2.3. These methods are elaborated in the subsections below.

2.2.1 Perform a Home Page Search

The home page search feature available in the center of the home page (Figure 2.2) is designed to simplify the search process for many commonly asked queries by immunologists. It is the most frequently used query mode. The approach it takes is analogous to many travel and shopping websites. IEDB users can start their search by specifying a number of fundamental and common search parameters on the home page. On the subsequent results page, users can then apply additional and more specific filters. The epitope structure choices include linear epitopes, discontinuous epitopes, or non-peptidic epitopes. For the linear epitope search, the user can prescribe the type of search desired - an exact match to the entered sequence, a substring search (described below), or a homologous peptides at sequence at identity levels of 70%, 80%, or 90% as determined by BLAST. The IEDB categorizes all assays as T cell, B cell, or MHC ligand. The MHC ligand includes binding and elution assays. Users can also select the MHC restriction for non-B cell searches. Finally, users can select the host species and the disease.

The results of the query are displayed in four tabs – Epitopes, Antigens, Assays, and References. The Epitopes tab lists the epitope description, such as the amino acid sequence for linear epitopes, its associated antigen and source organism, the number of references in which it appears, and the number of assays in which it is used. The Antigen tab lists the antigen, its source organism, and the number of related epitopes, assays, and references. The Assays tab contains three tabs, one each for T cell, B cell, and MHC ligand assays. All tabs list the IEDB-specific assay identifier, the reference in which it appears, and the related epitope. The other fields listed are those relevant for each assay type. For example, MHC restriction does not appear for B cell assays. The References tab lists the IEDB-specific reference identifier, the authors, title, abstract, and year of publication or submission. In all cases, the user can click on the IEDB-specific identifier to drill down to get additional information about the epitope, assay, or reference.



START YOUR SEARCH HERE

Epitope
● Any Epitopes
○ Linear Epitope
Exact M: Ex: SIINFEKL
○ Discontinuous Epitopes
○ Non-peptidic Epitopes

Assay
☑ Positive Assays Only
☑ T Cell Assays
☑ B Cell Assays
☑ MHC Ligand Assays
Ex: neutralization — Find

Antigen
Organism
Ex: influenza, peanut
Antigen Name
Ex: core, capsid, myosin

MHC Restriction
● Any MHC Restriction
○ MHC Class I
○ MHC Class II
○ MHC Nonclassical
○ Ex: HLA-A*02:01 — Find

Host
● Any Host
○ Humans
○ Mice
○ Non-human Primates
○ Ex: dog, camel — Find

Disease
● Any Disease
○ Infectious Disease
○ Allergic Disease
○ Autoimmune Disease
○ Ex: asthma, diabet — Find

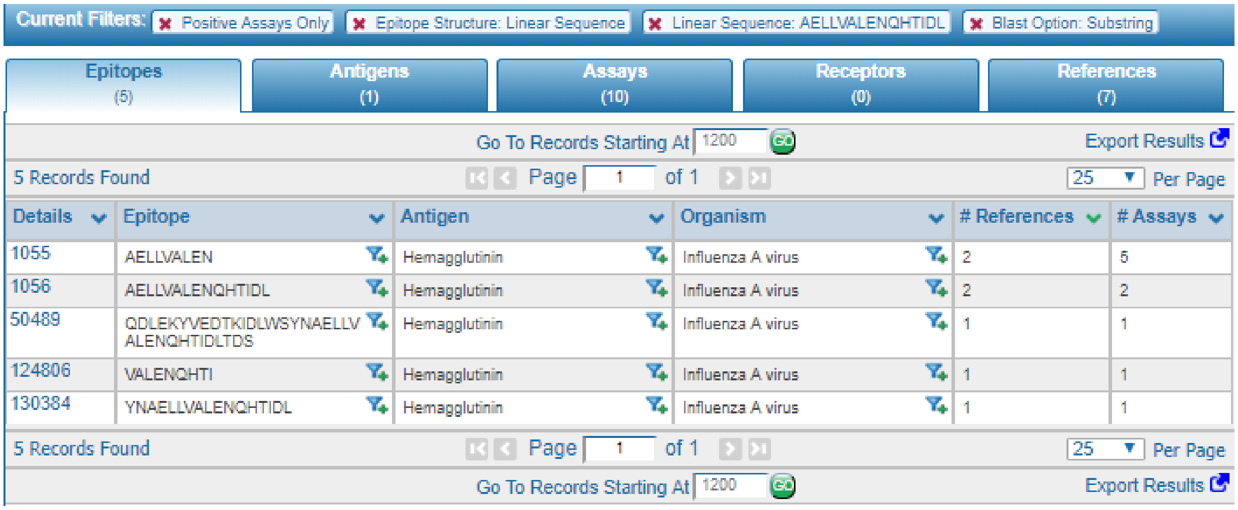
Figure 2.2 Home page Simple Search

Once the initial results are generated, the user can filter the results using additional filtering criteria. Auto-complete fields and associated hierarchical tree views reveal the available parameter choices. In this way, users can narrow their query to specific non-peptidic epitopes, assay types, MHC alleles, hosts, or diseases. Users can also specify article type (journal article and/or submission), the author, title, PubMed ID, and year. All filters that are applied are displayed at the top of the page. Results on most pages can be downloaded as comma separated value (CSV) files that can be read using a text editor or spreadsheet application. Users also have the ability to map positive and negative results to reference proteomes as a means of visualizing immunogenic regions using the Immunome Browser (Section 2.2.3.2).

An autocomplete feature is available for many of the fields on the lefthand side of the results page that contain additional filter criteria. This includes the non-peptidic epitope field in the Epitope box, the organism and antigen name fields in the Antigen box, the T cell, B cell, and MHC ligand assay fields in the Assay box, the specific MHC restriction field in the MHC Restriction box, the specific host field in the Host box, the specific disease field in the Disease box, and the author, title, and data fields in the Reference box. For example, as one types “hep” in the organism field in the Antigen box, several choices start to appear in a list below the text field, including “hepatitis C virus”. The user can click on a selection from the list or can continue typing to further narrow down choices. Likewise, a user may type “human” or “homo” to select “homo sapiens” in the Organism field. The list of matches includes scientific names and synonyms. These actions enable users to quickly specify their search parameters without using the finders. Use of the autocomplete circumvents the need to use the finders.

If the user decides not to use the autocomplete feature for a search field, they will need to use the finders. The epitope source can be prescribed for the source organism and source antigen by using the organism finder (Section 2.2.4.5) and molecule finder (Section 2.2.4.4), respectively. The user can decide whether to include B cell responses, T cell responses, and/or MHC ligand results in the search (at least one must be checked). The host organism, the MHC restriction, and the MHC class can also be specified with the help of the organism finder and the allele finder (Section 2.2.4.1). The fields using finders will allow multiple selections as search criteria. In these cases the selections are treated as a set. Records will be considered a match if they include at least one of the selected values in the set. The search is executed by clicking the Search button and the query results can be viewed on the updated results page described in Section 2.2.3.

In addition to finding peptides in the database that contain the specified amino acid sequence, the substring search also finds epitopes within the input sequence itself. For example, when the sequence AELLVALENQHTIDL is submitted for a substring search, the query results, shown in Figure 2.3, yields five peptide sequences. Three of them (the second, third, and fifth) contain the input sequence. The two others (the first and fourth) are substrings of the input sequence that are also epitopes contained in the IEDB.



Current Filters: Positive Assays Only; Epitope Structure: Linear Sequence; Linear Sequence: AELLVALENQHTIDL; Blast Option: Substring

5 Records Found

Details	Epitope	Antigen	Organism	# References	# Assays
1055	AELLVALEN	Hemagglutinin	Influenza A virus	2	5
1056	AELLVALENQHTIDL	Hemagglutinin	Influenza A virus	2	2
50489	QDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDS	Hemagglutinin	Influenza A virus	1	1
124806	VALENQHTI	Hemagglutinin	Influenza A virus	1	1
130384	YNAELLVALENQHTIDL	Hemagglutinin	Influenza A virus	1	1

5 Records Found

Figure 2.3 Query results for a substring search performed on the input sequence AELLVALENQHTIDL

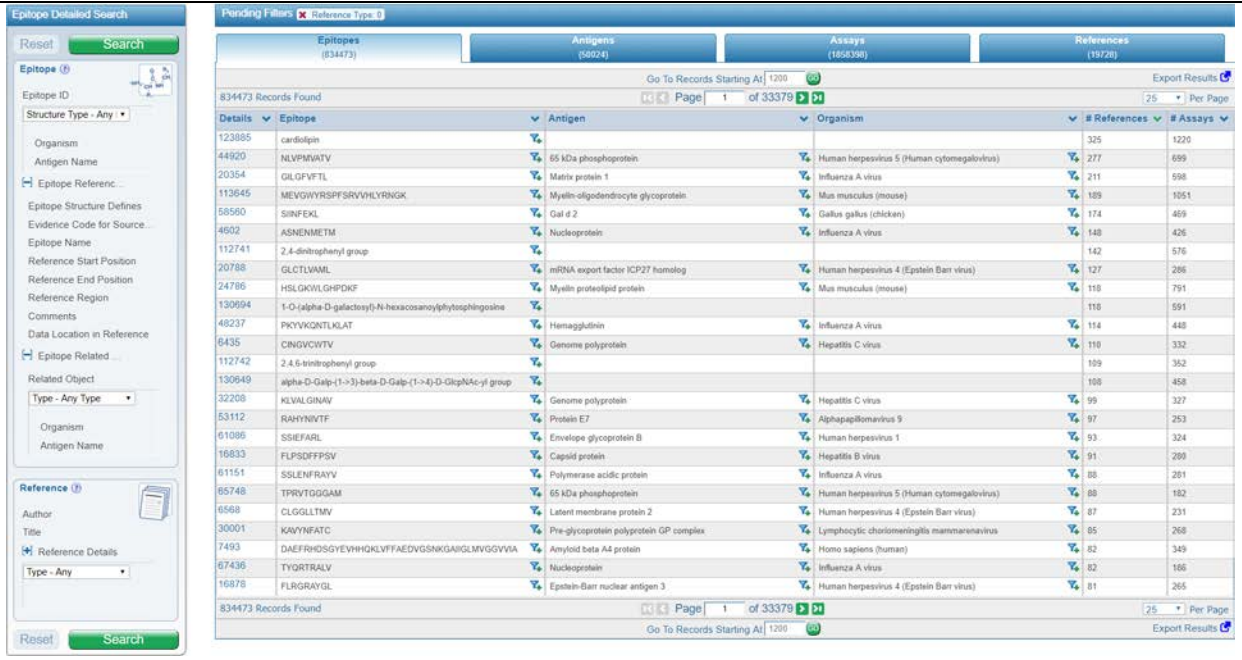
2.2.2 Specialized Searches

The Specialized queries are based on a standard Query by Example (QBE) approach, which is a method of forming queries where a user can enter conditions for each data field they want included in the query. The Specialized queries allow users to define example criteria for each field in the system. As there are over 300 fields, the Specialized queries are both powerful and comprehensive.

The fully expanded input screen for the Epitope Details Search is shown in Figure 2.4. The user can specify criteria in the left-hand panels for Epitope and Reference. These sections expand to the right to expose more detailed criteria for the search, including autocomplete fields and finders. An example of the expanded Epitope box is found in Figure 2.5. Users can specify search criteria for the epitope, such as epitope type (e.g. peptide from protein, carbohydrate), source molecule and organism, and various reference details. Further explanation of the search terms can be found in the Curation Manual. Using the bottom Reference section, the user can search on several reference criteria, such as author name, article title, the IEDB Reference ID, keywords in the reference abstract, year, author affiliation, and reference type. References are either published literature articles that have been curated by the IEDB curation staff or data submitted directly by researchers. This query type returns T cell, B cell, and MHC ligand data.

Auto-complete functionality is available for all the finder fields, as denoted by the greyed text that provide example inputs. The “?” provides a brief explanation and a “Learn More” link that connects to the appropriate help page in the IEDB Solutions Center. Finders are described in further detail in Section 2.2.4.

Figure 2.5 shows the fields when “Structure Type - Any” is selected in the Epitope filter. The fields for the other epitope type selections are shown in Figure 2.6 (linear epitopes), Figure 2.7 (Discontinuous epitopes), Figure 2.8 (Discontinuous peptides on Multichain), and Figure 2.9 (Non-peptidic epitopes).

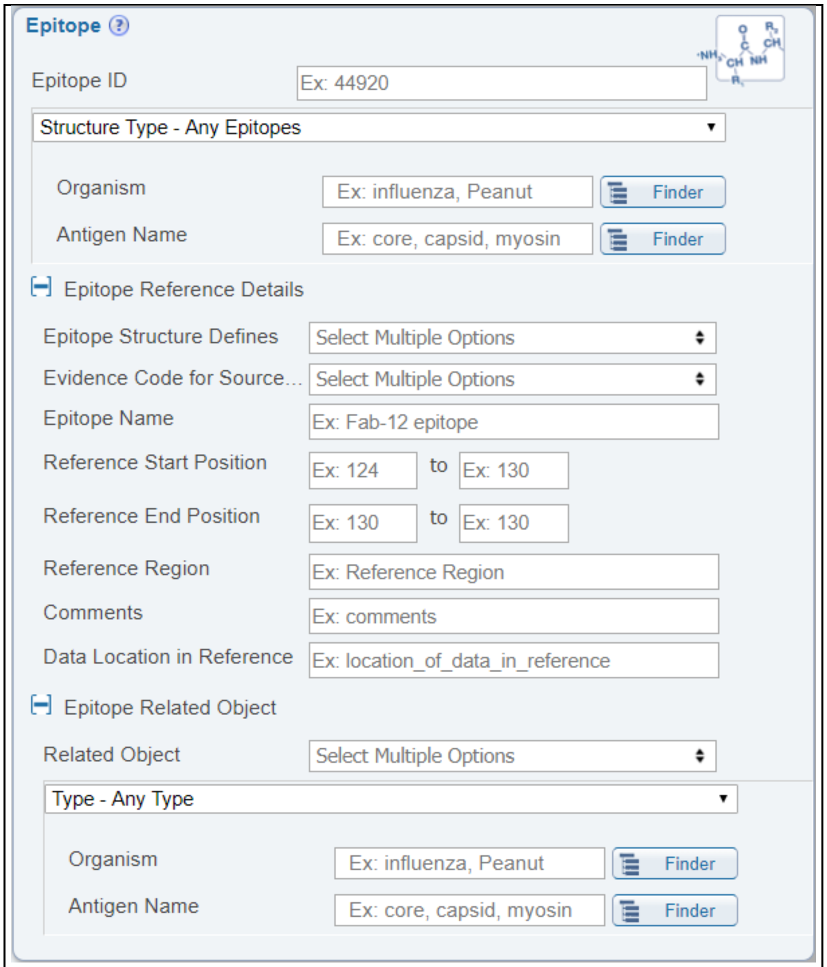


834473 Records Found

Details	Epitope	Antigen	Organism	# References	# Assays
123885	cardiolipin			325	1220
44920	NLVPMVATV	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	277	699
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	211	598
113645	MEVGWYRSPFSRVVHLYRNGK	Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	189	1051
58560	SIINFEKL	Gal d 2	Gallus gallus (chicken)	174	469
4602	ASNENMETM	Nucleoprotein	Influenza A virus	148	426
112741	2,4-dinitrophenyl group			142	576
20788	GLCTLVAML	mRNA export factor ICP27 homolog	Human herpesvirus 4 (Epstein Barr virus)	127	286
24786	HSLGKWLGHPDKF	Myelin proteolipid protein	Mus musculus (mouse)	118	791
130694	1-O-(alpha-D-galactosyl)-N-hexacosanoylphytosphingosine			118	591
48237	PKYVKQNTLKLAT	Hemagglutinin	Influenza A virus	114	448
6435	CINGVCWTV	Genome polyprotein	Hepatitis C virus	110	332
112742	2,4,6-trinitrophenyl group			109	352
130649	alpha-D-Galp-(1->3)-beta-D-Galp-(1->4)-D-GlcpNAc-yl group			108	458
32208	KLVALGINAV	Genome polyprotein	Hepatitis C virus	99	327
53112	RAHYNIVTF	Protein E7	Alphapapillomavirus 9	97	253
61086	SSIEFARL	Envelope glycoprotein B	Human herpesvirus 1	93	324
16833	FLPSDFFPSV	Capsid protein	Hepatitis B virus	91	280
61151	SSLENFRAYV	Polymerase acidic protein	Influenza A virus	88	281
65748	TPRVTGGGAM	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	88	182
6568	CLGGLLTMV	Latent membrane protein 2	Human herpesvirus 4 (Epstein Barr virus)	87	231
30001	KAVYNFATC	Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus	85	268
7493	DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA	Amyloid beta A4 protein	Homo sapiens (human)	82	349
67436	TYQRTRALV	Nucleoprotein	Influenza A virus	82	186
16878	FLRGRAYGL	Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	81	265

834473 Records Found

Figure 2.4 Epitope Detail Search input screen



Epitope

Epitope ID: Ex: 44920

Structure Type - Any Epitopes

Organism: Ex: influenza, Peanut — Finder

Antigen Name: Ex: core, capsid, myosin — Finder

Epitope Reference Details

Epitope Structure Defines: Select Multiple Options

Evidence Code for Source...: Select Multiple Options

Epitope Name: Ex: Fab-12 epitope

Reference Start Position: Ex: 124 to Ex: 130

Reference End Position: Ex: 130 to Ex: 130

Reference Region: Ex: Reference Region

Comments: Ex: comments

Data Location in Reference: Ex: location_of_data_in_reference

Epitope Related Object

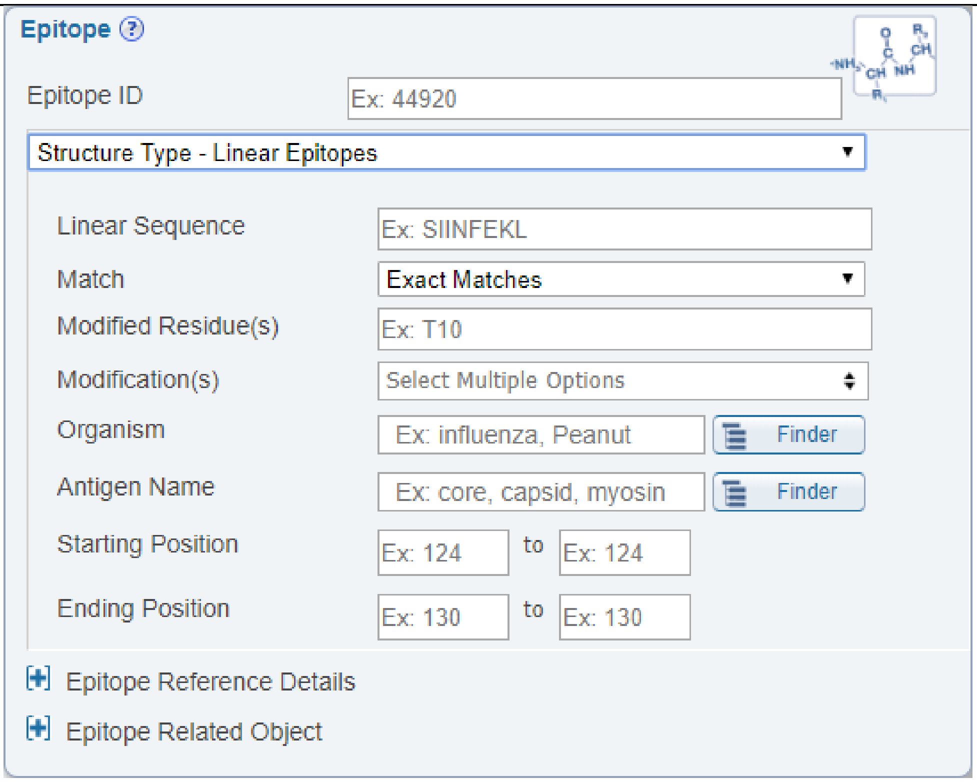
Related Object: Select Multiple Options

Type - Any Type

Organism: Ex: influenza, Peanut — Finder

Antigen Name: Ex: core, capsid, myosin — Finder

Figure 2.5 Epitope panel on the Specialized Search page expanded to show input fields



Epitope ?

Epitope ID: Ex: 44920

Structure Type - Linear Epitopes

Linear Sequence: Ex: SIINFEKL

Match: Exact Matches

Modified Residue(s): Ex: T10

Modification(s): Select Multiple Options

Organism: Ex: influenza, Peanut — Finder

Antigen Name: Ex: core, capsid, myosin — Finder

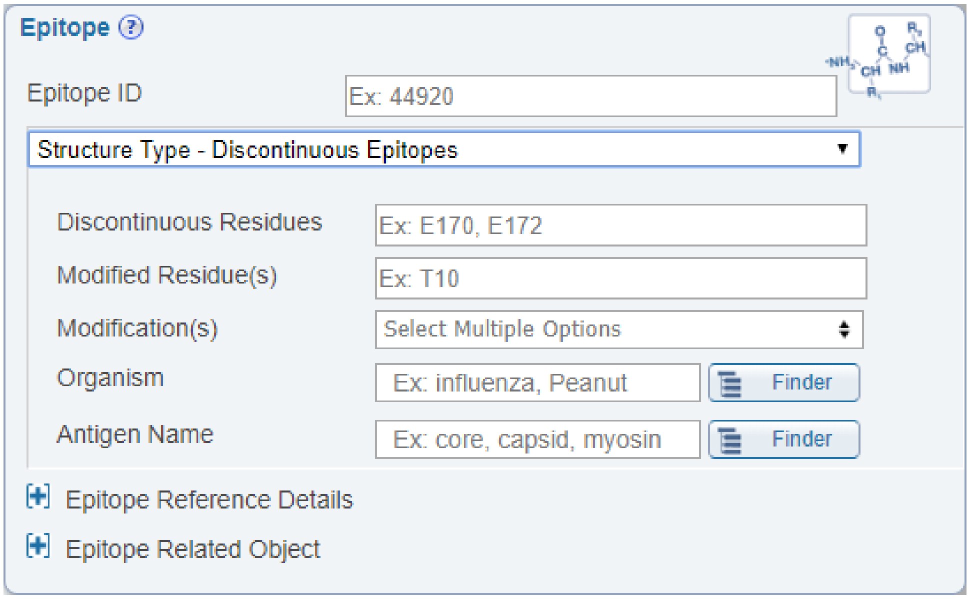
Starting Position: Ex: 124 to Ex: 124

Ending Position: Ex: 130 to Ex: 130

[+] Epitope Reference Details

[+] Epitope Related Object

Figure 2.6 Epitope query fields in the Advanced Search for Linear peptide epitopes



Epitope ?

Epitope ID: Ex: 44920

Structure Type - Discontinuous Epitopes

Discontinuous Residues: Ex: E170, E172

Modified Residue(s): Ex: T10

Modification(s): Select Multiple Options

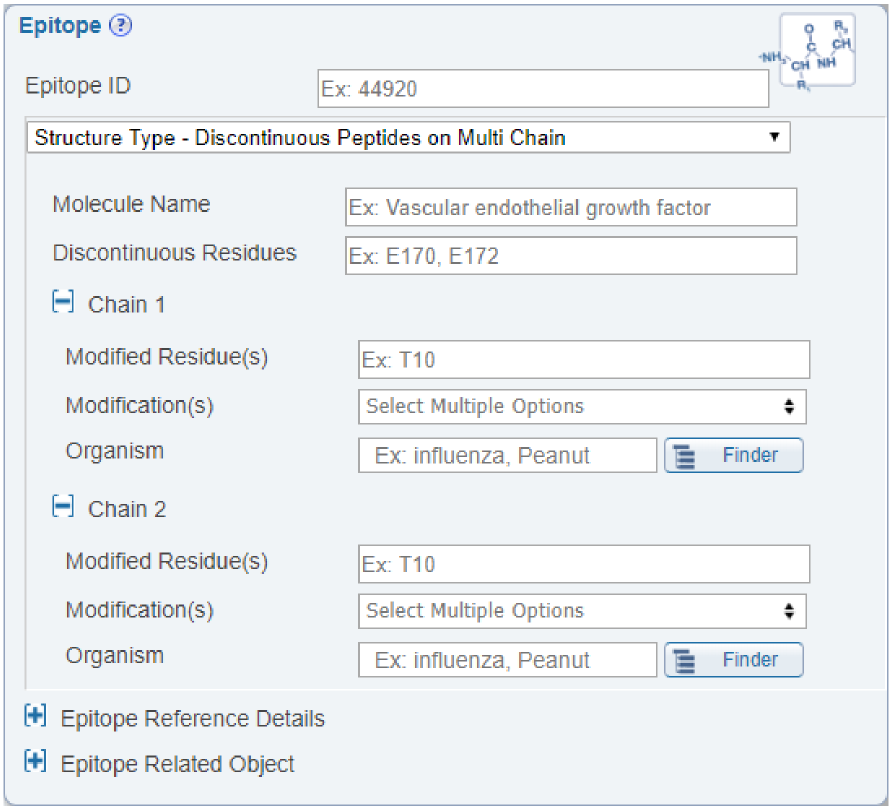
Organism: Ex: influenza, Peanut — Finder

Antigen Name: Ex: core, capsid, myosin — Finder

[+] Epitope Reference Details

[+] Epitope Related Object

Figure 2.7 Epitope query fields in the Advanced Search for Discontinuous peptide epitopes


Epitope ?

Epitope ID: Ex: 44920

Structure Type - Discontinuous Peptides on Multi Chain

Molecule Name: Ex: Vascular endothelial growth factor

Discontinuous Residues: Ex: E170, E172

Chain 1

Modified Residue(s): Ex: T10

Modification(s): Select Multiple Options

Organism: Ex: influenza, Peanut

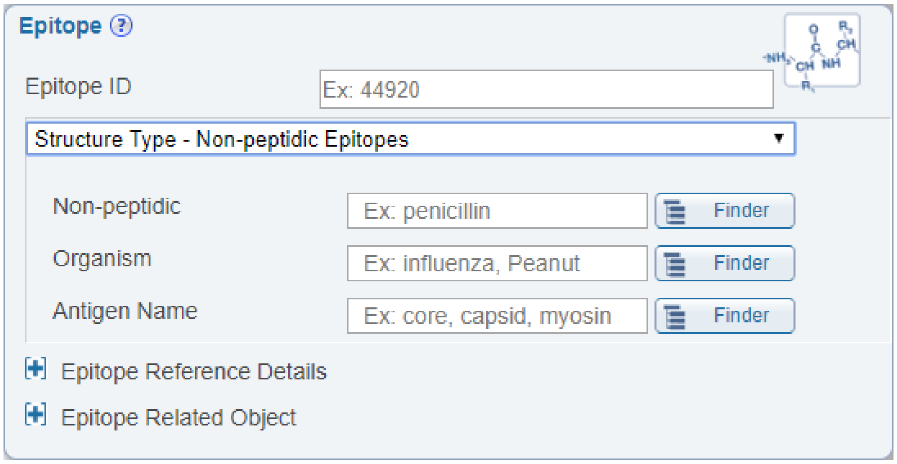
Chain 2

Modified Residue(s): Ex: T10

Modification(s): Select Multiple Options

Organism: Ex: influenza, Peanut

Figure 2.8 Epitope query fields in the Advanced Search for Discontinuous peptide on multi-chain epitopes


Epitope ?

Epitope ID: Ex: 44920

Structure Type - Non-peptidic Epitopes

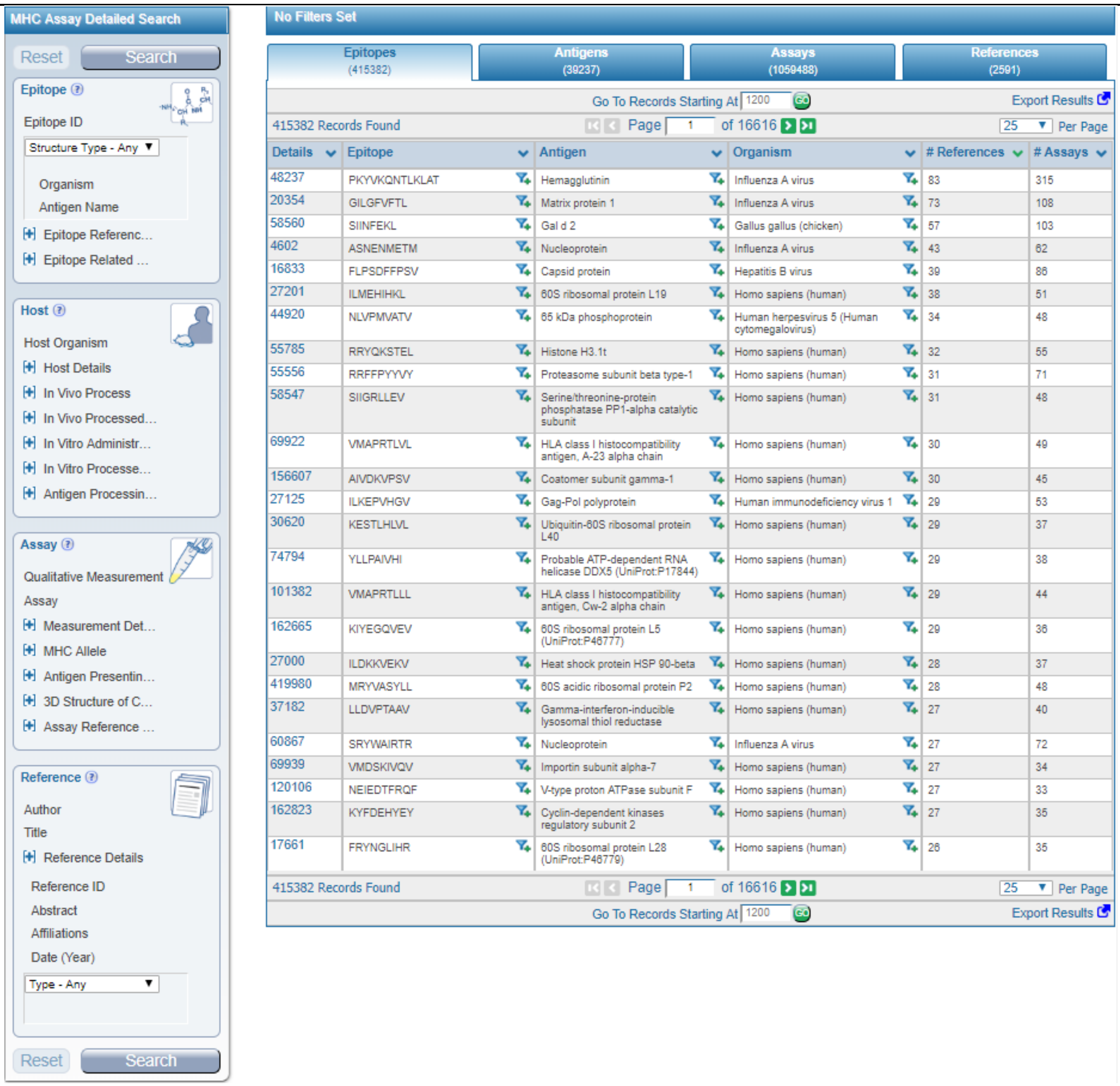
Non-peptidic: Ex: penicillin

Organism: Ex: influenza, Peanut

Antigen Name: Ex: core, capsid, myosin

Figure 2.9 Epitope query fields in the Advanced Search for Non-peptidic epitopes

There are four other Specialized queries that can be used to select search criteria for references, epitopes, and assays. These are T Cell Assay Details, B Cell Assay Details, MHC Assay Details, and Identifier Search. As an example, the MHC Assay Detailed Search page is shown in Figure 2.10. As is the case for all three assay search pages, the Epitope and Reference criteria fields are listed first and last, respectively, with the other relevant filter criteria specific for each assay type listed between them.



415382 Records Found

Details	Epitope	Antigen	Organism	# References	# Assays
48237	PKYVKQNTLKLAT	Hemagglutinin	Influenza A virus	83	315
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	73	108
58560	SIINFEKL	Gal d 2	Gallus gallus (chicken)	57	103
4602	ASNENMETM	Nucleoprotein	Influenza A virus	43	62
16833	FLPSDFFPSV	Capsid protein	Hepatitis B virus	39	86
27201	ILMEHIHKL	60S ribosomal protein L19	Homo sapiens (human)	38	51
44920	NLVPMVATV	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	34	48
55785	RRYQKSTEL	Histone H3.1t	Homo sapiens (human)	32	55
55556	RRFFPYYVY	Proteasome subunit beta type-1	Homo sapiens (human)	31	71
58547	SIIGRLLEV	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	Homo sapiens (human)	31	48
69922	VMAPRTLVL	HLA class I histocompatibility antigen, A-23 alpha chain	Homo sapiens (human)	30	49
156607	AIVDKVPSV	Coatomer subunit gamma-1	Homo sapiens (human)	30	45
27125	ILKEPVHGV	Gag-Pol polyprotein	Human immunodeficiency virus 1	29	53
30620	KESTLHLVL	Ubiquitin-60S ribosomal protein L40	Homo sapiens (human)	29	37
74794	YLLPAIVHI	Probable ATP-dependent RNA helicase DDX5 (UniProt:P17844)	Homo sapiens (human)	29	38
101382	VMAPRTLLL	HLA class I histocompatibility antigen, Cw-2 alpha chain	Homo sapiens (human)	29	44
162665	KIYEGQVEV	60S ribosomal protein L5 (UniProt:P46777)	Homo sapiens (human)	29	36
27000	ILDKKVEKV	Heat shock protein HSP 90-beta	Homo sapiens (human)	28	37
419980	MRYVASYLL	60S acidic ribosomal protein P2	Homo sapiens (human)	28	48
37182	LLDVPTAAV	Gamma-interferon-inducible lysosomal thiol reductase	Homo sapiens (human)	27	40
60867	SRYWAIRTR	Nucleoprotein	Influenza A virus	27	72
69939	VMDSKIVQV	Importin subunit alpha-7	Homo sapiens (human)	27	34
120106	NEIEDTFRQF	V-type proton ATPase subunit F	Homo sapiens (human)	27	33
162823	KYFDEHYEY	Cyclin-dependent kinases regulatory subunit 2	Homo sapiens (human)	27	35
17661	FRYNGLIHR	60S ribosomal protein L28 (UniProt:P46779)	Homo sapiens (human)	26	35

415382 Records Found

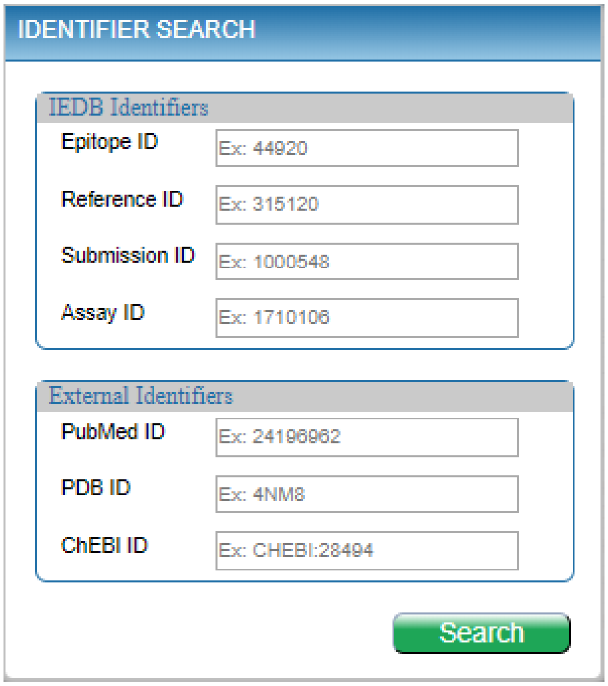
Figure 2.10 MHC Assay Detailed Search web page

The B cell response assay category captures B cell-mediated immunity information and describes antibody responses related to the epitope/antigen. In a B cell response, B lymphocytes (a type of white blood cell) produce proteins called antibodies that bind to antigens. Antibodies are present on the surface on B lymphocytes and are also secreted. Once an antibody binds an antigen, the bound antigen molecule can be engulfed by phagocytes and broken into fragments.

The T Cell Response assay category captures T cell-mediated immunity information where the MHC molecule/antigen complex is recognized by T cells in the context of presentation by an antigen presenting cell.

The MHC Ligand assay category combines assays that were previously in the MHC Binding and MHC Ligand Elution assay categories. As such, the MHC Ligand category captures details relating to the in vitro interaction of the epitope with specific MHC molecules along with available Epitope-MHC complex structure details, that is the epitope's binding capacity to the MHC molecule. It also captures data related to epitopes that are naturally processed and presented on the surface of an antigen presenting cell. The MHC

Ligand Elution subcategory differs from the MHC Binding subcategory in that for the former, antigen bound to the MHC molecule on the cell surface has been taken up and processed internally for presentation by the antigen presenting cell, where as for the latter, antigen in solution is bound to MHC molecules on the surface of the antigen presenting cells.



IEDB Identifiers

Epitope ID: Ex: 44920
Reference ID: Ex: 315120
Submission ID: Ex: 1000548
Assay ID: Ex: 1710106

External Identifiers

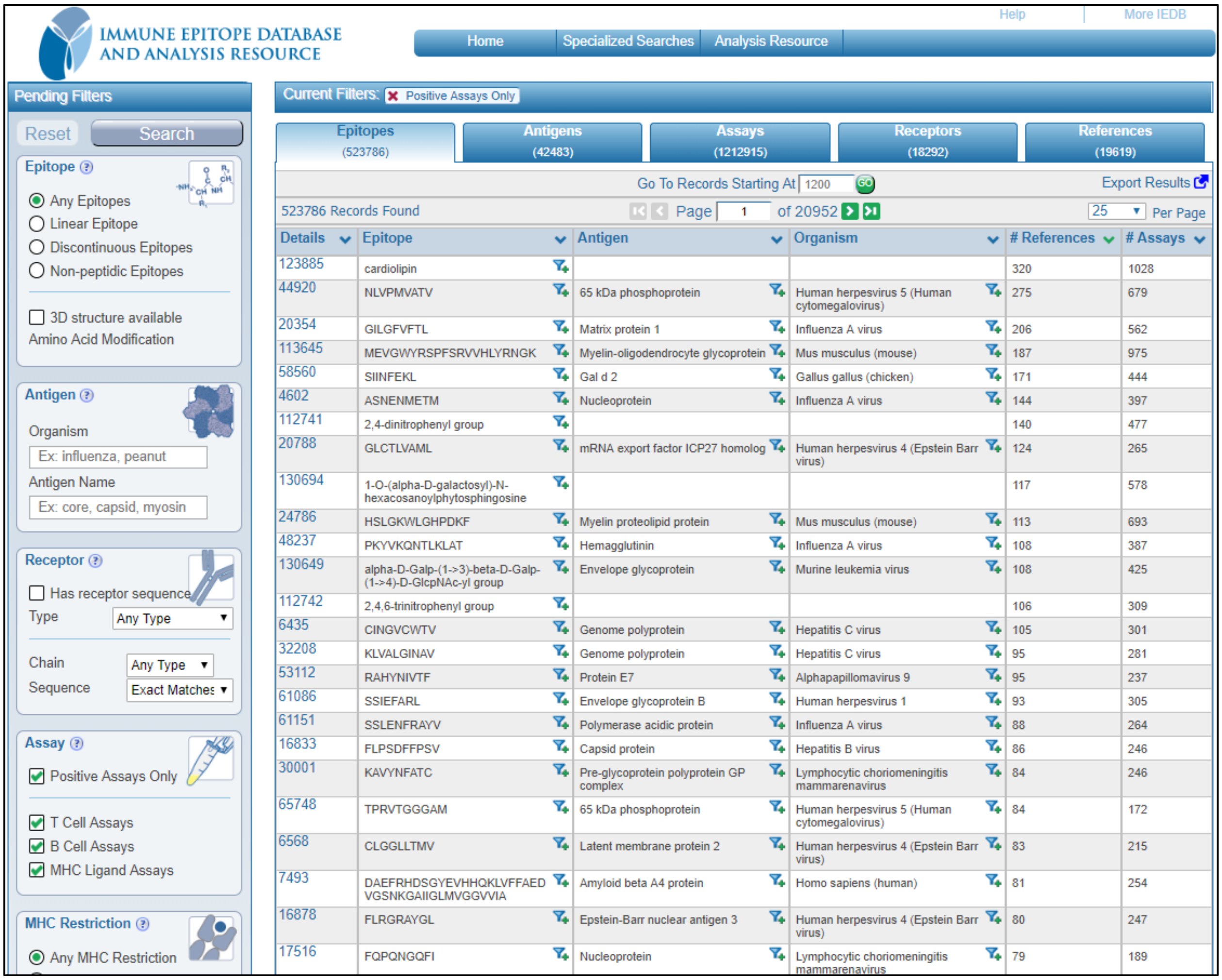
PubMed ID: Ex: 24196962
PDB ID: Ex: 4NM8
ChEBI ID: Ex: CHEBI:28494

Figure 2.11 Identifier Search input screen

The Identifier Search input screen is shown in Figure 2.11. If users know the epitope, reference, submission, or assay identifier they are seeking, they can enter that information into one of the four IEDB Identifiers fields. Users can also look for information based on the PubMed ID of a reference, the PDB ID of a structure, or the ChEBI ID of a nonpeptidic ligand by using the External Identifiers fields.

2.2.3 Search Results Page

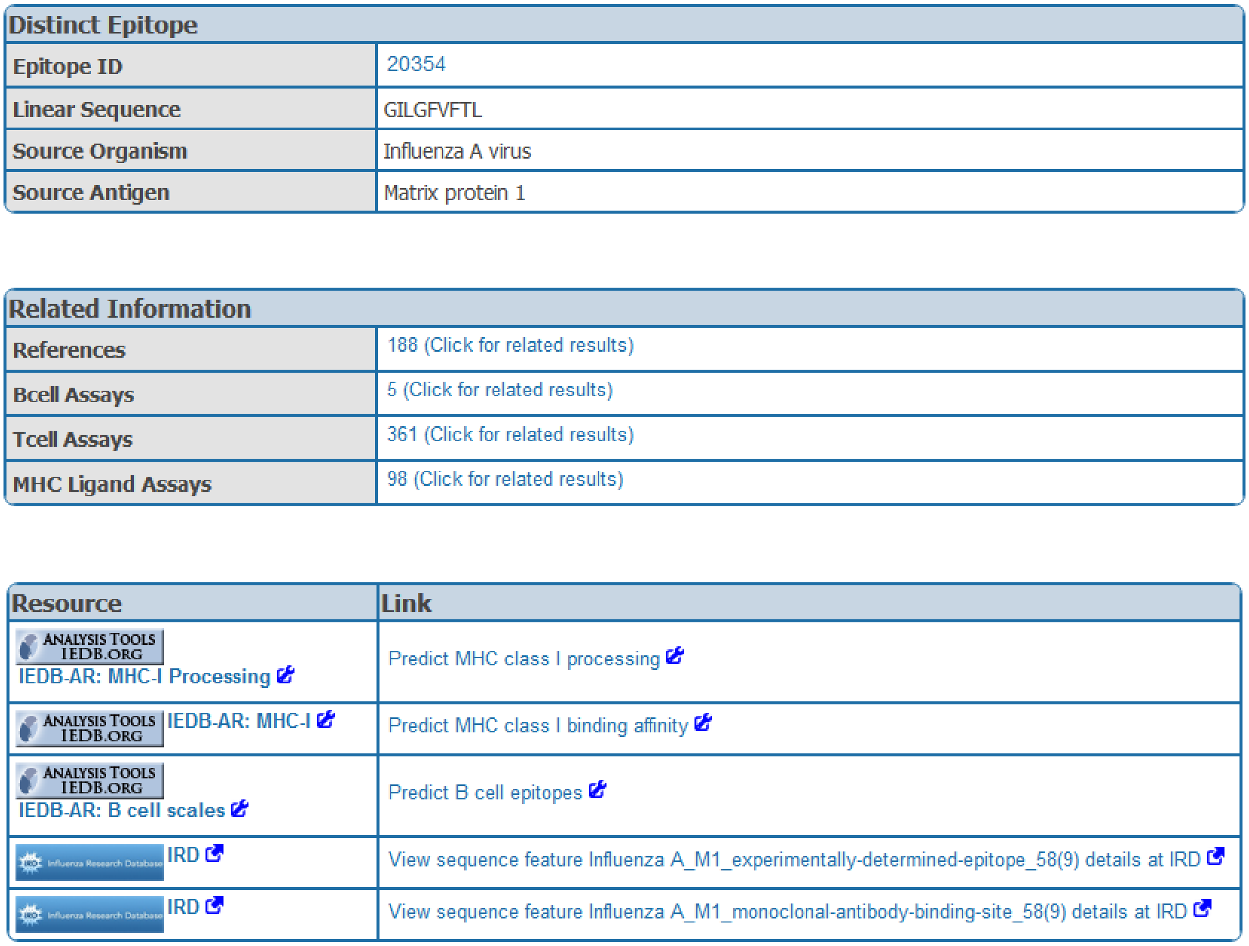
The results of a search or query appear on the Results page. An example is shown in Figure 2.12. The search criteria are listed in the Current Filters section above the results table. There are four tabs for the results. Figure 2.12 displays the Epitopes tab. Results are initially sorted by the number of assays, but the user can click on the column header to change the sort order. A second click will reverse the sort order of the selected column. The table includes the epitope structure description, the corresponding antigen, source organism, the number of references in which the epitope appears, and the number of assays (positive and negative) that reside in the database. Clicking on the Epitope ID number in the far left column will take the user to a Distinct Epitope detail page, as seen in Figure 2.13. The bottom section of the figure contains links to relevant tools in the Analysis Resource. Links can also appear to the Bioinformatics Resource Centers (BRC), such as the Influenza Research Database (IRD). The user can also refine the search results by clicking on the filter icon in the epitope, antigen, and organism fields.



523786 Records Found

Details	Epitope	Antigen	Organism	# References	# Assays
123885	cardiolipin			320	1028
44920	NLVPMVATV	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	275	679
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	206	562
113645	MEVGWYRSPFSRVVHLYRNGK	Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	187	975
58560	SIINFEKL	Gal d 2	Gallus gallus (chicken)	171	444
4602	ASNENMETM	Nucleoprotein	Influenza A virus	144	397
112741	2,4-dinitrophenyl group			140	477
20788	GLCTLVAML	mRNA export factor ICP27 homolog	Human herpesvirus 4 (Epstein Barr virus)	124	265
130694	1-O-(alpha-D-galactosyl)-N-hexacosanoylphytosphingosine			117	578
24786	HSLGKWLGHPDKF	Myelin proteolipid protein	Mus musculus (mouse)	113	693
48237	PKYVKQNTLKLAT	Hemagglutinin	Influenza A virus	108	387
130649	alpha-D-Galp-(1->3)-beta-D-Galp-(1->4)-D-GlcpNAc-yl group	Envelope glycoprotein	Murine leukemia virus	108	425
112742	2,4,6-trinitrophenyl group			106	309
6435	CINGVCWTV	Genome polyprotein	Hepatitis C virus	105	301
32208	KLVALGINAV	Genome polyprotein	Hepatitis C virus	95	281
53112	RAHYNIVTF	Protein E7	Alphapapillomavirus 9	95	237
61086	SSIEFARL	Envelope glycoprotein B	Human herpesvirus 1	93	305
61151	SSLENFRAYV	Polymerase acidic protein	Influenza A virus	88	264
16833	FLPSDFFPSV	Capsid protein	Hepatitis B virus	86	246
30001	KAVYNFATC	Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus	84	246
65748	TPRVTGGGAM	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	84	172
6568	CLGGLLTMV	Latent membrane protein 2	Human herpesvirus 4 (Epstein Barr virus)	83	215
7493	DAEFRHDSGYEVHHQKLVFFAED VGSNKGAIIGLMVGGVVIA	Amyloid beta A4 protein	Homo sapiens (human)	81	254
16878	FLRGRAYGL	Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	80	247
17516	FQPQNGQFI	Nucleoprotein	Lymphocytic choriomeningitis mammarenavirus	79	189

Figure 2.12 The Epitope tab of the search results page



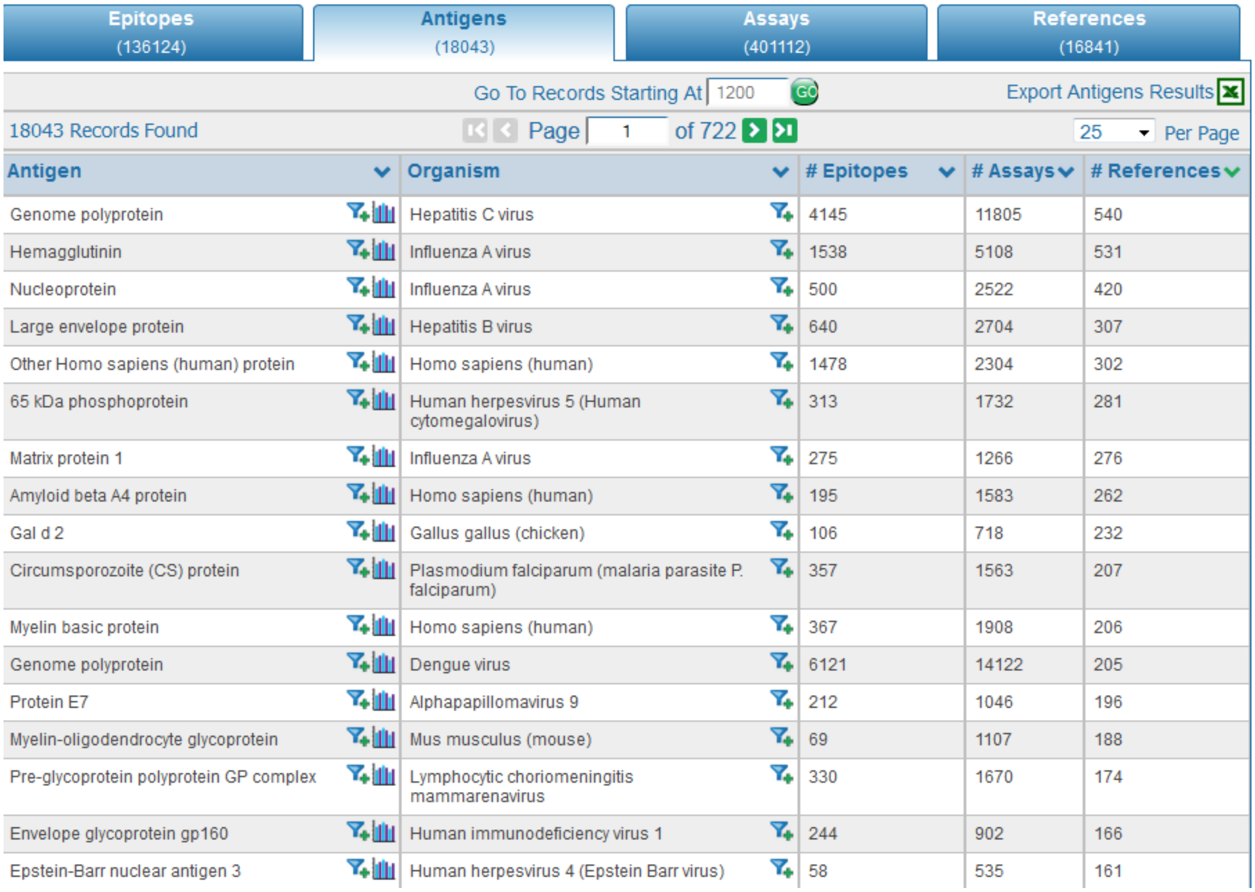
Distinct Epitope	
Epitope ID	20354
Linear Sequence	GILGFVFTL
Source Organism	Influenza A virus
Source Antigen	Matrix protein 1

Related Information	
References	188 (Click for related results)
Bcell Assays	5 (Click for related results)
Tcell Assays	361 (Click for related results)
MHC Ligand Assays	98 (Click for related results)

Resource	Link
ANALYSIS TOOLS IEDB.ORG IEDB-AR: MHC-I Processing	Predict MHC class I processing
ANALYSIS TOOLS IEDB.ORG IEDB-AR: MHC-I	Predict MHC class I binding affinity
ANALYSIS TOOLS IEDB.ORG IEDB-AR: B cell scales	Predict B cell epitopes
Influenza Research Database IRD	View sequence feature Influenza A_M1_experimentally-determined-epitope_58(9) details at IRD
Influenza Research Database IRD	View sequence feature Influenza A_M1_monoclonal-antibody-binding-site_58(9) details at IRD

Figure 2.13 An example of the epitope detail page

The second tab on the results page is the Antigens tab (Figure 2.14). Results are initially sorted by the number of assays, but the user can click on the column header to change the sort order. The table includes the antigen name, the corresponding source organism, the number of associated antigen epitopes in the IEDB, and the number of assays (positive and negative) that reside in the database. The user can explore the data related to a particular antigen by clicking on the funnel icon in the righthand side of the Antigen column. The data in the other three tabs will change accordingly as seen in Figure 2.15.



Go To Records Starting At: 1200

18043 Records Found

Page: 1 of 722

25 Per Page

Antigen	Organism	# Epitopes	# Assays	# References
Genome polyprotein	Hepatitis C virus	4145	11805	540
Hemagglutinin	Influenza A virus	1538	5108	531
Nucleoprotein	Influenza A virus	500	2522	420
Large envelope protein	Hepatitis B virus	640	2704	307
Other Homo sapiens (human) protein	Homo sapiens (human)	1478	2304	302
65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	313	1732	281
Matrix protein 1	Influenza A virus	275	1266	276
Amyloid beta A4 protein	Homo sapiens (human)	195	1583	262
Gal d 2	Gallus gallus (chicken)	106	718	232
Circumsporozoite (CS) protein	Plasmodium falciparum (malaria parasite P. falciparum)	357	1563	207
Myelin basic protein	Homo sapiens (human)	367	1908	206
Genome polyprotein	Dengue virus	6121	14122	205
Protein E7	Alphapapillomavirus 9	212	1046	196
Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	69	1107	188
Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus	330	1670	174
Envelope glycoprotein gp160	Human immunodeficiency virus 1	244	902	166
Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	58	535	161

Figure 2.14 The Antigens tab of the search results page

Go To Records Starting At: 1200

1 Records Found

Page: 1 of 1

25 Per Page

Antigen	Organism	# Epitopes	# Assays	# References
Nucleoprotein	Influenza A virus	500	2522	420

1 Records Found

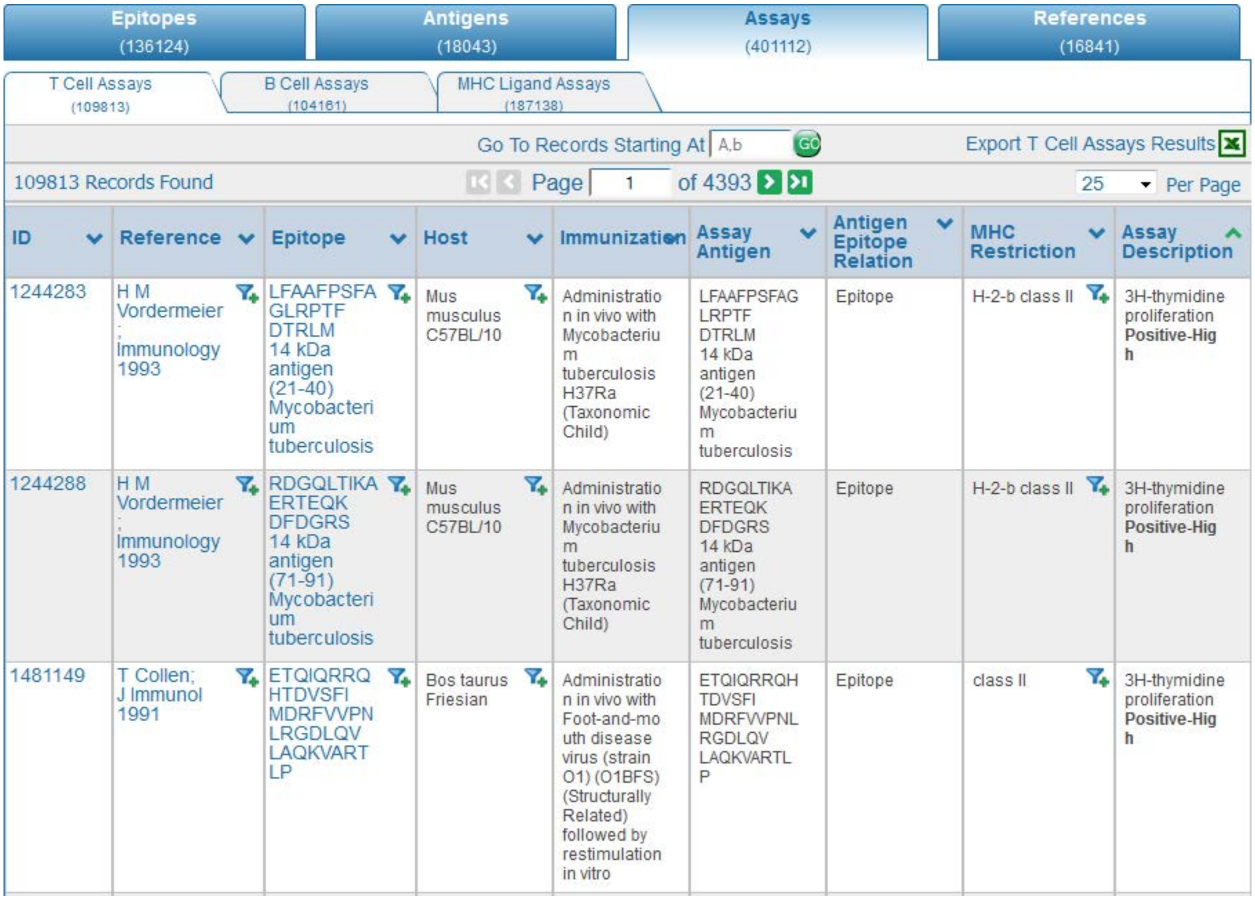
Page: 1 of 1

25 Per Page

Go To Records Starting At: 1200

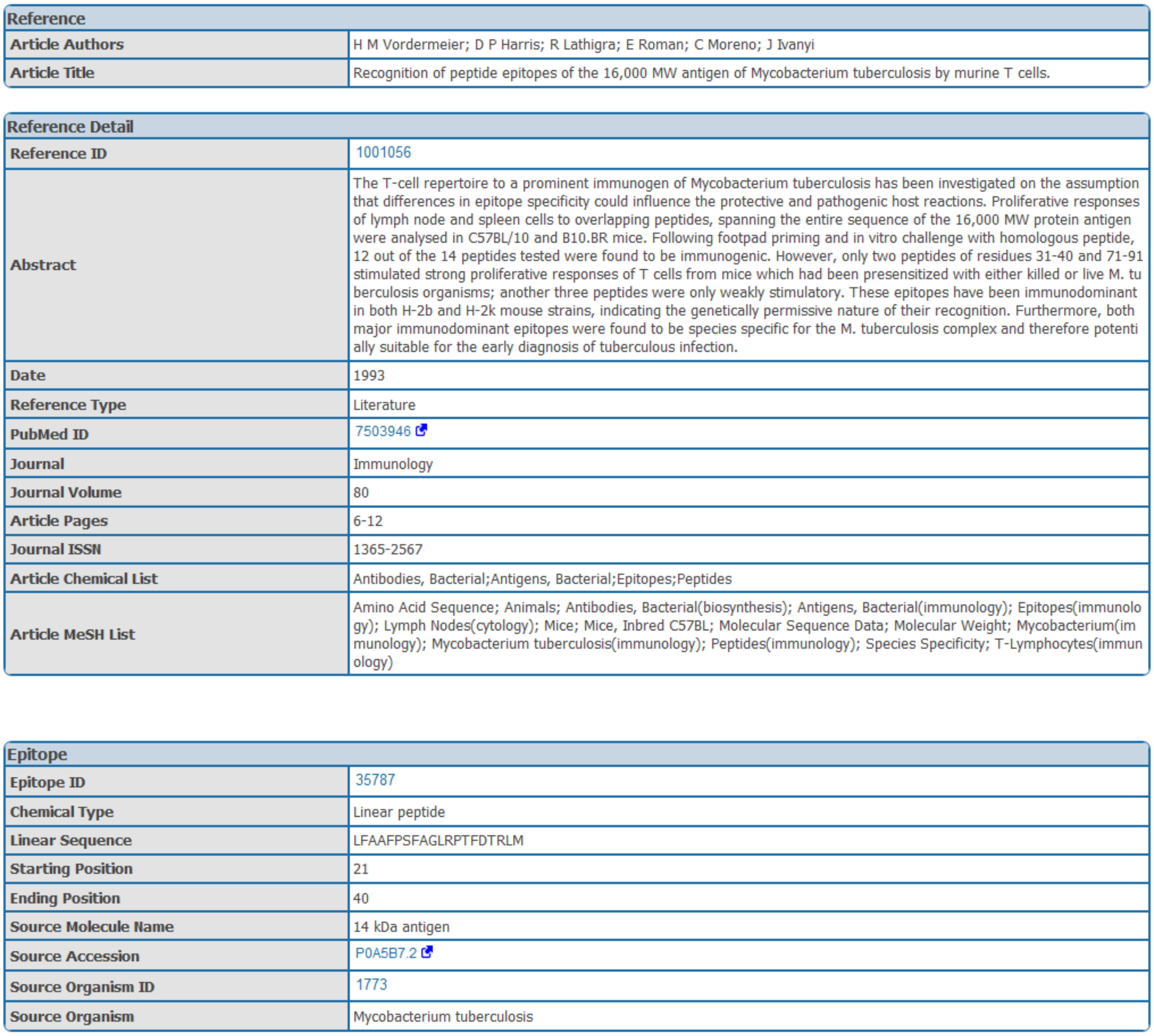
Figure 2.15 The Results filtered by the Nucleoprotein of the Influenza A virus. This was achieved by clicking on the filter icon in the antigen column. The content of the other tabs contain data specific to this antigen.

The third tab on the results page is the Assays tab (Figure 2.16). Results are initially sorted by the Assay Description, but the user can click on the column header to change the sort order. The table contains three additional tabs, one each for the three assay categories – T cell, B cell, and MHC Ligand. The table for the T cell assays includes the assay ID, the reference, epitope, host organism, immunization, assay antigen, antigen epitope relation, MHC restriction, and assay description. The content of the B cell assay tab is the same except it omits the MHC restriction column. The MHC ligand assay tab contains fields for assay ID, reference, epitope, antigen processing, MHC restriction, assay description, and quantitative measure. Clicking on the Assay ID in the far left lane will take the user to an Assay Detail page. An example is given in Figure 2.17. The actual page contains additional fields below what is shown in the figure, including sections for Epitope Reference Details, Immunization, Host Details, 1st In Vivo Process, Administation Details, 1st Immunogen, Immunogen Details, Immunization Comments, T Cell Assay, Effector Cells, Antigen Presenting Cells, MHC Allele, Antigen, Antigen Details, and Assay Reference Details. Hyperlinks were added to several fields in 2016: Reference ID, PubMed ID, Epitope ID, Source Accession, Source Organism ID, and MHC Allele Name. The user can also refine the results further by clicking on the filter icon that is available in seveal of the fields, such as reference, epitope, and host.



ID	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	MHC Restriction	Assay Description
1244283	H M Vordermeier; Immunology 1993	LFAAFPSFAGLRPTFDTRLM 14 kDa antigen (21-40) Mycobacterium tuberculosis	Mus musculus C57BL/10	Administration in vivo with Mycobacterium tuberculosis H37Ra (Taxonomic Child)	LFAAFPSFAGLRPTFDTRLM 14 kDa antigen (21-40) Mycobacterium tuberculosis	Epitope	H-2-b class II	3H-thymidine proliferation **Positive-High**
1244288	H M Vordermeier; Immunology 1993	RDGQLTIKAERTEQKDFDGRS 14 kDa antigen (71-91) Mycobacterium tuberculosis	Mus musculus C57BL/10	Administration in vivo with Mycobacterium tuberculosis H37Ra (Taxonomic Child)	RDGQLTIKAERTEQKDFDGRS 14 kDa antigen (71-91) Mycobacterium tuberculosis	Epitope	H-2-b class II	3H-thymidine proliferation **Positive-High**
1481149	T Collen; J Immunol 1991	ETQIQRRQHTDVSFIMDRFVVPNLRGDLQVLAQKVARTLP	Bos taurus Friesian	Administration in vivo with Foot-and-mouth disease virus (strain O1) (O1BFS) (Structurally Related) followed by restimulation in vitro	ETQIQRRQHTDVSFIMDRFVVPNLRGDLQVLAQKVARTLP	Epitope	class II	3H-thymidine proliferation **Positive-High**

Figure 2.16 The Assays tab of the search results page. The page contains three additional tabs for T Cell, B Cell, and MHC Ligand Assays



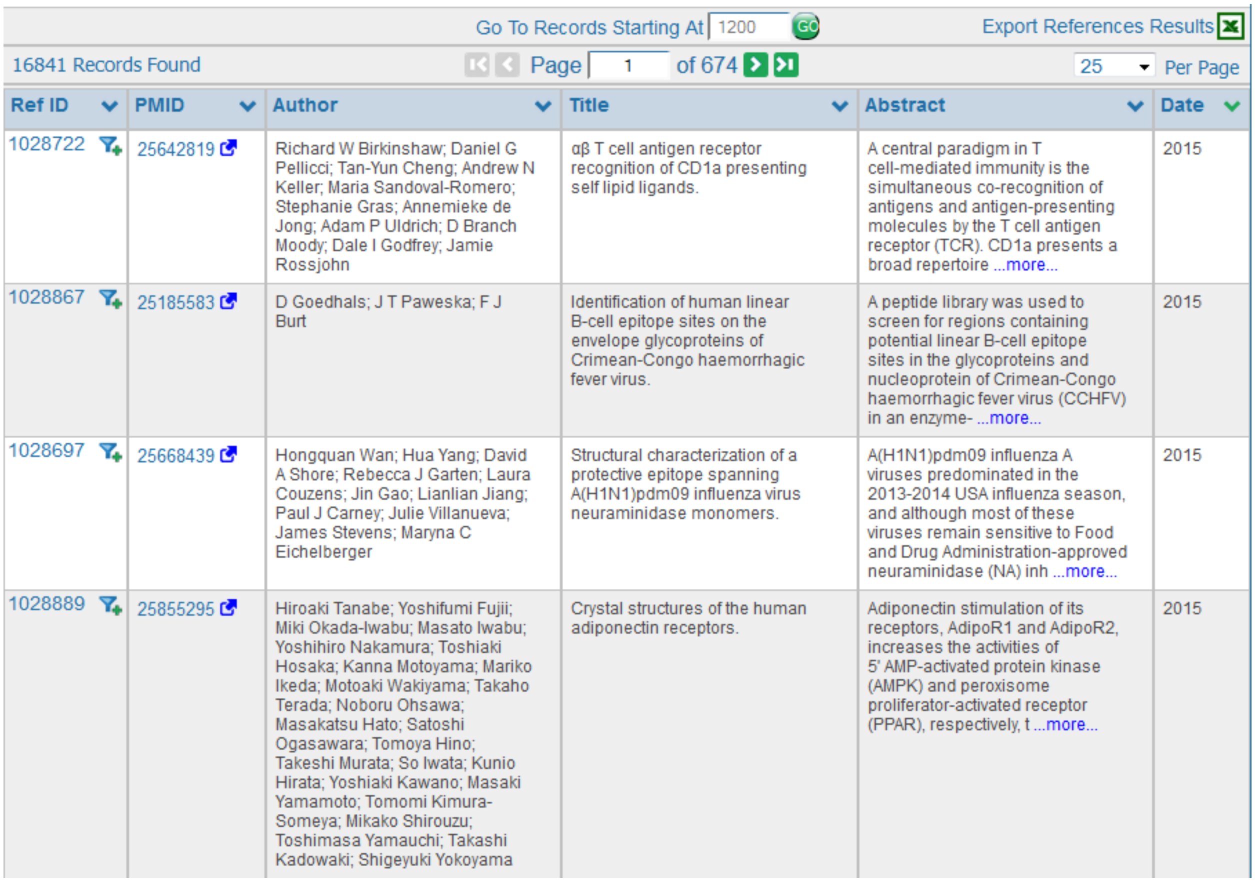
Reference	
Article Authors	H M Vordermeier; D P Harris; R Lathigra; E Roman; C Moreno; J Ivanyi
Article Title	Recognition of peptide epitopes of the 16,000 MW antigen of Mycobacterium tuberculosis by murine T cells.

Reference Detail	
Reference ID	1001056
Abstract	The T-cell repertoire to a prominent immunogen of Mycobacterium tuberculosis has been investigated on the assumption that differences in epitope specificity could influence the protective and pathogenic host reactions. Proliferative responses of lymph node and spleen cells to overlapping peptides, spanning the entire sequence of the 16,000 MW protein antigen were analysed in C57BL/10 and B10.BR mice. Following footpad priming and in vitro challenge with homologous peptide, 12 out of the 14 peptides tested were found to be immunogenic. However, only two peptides of residues 31-40 and 71-91 stimulated strong proliferative responses of T cells from mice which had been presensitized with either killed or live M. tuberculosis organisms; another three peptides were only weakly stimulatory. These epitopes have been immunodominant in both H-2b and H-2k mouse strains, indicating the genetically permissive nature of their recognition. Furthermore, both major immunodominant epitopes were found to be species specific for the M. tuberculosis complex and therefore potentially suitable for the early diagnosis of tuberculous infection.
Date	1993
Reference Type	Literature
PubMed ID	7503946
Journal	Immunology
Journal Volume	80
Article Pages	6-12
Journal ISSN	1365-2567
Article Chemical List	Antibodies, Bacterial;Antigens, Bacterial;Epitopes;Peptides
Article MeSH List	Amino Acid Sequence; Animals; Antibodies, Bacterial(biosynthesis); Antigens, Bacterial(immunology); Epitopes(immunology); Lymph Nodes(cytology); Mice; Mice, Inbred C57BL; Molecular Sequence Data; Molecular Weight; Mycobacterium(immunology); Mycobacterium tuberculosis(immunology); Peptides(immunology); Species Specificity; T-Lymphocytes(immunology)

Epitope	
Epitope ID	35787
Chemical Type	Linear peptide
Linear Sequence	LFAAFPSFAGLRPTFDTRLM
Starting Position	21
Ending Position	40
Source Molecule Name	14 kDa antigen
Source Accession	P0A5B7.2
Source Organism ID	1773
Source Organism	Mycobacterium tuberculosis

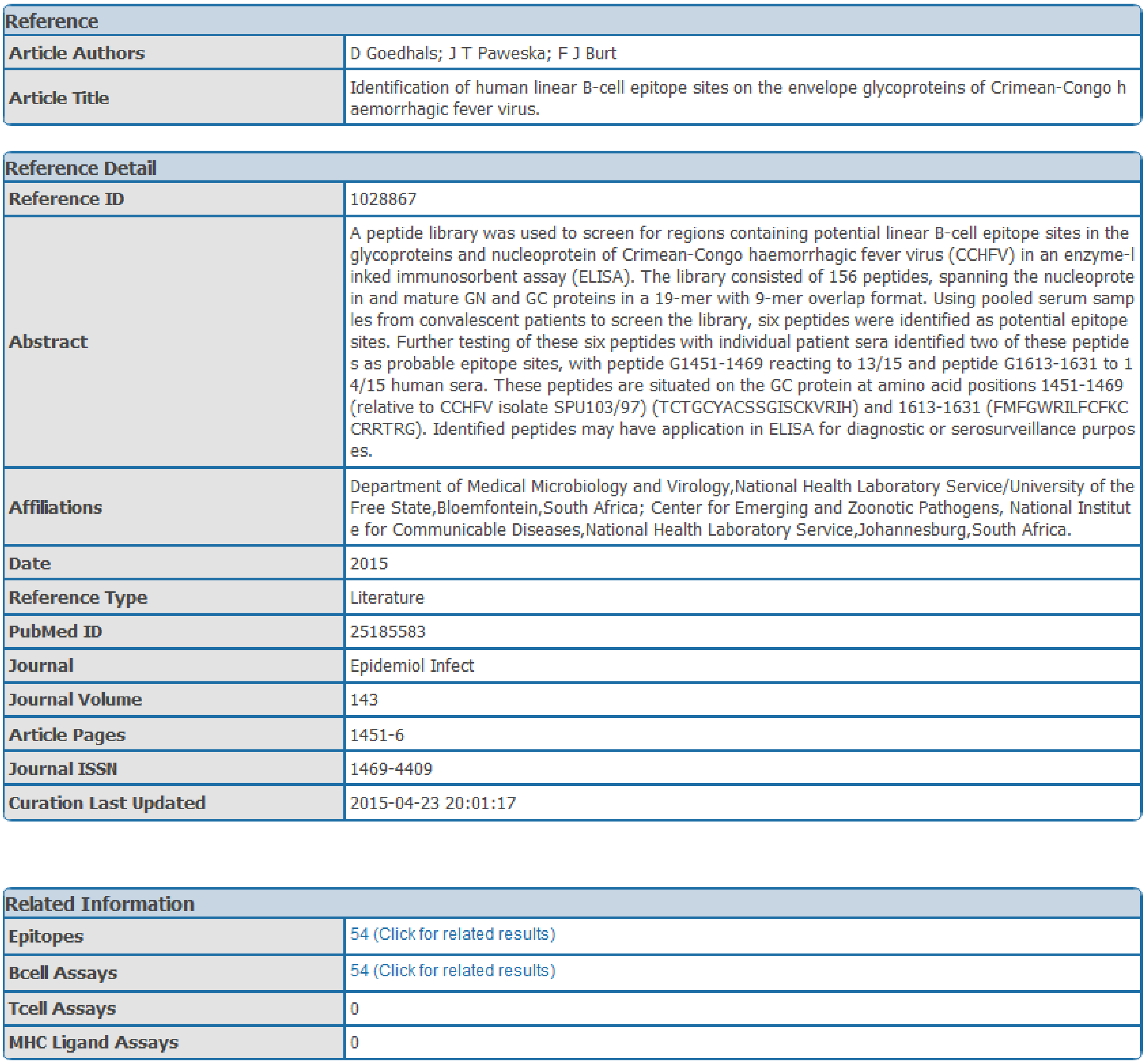
Figure 2.17 The top three sections of a sample T cell assay detail page.

The fourth tab on the results page is the References tab (Figure 2.18). Results are initially sorted by the year of publication or submission, the most recent references first. Again, the user can click on the column header to change the sort order. The table includes the IEDB-assigned reference ID, the PubMed ID, authors, article title, abstract, and the date. For journal articles, the information is downloaded directly from PubMed. Clicking on the Ref ID in the far left lane will take the user to a Reference Detail page. An example is given in Figure 2.19.



Ref ID	PMID	Author	Title	Abstract	Date
1028722	25642819	Richard W Birkinshaw; Daniel G Pellicci; Tan-Yun Cheng; Andrew N Keller; Maria Sandoval-Romero; Stephanie Gras; Annemieke de Jong; Adam P Uldrich; D Branch Moody; Dale I Godfrey; Jamie Rossjohn	αβ T cell antigen receptor recognition of CD1a presenting self lipid ligands.	A central paradigm in T cell-mediated immunity is the simultaneous co-recognition of antigens and antigen-presenting molecules by the T cell antigen receptor (TCR). CD1a presents a broad repertoire ...more...	2015
1028867	25185583	D Goedhals; J T Paweska; F J Burt	Identification of human linear B-cell epitope sites on the envelope glycoproteins of Crimean-Congo haemorrhagic fever virus.	A peptide library was used to screen for regions containing potential linear B-cell epitope sites in the glycoproteins and nucleoprotein of Crimean-Congo haemorrhagic fever virus (CCHFV) in an enzyme- ...more...	2015
1028697	25668439	Hongquan Wan; Hua Yang; David A Shore; Rebecca J Garten; Laura Couzens; Jin Gao; Lianlian Jiang; Paul J Carney; Julie Villanueva; James Stevens; Maryna C Eichelberger	Structural characterization of a protective epitope spanning A(H1N1)pdm09 influenza virus neuraminidase monomers.	A(H1N1)pdm09 influenza A viruses predominated in the 2013-2014 USA influenza season, and although most of these viruses remain sensitive to Food and Drug Administration-approved neuraminidase (NA) inh ...more...	2015
1028889	25855295	Hiroaki Tanabe; Yoshifumi Fujii; Miki Okada-Iwabu; Masato Iwabu; Yoshihiro Nakamura; Toshiaki Hosaka; Kanna Motoyama; Mariko Ikeda; Motoaki Wakiyama; Takaho Terada; Noboru Ohsawa; Masakatsu Hato; Satoshi Ogasawara; Tomoya Hino; Takeshi Murata; So Iwata; Kunio Hirata; Yoshiaki Kawano; Masaki Yamamoto; Tomomi Kimura-Someya; Mikako Shirouzu; Toshimasa Yamauchi; Takashi Kadowaki; Shigeyuki Yokoyama	Crystal structures of the human adiponectin receptors.	Adiponectin stimulation of its receptors, AdipoR1 and AdipoR2, increases the activities of 5' AMP-activated protein kinase (AMPK) and peroxisome proliferator-activated receptor (PPAR), respectively, t ...more...	2015

Figure 2.18 The References tab of the search results page



Reference	
Article Authors	D Goedhals; J T Paweska; F J Burt
Article Title	Identification of human linear B-cell epitope sites on the envelope glycoproteins of Crimean-Congo haemorrhagic fever virus.

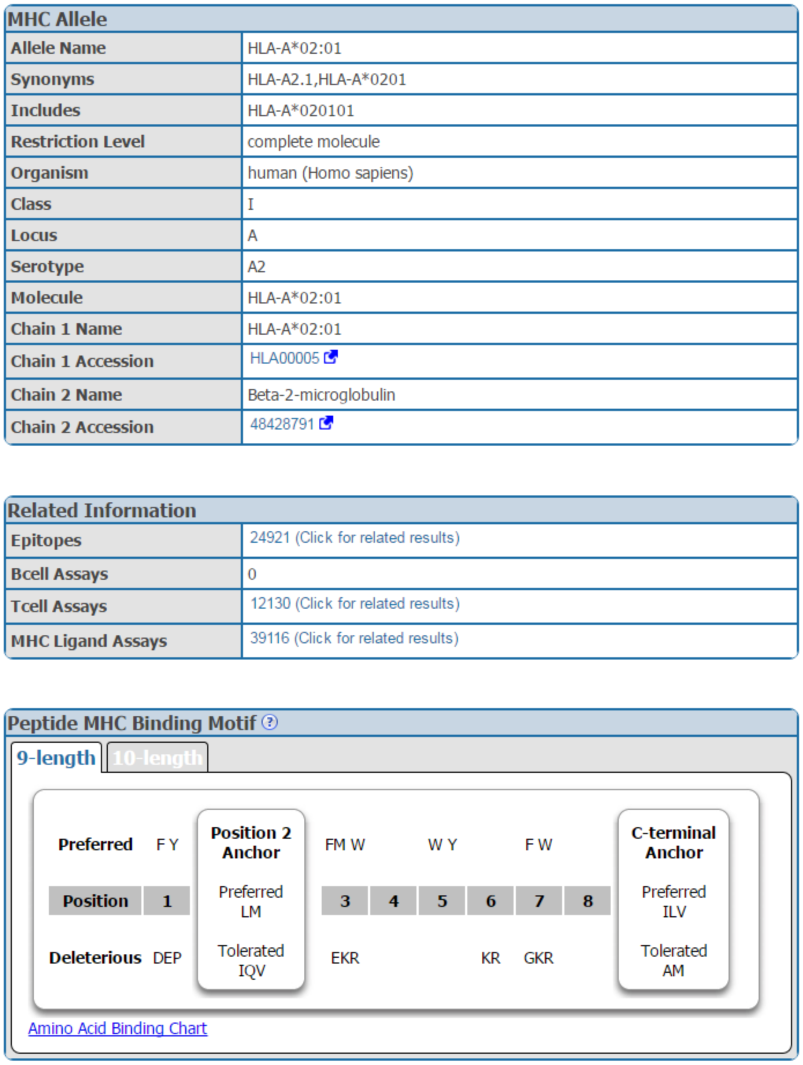
Reference Detail	
Reference ID	1028867
Abstract	A peptide library was used to screen for regions containing potential linear B-cell epitope sites in the glycoproteins and nucleoprotein of Crimean-Congo haemorrhagic fever virus (CCHFV) in an enzyme-linked immunosorbent assay (ELISA). The library consisted of 156 peptides, spanning the nucleoprotein and mature GN and GC proteins in a 19-mer with 9-mer overlap format. Using pooled serum samples from convalescent patients to screen the library, six peptides were identified as potential epitope sites. Further testing of these six peptides with individual patient sera identified two of these peptides as probable epitope sites, with peptide G1451-1469 reacting to 13/15 and peptide G1613-1631 to 14/15 human sera. These peptides are situated on the GC protein at amino acid positions 1451-1469 (relative to CCHFV isolate SPU103/97) (TCTGCYACSSGISCKVRIH) and 1613-1631 (FMFGWRILFCFKCCRRTRG). Identified peptides may have application in ELISA for diagnostic or serosurveillance purposes.
Affiliations	Department of Medical Microbiology and Virology,National Health Laboratory Service/University of the Free State,Bloemfontein,South Africa; Center for Emerging and Zoonotic Pathogens, National Institute for Communicable Diseases,National Health Laboratory Service,Johannesburg,South Africa.
Date	2015
Reference Type	Literature
PubMed ID	25185583
Journal	Epidemiol Infect
Journal Volume	143
Article Pages	1451-6
Journal ISSN	1469-4409
Curation Last Updated	2015-04-23 20:01:17

Related Information	
Epitopes	54 (Click for related results)
Bcell Assays	54 (Click for related results)
Tcell Assays	0
MHC Ligand Assays	0

Figure 2.19 An example of the Reference detail page

2.2.3.1 Peptide MHC Binding Motif Displays

A display of peptide MHC binding motif diagrams and amino acid binding charts for a subset of MHC allele records appears on the MHC Allele Details page. Clicking on the allele name in the MHC Restriction column on the Assays tab for T Cells and MHC Ligand will bring the user to an MHC Allele Details page (Figure 2.20). As can be seen by the tabs in the binding motif display, the Peptide MHC Binding Motif diagrams on MHC Allele Information pages support diagrams for multiple lengths.



MHC Allele

Allele Name	HLA-A*02:01
Synonyms	HLA-A2.1,HLA-A*0201
Includes	HLA-A*020101
Restriction Level	complete molecule
Organism	human (Homo sapiens)
Class	I
Locus	A
Serotype	A2
Molecule	HLA-A*02:01
Chain 1 Name	HLA-A*02:01
Chain 1 Accession	HLA00005
Chain 2 Name	Beta-2-microglobulin
Chain 2 Accession	48428791

Related Information

Epitopes	24921 (Click for related results)
Bcell Assays	0
Tcell Assays	12130 (Click for related results)
MHC Ligand Assays	39116 (Click for related results)

Peptide MHC Binding Motif

9-length 10-length

Position	**1**	**Position 2 Anchor**	**3**	**4**	**5**	**6**	**7**	**8**	**C-terminal Anchor**
Preferred	F Y	Preferred LM	FM W		W Y		F W		Preferred ILV
Deleterious	DEP	Tolerated IQV	EKR			KR	GKR		Tolerated AM

Amino Acid Binding Chart

Figure 2.20 Sample MHC Allele Details page with Peptide MHC Binding Motif diagram for HLA-A*02:01. Note the link to the corresponding Amino Acid Binding Chart on the bottom left of the diagram

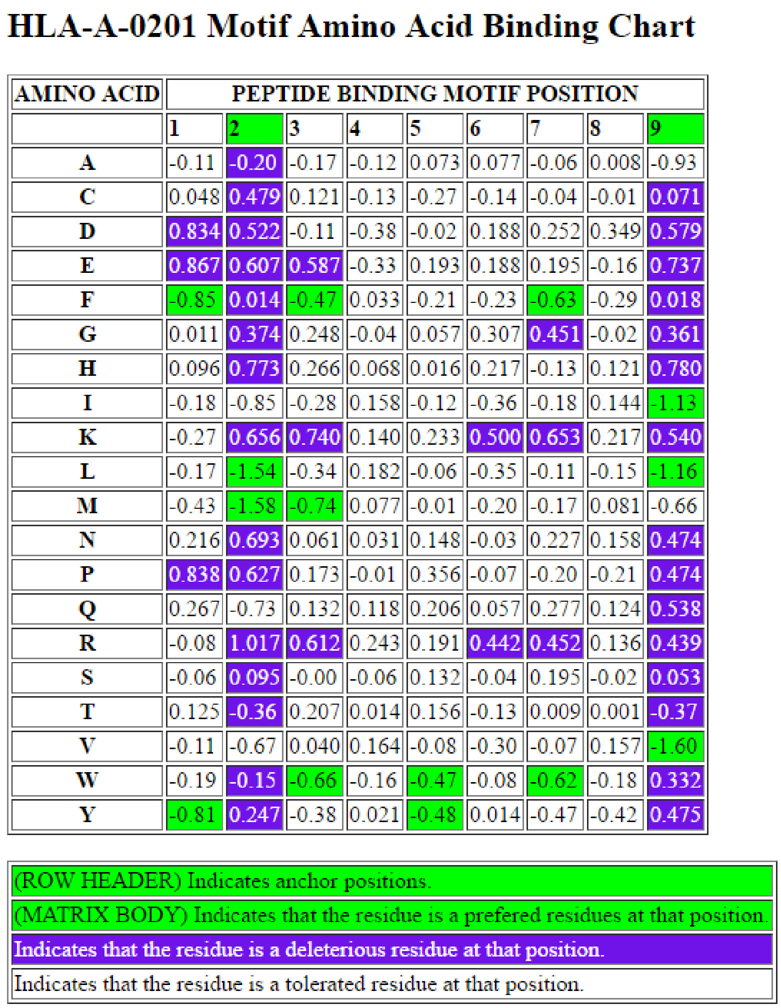
The Peptide MHC Binding Motif diagram summarizes the results of the amino acid binding for each position, which is shown in Figure 2.21. The amino acids are color-coded for each position, where green indicates the residue is preferred for binding, purple indicates it is deleterious for binding, and white indicates the residue is tolerated at that position. The motif diagram shows which residues are preferred and tolerated at the anchor positions, and which residues are preferred and deleterious at the non-anchor positions.

The residue preference is calculated from the SMM prediction matrix, which is described in Section 2.3.1.1. The following steps are taken in determining the residue preference at each position:

For anchor position:

1. determine the best value of this position from corresponding column of the SMM matrix
2. if a residue's value in this column of the SMM matrix is within 3 fold of the best value, designate this residue as prefered
3. if a residue's value in this column of the SMM matrix is within 10 fold of the best value, designate this residue as tolerated

4. The remaining residues are designated as deleterious



HLA-A-0201 Motif Amino Acid Binding Chart

AMINO ACID	PEPTIDE BINDING MOTIF POSITION								
	1	2	3	4	5	6	7	8	9
A	-0.11	-0.20	-0.17	-0.12	0.073	0.077	-0.06	0.008	-0.93
C	0.048	0.479	0.121	-0.13	-0.27	-0.14	-0.04	-0.01	0.071
D	0.834	0.522	-0.11	-0.38	-0.02	0.188	0.252	0.349	0.579
E	0.867	0.607	0.587	-0.33	0.193	0.188	0.195	-0.16	0.737
F	-0.85	0.014	-0.47	0.033	-0.21	-0.23	-0.63	-0.29	0.018
G	0.011	0.374	0.248	-0.04	0.057	0.307	0.451	-0.02	0.361
H	0.096	0.773	0.266	0.068	0.016	0.217	-0.13	0.121	0.780
I	-0.18	-0.85	-0.28	0.158	-0.12	-0.36	-0.18	0.144	-1.13
K	-0.27	0.656	0.740	0.140	0.233	0.500	0.653	0.217	0.540
L	-0.17	-1.54	-0.34	0.182	-0.06	-0.35	-0.11	-0.15	-1.16
M	-0.43	-1.58	-0.74	0.077	-0.01	-0.20	-0.17	0.081	-0.66
N	0.216	0.693	0.061	0.031	0.148	-0.03	0.227	0.158	0.474
P	0.838	0.627	0.173	-0.01	0.356	-0.07	-0.20	-0.21	0.474
Q	0.267	-0.73	0.132	0.118	0.206	0.057	0.277	0.124	0.538
R	-0.08	1.017	0.612	0.243	0.191	0.442	0.452	0.136	0.439
S	-0.06	0.095	-0.00	-0.06	0.132	-0.04	0.195	-0.02	0.053
T	0.125	-0.36	0.207	0.014	0.156	-0.13	0.009	0.001	-0.37
V	-0.11	-0.67	0.040	0.164	-0.08	-0.30	-0.07	0.157	-1.60
W	-0.19	-0.15	-0.66	-0.16	-0.47	-0.08	-0.62	-0.18	0.332
Y	-0.81	0.247	-0.38	0.021	-0.48	0.014	-0.47	-0.42	0.475

(ROW HEADER) Indicates anchor positions.

(MATRIX BODY) Indicates that the residue is a prefered residues at that position.

Indicates that the residue is a deleterious residue at that position.

Indicates that the residue is a tolerated residue at that position.

Figure 2.21 Amino acid binding matrix for MHC allele HLA-A*02:01

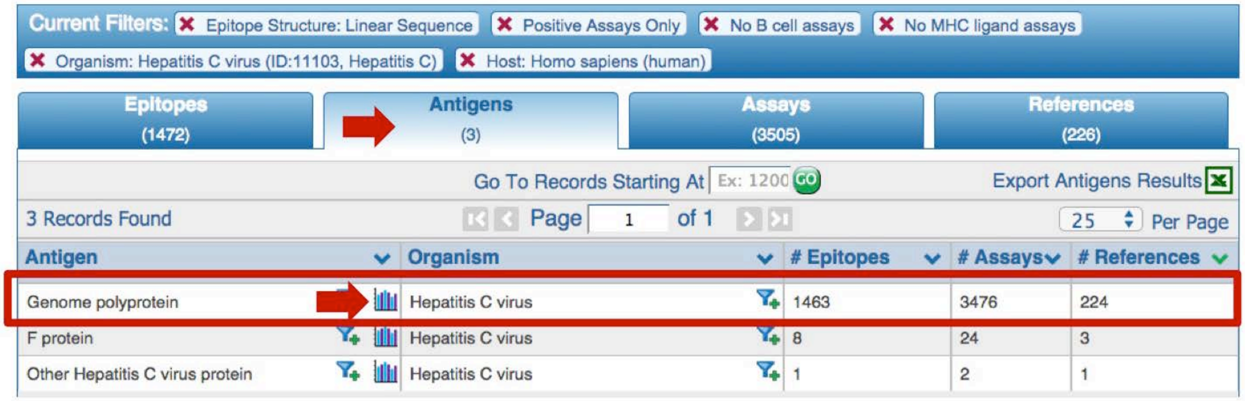
For non-anchor position:

1. determine the median value of this position from corresponding column of the SMM matrix
2. if a residue's value in this column of the SMM matrix is within 3 fold of the median value, designate this residue as tolerated
3. if a residue's value in this column of the SMM matrix is above 3 fold of the median value, designate this residue as prefered
4. if a residue's value in this column of the SMM matrix is below 3 fold of the median value, designate this residue as deleterious

2.2.3.2 Immunome Browser

The Immunome Browser is a feature integrated into the IEDB to more efficiently display large sets of immune epitope data. The purpose of the tool is to allow users to explore how often each protein region has been studied in immune assays and in how many assays the immune response was positive or negative. The Immunome Browser “maps” query results from the IEDB onto a reference proteome. A reference proteome is used because (1) epitopes reported in IEDB were identified for different strains and protein isoforms –

mapping to the reference protein allows to visualize and study such epitopes as they would have the same antigen; (2) different mutant variants of the same epitope were tested and reported; and (3) immune response varies among studies and assays due to heterogeneity of samples and complexity of immune response. The Immunome Browser presents the mapped data along with calculated 'epitope prominence scores' that rank known epitopes based on how frequently subjects responded to each epitope, allowing identification of immunodominance. Both linear and discontinuous linear peptide epitopes with T cell or B cell responses are supported for viewing using the Immunome Browser. It is accessible via the Immunome Browser icon on the Antigen tab on the results page, as seen in Figure 2.22.



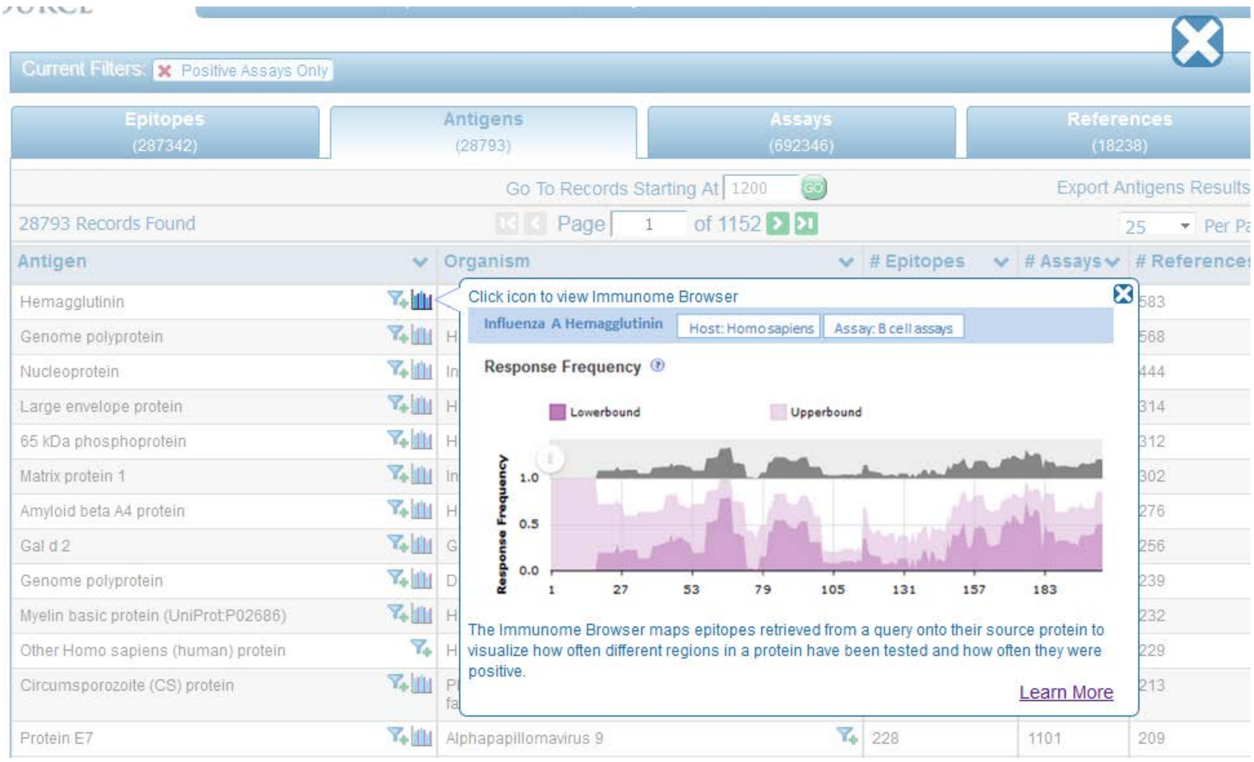
Current Filters: ✖ Epitope Structure: Linear Sequence ✖ Positive Assays Only ✖ No B cell assays ✖ No MHC ligand assays ✖ Organism: Hepatitis C virus (ID:11103, Hepatitis C) ✖ Host: Homo sapiens (human)

3 Records Found

Antigen	Organism	# Epitopes	# Assays	# References
Genome polyprotein	Hepatitis C virus	1463	3476	224
F protein	Hepatitis C virus	8	24	3
Other Hepatitis C virus protein	Hepatitis C virus	1	2	1

Figure 2.22 The Immunome Browser is accessed by clicking on the icon shown on the Antigen tab on the results page of a query

In order to make the Immunome Browser capability more prominent, a pop-up window was added that appears the first time a user goes to the Antigen tab after making a search, as seen in Figure 2.23. It can be easily dismissed by clicking on the large X in the upper right-hand corner or clicking anywhere else on the window.



Current Filters: Positive Assays Only

Epitopes (287342) | Antigens (28793) | Assays (692346) | References (18238)

Go To Records Starting At 1200 GO

Export Antigens Results

28793 Records Found

Page 1 of 1152

25 Per Pa

Antigen	Organism	# Epitopes	# Assays	# References
Hemagglutinin				583
Genome polyprotein	H			568
Nucleoprotein	In			444
Large envelope protein	H			314
65 kDa phosphoprotein	H			312
Matrix protein 1	In			302
Amyloid beta A4 protein	H			276
Gal d 2	G			256
Genome polyprotein	D			239
Myelin basic protein (UniProt:P02686)	H			232
Other Homo sapiens (human) protein	H			229
Circumsporozoite (CS) protein	P fa			213
Protein E7	Alphapapillomavirus 9	228	1101	209

Click icon to view Immunome Browser

Influenza A Hemagglutinin | Host: Homo sapiens | Assay: B cell assays

Response Frequency

The Immunome Browser maps epitopes retrieved from a query onto their source protein to visualize how often different regions in a protein have been tested and how often they were positive.

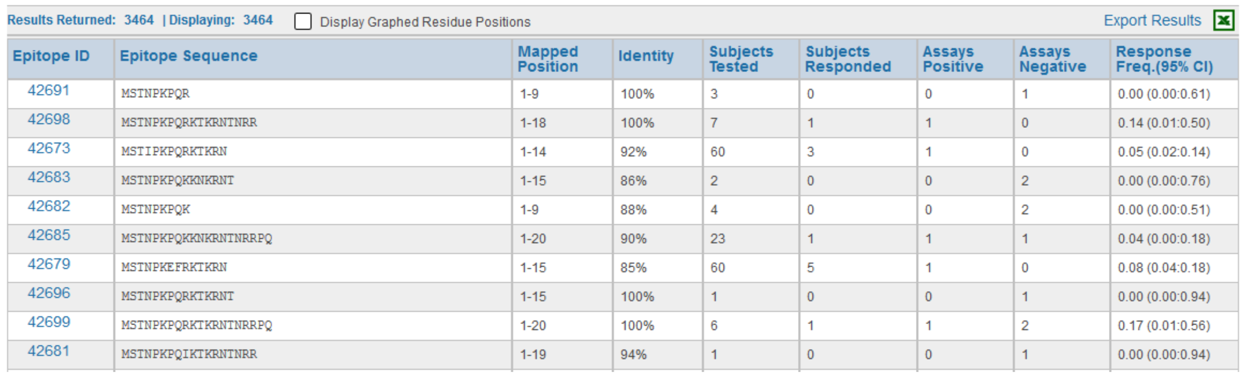
Learn More

Figure 2.23 **A pop-up window appears each time the user clicks on the Antigen tab on the Results page. It highlights the Immunome Browser icon and briefly explains the Immunome Browser's functionality.**

In the Immunome Browser, each selected antigen is considered to be a target protein, and the tool by default maps and visualizes all epitopes in the query result that are from the source antigen, which is the target protein or any of its taxonomic child. The mapping is done using the alignment between the source antigen and the target protein, and matching the epitope positions in the source antigen with the residue positions in the target protein. By default, epitopes that were tested as negative for the correspondent query will be mapped as well, even if the user queried only for positive assays. Also, the epitopes that failed to satisfy the default mapping criteria won't be mapped and visualized. The Immunome Browser output for query criteria of T cell assays, linear epitopes, Hepatitis C virus, and human host is shown in Figure 2.24.

Figure 2.24 Immunome Browser graphical output displaying assay results mapped onto a reference proteome by residue position

Two graphs are generated in the Immunome Browser. The upper plot titled "Response Frequency" renders the lower (dark color) and upper (light color) bounds of the 95% confidence interval (CI) of the response frequency (RF) for each position target protein position, averaged over all epitopes mapped to that position. RF is calculated as the number of positively responded subjects (or individuals in this case) relative to the total number of those tested summed up by mapped epitopes. The graph, however, displays only the upper and lower bounds of the 95% confidence interval (CI) for the RF score and not the RF score itself. The lower plot, titled "Epitope Assay Counts," indicates the number of positive and negative assays for each residue position.


Results Returned: 3464 | Displaying: 3464 ☐ Display Graphed Residue Positions Export Results

Epitope ID	Epitope Sequence	Mapped Position	Identity	Subjects Tested	Subjects Responded	Assays Positive	Assays Negative	Response Freq.(95% CI)
42691	MSTNPKPQR	1-9	100%	3	0	0	1	0.00 (0.00:0.61)
42698	MSTNPKPQRKTKRNTNRR	1-18	100%	7	1	1	0	0.14 (0.01:0.50)
42673	MSTIPKPQRKTKRN	1-14	92%	60	3	1	0	0.05 (0.02:0.14)
42683	MSTNPKPQKKNKRNT	1-15	86%	2	0	0	2	0.00 (0.00:0.76)
42682	MSTNPKPQK	1-9	88%	4	0	0	2	0.00 (0.00:0.51)
42685	MSTNPKPQKKNKRNTNRRPQ	1-20	90%	23	1	1	1	0.04 (0.00:0.18)
42679	MSTNPKEFRKTKRN	1-15	85%	60	5	1	0	0.08 (0.04:0.18)
42696	MSTNPKPQRKTKRNT	1-15	100%	1	0	0	1	0.00 (0.00:0.94)
42699	MSTNPKPQRKTKRNTNRRPQ	1-20	100%	6	1	1	2	0.17 (0.01:0.56)
42681	MSTNPKPQIKTKRNTNRR	1-19	94%	1	0	0	1	0.00 (0.00:0.94)

Figure 2.25 Immunome Browser tabular output.

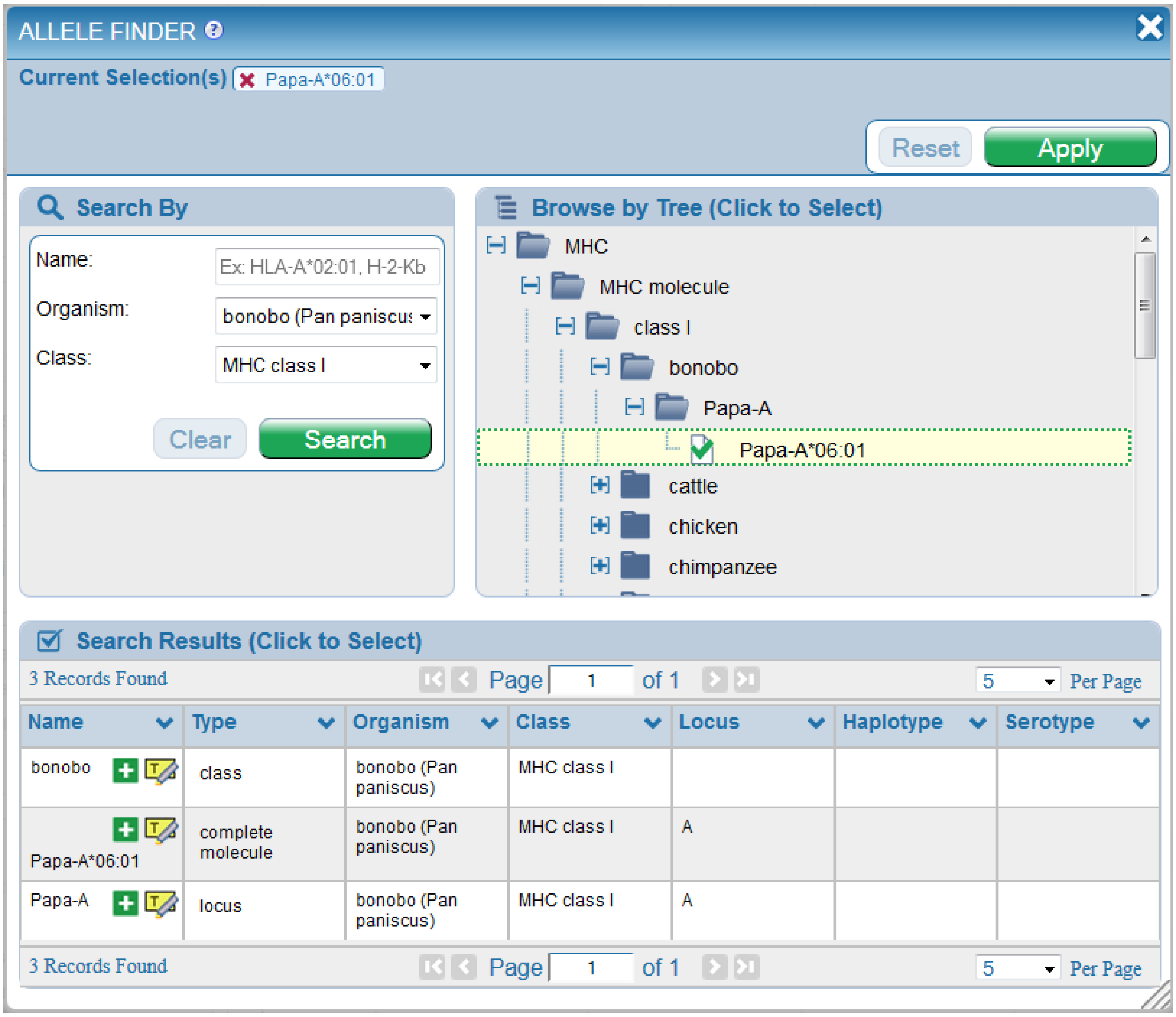
In addition to the plots, a table is generated that displays the epitope ID, sequence, position, and identity, as well as the number of subjects tested, the number who responded, and number of positive and negative assays, and the response frequency (Figure 2.25). The user can interactively zoom in and out onthe plots to a specific protein region and, if the check box for the table to correspond the plots is selected, the table is automatically updated to show only epitope from the selected region. Alternatively, the user can specify the residue start and end positions at the bottom of plots and click Update Display.

2.2.4 Finders Overview

Several finders (Allele, Assay, Disease, Molecule, Geolocation, and Organism) are available to help facilitate selections and control vocabulary usage, thus improving query results. At times the potential list of selections can be quite extensive, and the finders help users make selections from large lists. The finders can be utilized when performing all queries. Multiple selections can be made when utilizing finders during a query.

2.2.4.1 Allele Finder

The MHC Allele Finder facilitates the selection of one or more MHC alleles. The finder consists of four sections as shown in Figure 2.26. The top section lists the alleles that the user selects. The selections can be removed by clicking on the red X of an allele name or by clicking on the Reset button to delete all selected alleles. When the user has completed the selection process, the user needs to click the green Apply button. The middle left section of the finder contains the “Search By” panel. Users can search by allele name, source organism, and/or class (I, II, or non-classical). After the user supplies their search criteria and clicks the Search button, the system will filter the list of MHC alleles using the organism, class, and allele provided. The allele finder uses wild card characters by default on both ends of criteria entered into the allele field. The system then returns in the bottom “Search Results” panel a list of any alleles that contain the value in the name field and match the class selected. Users can click on the green “+” icon to select an allele. Users can also click on the yellow highlighter icon to highlight the allele in the allele tree in the middle right section of the finder. Alternatively, a user can browse the hierarchical allele tree. Clicking on a node in this tree will add the allele to the Current Selections section of the finder.



Current Selection(s) Papa-A*06:01

Name: Ex: HLA-A*02:01, H-2-Kb
Organism: bonobo (Pan paniscus
Class: MHC class I

3 Records Found Page 1 of 1 5 Per Page

Name	Type	Organism	Class	Locus	Haplotype	Serotype
bonobo	class	bonobo (Pan paniscus)	MHC class I			
Papa-A*06:01	complete molecule	bonobo (Pan paniscus)	MHC class I	A		
Papa-A	locus	bonobo (Pan paniscus)	MHC class I	A		

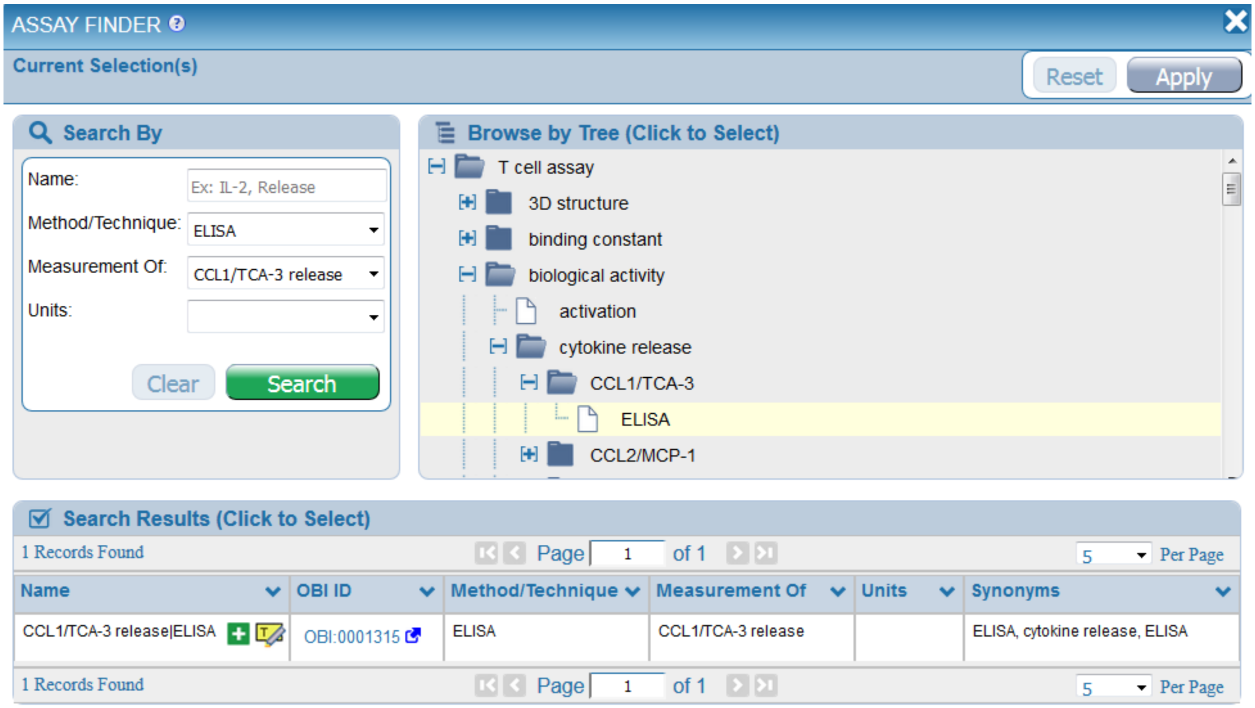
3 Records Found Page 1 of 1 5 Per Page

Figure 2.26 Allele Finder. Alleles are displayed in a tree structure and users can sdearch by allele name, source organism, and MHC class (I, II, or non-classical)

2.2.4.2 Assay Finder

The IEDB contains experimental data characterizing antibody and T cell epitopes studied in humans, non-human primates, and other animal species. Search results may easily be narrowed to include only the specific assay categories of T Cell Assays, B Cell Assays, and MHC Ligand Assays. Additionally, one may further narrow search results to very specific experimental methods using the Assay Finder.

The Assay Finder is used to facilitate the selection of one or more assay types and lists all assay types in the selected assay category. The Assay Finder for T Cell, B cell, and MHC Ligand assays can be found in the Assay section on the the home page search interface, the left-hand side of the Results page, and on their respective Specialized Search pages. These versions of the Assay Finder organize and display assays in a tree structure, as seen in Figure 2.27 for the T Cell assays. Users can also search for assays by their method/technique and by the characters within the assay's name. The figure shows the results for ELISA type assays for "CCL1/TCA-3 release". Users can click on the green "+" icon to select an assay. Users can also click on the yellow highlighter icon to highlight the assay in the assay tree in the middle right section of the finder, as is shown in the figure. Alternatively, a user can browse the hierarchical assay tree. Clicking on a node in this tree will add the assay to the Current Selections section of the finder.



Name: Ex: IL-2, Release
Method/Technique: ELISA
Measurement Of: CCL1/TCA-3 release
Units:

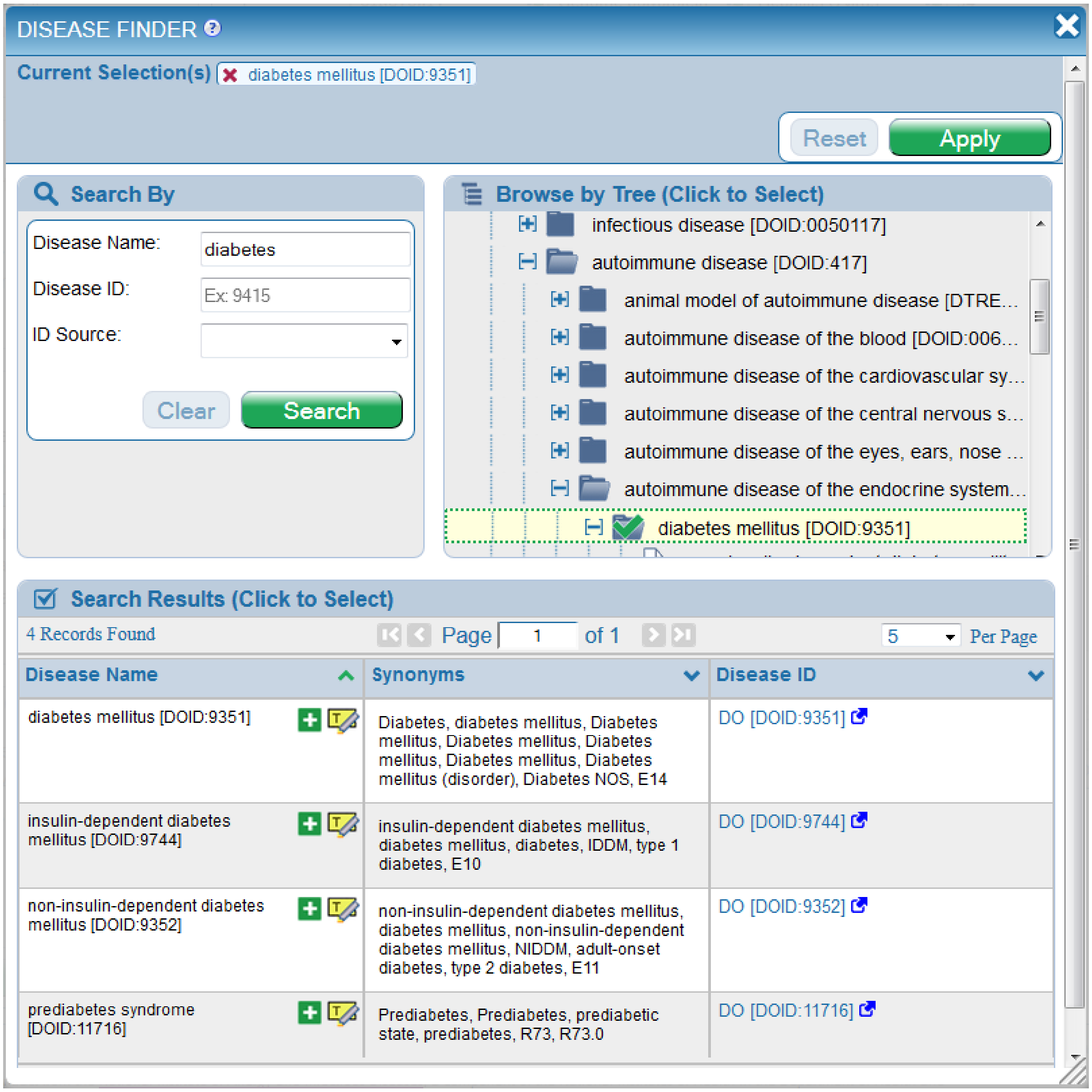
Name	OBI ID	Method/Technique	Measurement Of	Units	Synonyms
CCL1/TCA-3 release|ELISA	OBI:0001315	ELISA	CCL1/TCA-3 release		ELISA, cytokine release, ELISA

Figure 2.27 Assay Finder on the T Cell Advanced Search page. Assays are displayed in a tree structure and users can find displays by their method/technique and by the characters with which the assay name starts

2.2.4.3 Disease Finder

This query feature allows users to select a disease association based on the host disease state or status as captured in curation. Diseases are organized into a browsable tree structure. Upon the selection of host disease state/status, the system provides the user with a hierarchical *Disease Tree* that organizes the data at the highest level according to the five disease categories (Allergy, Autoimmunity, Infectious Disease, Additional Diseases by category, and Transplant-related Disease and Allo-reactivity) and then by the anatomical location of the disease (e.g. respiratory tract, gastrointestinal tract). In this way the user can either type in the disease name or synonym of interest, or navigate the Disease Tree by disease manifestation and physical location to see what is available. A node for healthy subjects is also included. The Disease Finder is fully functional for only Autoimmunity. The finder will be revised with an updated disease ontology and hierarchical tree during 2017 based on the Disease Ontology that will make it functional for the other disease categories. Infectious disease searches are best accommodated using the Organism Finder to specify the antigen.

Figure 2.28 shows the Disease Tree with diabetes highlighted. DOID refers to the Disease Ontology identifier. The DTREE designates an IEDB-specific identifier that will be updated later with a DOID number when the Disease Ontology incorporates the terms.



Current Selection(s): ☒ diabetes mellitus [DOID:9351]

Disease Name: diabetes
Disease ID: Ex: 9415
ID Source:

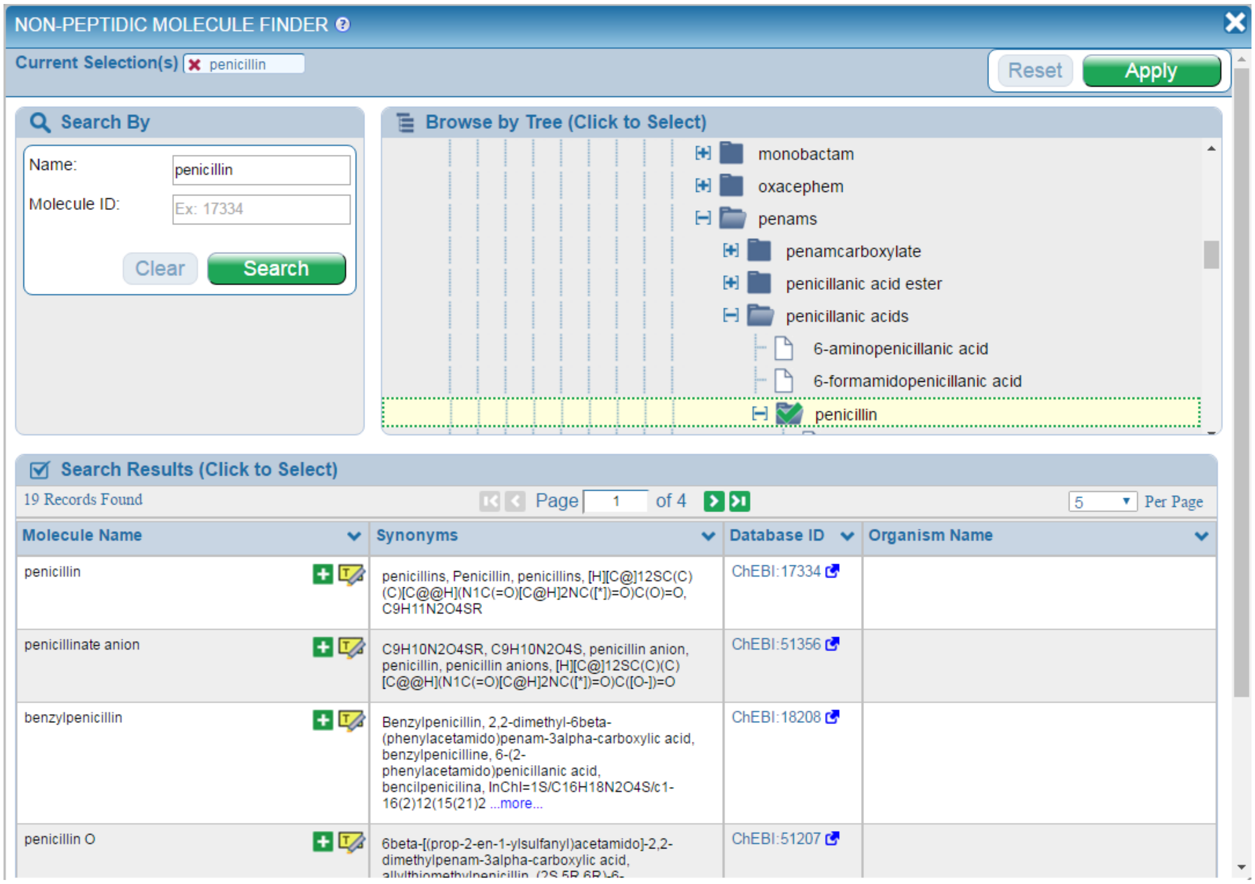
- infectious disease [DOID:0050117]
- autoimmune disease [DOID:417]
  - animal model of autoimmune disease [DTRE…
  - autoimmune disease of the blood [DOID:006…
  - autoimmune disease of the cardiovascular sy…
  - autoimmune disease of the central nervous s…
  - autoimmune disease of the eyes, ears, nose …
  - autoimmune disease of the endocrine system…
    - ☑ diabetes mellitus [DOID:9351]

Disease Name	Synonyms	Disease ID
diabetes mellitus [DOID:9351]	Diabetes, diabetes mellitus, Diabetes mellitus, Diabetes mellitus, Diabetes mellitus, Diabetes mellitus, Diabetes mellitus (disorder), Diabetes NOS, E14	DO [DOID:9351]
insulin-dependent diabetes mellitus [DOID:9744]	insulin-dependent diabetes mellitus, diabetes mellitus, diabetes, IDDM, type 1 diabetes, E10	DO [DOID:9744]
non-insulin-dependent diabetes mellitus [DOID:9352]	non-insulin-dependent diabetes mellitus, diabetes mellitus, non-insulin-dependent diabetes mellitus, NIDDM, adult-onset diabetes, type 2 diabetes, E11	DO [DOID:9352]
prediabetes syndrome [DOID:11716]	Prediabetes, Prediabetes, prediabetic state, prediabetes, R73, R73.0	DO [DOID:11716]

Figure 2.28 The disease finder is particularly helpful in specifying epitopes related to autoimmune diseases. In the example shown, diabetes is highlighted and selected.

2.2.4.4 Molecule Finder

The Molecule Finder is used to facilitate the selection of source antigens, immunogens, and epitopes. There are two versions of the Molecule Finder – one specifically for non-peptidic molecules found in the Epitope box in the results page, and another that includes peptidic and non-peptidic branches, found in the Antigen box in the results page. The former contains the structures curated by the Chemical Entities of Biological Interest (ChEBI) database. An example of the non-peptidic finder is shown in Figure 2.29.



Current Selection(s) penicillin

Name: penicillin

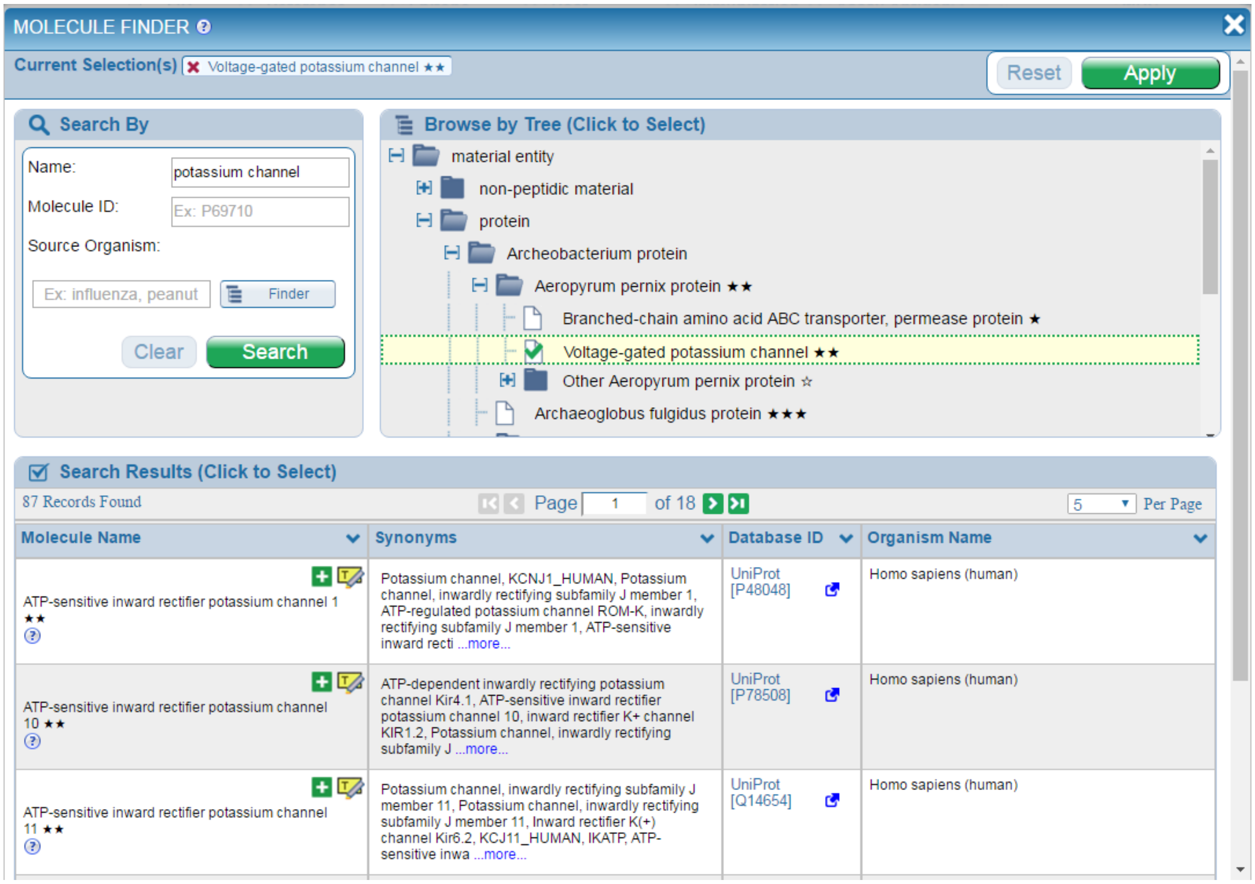
Molecule ID: Ex: 17334

19 Records Found — Page 1 of 4 — 5 Per Page

Molecule Name	Synonyms	Database ID	Organism Name
penicillin	penicillins, Penicillin, penicillins, [H][C@]12SC(C)(C)[C@@H](N1C(=O)[C@H]2NC([*])=O)C(O)=O, C9H11N2O4SR	ChEBI:17334	
penicillinate anion	C9H10N2O4SR, C9H10N2O4S, penicillin anion, penicillin, penicillin anions, [H][C@]12SC(C)(C)[C@@H](N1C(=O)[C@H]2NC([*])=O)C([O-])=O	ChEBI:51356	
benzylpenicillin	Benzylpenicillin, 2,2-dimethyl-6beta-(phenylacetamido)penam-3alpha-carboxylic acid, benzylpenicilline, 6-(2-phenylacetamido)penicillanic acid, bencilpenicilina, InChI=1S/C16H18N2O4S/c1-16(2)12(15(21)2 ...more...	ChEBI:18208	
penicillin O	6beta-[(prop-2-en-1-ylsulfanyl)acetamido]-2,2-dimethylpenam-3alpha-carboxylic acid,	ChEBI:51207	

Figure 2.29 The non-peptidic version of the Molecule Finder. This finder is accessed in the Epitope filter on the search results page.

With regard to the protein or peptidic branch of the Molecule Finder, individual GenPept proteins utilized by IEDB data are assigned to parent proteins from reference proteomes by sequence homology. These reference proteomes are graded by a star system described below that reflects the quality and completeness of each. An example of the star system and the protein tree can be seen in Figure 2.30.



Current Selection(s) ☒ Voltage-gated potassium channel ★★

Name: potassium channel
Molecule ID: Ex: P69710
Source Organism: Ex: influenza, peanut

- material entity
  - non-peptidic material
  - protein
    - Archeobacterium protein
      - Aeropyrum pernix protein ★★
        - Branched-chain amino acid ABC transporter, permease protein ★
        - ☑ Voltage-gated potassium channel ★★
        - Other Aeropyrum pernix protein ☆
      - Archaeoglobus fulgidus protein ★★★

87 Records Found — Page 1 of 18 — 5 Per Page

Molecule Name	Synonyms	Database ID	Organism Name
ATP-sensitive inward rectifier potassium channel 1 ★★	Potassium channel, KCNJ1_HUMAN, Potassium channel, inwardly rectifying subfamily J member 1, ATP-regulated potassium channel ROM-K, inwardly rectifying subfamily J member 1, ATP-sensitive inward recti ...more...	UniProt [P48048]	Homo sapiens (human)
ATP-sensitive inward rectifier potassium channel 10 ★★	ATP-dependent inwardly rectifying potassium channel Kir4.1, ATP-sensitive inward rectifier potassium channel 10, inward rectifier K+ channel KIR1.2, Potassium channel, inwardly rectifying subfamily J ...more...	UniProt [P78508]	Homo sapiens (human)
ATP-sensitive inward rectifier potassium channel 11 ★★	Potassium channel, inwardly rectifying subfamily J member 11, Potassium channel, inwardly rectifying subfamily J member 11, Inward rectifier K(+) channel Kir6.2, KCJ11_HUMAN, IKATP, ATP-sensitive inwa ...more...	UniProt [Q14654]	Homo sapiens (human)

Figure 2.30 An example of the protein branch of the Molecule Finder

Proteomes

★★★ For some well-studied species UniProt provides reference proteomes that contain a full set of all proteins expressed by the species. For some bacterial species having inconsistent protein expression, additional proteins have been added to the reference proteome to create metaproteomes. These reference proteomes or metaproteomes are designated by **three stars**.

★★ For other species that have been completely sequenced, UniProt provides complete proteomes. In addition, for some species expressing allergens, formal nomenclature designated by the International Union of Immunological Societies (IUIS) exists to describe these allergens. Complete proteomes that are not considered reference proteomes, or ones that contain formal IUIS allergen nomenclature for a subset of proteins, are designated by **two stars**.

★ For some species, a proteome does not currently exist in UniProt, but GenBank provides a set of proteins representative of the species. These GenBank proteomes are designated by a **single star**.

☆ For species that have no proteome in UniProt or GenBank, and no IUIS nomenclature, UniProt may still contain some records that can be used as parents. This case is designated with an **unfilled star**.

No Star. Species having no proteome in either UniProt or GenBank are designated by **no stars**.

Proteins

Within each species' proteome, individual, "parent" proteins serve to group multiple distinct GenPept sequences. These GenPept entries are the "children" for each proteome protein in the Molecule Tree. This allows users to search IEDB data by selecting the parent protein from the reference proteome, rather than having to select each individual GenPept entry. The "parent" proteins within each proteome also use stars to denote the quality of information provided by each.

★★ UniProt reviewed proteins or proteins having official IUIS allergen nomenclature have **two stars**.

★ UniProt unreviewed proteins or proteins from GenBank have a **single star**.

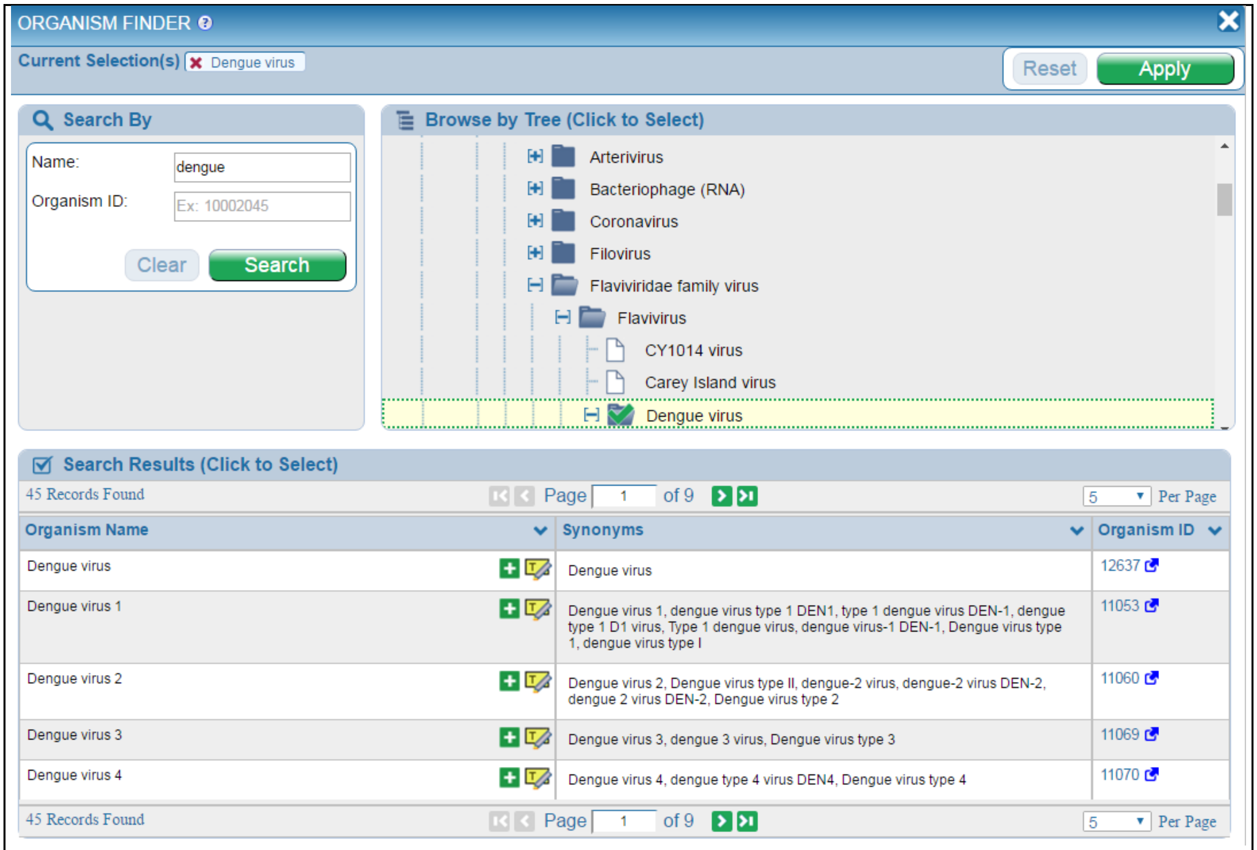
☆ Nodes of the protein branch of the molecule tree containing GenPept and IEDB internal protein accessions having no homology to any protein within a reference proteome are designated with an **unfilled star**.

Organizational nodes, utilized by the Molecule tree to clarify the relationship between groups of similar proteins have **no stars**. An example of these nodes is "Immunoglobulin" used to group all immunoglobulin proteins from a single species.

As one can see in Figure 2.29, a user can search the molecule tree by entering text, including synonyms, in the Name field in the upper lefthand corner of the finder. The user can also specify the source organism of the molecule of interest using the autocomplete field or the organism finder. For example, this can facilitate the specification of a hemagglutinin is a particular strain of Influenza.

2.2.4.5 Organism Finder

The organism finder is used to facilitate the selection of a species or strain from the NCBI Taxonomy Database. The Organism finder allows the user to find species using their name, synonyms, or taxonomy identifier (assigned by NCBI). When the user performs a search, the system will display a tree structure. The user can search for a name or Organism ID in the "Search By" panel in the upper lefthand portion of the Finder. In the example shown in Figure 2.31, a search for "dengue" is performed, which results in 45 items being found. The user can select one or more of the items by clicking on the green "+" icon or clicking a branch in the tree. The user can also choose to highlight the item in the tree, as shown in the figure, by clicking the corresponding yellow highlighter icon. Synonyms for a selection are listed next to the organism name column in the search results table. When the Organism Finder is adjacent to a Host Organism field, only the source organisms for which data exist in the IEDB are displayed in the tree structure.



Name: dengue

Organism ID: Ex: 10002045

45 Records Found — Page 1 of 9 — 5 Per Page

Organism Name	Synonyms	Organism ID
Dengue virus	Dengue virus	12637
Dengue virus 1	Dengue virus 1, dengue virus type 1 DEN1, type 1 dengue virus DEN-1, dengue type 1 D1 virus, Type 1 dengue virus, dengue virus-1 DEN-1, Dengue virus type 1, dengue virus type I	11053
Dengue virus 2	Dengue virus 2, Dengue virus type II, dengue-2 virus, dengue-2 virus DEN-2, dengue 2 virus DEN-2, Dengue virus type 2	11060
Dengue virus 3	Dengue virus 3, dengue 3 virus, Dengue virus type 3	11069
Dengue virus 4	Dengue virus 4, dengue type 4 virus DEN4, Dengue virus type 4	11070

45 Records Found — Page 1 of 9 — 5 Per Page

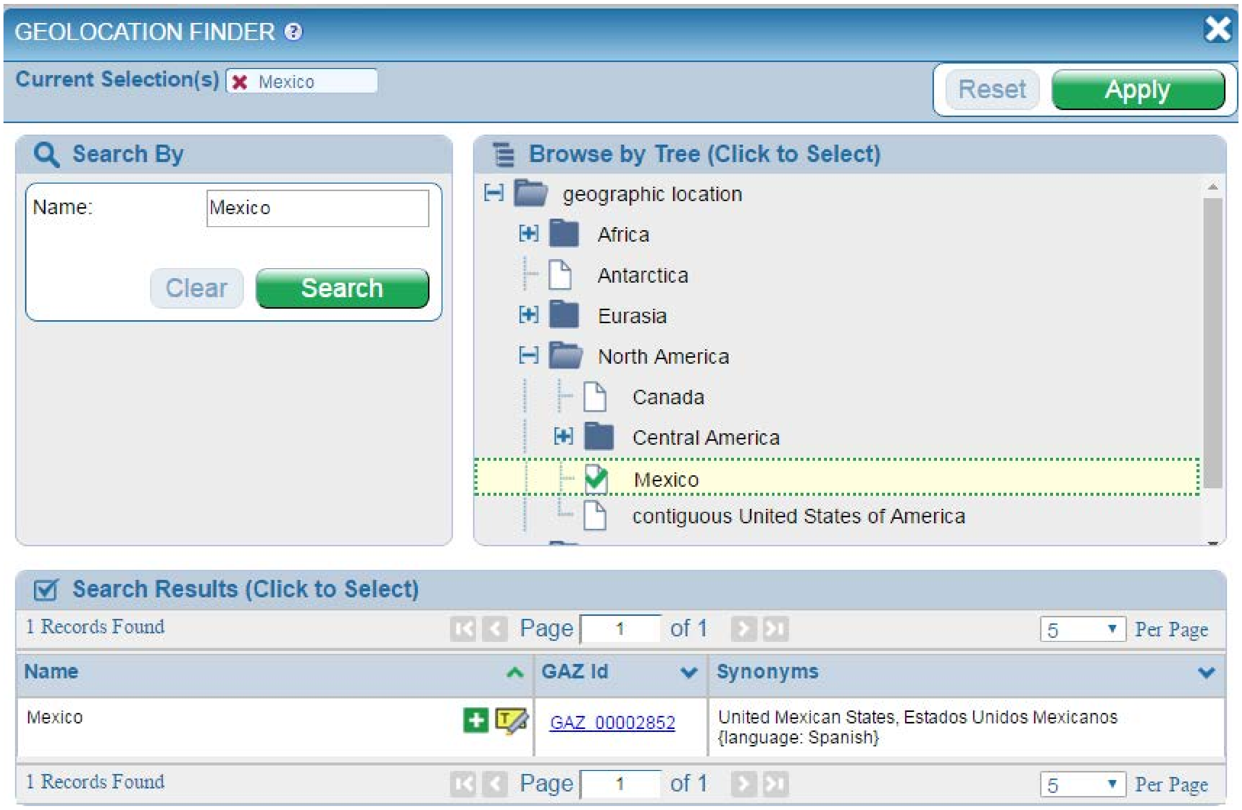
Figure 2.31 Organism Finder showing a search for dengue with dengue highlighted in the tree

2.2.4.6 Geolocation Finder

This feature combines the locations where study subjects were studied and the external ontology known as Gazetteer (http://bioportal.bioontology.org/ontologies/1397). It can be found on the B Cell Search, T Cell Search, and MHC Ligand Specialized search pages under the Host Details subsection within the Immunization section. Gazetteer represents geographic locations in a formal ontological hierarchy. The IEDB's Geographic Location Finder was created by taking the geographic locations mentioned in the manuscripts containing data curated by the IEDB and presenting them in the formal ontological hierarchy of Gazetteer. Thus, every geographic location in the Finder links out to a GAZ ID, where additional information provided by Gazetteer such as definitions and synonyms can be found.

To use the Finder, simply navigate the tree by clicking open the continent of choice to find the country(ies) where study subjects were exposed to the immunogen tested in the immune epitope assays. Alternatively, one may use the "Search By" feature and type free text to search the tree. The Search By feature accepts synonyms as search criteria. Its use is shown in Figure 2.32for the term “Mexico”.

It must be noted that curators only capture geographic location information when authors explicitly state that subjects were recruited in a specific country. The location of authors' affiliations is not used to populate this field.



Current Selection(s): Mexico

Name: Mexico

1 Records Found

Name	GAZ Id	Synonyms
Mexico	GAZ_00002852	United Mexican States, Estados Unidos Mexicanos {language: Spanish}

1 Records Found

Figure 2.32 Geolocation finder. This example shows the tree structure by continent, region, and country. A search was made for Mexico within the tree using the Search By box on the left, which produced one result. This was then highlighted in the tree, as shown. Clicking on "Mexico" in the tree populated the Current Selection field in the upper left corner of the finder.

2.3 Tools

The Analysis Resource pull-down menu at www.iedb.org accesses the IEDB Analysis Resource and has five items – Analysis Resource Overview, T Cell Epitope Prediction, B Cell Epitope Prediction, Epitope Analysis Tools, and Tool Licensing Information. The purpose of the Analysis Resource of the IEDB is to provide computational tools that enhance the value of the IEDB database to the user. Providing access to tools in one centralized location helps make users aware of available solutions to their problems. All of the information contained within the Analysis Resource, including analysis tools and algorithms developed by the IEDB staff, are freely available to the scientific community. For commercial entitites that wish to access the tools in-house, licensing information for the tools can be accessed from the pull-down menu. The Analysis Resource can also be accessed via the rightmost panel on the IEDB home page, although only the most frequently used tools are listed.

The tools provided in the analysis resource fall into two categories – prediction tools and analysis tools. Prediction tools extrapolate beyond data held in the database. They can be used to predict epitopes in protein sequences or predict properties of known epitopes, such as their MHC binding affinity. Analysis tools help extract and interpret data contained in the database.

For prediction tools, it is important to differentiate between the **tool** making predictions, and the **method** used to generate that tool, given a set of training data. For example, the artificial neural network method or approach, when trained on a particular data set, will yield a prediction tool. As the ANN method is trained on different data sets, different corresponding prediction tools will result. In this way, the ANN method can be used to develop an MHC class I prediction tool and a separate MHC class II prediction tool. These tools can be refined as more data are available for training. One benefit of the IEDB is that it allows implementing methods to automatically generate new prediction tools as the database grows.

Prediction tools can be subdivided into categories by what they predict. The current tools fall into the subcategories listed below:

- T cell epitopes – MHC class I and II binding prediction
- T cell epitopes – Processing prediction
- T cell epitopes – Immunogenicity prediction
- B-cell epitope prediction

The AR Labs page (http://tools.iedb.org/main/labs/) was introduced in early 2016. Tools under AR Labs are experimental and are considered to be beta versions, not quite ready for production yet. They are intended for further research, updates and testing. This means they are functional, but the team is still actively developing on improving them and more substantial changes are expected in upcoming releases.

The next subsections will describe each prediction and analytical tool in more detail.

2.3.1 T Cell Epitope Prediction

2.3.1.1 T Cell Epitopes - MHC binding prediction

The Analysis Resource provides tools for predicting peptide binding to MHC class I and II molecules. For class I binding predictions, users can select predictions performed with tools derived from ten different methods – IEDB Recommended, artificial neural network (ANN), stabilized matrix method (SMM), SMM with a peptide:MHC binding energy covariance matrix (SMMPMBEC), Scoring matrices derived from combinatorial peptide libraries (Comblib_Sidney2008), Consensus, NetMHCpan, PickPocket, NetMHCcons, and NetMHCstabpan. The Consensus method is derived from the ANN, SMM, and

CombLib methods. For class II binding predictions, users can select IEDB Recommended, the Combinatorial Library method, the NN_align, the SMM_align method, a method devised by Sturniolo et al. and used in TEPITOPE, NetMHCIIpan, and a consensus method derived from the NN-align, SMM_align, Sturniolo methods, and the Combinatorial Library. Tutorials and example data are available for both the class I and II tools.

A RESTful interface is available for the MHC class I and class II prediction tools. This allows users to perform predictions on the IEDB server in batch mode without having to install any software on their own systems. Additionally, users will always be assured that they are using the latest version of the tools. More information is available in Section 2.3.5. These tools are also available in standalone form on the Download tab and can be downloaded at http://tools.iedb.org/main/download/.

2.3.1.1.1 Peptide Binding to MHC Class I Molecules

Users can select from ten different methods for predicting class I epitopes – ANN, SMM, SMMPMBEC, Comblib_Sidney2008, Consensus, NetMHCpan, NetMHCcons, PickPocket, NetMHCstabpan, and IEDB recommended, which are described further below. A check box can be used to show only frequently occurring alleles. This allows the selection of only those alleles that occur in at least 1% of the human population or allele frequency of 1% or higher. However, un-checking the check-box will allow selection of all the alleles and corresponding peptide lengths for a particular species. Users can also upload an allele file instead of entering allele on the page one at a time.

Artificial Neural Network

Artificial neural networks (ANN) are computer algorithms modeled after the brain. They consist of many simple processing units which are wired together in a communication network. Each unit is a simplified model of a neuron which sends off a new signal if it receives a sufficiently strong input signal from the other units to which it is connected. The strength of these connections can be varied in order for the network to perform a desired pattern of node signal activity, which is learned from a set of input training data.

ANNs have been trained for 81 different Human MHC alleles including HLA-A, -B, -C and -E. Furthermore, predictions for 41 animal (Monkey, Cattle, Pig, and Mouse) alleles are available. The current version of ANN is based on NetMHC 4.0. The method is describe in Nielsen et al. (Protein Science, 2003) and Andreatta and Nielsen (Bionformatics, 2016).

Stabilized Matrix Method (SMM)

The Stabilized Matrix Method (SMM) described by Peters and Sette (BMC Bioinformatics, 2005) can be applied to calculate matrices from quantitative affinity data of peptides binding to MHC molecules. The advantage of this method is that it suppresses the noise present in the training data, caused by the inevitable experimental error as well as the limited number of data points.

Stabilized matrix Method with a Peptide:MHC Binding Energy Covariance matrix (SMMPMBEC)

SMMPMBEC is an improved version of SMM. It is different from SMM in that it addresses sparseness of peptide sequence coverage that is often found in binding data sets by using Peptide:MHC Binding Energy Covariance (PMBEC). The PMBEC matrix was derived from experimentally determined binding affinity measurements using combinatorial peptide libraries. SMMPMBEC is described in Kim et al. BMC Bioinformatics 2009.

Scoring matrices derived from combinatorial peptide libraries (Comblib_Sidney2008)

Comblib_Sidney2008 refers to a set of predictors (i.e. scoring matrices) that were derived from binding affinity measurements of combinatorial peptide libraries against a panel of MHC alleles. This work is described in Sidney et al. (Immunome Res. 2008). This class of predictors is unique in that average binding energy contribution of a given residue at a position is directly measured, without worrying about limited peptide sequence coverage.

Consensus

The Consensus predictor was motivated by an idea that predictions made by consulting "consensus" of individual predictions from multiple predictors may result in improved performance over that of any individual ones. For MHC-I, a work describing an early implementation can be found in Moutaftsi M et al. (Nat Biotech 2006). The methods used for Consensus are ANN, SMM, and CombLib_Sidney2008. The Consensus method uses as many of these three component methods as possible, depending on their applicability for the chosen allele and length.

NetMHCpan

NetMHCpan version 3.0 predicts binding of peptides to any MHC class I molecule of known sequence using artificial neural networks (ANNs). The method is trained on more than 180,000 quantitative binding data covering 172 MHC molecules from human (HLA-A, B, C, E), mouse (H-2), cattle (BoLA), primates (Patr, Mamu, Gogo) and swine (SLA). It has been trained on an extended data set of 8 – 13mer peptides using a method described by Andreatta and Nielsen (Bioinformatics, 2016). Further information about the method can be found in Hoof I et al. (Immunogenetics 2009) and Nielsen and Andreatta (Genome Medicine, 2016).

PickPocket

PickPocket predicts binding of peptides to any known MHC molecule using positiion specific weight matrices. The method is trained on more than 150,000 quantitative binding data covering more than 150 different MHC molecules. Predictions can be made for HLA-A, B, C, E and G alleles, as well as for non-human primates, mouse, cattle, and pig. Version 1.1 has been retrained on extented data set including 10 prevalent HLA-C and 7 prevalent BoLA MHC-I molecules. The matrices of pocket-library are generated using the SMM_pmbec method described in Kim et al. (BMC Bioinformatics, 2009). Predictions can be made for 8 – 12mer peptides. All non-9mer predictions are made using approximations. The prediction values are given in nM IC50 values. The algorithm is described in Zhang et al. (Bioinformatics, 2009).

NetMHCcons

NetMHCcons predicts binding of peptides to any known MHC class I molecule. This is a consensus method for MHC class I predictions integrating three state-of-the-art methods, NetMHC, NetMHCpan, and PickPocket, to give the most accurate predictions. NetMHC is an artificial neural network-based (ANN) allele-specific method which has been trained using 94 MHC class I alleles. Version 3.4 is used as part of NetMHCcons-1.1. NetMHCpan is a pan-specific ANN method trained on more than 115,000 quantitative binding data covering more than 120 different MHC molecules. Version 2.8 is used as part of NetMHCcons-1.1. PickPocket Version 1.1 is described above. NetMHCcons can generate predictions for peptides of 8 – 15 residues in length. The prediction values are given in nM IC50 values. The method is described in detail in Karosiene et al. (Immunogenetics, 2012).

NetMHCstabpan

NetMHCstabpan was introduced in 2016. It predicts binding stability of peptides to any known MHC molecule using artificial neural networks (ANNs). The method is trained on more than 25,000 quantitative stability data covering 75 different HLA molecules. The user can upload full length MHC protein sequences, and have the server predict MHC restricted peptides from any given protein of interest. Predictions can be made for 8-14 mer peptides, although all non 9mer predictions are made using approximations. Most HLA molecules have a strong preference for binding 9mers. The prediction values are given in half life time in hours values and as %-Rank to a set of 200,000 random natural peptides. The method is described in Rasmussen et al. (Journal of Immunology, 2016).

IEDB Recommended
IEDB recommended is the default prediction method selection. It considers all alleles and their corresponding peptide lengths for a particular species. For each allele-length combination, consensus method is used, which includes ANN, SMM, and CombLib. If none of these methods are available for the allele, NetMHCpan is used.

2.3.1.1.2 Peptide Binding to MHC Class II Molecules

Users can select from seven different methods for predicting class II epitopes – IEDB recommended, SMM-align, Sturniolo, Combinatorial Library, Consensus, NN-align, and NetMHCIIpan. By default, the overall best method (IEDB recommended) is selected. However, not all methods can currently make predictions for all alleles, so only the alleles available will be displayed. The seven methods are described further below.

SMM-align
The MHC class II binding groove is open at both ends making the correct alignment of a peptide in the binding groove a crucial part of identifying the core of an MHC class II binding motif. The stabilization matrix alignment method, SMM-align, allows for direct prediction of peptide:MHC binding affinities. The method uses amino terminal peptide flanking residues (PFR) to get a consistent gain in predictive performance by favoring binding registers with a minimum PFR length of two amino acids. The method predicts quantitative peptide:MHC binding affinity values. The method has been trained and evaluated on a data set that covers the nine HLA-DR supertypes suggested and three mouse H2-IA allele. The method is described by Nielsen et al. (BMC Bioinformatics, 2007).

Sturniolo
This matrix-based approach is used in the TEPITOPE class II epitope prediction program. It is described in Sturniolo et al. (Nat. Biotechnol., 1999).

Combinatorial Library
The positional scanning combinatorial libraries approach utilized a pool of random peptide libraries to systematically measure the contribution to MHC binding from each amino acid at each of the nine positions at the binding peptide. Each pool in the library contains 9-mer peptides with one fixed residue at a single position. With each of the 20 naturally occurring residues represented at each position along the 9-mer backbone, the entire library consisted of 180 peptide mixtures. Competitive binding assays were then carried out to determine the IC50 values for each pool. IC50 values for each mixture were standardized as a ratio to the geometric mean IC50 value of the entire set of 180 mixtures, and then normalized at each position so that the value associated with the optimal value at each position corresponds to 1. For each position, an average (geometric) relative binding affinity (ARB) was calculated, and then the ratio of the ARB for the entire library to the ARB for each position was derived. The final results are a set of 9 by 20 scoring matrices which could predict the binding of novel peptides to MHC molecules.

The methodology is the same as that used for the MHC class I combinatorial library tool as described in Sidney et al. Immunome Res. 2008. A description of the ARB method is contained in Bui et al., Immunogenetics, 2005.

Consensus
The consensus method was developed by the IEDB team by exploiting features of three aforementioned methods. The Consenus method uses NN-align, SMM-align, and the combinatorial peptide scanning library. When the scanning library is not available for an allele, the Sturniolo method is used instead. A paper describing the original method was published by Wang et al. (PLoS Comput Biol, 2008), and a subsequent paper was published by Wang et al. (BMC Bioinformatics, 2010). The datasets used in assessing the performance of the NN-align, SMM-align, and Sturniolo methods and in developing the Consensus method, as described in Wang et al. (2010), can be found at http://tools.iedb.org/main/datasets/.

NN-align
NN-align is an artificial neural network-based alignment algorithm for MHC class II peptide binding prediction. It simultaneously identifies the MHC class II binding core and binding affinity. The method is trained using an algorithm that corrects bias in the training data caused by redundancy in binding core representation. Prediction accuracy has been shown to improve significantly when information about the residues flanking the peptide-binding core is taken into account. A 2009 paper in BMC Bioinformatics by Nielsen and Lund describes the method in detail (PMID: 19765293).

NetMHCIIpan
NetMHCIIpan predicts binding of peptides for all three human MHC class II isotypes- HLA-DR, HLA-DP, and HLA-DQ, in addition to mouse H-2-I molecules. A paper describing the method was published by Nielsen et al. in PLoS Computational Biology, 2008, and a paper describing the latest version 3.1 was published by Andreatta et al. in Immunogenetics, 2015.

IEDB Recommended
IEDB recommended is the default prediction method selection. It considers all alleles and their corresponding peptide lengths for a particular species. For each allele-length combination, consensus method is used, as described above. If none of these methods are available for the allele, NetMHCIIpan is used.

2.3.1.2 T Cell Epitopes – MHC I Processing Prediction

2.3.1.2.1 Proteasomal cleavage/TAP transport/MHC class I combined predictor

For the prediction of antigen processing through the MHC class I antigen presentation pathway, we incorporated predictions of proteasomal cleavage and TAP transport similar to the MHCPathway website described in (Tenzer et al, CMLS, 2005). The predictions are based on in vitro experiments characterizing the sequence specificity of proteasomal cleavage and TAP transport. The goal of the prediction is to identify MHC-I ligands (peptides that are naturally processed from their source proteins and presented by MHC class I molecules).

The proteasomal cleavage predictions evaluate how efficiently a peptide or its N-terminally prolonged precursors can be liberated from its source protein. The TAP transport predictions evaluate how efficiently a peptide or its N-terminal prolonged precursors are transported into the ER by TAP (Peters et al., Immunol, 2003). When this information is taken together and combined with MHC class I binding predictions, the tool yields a prediction of the efficiency with which a peptide is presented on the cell surface. The methods available are ANN, SMM, SMMPMBEC, Comblib_Sidney2008, NetMHCpan, PickPocket, NetMHCcons, and IEDB Recommended, which are described in Section 2.3.1.1.1.

A check box can be used to show only frequently occurring alleles. This allows the selection of only those alleles that occur in at least 1% of the human population or allele frequency of 1% or higher. However, un-checking the check-box will allow selection of all the alleles and corresponding peptide lengths for a particular species. Users can also upload an allele file instead of entering allele on the page one at a time.

2.3.1.2.2 Neural network based prediction of proteasomal cleavage sites (NetChop) and T cell epitopes (NetCTL/NetCTLpan)

NetChop produces neural network predictions for cleavage sites of the human proteasome (Kesmir et al., 2002). NetChop takes into account the characteristics of the structurally modified proteasomes found in cells stimulated by gamma-interferon under physiological conditions. The NetChop algorithm was trained on in vitro data and MHC Class I ligand data. The use of this training set, combined with the artificial neural network methodology, makes the prediction of cleavage sites more accurate. NetChop has been trained only on human data, but since the proteasome structure is quite conserved, the algorithm developers believe that the tool is capable of making reliable predictions for at least the other mammalian proteasomes.

NetCTL predicts CTL epitopes in protein sequences integrating prediction of peptide MHC binding, proteasomal C terminal cleavage and TAP transport efficiency. The method is described in detail in Larsen et al. (Eur J Immunol., 2005). NetCTLpan is an update to the original NetCTL server that allows for prediction of CTL epitope with restriction to any MHC molecules of known protein sequence (Stranzl et al., Immunogenetics, 2010). This tool is also available in a standalone form on the Download tab and can be downloaded at http://tools.iedb.org/main/download/.

2.3.1.2.3 MHC-NP – Prediction of peptides naturally processed by the MHC

MHC-NP is a tool for predicting peptides naturally processed by the MHC pathway and was introduced to the Analysis Resource in 2013. MHC-NP employs data obtained from MHC elution experiments in order to assess the probability that a given peptide is naturally processed and binds to a given MHC molecule. This tool was the winner of the 2nd Machine Learning Competition in Immunology, where it yielded state-of-the-art accuracy for the prediction of peptides eluted from human HLA-A*02:01, HLA-B*07:02, HLA-B*35:01, HLA-B*44:03, HLA-B*53:01, HLA-B*57:01 and mouse H2-D(b) and H2-K(b) MHC molecules. The method is described in Giguère et al. (J Immunol Methods, 2013). Because the tool was developed by researchers external to the IEDB team, it is not included in the virtual machine image.

2.3.1.3 T cell class I pMHC immunogenicity predictor

An MHC class I immunogenicity tool was introduced in 2013. T-cells have to recognize peptides presented on MHC molecules to be activated and elicit their effector functions. Several studies have demonstrated that some peptides are more immunogenic than others and therefore more likely to be T-cell epitopes. This tool is based on an analysis of a large set of data describing the immunogenicity of peptides presented on various MHC-I molecules.

Two main conclusions could be drawn from this analysis. First, in line with previous observations, the developers showed that positions P4-6 of a presented peptide are more important for immunogenicity. Second, some amino acids, especially those with large and aromatic side chains, are associated with immunogenicity. This information was combined into a simple model that was used to demonstrate that immunogenicity is, to a certain extent, predictable. This model was validated with data from two independent epitope discovery studies. This model indicated that T-cells are equipped to better recognize viral than human (self) peptides. The method is described in Calis et al. (PLoS Comput Biol., 2013). This tool is also available in a standalone form on the Download tab and can be downloaded at http://tools.iedb.org/main/download/.

2.3.2 B Cell Epitope Prediction

2.3.2.1 Prediction of linear epitopes from protein sequence

Six different tools are provided that predict antibody epitope candidates from amino acid sequences. Five are based on amino acid property scales and a sixth method uses a Hidden Markov Model. Parameters such as hydrophilicity, flexibility, accessibility, and antigenic propensity of polypeptides chains have been correlated with the location of continuous epitopes in a few well-characterized proteins. Based on these observations, amino acid property scales have been developed to predict antigenic determinants. Each scale consists of 20 values assigned to each of the amino acid residues on the basis of their relative propensity to possess the property described by the scale. The following amino acid property scales have been selected and implemented based on their popularity and coverage of different categories.

- Secondary structure - Chou and Fasman beta turn prediction
- Surface exposure - Emini surface accessibility prediction
- Flexibility - Karplus and Schulz flexibility prediction
- Antigenicity - Kolaskar and Tongaonkar antigenicity prediction
- Hydrophobicity/hydrophilicity - Parker hydrophilicity prediction

BepiPred combines the predictions of a hidden Markov model and the propensity scale of Parker et al. (Biochemistry, 1986). It is described in Larsen et al. (Immunome Research, 2006). The linear B cell epitope predictor is also available as a standalone tool. In 2017, BepiPred 2.0 was developed and published (Nucleic Acids Res, 2017), PMID: 28472356. BepiPred-2.0 uses structural predictions, such as surface accessibility and secondary structure as part of the feature space. Using a Random Forest machine-learning algorithm trained on structural epitopes obtained from 160 3D-structures, they improved the performance significantly compared to the prior version and other state-of-the-art prediction tools.

Further information can be found on the Download tab at http://tools.iedb.org/main/download/.

2.3.2.2 DiscoTope - Prediction of epitopes from protein structure

DiscoTope was augmented in 2013 to include include version 2.0 as well as version 1.1. DiscoTope is designed specifically to predict discontinuous epitopes. It uses protein three-dimensional structural data in addition sequence data. The method is based on amino acid statistics, spatial information, and surface accessibility in a compiled data set of discontinuous epitopes determined by X-ray crystallography of antibody/antigen protein complexes. DiscoTope 2.0 works with a novel definition of the spatial neighborhood used to sum propensity scores and half-sphere exposure as a surface measure. The results are more accurate than version 1.1 but involve more complex calculations that increase run times by a factor of approximately 30.

DiscoTope 1.1 is described in Haste Andersen et al. (Protein Sci., 2006), and DiscoTope 2.0 is described in Kringelum et al. (PLoS Comp. Bio, 2012).

2.3.2.3 ElliPro - Epitope prediction based upon structural protrusion

ElliPro predicts linear and discontinuous antibody epitopes based on a protein antigen's 3D structure. ElliPro accepts either a protein structure (preferred) or a protein sequence as an input. If a protein sequence is used, ElliPro will predict its 3D structure by homology modeling. Its use if described in the Tutorial tab of the ElliPro section of the Analysis Resource. The method is described in Julia Ponomarenko et al. (BMC Bioinformatics, 2008). It is also available as a standalone tool. Further information can be found on the Download tab at http://tools.immuneepitope.org/ellipro/download/.

2.3.2.4 Prediction of ImmunoGlobulin Structure (PIGS)

PIGS is a web server for the automatic modeling of immunoglobulin variable domains based on the canonical structure method. It takes heavy and light chain sequences as input, automatically selects the best template, and provides a complete three-dimensional model of the target antibody as an output that can be downloaded or displayed on-line. PIGS was developed by Paolo Marcatili and Anna Tramontano at the Biocomputing Unit of Sapienza University in Rome. A detailed description of PIGS can be found in Marcatili et al. (Bioinformatics, 2008).

In 2017, PIGS was replaced by LYRA.

2.3.2.5 LYmphocyte Receptor Automated modeling (LYRA)

The LYRA web server implements a complete and automated method for building of B- and T-cell receptor structural models starting from their amino acid sequence alone. The webserver is freely available and easy to use for non-specialists. Upon submission, LYRA automatically generates alignments using ad hoc profiles, predicts the structural class of each hypervariable loop, selects the best templates in an automatic fashion, and provides within minutes a complete 3D model that can be downloaded or inspected online. Experienced users can manually select or exclude template structures according to case specific information. LYRA is based on the canonical structure method, that in the last 30 years has been successfully used to generate antibody models of high accuracy, and in our benchmarks this approach proves to achieve similarly good results on TCR modeling, with a benchmarked average RMSD accuracy of 1.29 and 1.48 Å for B- and T-cell receptors, respectively.

2.3.2.6 Methods for modeling and docking of antibody and protein 3D structures

This web page provides information on methods for modeling and docking of antibody and protein 3D structures. The methods are available as web servers and are hosted outside the IEDB except one method, LYRA, described above. One of the approaches at B-cell epitope prediction involves antibody-antigen docking, or 3D modeling of an antibody-antigen complex, for known 3D structures of both antibody and antigen. When the structures of either antibody or protein or both are unknown (that is, not available in PDB) but sequences are known, the user can attempt to obtain the 3D structural models of the antibody and the antigen, following the chart displayed on the web page and using the described web servers. Links are provided to these servers for the user’s convenience.

2.3.3 Epitope Analysis Tools

2.3.3.1 Population coverage

T cells recognize a complex between a specific MHC type and a particular pathogen-derived epitope and thus a given epitope will elicit a response only in individuals that express an MHC molecule capable of binding that particular epitope. MHC molecules are extremely polymorphic (over a thousand different variants are known in humans). Therefore, selecting multiple peptides with different MHC binding specificities will afford increased coverage of the patient population targeted as vaccine recipients. The issue of population coverage in relation to MHC polymorphism is further complicated by the fact that different MHC types are expressed at dramatically different frequencies in different ethnicities. Thus, without careful consideration, a vaccine with ethnically biased population coverage could result. To address this issue, the actual/predicted binding capacity of potential epitopes to as many different MHC molecules possible (and when available, also restriction data of T cell responses recognizing the epitope) can be used to project the population coverage in different ethnicities of different vaccine candidates or epitope sets. Accordingly, epitope-based vaccines or diagnostics can be designed to maximize population coverage, while minimizing complexity (that is, the number of different epitopes included in the diagnostic or vaccine), and also minimizing the variability of coverage obtained or projected in different ethnic groups.

An important consideration in the process of epitope selection is that the patient population coverage afforded by a given set is not simply corresponding to the sum of the coverage of its individual components. Thus, to calculate the coverage afforded by a given mixture of epitopes, a more comprehensive approach and a suitable algorithm has been developed for this specific purpose (Bui et al. BMC Bioinformatics 2006). This method calculates the fraction of individuals predicted to respond to a given epitope set on the basis of HLA genotypic frequencies, assuming non-linkage disequilibrium between HLA loci, and on the basis of MHC binding and/or T cell restriction data. The algorithm is briefly explained here. First, genotypic frequencies of various MHC are tabulated. Each time a peptide binds to a given MHC, a “hit” is recorded for that MHC. The process is repeated for all peptides. Then the hits for MHC are tallied. Next, the frequency of each possible diploid MHC combination (phenotype) is calculated. For *n* MHC types, this corresponds to an *n* x *n* tabulation of the frequency at which each specific pair of MHCs will be found in the population from which the MHC frequencies are derived. A similar table is generated to contain the number of hits per each of the MHC combinations by adding the number of hits associated with each of the two alleles of MHC in the combination (a simple exception is the case of homozygous combinations, where the number of hits is simply the number of hits of the given MHC). From these two tables, a frequency distribution is assembled, tabulating the genotypic frequency of all MHC combinations associated with a certain number of hits. The result of the analysis is displayed as a frequency distribution histogram and a cumulative frequency plot.

HLA allele genotypic frequencies were obtained from Allele Frequency Net Database (http://www.allelefrequencies.net/). At present, Allele Frequency Net Database (Gonzalez-Galarza FF et al., Nucleic Acids Res. 2015) provides allele frequencies for 115 countries and 20 different ethnicities grouped into 16 different geographical areas. In addition, the program also accepts custom populations with allele frequencies defined by users. Multiple population coverages can be simultaneously calculated and an average population coverage is generated. Since MHC class I and MHC class II restricted T cell epitopes elicit immune responses from two different T cell populations (CTL and HTL, respectively), the program provides three calculation options to accommodate different coverage modes: (1) class I separate, (2) class II separate, and (3) class I and class II combined. For each population coverage, the tool computes the following: (1) projected population coverage, (2) average number of epitope hits / HLA combinations recognized by the population, and (3) minimum number of epitope hits / HLA combinations recognized by 90% of the population (PC90).

2.3.3.2 Epitope conservancy

In a diagnostic or epitope-based vaccine setting, focusing on conserved epitopes allows for targeting responses around pathogen variability, whether it exists prior to infection, or develops in the natural course of disease. The use of conserved epitopes would be expected to focus the immune response on sequences crucial for retaining biological function of the pathogen proteins, and thus with intrinsically lower variability, even under immune pressure. The epitope conservancy analysis tools implemented here aims to address the issue of variability (or conservation) of epitopes, and to assist in the selection of epitopes with the desired pattern of conservation. The algorithm has been implemented to calculate the degree of conservancy of an epitope within a given protein sequence set at different degree of identities. The degree of conservation is defined as the number of protein sequences that contain the epitope at a given identity level, divided by the total number of protein sequences found in the dataset analyzed (Bui et al. BMC Bioinformatics 2007).

A new feature was added in the past year. User can now indicate whether they want duplicated protein sequences removed from the results set by checking a box in the “Specify calculation options” section of the input page. Previously redundant results were removed. For users wanting to study different populations, keeping redundant sequences can be very informative.

2.3.3.3 Epitope Cluster Analysis

The Epitope Cluster Analysis tool (Kim et al., Nucleic Acids Res. 2012) groups epitopes into clusters based on sequence identity. A cluster is defined as a group of sequences that has a sequence similarity greater than the minimum sequence identity threshold specified. Epitope sequences can be either directly entered in the text area or uploaded from a file. Two acceptable sequence formats are PLAIN and FASTA. The user can select the sequence identity threshold at which they want to calculate epitope clusters. Clusters are displayed in a table format where clusters are indicated by table rows which have the same color. All calculated cluster results can be saved to a file by clicking on the "Download data to file" button.

2.3.3.4 Computational Methods for Mapping Mimotopes to Protein Antigens

A web page devised by Dr. Julia Ponomarenko was added to the Analysis Tools section in 2014 that provides guidelines for mapping mimotopes to protein antigens. Mimotopes are molecules, often peptides, which are recognized by antibodies or T cells that were primed to recognize a different epitope. For antibody epitope mapping, peptide mimotopes can be selected from a combinatorial library (usually peptides from a specific protein antigen) on binding to a specific monoclonal antibody with high affinity. They are commonly obtained using phage display. Experimental data on mimotopes can be found in the IEDB, MimoDB (http://immunet.cn/mimodb/index.html), and journal publications. Mimotopes can mimic essential features of genuine epitopes and therefore their mapping to the antigen is a logical and essential step of the mimotope analysis. This web page provides information on available methods for mimotope mapping, how to search the IEDB for mimotopes, and an example of a mimotope dataset and the results of its mapping, using the available web servers hosted outside the IEDB.

Methods available as web servers and operational as of July 2014 (they all require the user submitting an antigen protein 3D structure, providing either PDB ID of the structure or the pdb file) are as follows:

- **MIMOX** (http://immunet.cn/mimox/)
- **Pepitope server** (http://pepitope.tau.ac.il/) provides three algorithms: Mapitope, PepSurf, or combined
- **EpiSearch** (http://curie.utmb.edu/episearch.html)

The web page also lists other published methods that are unavailable as web servers. They include the following:

- **PepMapper** (http://www.ncbi.nlm.nih.gov/pubmed/22701536) (2012) - provided URL didn't respond
- **MimoPro** (http://www.ncbi.nlm.nih.gov/pubmed/21609501) (2011) - provided URL didn't respond
- **Pep-3D-Search** (http://www.ncbi.nlm.nih.gov/pubmed/19087303) (2008) - available for download at http://kyc.nenu.edu.cn/Pep3DSearch/
- **MEPS** (http://www.ncbi.nlm.nih.gov/pubmed/17430573) (2007)
- **MIMOP** (http://www.ncbi.nlm.nih.gov/pubmed/16434442) (2006)
- **3D-Epitope-Explorer (3DEX)** (http://www.ncbi.nlm.nih.gov/pubmed/15834923) (2005) - available for download at http://www.schreiber-abc.com/3dex/
- **Enshell-Seijffers et al.** (http://www.ncbi.nlm.nih.gov/pubmed/14596802) (2003)
- **FINDMAP** (http://www.ncbi.nlm.nih.gov/pubmed/12935344) (2003)
- **SiteLight** (http://www.ncbi.nlm.nih.gov/pubmed/12824481) (2003)

The webpage also contains instructions on how to search for mimotopes in the IEDB.

2.3.4 IEDB Analysis Resource Labs

The AR Labs page (http://tools.iedb.org/main/labs/) was introduced in early 2016. Tools under AR Labs are experimental and are considered to be beta versions, not quite ready for production yet. They are intended for further research, updates and testing. This means they are functional, but the team is still actively developing on improving them and more substantial changes are expected in upcoming releases. Therefore users are asked not to expect the same level of stability for these tools as for other tools in the IEDB analysis resource. Users are welcome to send bug reports and suggestions for improvements for these tools via http://help.iedb.org/hc/en-us/requests.

Two tools are currently available on the Labs web page:

RATE (Restrictor Analysis Tool for Epitopes): is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles. A description of the tool can be found in Paul et al. (Journal of Immunology, 2015).
In 2017, RATE was validated using experimentally defined restriction data from a set of 191 tuberculosis-derived epitopes and 63 healthy individuals with MTB infection from the Western Cape Region of South Africa. Additionally, the parameters used by the RATE tool to infer restriction were optimized. New HLA restrictions were identified using the optimized RATE tool. A description of this study can be found in Paul et al. (BMC Immunol, 2017).

TepiTool: The TepiTool provides prediction of peptides binding to MHC class I and class II molecules. The tool is designed as a wizard with six steps. Each field (except sequences and alleles) is filled with default recommended settings for prediction and selection of optimum peptides. The input parameters can be adjusted as per the user’s specific needs. Users can go back to previous steps to change your selection before submission of the job. Once the user submits the job (at the end of step-6), they will not be able to make any more changes and will have to start the prediction all over again with updated input parameters. A description of the tool can be found in Paul et al. (Current Protocols in Immunology, 2016).

2.3.5 Benchmark references and data sets

The “Datasets” tab contains data sets and references related to benchmarking results of the IEDB’s epitope prediction tools. There are three accordion sliders that can be expanded to reveal details. The three are for MHC class I binding prediction, MHC class II binding prediction, and B cell epitope prediction. In each case, the journal article title, authors, journal name, and year are listed along with a description of the data set, the date of its generation, details on the data set generation, the data format, and where the data set is available.

For the MHC class I binding predictions, the references are:

- Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M. Automated benchmarking of peptide-MHC class I binding predictions. Bioinformatics. 2015 Jul 1;31(13):2174-81. doi: 10.1093/bioinformatics/btv123. Epub 2015 Feb 25. PubMed PMID: 25717196; PubMed Central PMCID: PMC4481849
- Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B. Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. BMC Bioinformatics. 2014 Jul 14;15:241. doi: 10.1186/1471-2105-15-241. PubMed PMID: 25017736; PubMed Central PMCID: PMC4111843
- Kim Y, Sidney J, Pinilla C, Sette A, Peters B. Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior. BMC Bioinformatics. 2009 Nov 30;10:394. PubMed PMID: 19948066.
- Peters B, Bui HH, Frankild S, Nielson M, Lundegaard C, Kostem E, Basch D, Lamberth K, Harndahl M, Fleri W, Wilson SS, Sidney J, Lund O, Buus S, Sette A., A community resource benchmarking predictions of peptide binding to MHC-I molecules, PLoS Comput Biol. 2006 Jun 9;2(6):e65. Epub 2006 Jun 9. PMID: 16789818

For the MHC class II binding predictions, the references are:

- Wang P, Sidney J, Kim Y, Sette A, Lund O, Nielsen M, Peters B. Peptide binding predictions for HLA DR, DP and DQ molecules. BMC Bioinformatics. 2010 Nov 22;11:568. PubMed PMID: 21092157; PubMed Central PMCID: PMC2998531.
- Wang, P., J. Sidney, C. Dow, B. Mothe, A. Sette, B. Peters. (2008). "A Systematic Assessment of MHC Class II Peptide Binding Predictions and Evaluation of a Consensus Approach." PLoS Computational Biology 4(4). PMID: 18389056

For the B cell predictions, the references are:

- Kringelum JV, Nielsen M, Padkjær SB, Lund O. Structural analysis of B-cell epitopes in antibody:protein complexes. Mol Immunol. 2013 Jan;53(1-2):24-34. doi: 10.1016/j.molimm.2012.06.001. Epub 2012 Jul 10. PubMed PMID: 22784991; PubMed Central PMCID: PMC3461403
- Kringelum JV, Lundegaard C, Lund O, Nielsen M. Reliable B cell epitope predictions: impacts of method development and improved benchmarking. PLoS Comput Biol. 2012;8(12):e1002829. doi: 10.1371/journal.pcbi.1002829. Epub 2012 Dec 27. PubMed PMID: 23300419; PubMed Central PMCID: PMC3531324.
- Rubinstein ND, Mayrose I, Martz E, Pupko T. Epitopia: a web-server for predicting B-cell epitopes. BMC Bioinformatics. 2009 Sep 14;10:287. doi: 10.1186/1471-2105-10-287. PubMed PMID: 19751513; PubMed Central PMCID: PMC2751785.
- Liang S, Zheng D, Standley DM, Yao B, Zacharias M, Zhang C. EPSVR and EPMeta: prediction of antigenic epitopes using support vector regression and multiple server results. BMC Bioinformatics. 2010 Jul 16;11:381. doi: 10.1186/1471-2105-11-381. PubMed PMID: 20637083; PubMed Central PMCID: PMC2910724.
- Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. BMC Struct Biol. 2007 Oct 2;7(1):64. PMID: 17910770

2.3.6 Other Ways to Access Tools

There are several ways that users can access many of the tools in the Analysis Resource in addition to using the tools directly on the Analysis Resource website. On the Analysis Resource home page (http://tools.iedb.org), there are tabs for Tools-API and Download. The former takes the user to information about the RESTful interface. The RESTful (Representational State Transfer) web service is available for the MHC class I and II binding predictions, MHC class I processing predictions, and MHC-NP for T cell epitopes, and linear epitope prediction methods for B cells. The service sends POST request to the tools server, and relies on user supplied parameters. The Tools-API web page contains examples for accessing the service using the 'curl' program, although any program that sends POST requests to the server will work just as well (including a web browser). This feature allows users to perform predictions on the IEDB server in batch mode without having to install any software on their own systems. Additionally, users will always be assured that they are using the latest version of the tools.

The Download tab takes the user to the IEDB Tools Download web page. For users from non-commercial organizations with batch processing needs, the MHC class I and II binding prediction tools, linear B cell epitope prediction tool, ElliPro, the epitope cluster analysis tool, the MHC class I immunogencity tool, and proteasomal cleavage prediction tool (added in 2016) are available as standalone scripts for download. These command line tools are kept in sync with the web tools and should therefore produce the same results as clicking through the web interface. They are freely available to non-profit/academic users through an open source license.

For commercial users that would like to run the analysis resource locally, licenses for a virtual machine image file or standalone downloads are available upon request for a modest annual fee. For the virtual machine, all tools are included except MHC-NP, and PIGS, which were not developed by the IEDB team. The virtual machine image is kept in sync with the current version of the IEDB Analysis Resource and is updated approximately every six months. Commercial licenses are also available. Requests for either license can be sent to license@iedb.org.

2.4 Help Overview

The Help pull-down menu contains items that aid the user to understand and utilize the features of the website. Users can access relevant documentation, request help, and provide feedback.

2.4.1 Support

The IEDB Solutions Center is the primary resource for information on using the website's features. The user can submit help requests, check on the status of requests, browse and search the knowledge base and forums, and link to help documentation, such as the Curation Manual. In order to submit a help request via the Solutions Center, users must provide an email address, a subject line, and a description of the issue password. The Solutions Center can also be accessed by a link at the bottom of each web page.

The Solutions Center has extensive documentation organized in forums that address a variety of topics, including the epitope analysis and prediction tools, submitting data to the IEDB, querying the database, and general announcements and updates. The Solutions Center is also the repository for the Annual Compendia, the list of meta-analyses and other papers published by the IEDB team, release notes for the main website and the Analysis Resource, and the News and Noteworthy forum. In addition, written and video tutorials, including the presentations from the 2015 IEDB User Workshop can be found there.

2.4.2 Help Request

Users can submit help requests in two ways. At the bottom of most pages is a "Help request" link. This will initiate a submission to the IEDB Solutions Center. The second method also utilizes the IEDB Solutions Center. The top menu bar on the IEDB Solutions Center web page has a "Help Request" link. Selecting this link brings the user to a "Submit a request" web page. The user must fill in their email address, the subject line, and a description of the help request. All help requests are forwarded to the same help desk.

Help requests should consist of problems that users have with the application, such as a certain function of the system not working. Questions on how to use features of the application should be covered in the online help available in the Solutions Center. After submitting a help request, a confirmation e-mail will be sent to the user's e-mail address, which will include the help request number. When the help request issue has been resolved, an e-mail will be sent to notify the user that the help request has been satisfied.

Help requests are generally responded to within one business day and solved within two business days. Requests that are actually bug reports by users are answered initially to inform the requestor that their issue is being forwarded to the appropriate developers and they will be notified when a fix is released. Requests involving the curation or re-curation of articles will typically take longer to resolve.

2.4.3 Provide Feedback

All users are able to submit feedback, which will transmit an email message to the IEDB team. Feedback is intended for questions, input, and suggestions, such as new features they would like to see added in the future. Feedback helps the IEDB team update the system to provide users with the best possible experience. If users need help using the system or handling an unexpected result, a Help Request is more appropriate. The feedback feature can be accessed with the Support pull-down menu and the "Provide Feedback" at the bottom of each web page. Both initiate a submission to the IEDB Solutions Center.

2.4.4 Video Tutorials

There is a link to the IEDB video tutorials under the Help menu at the top of each web page. This link takes the user to the "How-to Videos" article in the Solutions Center in the Tutorials and Reference Materials folder. Most of the videos are edited versions of live presentations made at the 2015 IEDB User Workshop held in October 2015 at the NIAID facility in Rockville, Maryland. The videos are listed in Table 2.1. An overview of the resource and information regarding the data structure and curation are presented first. The next category addresses the query and reporting features. Videos for all the tools in the Analysis Resource are listed next. Videos for the legacy website have been removed because the legacy site has been retired and can no longer be accessed by users.

Category	**Topic**
IEDB Overview, data curation, and data structure	Overview of the IEDB resource (19 minutes)
	IEDB data structure and curation (17 minutes)
Data query and reporting features	Finding Data Using the Home Page Search (29 minutes)
	Finding Data Using the Specialized Searches (12 minutes)
	The Immunome Browser (26 minutes)
	Home page search examples (20 minutes)
	Specialized search examples (20 minutes)
	Four infectious disease related queries (23 minutes)
	Two autoimmune disease relted queries (15 minutes)
	Finding T and B cell epitopes in a given protein of interest (5 minutes)
	Example allergy query (3 minutes)
	IEDB and cancer epitopes (2 minutes)
	Queries and IEDB features relevant to vaccine development (2 minutes)
	Help and support features; database export options (25 minutes)
IEDB Analysis Resource - Epitope Prediction and Analysis Tools, including epitope visualization	Introduction to the Analysis Resource (29 minutes)
	MHC class I binding prediction tools (41 minutes)
	MHC class I processing and immunogenicity tools (27 minutes)
	MHC class II binding prediction tools and API, including TepTool (62 minutes)
	TepiTool – a wizard interface for predicting MHC class I and II binding (20 minutes)
	B cell epitope prediction tools (67 minutes)
	Homology mapping tool and Epitope Viewer (23 minutes)
	B Cell Epitope Modeling and Docking, including Prediction of ImmunoGlobulin Structure (PIGS) (10 minutes)
	Analysis Tools (9 minutes)
	Tool downloads, epitope prediction references and benchmarks, and how to contribute tools to the IEDB (4 minutes)

Table 2.1 Available IEDB video tutorials

2.5 More IEDB

The "More IEDB" pull-down menu contains links to other relevant information that may be of interest to users. Its component links are described below.

2.5.1 Database Export

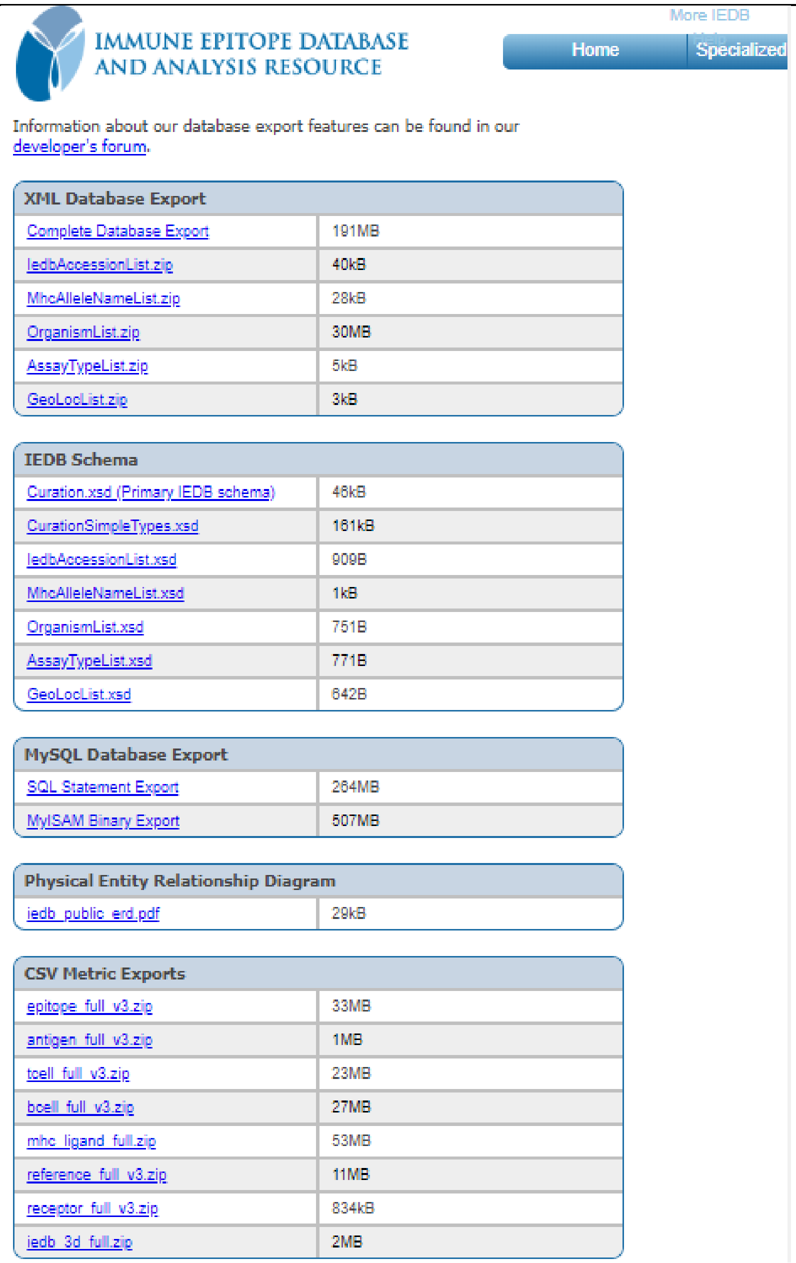
The contents of the Immune Epitope Database are exported weekly to files in XML format. The database export page (Figure 2.32) contains a complete database export in XML format along with exports of the various records that are referenced in the complete database export. The complete dataset export is provided as a ZIP archive (iedb_export.zip) containing one XML file for each reference contained in the database. The export also contains ZIP archives of XML files that provide users with the full record for the various identifiers that are referenced in the full database export, such as the IEDB source organism accession identifier list, the MHC allele name list, and the organism list. The supporting XML files only contain full records when the record is not otherwise available from the original source.

The database export page also provides the relevant XML Schema Definition (XSD) files for each of the XML files provided. The XSD file(s) for a particular XML file are located in the IEDB Schema box in the export table. In the case of the complete database export, multiple schemas are provided, with the primary schema being listed first, followed by any supporting schemas.

In addition to the XML export, the contents of the IEDB are exported weekly as a MySQL Structure Query Language (SQL) database. The database export page contains the complete database export in two formats, a single SQL script (iedb_public.sql.gz), and a TAR archive of MyISAM binary tables (iedb_public.tar.gz). Both export formats are generated from a 5.5.52-MariaDB database server. The database export page also provides an entity-relationship diagram (ERD) for the MySQL database.

Archives of the data as they appeared in IEDB 1.0, 2.0, 2.1, and 2.3 are available by clicking on the *Archived Versions*. For each version, there is a compressed file that contains an XML for each reference. The corresponding XSD files are also available for download.

Select compilations of data are available for download from the Database Export web page in CSV format in the section titled CSV Metric Exports. Users can download these files to conveniently obtain all the information in the IEDB for specific categories. Files are available for all epitopes, antigens, T cell assays, B cell assays, MHC ligand assays, and references. In addition, an export for antibody and T cell receptors was added in 2016. In addition to the files available on the Database Export web page, comma separated values (CSV) file exports are available on-demand from all list pages and list tabs throughout the site.



Information about our database export features can be found in our developer's forum.

XML Database Export	
Complete Database Export	191MB
IedbAccessionList.zip	40kB
MhcAlleleNameList.zip	28kB
OrganismList.zip	30MB
AssayTypeList.zip	5kB
GeoLocList.zip	3kB

IEDB Schema	
Curation.xsd (Primary IEDB schema)	46kB
CurationSimpleTypes.xsd	161kB
IedbAccessionList.xsd	909B
MhcAlleleNameList.xsd	1kB
OrganismList.xsd	751B
AssayTypeList.xsd	771B
GeoLocList.xsd	642B

MySQL Database Export	
SQL Statement Export	264MB
MyISAM Binary Export	507MB

Physical Entity Relationship Diagram	
iedb_public_erd.pdf	29kB

CSV Metric Exports	
epitope_full_v3.zip	33MB
antigen_full_v3.zip	1MB
tcell_full_v3.zip	23MB
bcell_full_v3.zip	27MB
mhc_ligand_full.zip	53MB
reference_full_v3.zip	11MB
receptor_full_v3.zip	834kB
iedb_3d_full.zip	2MB

Figure 2.33 IEDB Database Export web page

2.5.2 Meta-Analyses

The IEDB team has conducted a variety of analyses that examine data in the IEDB for several disease conditions and have been published in scientific journals. Over 20 papers have been published covering topics ranging from allergies, diabetes, and multiple sclerosis, to influenza, tuberculosis, malaria. When a user selects this menu item, they are directed to the Meta-analyses folder in the Knowledgebase and Forums section of the IEDB Solutions Center. The forum is updated as new meta-analyses are published. Users who subscribe to the folder will be automatically informed when content is added.

2.5.3 Citing the IEDB

Data and tools within the IEDB are presented as a public resource. Users are requested to consider citing the IEDB when they present information obtained from the IEDB or use tools contained in the Analysis

Resource. It is expected that the authors of an entry as well as the IEDB are properly cited whenever their work is referred to:

1. The IEDB website should be cited using the URL: http://www.iedb.org

2. The journal reference for the IEDB was updated after the release of IEDB 3.0. The IEDB should be cited as:

   Vita R, Overton JA, Greenbaum JA, Ponomarenko J, Clark JD, Cantrell JR, Wheeler DK, Gabbard JL, Hix D, Sette A, Peters B. The immune epitope database (IEDB) 3.0. Nucleic Acids Res. 2014 Oct 9. pii: gku938. [Epub ahead of print] PubMed PMID: 25300482.

2.5.4 Release Notes

Release notes are provided whenever a new release of the main website or the Analysis Resource is deployed to the public. When a user selects this menu item, they are directed to the Release Notes folder in the Knowledgebase and Forums section of the IEDB Solutions Center. The forum is updated as new releases are deployed. Users who subscribe to the folder will be automatically informed when content is added.

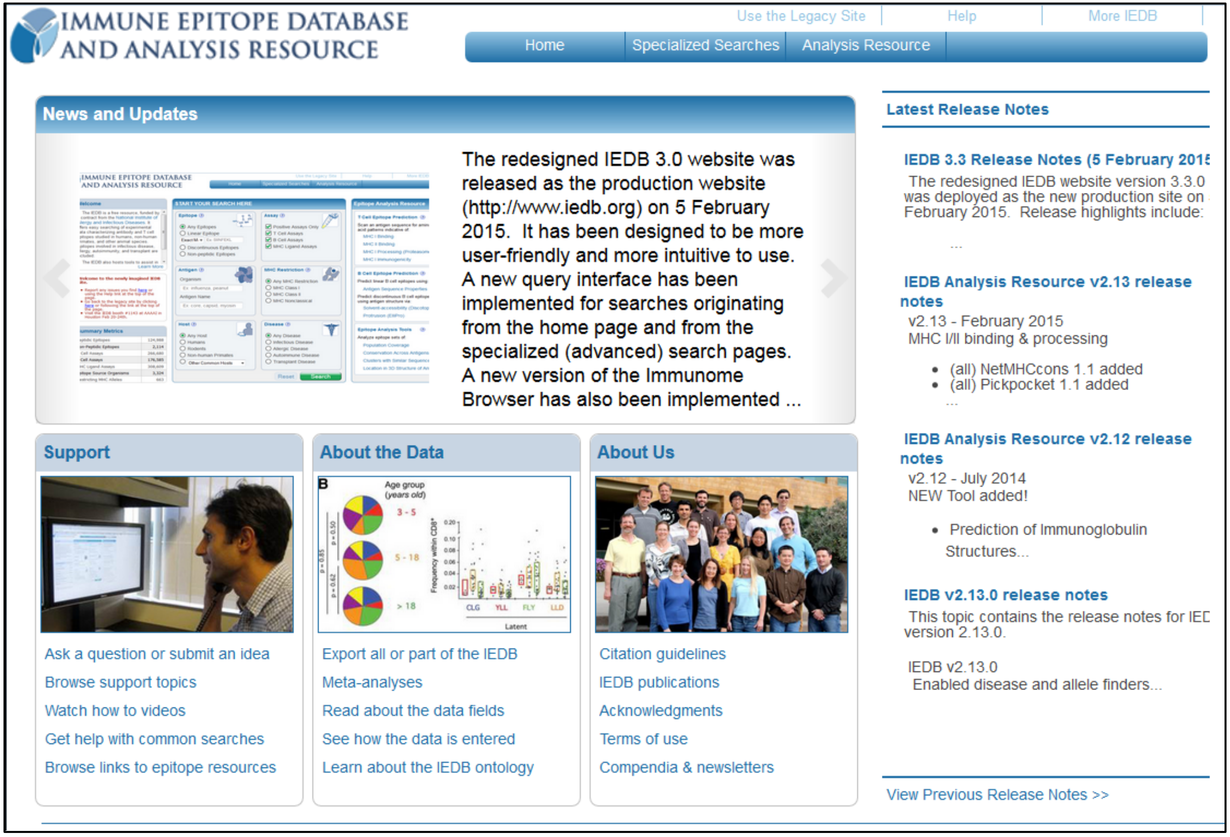
2.5.5 Links to External Sources

The IEDB system provides a list of links to external resources solely for the convenience of Immune Epitope Database visitors. The Immune Epitope Database has no interest in, responsibility for, or control over the linked-site. The Immune Epitope Database makes no promises or warranties of any kind, express or implied, including those of fitness for any particular purpose, as to the content of the linked-site. To view the links available, select the Links menu item. The hyperlinks on the links page are grouped by category:

- Public Databases, Prediction Algorithms, and Other Tools
- Antibody Related Links
- Bioinformatics Resource Centers
- MHC and TCR Related Links
- Protein Related Links
- Laboratory Resources
- Biodefense Resources

2.6 Learn More

The Learn More web page can be accessed from the link at the bottom of the Welcome box in the upper left-hand corner of the IEDB home page. The Learn More page has five major sections, as seen in Figure 2.33. The upper left section has a carousel of content from the New and Noteworthy forum in the Solutions Center. A graphic is usually included in the forum article that is displayed in the left-hand portion of the section. Below this section are three other sections titled Support, About the Data, and About Us. The Support section has links to submit a help request or feedback. The right-hand panel of the page lists the release notes for the most recent versions of the main website and the Analysis Resource.



The redesigned IEDB 3.0 website was released as the production website (http://www.iedb.org) on 5 February 2015. It has been designed to be more user-friendly and more intuitive to use. A new query interface has been implemented for searches originating from the home page and from the specialized (advanced) search pages. A new version of the Immunome Browser has also been implemented ...

IEDB 3.3 Release Notes (5 February 201

The redesigned IEDB website version 3.3.0 was deployed as the new production site on February 2015. Release highlights include:

...

IEDB Analysis Resource v2.13 release notes

v2.13 - February 2015
MHC I/II binding & processing

- (all) NetMHCcons 1.1 added
- (all) Pickpocket 1.1 added

...

IEDB Analysis Resource v2.12 release notes

v2.12 - July 2014
NEW Tool added!

- Prediction of Immunoglobulin Structures...

IEDB v2.13.0 release notes

This topic contains the release notes for IED version 2.13.0.

IEDB v2.13.0
Enabled disease and allele finders...

Figure 2.34 The Learn More page, accessed from the Welcome message in the upper left corner of the IEDB home page

2.6.1 Support

Each link is briefly described below.

Ask a question or submit an idea

This link allows the user to submit a help request or suggestion via the IEDB Solutions Center. The user must specify their email address, the subject of their request, and description of the problem or suggestion. Users can also attach relevant files.

Browse support topics

The IEDB Solutions Center home page has a variety of user help, including several resources for getting started with the IEDB, recent Release Notes, and timely articles.

Watch how to videos

Videos describing the use of the main website and the Analysis Resource are located in the Solutions Center at http://help.iedb.org/entries/140865-How-To-Videos. See Section 2.4.4 for further details.

Get help with common searches

There is a category in the Solutions Center that contains a list of common queries. These queries have been designed to parallel the IEDB meta-analysis efforts. Meta-analyses are performed at intervals to query the database for all data relating to subjects of interest (ex. Influenza, Malaria, Tuberculosis). These queries represent a simplified version of such analysis.

Browse links to epitope resources

The IEDB system provides a list of links to external resources solely for the convenience of Immune Epitope Database visitors as described in Section 2.5.5.

2.6.2 About the Data

Each link is briefly described below.

Export all or part of the IEDB

Clicking on this link will bring the user to the Database Export page that is described in Section 2.5.1.

Meta-analyses

The meta-analyses conducted by the IEDB team are described in Section 2.5.2.

Read about the data fields

This link gives the user access to a subset of the Curation Manual hosted in a Wiki that describes and defines the various data fields. Using the Find function of their web browser, users can search for the data field name of interest in order to gain a fuller understanding of the field definition and the possible values.

See how the data is entered

Users can access the full IEDB Curation Manual. The rules for curating all data fields are described in this Wiki.

Learn about the IEDB ontology

Selecting IEDB Ontology takes the user to http://ontology.iedb.org, the home page for the Ontology of Immune Epitopes (ONTIE). The IEDB ontology is available to download in a format that can be viewed with the Protégé OWL editor. The file ONTIE.owl contains the classes and relations used in the IEDB export. IEDB-export.owl is the ONTIE-annotated export of the IEDB T cell epitope data. Smaller versions of the file are available for download. The ONTIE home page also lists related ontologies that are used in constructing ONTIE.

2.6.3 About Us

Citation Guidelines

This link brings the user to the "Citing the IEDB" web page described in Section 2.5.3.

IEDB Publications

A list of publications relevant to the IEDB can be found on the Publications page. They have been grouped into four categories – General IEDB, Epitope Meta-analyses, Analysis Resource, and Curation. This list is updated with each new release of the main website. A list of IEDB related publications can also be found in the Publications folder in the IEDB Solutions Center at http://help.iedb.org/hc/en-us/sections/114094004371-Publications.

Acknowledgements

A host of talented individuals have worked hard to make the Immune Epitope Database a reality. A roster of the current team members can be viewed on this page.

Terms of Use

The Terms of Use page is a collection of statements that outline the conditions related to using the IEDB system. The Terms of use includes our privacy notice, copyright information, and various disclaimers. The IEDB privacy policy describes what user information is collected, the circumstances for collecting it, and how it is used. Personal information about users is not collected unless the users choose to provide it.

Annual Compendia

An archive of the IEDB Annual Compendia can be found at this link to the IEDB Solutions Center. The list includes all Annual Compendia going back to 2005. The section also includes the IEDB System and Architecture Design document.

3 Scientific Publications

This section lists the scientific publications for which the IEDB played a contributory role. The first section lists publications authored by the IEDB contractor team over the past 13 years. The second section lists references that cited the IEDB. This list was compiled by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the IEDB team authored papers.

3.1 Publications of the IEDB team by Year

Scientific articles written by the IEDB team members that are relevant to the IEDB are listed below by year of publication. In 2017, seventeen articles were published, 10 in 2016, 12 in 2015, seven in 2014, ten in 2013, six were published in 2012, three in 2011, nine in 2010, seven in 2009, nine in 2008, twelve in 2007, five in 2006, six in 2005, and one in 2004. In all, the team has written 114 scientific articles about the IEDB since program initiation in 2003.

3.1.1 2017

1. Vita R, Overton JA, Sette A, Peters B. Better living through ontologies at the Immune Epitope Database. Database (Oxford). 2017 Jan 1;2017(1). doi: 10.1093/database/bax014. PubMed PMID: 28365732.

2. Remesh SG, Andreatta M, Ying G, Kaever T, Nielsen M, McMurtrey C, Hildebrand W, Peters B, Zajonc DM. Unconventional Peptide Presentation by Major Histocompatibility Complex (MHC) Class I Allele HLA-A*02:01: BREAKING CONFINEMENT. J Biol Chem. 2017 Mar 31;292(13):5262-5270. doi: 10.1074/jbc.M117.776542. Epub 2017 Feb 8. PubMed PMID: 28179428.

3. Fleri W, Paul S, Dhanda SK, Mahajan S, Xu X, Peters B, Sette A. The Immune Epitope Database and Analysis Resource in Epitope Discovery and Synthetic Vaccine Design. Front Immunol. 2017 Mar 14;8:278. doi: 10.3389/fimmu.2017.00278. eCollection 2017. Review. PubMed PMID: 28352270; PubMed Central PMCID: PMC5348633.

4. Nielsen M, Andreatta M. NNAlign: a platform to construct and evaluate artificial neural network models of receptor-ligand interactions. Nucleic Acids Res. 2017 Apr 12. doi: 10.1093/nar/gkx276. [Epub ahead of print] PubMed PMID: 28407117.

5. Andreatta M, Alvarez B, Nielsen M. GibbsCluster: unsupervised clustering and alignment of peptide sequences. Nucleic Acids Res. 2017 Apr 12. doi: 10.1093/nar/gkx248. [Epub ahead of print] PubMed PMID: 28407089.

6. Jespersen MC, Peters B, Nielsen M, Marcatili P. BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes. Nucleic Acids Res. 2017 May 2. doi: 10.1093/nar/gkx346. [Epub ahead of print] PubMed PMID: 28472356.

7. Sidney J, Becart S, Zhou M, Duffy K, Lindvall M, Moore EC, Moore EL, Rao T, Rao N, Nielsen M, Peters B, Sette A. Citrullination only infrequently impacts peptide binding to HLA class II MHC. PLoS One. 2017 May 8;12(5):e0177140. doi: 10.1371/journal.pone.0177140. eCollection 2017. PubMed PMID: 28481943; PubMed Central PMCID: PMC5421785.

8. Andreatta M, Jurtz VI, Kaever T, Sette A, Peters B, Nielsen M. Machine learning reveals a non-canonical mode of peptide binding to MHC class II molecules. Immunology. 2017 May 24. doi: 10.1111/imm.12763. [Epub ahead of print] PubMed PMID: 28542831.

9. Fleri W, Vaughan K, Salimi N, Vita R, Peters B, Sette A. The Immune Epitope Database: How Data Are Entered and Retrieved. J Immunol Res. 2017;2017:5974574. doi: 10.1155/2017/5974574. Epub 2017 May 29. Review. PubMed PMID: 28634590; PubMed Central PMCID: PMC5467323.

10. Paul S, Arlehamn CSL, Schulten V, Westernberg L, Sidney J, Peters B, Sette A. Experimental validation of the RATE tool for inferring HLA restrictions of T cell epitopes. BMC Immunol. 2017 Jun 21;18(Suppl 1):20. doi: 10.1186/s12865-017-0204-1. PubMed PMID: 28681704.

11. Shao W, Pedrioli PGA, Wolski W, Scurtescu C, Schmid E, Vizcaíno JA, Courcelles M, Schuster H, Kowalewski D, Marino F, Arlehamn CSL, Vaughan K, Peters B, Sette A, Ottenhoff THM, Meijgaarden KE, Nieuwenhuizen N, Kaufmann SHE, Schlapbach R, Castle JC, Nesvizhskii AI, Nielsen M, Deutsch EW, Campbell DS, Moritz RL, Zubarev RA, Ytterberg AJ, Purcell AW, Marcilla M, Paradela A, Wang Q, Costello CE, Ternette N, van Veelen PA, van Els CACM, Heck AJR, de Souza GA, Sollid LM, Admon A, Stevanovic S, Rammensee HG, Thibault P, Perreault C, Bassani-Sternberg M, Aebersold R, Caron E. The SysteMHC Atlas project. Nucleic Acids Res. 2017 Jul 29. doi: 10.1093/nar/gkx664. [Epub ahead of print] PubMed PMID: 28985418.

12. Vaughan K, Xu X, Caron E, Peters B, Sette A. Deciphering the MHC-associated peptidome: a review of naturally processed ligand data. Expert Rev Proteomics. 2017 Sep;14(9):729-736. doi: 10.1080/14789450.2017.1361825. Epub 2017 Aug 11. PubMed PMID: 28756714.

13. Dhanda SK, Grifoni A, Pham J, Vaughan K, Sidney J, Peters B, Sette A. Development of a strategy and computational application to select candidate protein analogues with reduced HLA binding and immunogenicity. Immunology. 2017 Aug 22. doi: 10.1111/imm.12816. [Epub ahead of print] PubMed PMID: 28833085.

14. Jurtz VI, Rosenberg Johansen A, Nielsen M, Almagro Armenteros JJ, Nielsen H, Kaae Sønderby C, Winther O, Kaae Sønderby S. An introduction to Deep learning on biological sequence data - Examples and solutions. Bioinformatics. 2017 Aug 23. doi: 10.1093/bioinformatics/btx531. [Epub ahead of print] PubMed PMID: 28961695.

15. Jurtz V, Paul S, Andreatta M, Marcatili P, Peters B, Nielsen M. NetMHCpan-4.0: Improved Peptide-MHC Class I Interaction Predictions Integrating Eluted Ligand and Peptide Binding Affinity Data. J Immunol. 2017 Nov 1;199(9):3360-3368. doi: 10.4049/jimmunol.1700893. Epub 2017 Oct 4. PubMed PMID: 28978689; PubMed Central PMCID: PMC5679736.

16. Andreatta M, Trolle T, Yan Z, Greenbaum JA, Peters B, Nielsen M. An automated benchmarking platform for MHC class II binding prediction methods. Bioinformatics. 2017 Dec 21. doi: 10.1093/bioinformatics/btx820. [Epub ahead of print] PubMed PMID: 29281002.

17. Lanzarotti E, Marcatili P, Nielsen M. Identification of the cognate peptide-MHC target of T cell receptors using molecular modeling and force field scoring. Mol Immunol. 2017 Dec 27;94:91-97. doi: 10.1016/j.molimm.2017.12.019. [Epub ahead of print] PubMed PMID: 29288899.

3.1.2 2016

18. Bandrowski A, Brinkman R, Brochhausen M, Brush MH, Bug B, Chibucos MC, Clancy K, Courtot M, Derom D, Dumontier M, Fan L, Fostel J, Fragoso G, Gibson F, Gonzalez-Beltran A, Haendel MA, He Y, Heiskanen M, Hernandez-Boussard T, Jensen M, Lin Y, Lister AL, Lord P, Malone J, Manduchi E, McGee M, Morrison N, Overton JA, Parkinson H, Peters B, Rocca-Serra P, Ruttenberg A, Sansone SA, Scheuermann RH, Schober D, Smith B, Soldatova LN, Stoeckert CJ Jr, Taylor CF, Torniai C, Turner JA, Vita R, Whetzel PL, Zheng J. The Ontology for Biomedical

Investigations. PLoS One. 2016 Apr 29;11(4):e0154556. doi: 10.1371/journal.pone.0154556. eCollection 2016. PubMed PMID: 27128319; PubMed Central PMCID: PMC4851331.

19. Bresciani A, Paul S, Schommer N, Dillon MB, Bancroft T, Greenbaum J, Sette A, Nielsen M, Peters B. T-cell recognition is shaped by epitope sequence conservation in the host proteome and microbiome. Immunology. 2016 May;148(1):34-9. doi: 10.1111/imm.12585. Epub 2016 Feb 8. PubMed PMID: 26789414; PubMed Central PMCID: PMC4819143.

20. Fleri W, Salimi N, Vita R, Peters B, Sette A, Immune Epitope Database and Analysis Resource, Encyclopedia of Immunobiology, Vol. 2, Elsevier Ltd., 20 May 2016, doi:10.1016/B978-0-12-374279-7.06004-5

21. McMurtrey C, Trolle T, Sansom T, Remesh SG, Kaever T, Bardet W, Jackson K, McLeod R, Sette A, Nielsen M, Zajonc DM, Blader IJ, Peters B, Hildebrand W. Toxoplasma gondii peptide ligands open the gate of the HLA class I binding groove. Elife. 2016 Jan 29;5. pii: e12556. doi: 10.7554/eLife.12556. PubMed PMID: 26824387; PubMed Central PMCID: PMC4775218.

22. Nielsen M, Andreatta M, NetMHCpan-3.0; improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length data sets. Genome Medicine, March 2016, Mar 30;8(1):33. doi: 10.1186/s13073-016-0288-x. PubMed PMID: 27029192; PubMed Central PMCID: PMC4812631

23. Paul S, Sidney J, Sette A, Peters B. TepiTool: A Pipeline for Computational Prediction of T Cell Epitope Candidates. Curr Protoc Immunol. 2016 Aug 1;114:18.19.1-18.19.24. doi: 10.1002/cpim.12. PubMed PMID: 27479659; PubMed Central PMCID: PMC4981331

24. Ponomarenko J, Vaughan K, Paul S, Peters B, Sette A, Haeussler M, Maurer-Stroh S, Ebola: an analysis of immunity at the molecular level, 2015 International Workshop on Artificial Immune Systems (AIS), Taormina, 2015, pp. 1-8. doi: 10.1109/AISW.2015.7469230,published online at IEEE Xplore Digital Library, URL: http://ieeexplore.ieee.org/stamp/stamp.jsp?tp=&arnumber=7469230&isnumber=7469223

25. Trolle T, McMurtrey CP, Sidney J, Bardet W, Osborn SC, Kaever T, Sette A, Hildebrand WH, Nielsen M, Peters B. The Length Distribution of Class I-Restricted T Cell Epitopes Is Determined by Both Peptide Supply and MHC Allele-Specific Binding Preference. J Immunol. 2016 Feb 15;196(4):1480-7. doi: 10.4049/jimmunol.1501721. Epub 2016 Jan 18. PubMed PMID: 26783342; PubMed Central PMCID: PMC4744552.

26. Vita R, Overton JA, Seymour E, Sidney J, Kaufman J, Tallmadge RL, Ellis S, Hammond J, Butcher GW, Sette A, Peters B. An ontology for major histocompatibility restriction. J Biomed Semantics. 2016 Jan 11;7:1. doi:10.1186/s13326-016-0045-5. eCollection 2016. PubMed PMID: 26759709; PubMed Central PMCID: PMC4709943.

27. Xu X, Vaughan K, Weiskopf D, Grifoni A, Diamond MS, Sette A, Peters B. Identifying Candidate Targets of Immune Responses in Zika Virus Based on Homology to Epitopes in Other Flavivirus Species. PLoS Curr. 2016 Nov 15;8. pii: ecurrents.outbreaks.9aa2e1fb61b0f632f58a098773008c4b. doi: 10.1371/currents.outbreaks.9aa2e1fb61b0f632f58a098773008c4b. PubMed PMID: 28018746; PubMed Central PMCID: PMC5145810.

3.1.3 2015

28. Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M. “Automated benchmarking of peptide-MHC class I binding predictions”. Bioinformatics. 2015 Feb 25. pii: btv123. [Epub ahead of print] PubMed PMID: 25717196
29. Vita, R. The Much Overlooked “Materials and Methods” (Editorial), Immunome Research, March 23, 2015 (http://www.omicsonline.com/open-access/the-much-overlooked-materials-and-methods-1745-7580-1000e004.pdf)
30. Sela-Culang, I., 1, Ofran, Y., and Peters, B. “Antibody specific epitope prediction - emergence of a new paradigm”, Current Opinion in Virology, Volume 11, April 2015, Pages 98–102, PMID: 25837466
31. Paul S, Lindestam Arlehamn CS, Scriba TJ, Dillon MB, Oseroff C, Hinz D, McKinney DM, Carrasco Pro S, Sidney J, Peters B, Sette A. Development and validation of a broad scheme for prediction of HLA class II restricted T cell epitopes. J Immunol Methods. 2015 Jul;422:28-34. doi: 10.1016/j.jim.2015.03.022. Epub 2015 Apr 7. PubMed PMID: 25862607
32. Paul S, Dillon MB, Lindestam Arlehamn CS, Huang H, Davis MM, McKinney DM, Scriba TJ, Sidney J, Peters B, Sette A. A Population Response Analysis Approach To Assign Class II HLA-Epitope Restrictions. J Immunol. 2015 Jun 15;194(12):6164-76. doi: 10.4049/jimmunol.1403074. Epub 2015 May 6. PubMed PMID: 25948811; PubMed Central PMCID: PMC4458389
33. Vaughan K, Ponomarenko J, Peters B, Sette A. Analysis of Human RSV Immunity at the Molecular Level: Learning from the Past and Present. PLoS One. 2015 May 22;10(5):e0127108. doi: 10.1371/journal.pone.0127108. eCollection 2015. PubMed PMID: 26001197
34. Klausen MS, Anderson MV, Jespersen MC, Nielsen M, Marcatili P. LYRA, a webserver for lymphocyte receptor structural modeling. Nucleic Acids Res. 2015 Jul 1;43(W1):W349-W355. Epub 2015 May 24. PubMed PMID: 26007650
35. Andreatta M, Karosiene E, Rasmussen M, Stryhn A, Buus S, Nielsen M. Accurate pan-specific prediction of peptide-MHC class II binding affinity with improved binding core identification. Immunogenetics. 2015 Sep 29. [Epub ahead of print] PubMed PMID: 26416257
36. Carrasco Pro S, Sidney J, Paul S, Lindestam Arlehamn C, Weiskopf D, Peters B, Sette A. Automatic Generation of Validated Specific Epitope Sets. J Immunol Res. 2015;2015:763461. doi: 10.1155/2015/763461. Epub 2015 Oct 19. PubMed PMID: 26568965
37. Andreatta M, Nielsen M. Gapped sequence alignment using artificial neural networks: application to the MHC class I system. Bioinformatics. 2015 Oct 29. pii: btv639. [Epub ahead of print] PubMed PMID: 26515819
38. Sette A, Paul S, Vaughan K, Peters B. The Use of the Immune Epitope Database to Study Autoimmune Epitope Data Related to Alopecia Areata. J Investig Dermatol Symp Proc. 2015 Nov;17(2):36-41. doi: 10.1038/jidsymp.2015.39. Review. PubMed PMID: 26551944
39. Vita R, Vasilevsky N, Bandrowski A, Haendel M, Sette A, Peters B. Reproducibility and Conflicts in Immune Epitope Data. Immunology. 2015 Dec 17. doi: 10.1111/imm.12566. [Epub ahead of print] PubMed PMID: 26678806

3.1.4 2014

40. Ponomarenko J, Vaughan K, Sette A, Maurer-Stroh S. Conservancy of mAb Epitopes in Ebolavirus Glycoproteins of Previous and 2014 Outbreaks. PLOS Currents Outbreaks. 2014 Nov 3. Edition 1.

41. Vaughan K, Peters B, Mallone R, von Herrath M, Roep BO, Sette A. Navigating diabetes-related immune epitope data: resources and tools provided by the Immune Epitope Database (IEDB). Immunome Res. 2013;9(1). doi: 10.4172/1745-7580.1000063. PubMed PMID: 25140192; PubMed Central PMCID: PMC4134942.

42. Vaughan K, Seymour E, Peters B, Sette A. Substantial gaps in knowledge of Bordetella pertussis antibody and T cell epitopes relevant for natural immunity and vaccine efficacy. Hum Immunol. 2014 May;75(5):440-451. doi: 10.1016/j.humimm.2014.02.013. Epub 2014 Feb 12. Review. PubMed PMID: 24530743.

43. Trolle T, Nielsen M. NetTepi: an integrated method for the prediction of T cell epitopes. Immunogenetics. 2014 May 27. [Epub ahead of print] PubMed PMID: 24863339

44. Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B. Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. BMC Bioinformatics. 2014 Jul 14;15:241. doi: 10.1186/1471-2105-15-241. PubMed PMID: 25017736; PubMed Central PMCID: PMC4111843.

45. Shirai H, Prades C, Vita R, Marcatili P, Popovic B, Xu J, Overington JP, Hirayama K, Soga S, Tsunoyama K, Clark D, Lefranc MP, Ikeda K. Antibody informatics for drug discovery. Biochim Biophys Acta. 2014 Nov;1844(11):2002-2015. doi: 10.1016/j.bbapap.2014.07.006. Epub 2014 Aug 8. Review. PubMed PMID: 25110827.

46. Vita R, Overton JA, Greenbaum JA, Ponomarenko J, Clark JD, Cantrell JR, Wheeler DK, Gabbard JL, Hix D, Sette A, Peters B. The immune epitope database (IEDB) 3.0. Nucleic Acids Res. 2014 Oct 9. pii: gku938. [Epub ahead of print] PubMed PMID: 25300482.

3.1.5 2013

47. Kim Y, Yewdell JW, Sette A, Peters B. Positional bias of MHC class I restricted T-cell epitopes in viral antigens is likely due to a bias in conservation. PLoS Comput Biol. 2013 Jan;9(1):e1002884. doi: 10.1371/journal.pcbi.1002884. Epub 2013 Jan 24. PubMed PMID: 23357871; PubMed Central PMCID: PMC3554532.

48. Vita R, Overton JA, Greenbaum JA, Sette A; OBI consortium, Peters B. Query enhancement through the practical application of ontology: the IEDB and OBI. J Biomed Semantics. 2013 Apr 15;4 Suppl 1:S6. doi: 10.1186/2041-1480-4-S1-S6. Epub 2013 Apr 15. PubMed PMID: 23734660; PubMed Central PMCID: PMC3633001.

49. Jessen LE, Hoof I, Lund O, Nielsen M. SigniSite: Identification of residue-level genotype-phenotype correlations in protein multiple sequence alignments. Nucleic Acids Res. 2013 Jul 1;41(Web Server issue):W286-91. doi: 10.1093/nar/gkt497. Epub 2013 Jun 12. PMID: 23761454; PMCID: PMC3692133

50. Jørgensen KW, Rasmussen M, Buus S, Nielsen M. NetMHCstab - predicting stability of peptide:MHC-I complexes; impacts for CTL epitope discovery**.** Immunology. 2013 Aug 8. doi: 10.1111/imm.12160. PubMed PMID: 23927693; PubMed Central PMCID: PMC3893846

51. Schubert B, Lund O, Nielsen M. Evaluation of peptide selection approaches for epitope-based vaccine design. Tissue Antigens. 2013 Oct;82(4):243-51. doi: 10.1111/tan.12199. PubMed PMID: 24461003

52. Karosiene E, Rasmussen M, Blicher T, Lund O, Buus S, Nielsen M. NetMHCIIpan-3.0, a common pan-specific MHC class II prediction method including all three human MHC class II isotypes, HLA-DR, HLA-DP and HLA-DQ. Immunogenetics. 2013 Oct;65(10):711-24. doi: 10.1007/s00251-013-0720-y. Epub 2013 Jul 31. PubMed PMID: 23900783.

53. Vaughan K, Peters B, O'Connor KC, Martin R, Sette A. A molecular view of multiple sclerosis and experimental autoimmune encephalitis: What can we learn from the epitope data? J Neuroimmunol. 2013 Dec 12. pii: S0165-5728(13)00340-8. doi: 10.1016/j.jneuroim.2013.12.009. PubMed PMID: 24365494.

54. Paul S, Kolla RV, Sidney J, Weiskopf D, Fleri W, Kim Y, Peters B, Sette A. Evaluating the immunogenicity of protein drugs by applying in vitro MHC binding data and the immune epitope database and analysis resource. Clin Dev Immunol. 2013;2013:467852. doi: 10.1155/2013/467852. Epub 2013 Oct 8. PubMed PMID: 24222776; PubMed Central PMCID: PMC3816028.

55. Calis JJ, Maybeno M, Greenbaum JA, Weiskopf D, De Silva AD, Sette A, Kesmir C, Peters B. Properties of MHC class I presented peptides that enhance immunogenicity. PLoS Comput Biol. 2013 Oct;9(10):e1003266. doi: 10.1371/journal.pcbi.1003266. Epub 2013 Oct 24. PubMed PMID: 24204222; PubMed Central PMCID: PMC3808449.

56. Paul S, Weiskopf D, Angelo MA, Sidney J, Peters B, Sette A. HLA Class I Alleles Are Associated with Peptide-Binding Repertoires of Different Size, Affinity, and Immunogenicity. J Immunol. 2013 Dec 15;191(12):5831-9. doi: 10.4049/jimmunol.1302101. Epub 2013 Nov 4. PubMed PMID: 24190657; PubMed Central PMCID: PMC3872965.

3.1.6 2012

57. Kim Y, Ponomarenko J, Zhu Z, Tamang D, Wang P, Greenbaum J, Lundegaard C, Sette A, Lund O, Bourne PE, Nielsen M, Peters B. Immune epitope database analysis resource. Nucleic Acids Res. 2012 Jul;40 (Web Server issue):W525-30. Epub 2012 May 18. PubMed PMID: 22610854.

58. Kim Y, Vaughan K, Greenbaum J, Peters B, Law M, Sette A. A Meta-Analysis of the Existing Knowledge of Immunoreactivity against Hepatitis C Virus (HCV). PLoS One. 2012;7(5):e38028. Epub 2012 May 31. PubMed PMID: 22675428; PubMed Central PMCID: PMC3364976.

59. Kringelum JV, Nielsen M, Padkjær SB, Lund O. Structural analysis of B-cell epitopes in antibody:protein complexes. Mol Immunol. 2013 Jan;53(1-2):24-34. doi: 10.1016/j.molimm.2012.06.001. Epub 2012 Jul 10. PubMed PMID: 22784991; PubMed Central PMCID: PMC3461403

60. Salimi N, Fleri W, Peters B, Sette A. The Immune Epitope Database: A Historical Retrospective of the First Decade. Immunology. 2012 Jun 8. doi:10.1111/j.1365-2567.2012.03611.x. [Epub ahead of print] PubMed PMID: 22681406.

61. Vaughan K, Kim Y, Sette A. A comparison of epitope repertoires associated with myasthenia gravis in humans and nonhuman hosts. Autoimmune Dis. 2012;2012:403915. doi: 10.1155/2012/403915. Epub 2012 Dec 2. PubMed PMID: 23243503; PubMed Central PMCID: PMC3518085.

62. Vaughan K, Peters B, Larche M, Pomes A, Broide D, Sette A. Strategies to Query and Display Allergy-Derived Epitope Data from the Immune Epitope Database. Int Arch Allergy Immunol. 2012 Nov 21;160(4):334-345. [Epub ahead of print] PubMed PMID: 23172234.

3.1.7 2011

63. Seymour E., Damle R., Sette A., Peters B. (2011). “Cost sensitive hierarchical document classification to triage PubMed abstracts for manual curation.” BMC Bioinformatics 12(1): 482. [Epub ahead of print]. PMID: 22182279.

64. Vaughan K, Greenbaum J, Kim Y, Vita R, Chung J, Peters B, Broide D, Goodman R, Grey H, Sette A. Towards defining molecular determinants recognized by adaptive immunity in allergic disease:

an inventory of the available data. J Allergy (Cairo). 2010;2010:628026. Epub 2011 Feb 13. PubMed PMID: 21403821

65. Vita R, Peters B, Josephs Z, de Matos P, Ennis M, Turner S, Steinbeck C, Seymour E, Zarebski L, Sette A. (2011). “A Model for Collaborative Curation, The IEDB and ChEBI Curation of Non-peptidic Epitopes.” Immunome Res. 2011 Apr 1;7(1):1-8. PubMed PMID: 21897450

3.1.8 2010

66. Brinkman RR, Courtot M, Derom D, Fostel JM, He Y, Lord P, Malone J, Parkinson H, Peters B, Rocca-Serra P, Ruttenberg A, Sansone SA, Soldatova LN, Stoeckert CJ Jr, Turner JA, Zheng J; OBI consortium. Modeling biomedical experimental processes with OBI. J Biomed Semantics. 2010 Jun 22;1 Suppl 1:S7. PubMed PMID: 20626927

67. Diehl AD, Augustine AD, Blake JA, Cowell LG, Gold ES, Gondré-Lewis TA, Masci AM, Meehan TF, Morel PA, Nijnik A, Peters B, Pulendran B, Scheuermann RH, Yao QA, Zand MS, Mungall CJ. "Hematopoietic cell types: Prototype for a revised cell ontology. J Biomed Inform. 2010 Feb 1. [Epub ahead of print]PMID: 20123131

68. Kim Y, Sette A, Peters B. Applications for T-cell epitope queries and tools in the Immune Epitope Database and Analysis Resource. J Immunol Methods. 2010 Oct 31. [Epub ahead of print] PubMed PMID: 21047510.

69. Nielsen M, Lund O, Buus S, Lundegaard C. MHC class II epitope predictive algorithms. Immunology. 2010 Jul;130(3):319-28. Epub 2010 Apr 12. Review. PubMed PMID: 20408898;

70. Ponomarenko J, Papangelopoulos N, Zajonc DM, Peters B, Sette A, Bourne PE. IEDB-3D: structural data within the immune epitope database. Nucleic Acids Res. 2010 Oct 28. [Epub ahead of print] PubMed PMID: 21030437.

71. Salimi N, Fleri W, Peters B, Sette A. Design and utilization of epitope-based databases and predictive tools. Immunogenetics. 2010 Apr;62(4):185-96. Epub 2010 Mar 6. Review. PubMed PMID: 20213141; PubMed Central PMCID: PMC2843836.

72. Vaughan K, Greenbaum J, Blythe M, Peters B, Sette A. Meta-analysis of all immune epitope data in the Flavivirus genus: inventory of current immune epitope data status in the context of virus immunity and immunopathology. Viral Immunol. 2010 Jun;23(3):259-84. PubMed PMID: 20565291; PubMed Central PMCID: PMC2942863.

73. Wang P, Sidney J, Kim Y, Sette A, Lund O, Nielsen M, Peters B. Peptide binding predictions for HLA DR, DP and DQ molecules. BMC Bioinformatics. 2010 Nov 22;11:568. PubMed PMID: 21092157; PubMed Central PMCID: PMC2998531.

74. Zhang H, Wang P, Papangelopoulos N, Xu Y, Sette A, Bourne PE, Lund O, Ponomarenko J, Nielsen M, Peters B. Limitations of Ab initio predictions of peptide binding to MHC class II molecules. PLoS One. 2010 Feb 17;5(2):e9272. PubMed PMID: 20174654; PubMed Central PMCID: PMC2822856.

3.1.9 2009

75. Davies V, Vaughan K, Damle R, Peters B, Sette A. Classification of the universe of immune epitope literature: representation and knowledge gaps. PLoS One. 2009 Sep 14;4(9):e6948. PubMed PMID: 19774228;

76. Greenbaum JA, Kotturi MF, Kim Y, Oseroff C, Vaughan K, Salimi N, Vita R, Ponomarenko J, Scheuermann RH, Sette A, Peters B. Pre-existing immunity against swine-origin H1N1 influenza

viruses in the general human population. Proc Natl Acad Sci U S A. 2009 Dec 1;106(48):20365-70. Epub 2009 Nov 16. PubMed PMID: 19918065; PubMed Central PMCID: PMC2777968.

77. Hoof I, Peters B, Sidney J, Pedersen LE, Sette A, Lund O, Buus S, Nielsen M, NetMHCpan, a method for MHC class I binding prediction beyond humans. Immunogenetics. 2009 Jan;61(1):1-13. PMID: 19002680
78. Kim Y, Sidney J, Pinilla C, Sette A, Peters B. Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior. BMC Bioinformatics. 2009 Nov 30;10:394. PubMed PMID: 19948066.
79. Vaughan K, Blythe M, Greenbaum J, Zhang Q, Peters B, Doolan DL, Sette A, Meta-analysis of immune epitope data for all Plasmodia: overview and applications for malarial immunobiology and vaccine-related issues. Parasite Immunol. 2009 Feb;31(2):78-97. [PMID: 19149776]
80. Vita R, Zarebski L, Greenbaum JA, Emami H, Hoof I, Salimi N, Damle R, Sette A, Peters B. The Immune Epitope Database 2.0. Nucleic Acids Res. 2009 Nov 11. [Epub ahead of print] PubMed PMID: 19906713.
81. Zhang H, Lund O, Nielsen M. The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: Application to MHC-peptide binding. Bioinformatics. 2009 Mar 17. PMID: 19297351

3.1.10 2008

82. Lundegaard C., K. Lamberth, M. Harndahl, S. Buus, O. Lund, M. Nielsen. (2008). “NetMHC-3.0: accurate web accessible predictions of human, mouse and monkey MHC class I affinities for peptides of length 8-11.” Nucleic Acids Res. 2008 36:W509-12. PMID: 18996943
83. Nielsen, M., C. Lundegaard, T. Blicher, B. Peters, A. Sette, S. Justesen, S. Buus, O. Lund. (2008). "Quantitative Predictions of Peptide Binding to Any HLA-DR Molecule of Known Sequence: NetMHCIIpan." PLoS Computational Biology **4**(7). PMID: 18604266
84. Ponomarenko J, H. H. Bui, W. Li, N. Fusseder, P. E. Bourne, A. Sette, B. Peters. (2008). “ElliPro: a new structure-based tool for the prediction of antibody epitopes.” BMC Bioinformatics, 9(514). PMID: 19055730
85. Ponomarenko J. V., M. H. C. van Regenmortel (2008) “B-cell epitope prediction.” Structural Bioinformatics, Ed: Bourne PE, Gu J. Wiley-Liss; 2 edition.
86. Rapin N., I. Hoof, O. Lund, M. Nielsen. (2008). “MHC motif viewer.” Immunogenetics. 60(12): 759-65. PMID: 18766337
87. Vita R., B. Peters, A. Sette. (2008). “The Curation Guidelines of the Immune Epitope Database and Analysis Resource.” Cytometry A 73(11): 1066-1070. PMID: 18688821
88. Wang, P., J. Sidney, C. Dow, B. Mothe, A. Sette, B. Peters. (2008). "A Systematic Assessment of MHC Class II Peptide Binding Predictions and Evaluation of a Consensus Approach." PLoS Computational Biology **4**(4). PMID: 18389056
89. Zarebski L. M., K. Vaughan, J. Sidney, B. Peters, H. Grey, K. D. Janda, A. Casadevall, A. Sette. (2008). “Analysis of epitope information related to Bacillus anthracis and Clostridium botulinum.” Expert Rev Vaccines 7(1): 55-74. PMID: 18251694
90. Zhang, Q., P. Wang, et al. (2008). "Immune epitope database analysis resource (IEDB-AR)." Nucleic Acids Research **36**: W513-W518. PMID: 18515843

3.1.11 2007

91. Beaver JE, Bourne PE, Ponomarenko JV. EpitopeViewer: a Java application for the visualization and analysis of immune epitopes in the Immune Epitope Database and Analysis Resource (IEDB). Immunome Res. 2007 Feb 21;3:3. PMID: 17313688
92. Blythe MJ, Zhang Q, Vaughan K, de Castro R Jr, Salimi N, Bui HH, Lewinsohn DM, Ernst JD, Peters B, Sette A. An analysis of the epitope knowledge related to Mycobacteria. Immunome Res. 2007 Dec 14;3(1):10. PMID: 18081934
93. Bui HH, Peters B, Assarsson E, Mbawuike I, Sette A. Ab and T cell epitopes of influenza A virus, knowledge and opportunities. Proc Natl Acad Sci U S A. 2007 Jan 2;104(1):246-51. PMID: 17200302
94. Bui HH, Sidney J, Li W, Fusseder N, Sette A. Development of an epitope conservancy analysis tool to facilitate the design of epitope-based diagnostics and vaccines. BMC Bioinformatics. 2007 Sep 26;8(1):361. PMID: 17897458
95. Ernst JD, Lewinsohn DM, Behar S, Blythe M, Schlesinger LS, Kornfeld H, Sette A. Meeting Report: NIH Workshop on the Tuberculosis Immune Epitope Database. Tuberculosis (Edinb). 2007 Dec 6. PMID: 18068490
96. Greenbaum JA, Andersen PH, Blythe M, Bui HH, Cachau RE, Crowe J, Davies M, Kolaskar AS, Lund O, Morrison S, Mumey B, Ofran Y, Pellequer JL, Pinilla C, Ponomarenko JV, Raghava GP, van Regenmortel MH, Roggen EL, Sette A, Schlessinger A, Sollner J, Zand M, Peters B. Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. J Mol Recognit. 2007 Mar-Apr;20(2):75-82. PMID: 17205610
97. Lundegaard C, Lund O, Kesmir C, Brunak S, Nielsen M. Modeling the adaptive immune system: predictions and simulations. Bioinformatics. 2007 Dec 15;23(24):3265-75. PMID: 18045832
98. Nielsen M, Lundegaard C, Blicher T, Lamberth K, Harndahl M, Justesen S, Røder G, Peters B, Sette A, Lund O, Buus S. NetMHCpan, a method for quantitative predictions of peptide binding to any HLA-A and -B locus protein of known sequence. PLoS ONE. 2007 Aug 29;2(8):e796. PMID: 17726526
99. Peters B, Sette A. Integrating epitope data into the emerging web of biomedical knowledge resources. Nat Rev Immunol. 2007 Jun;7(6):485-90. PMID: 17479127
100. Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. BMC Struct Biol. 2007 Oct 2;7(1):64. PMID: 17910770
101. Sette A, Peters B., Immune epitope mapping in the post-genomic era: lessons for vaccine development. Curr Opin Immunol. 2007 Feb;19(1):106-10. PMID: 17113275
102. Wang P, Morgan AA, Zhang Q, Sette A, Peters B. Automating document classification for the Immune Epitope Database. BMC Bioinformatics. 2007 Jul 26;8:269. PMID: 17655769

3.1.12 2006

103. Bui HH, Sidney J, Dinh K, Southwood S, Newman MJ, Sette A. Predicting population coverage of T-cell epitope-based diagnostics and vaccines. BMC Bioinformatics. 2006 Mar 17;7(1):153. PMID: 16545123
104. Peters B, Bui HH, Frankild S, Nielson M, Lundegaard C, Kostem E, Basch D, Lamberth K, Harndahl M, Fleri W, Wilson SS, Sidney J, Lund O, Buus S, Sette A., A community resource benchmarking predictions of peptide binding to MHC-I molecules, PLoS Comput Biol. 2006 Jun 9;2(6):e65. Epub 2006 Jun 9. PMID: 16789818

105. Salimi N, R. Vita. (2006). "The biocurator: connecting and enhancing scientific data". PLoS Comput Biol 2(10) :e125. PMID: 17069454

106. Sette, A., H. H. Bui, S. Buus, W. Fleri, R. Kubo, O. Lund, D. Nemazee, J. V. Ponomarenko, M. Sathiamurthy, S. Stewart, S. Way, S. S. Wilson, B. Peters. (2006). “The Immune Epitope Database and Analysis Resource.” Pattern Recognition in Bioinformatics: International Workshop, Hong Kong, China, August 20, 2006 : Procedings, Springer, Jagath C. Rajapakse, Limsoon Wong, Raj Acharya (Eds). ISBN: 3540374469 9783540374466

107. Vita R, K. Vaughan, L. Zarebski, N. Salimi, W. Fleri , H. Grey, M. Sathiamurthy, J. Mokili, H. H. Bui, P. E. Bourne, J. V. Ponomarenko, R. de Castro Jr, R. K. Chan, J. Sidney, S. S. Wilson, S. Stewart, S. Way, B. Peters, A. Sette. (2006) "Curation of complex, context-dependent immunological data." BMC Bioinformatics. 12(7): 341. PMID: 16836764

3.1.13 2005

108. Bui HH, Sidney J, Peters B, Sathiamurthy M, Sinichi A, Purton KA, Mothé BR, Chisari FV, Watkins DI, Sette A. Automated generation and evaluation of specific MHC binding predictive tools: ARB matrix applications. Immunogenetics. 2005 Jun;57(5):304-14. Epub 2005 May 3. PMID: 15868141

109. Peters B, Sette A. Generating quantitative models describing the sequence specificity of biological processes with the stabilized matrix method. BMC Bioinformatics. 2005 May 31;6:132. PMID: 15927070

110. Peters, B., J. Sidney, P. Bourne, H. H. Bui, S. Buus, G. Doh, W. Fleri, M. Kronenberg, R.Kubo, O. Lund, D. Nemazee, J. V. Ponomarenko, M. Sathiamurthy, S. Schoenberger, S. Stewart, P. Surko, S. Way, S. Wilson, A. Sette. (2005). "The design and implementation of the immune epitope database and analysis resource." Immunogenetics 57(5): 326-336. PMID: 15895191

111. Peters, B., J. Sidney, P. Bourne, H. H. Bui, S. Buus, G. Doh, W. Fleri, M. Kronenberg, R.Kubo, O. Lund, D. Nemazee, J. V. Ponomarenko, M. Sathiamurthy, S. Schoenberger, S. Stewart, P. Surko, S. Way, S. Wilson, A. Sette. (2005). "The Immune Epitope Database and Analysis Resource: From Vision to Blueprint." PLoS Biology 3(3). PMID: 15760272

112. Sathiamurthy, M., B. Peters, H. H. Bui, J. Sidney, J. Mokili, S. S. Wilson, W. Fleri, D. McGuinness, P. Bourne, A. Sette. (2005). "An ontology for immune epitopes: application to the design of a broad scope database of immune reactivities." Immunome Res 1(2): 1745-7580. PMID: 16305755

113. Sette, A., W. Fleri, B. Peters, M. Sathiamurthy, H. H. Bui, S. Wilson. (2005). "A Roadmap for the Immunomics of Category A–C Pathogens." Immunity 22(2): 155-161. PMID: 15773067

3.1.14 2004

114. Sette A. (2004). “The immune epitope database and analysis resource: from vision to blueprint.” Genome Inform Ser Workshop Genome Inform 15(2):299. PMID: 16312048

3.2 Publications Citing the IEDB in 2017

In 2017, the IEDB or Analysis Resource received of total of 1,457 citations. This represents an increase of 223 citations over 1,224 from the previous year (2016). The citation list includes 621 references which formally cited one or more of the 114 papers written by the IEDB team over the past thirteen years, and an additional 220 references that cited the IEDB in-text but did not cite a specific reference. Of note, this total may increase over time since these databases may not include references published late in 2017.

The formal citation list was compiled by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the 114 papers and excludes self-citations. In contrast, often scientific reports quote the IEDB not as a formal citation, but by simply stating in the text that the IEDB was used or listing the website address. Here we developed and implemented a plan to address in-text citations (informal mentions of the IEDB, rather than a direct citation). For this purpose we utilized Publish or Perish, a software program that retrieves citations from Crossref, Google Scholar, Microsoft Academic, Scopus, and Web of Science, and returns output that can easily be converted to an excel file. The tool can capture citations that the document specialist's citation analysis, which includes Google Scholar and Web or Science, may have missed, and can capture references that cite the IEDB in text but do not cite a specific IEDB-related publication.

The papers have been categorized by the type of IEDB paper they cited – General IEDB (G), Analysis Resource (AR), or Meta-analysis (MA). All papers listed below denote their category or categories with these abbreviations since a paper can cite several IEDB papers that belong in different categories. For example, a paper that cites an analysis resource paper may also cite the primary IEDB Nucleic Acids Res (2014) paper, and thus is listed under General IEDB and has an [AR, G] to indicate the Analysis Resource citation. Any paper that has "General" as one of its categories has been listed in the General category below. All papers having "Meta-analysis" as a category and not having "General" have been listed in the "Meta-Analysis" list below. That means all papers listed under "Analysis Resource" below only belong to that category.

Adhering to the hierarchy, 621 references cited at least one of the 114 papers written by the IEDB team in the past thirteen years. General IEDB publications were cited by 213 papers, Analysis Resource publications were cited by 363 papers, and meta-analysis publications were cited by 45 papers. Additionally, the new category to capture informal citation of the IEDB includes 220 papers.

The hierarchical list is presented below.

3.2.1 General IEDB

1. Abelin, J.G., Keskin, D.B., Sarkizova, S., Hartigan, C.R., Zhang, W.D., Sidney, J., Stevens, J., Lane, W., Zhang, G.L., Eisenhaure, T.M., Clauser, K.R., Hacohen, N., Rooney, M.S., Carr, S.A., and Wu, C.J. (2017). "Mass Spectrometry Profiling of HLA-Associated Peptidomes in Mono-allelic Cells Enables More Accurate Epitope Prediction." Immunity 46(2): 315-326. **[G, AR, MA]**
2. Abu-haraz, A.H., bd-elrahman, K.A., Ibrahim, M.S., Hussien, W.H., Mohammed, M.S., Badawi, M.M., and Salih, M.A. (2017). "Multi epitope peptide vaccine prediction against Sudan Ebola virus using Immuno-informatics approaches." Advanced Techniques in Biology & Medicin e 5(1-22. [**G, AR]**
3. Ahmed, O.H., Abdelhalim, A., Obi, S., Ali, K., and Hamdi, A. (2017). "Immunoinformatic Approach for Epitope-Based Peptide Vaccine against Lagos Rabies Virus Glycoprotein G." Immunome Res 13(137): 2- **[G, AR]**
4. Albagi, S.O.A., Ahmed, O.H., Gumaa, M.A., Abd, e., and Abu-Haraz, A.H. (2017). "Immunoinformatics-Peptide Driven Vaccine and In silico Modeling for Duvenhage Rabies Virus Glycoprotein G." J Clin Cell Immunol 8(517): 2**- [G, AR]**
5. Aldous, A.R. and Dong, J.Z. (2017). "Personalized neoantigen vaccines: A new approach to cancer immunotherapy." Bioorganic & medicinal chemistry **[G, AR]**
6. Ali, M., Pandey, R.K., Khatoon, N., Narula, A., Mishra, A., and Prajapati, V.K. (2017). "Exploring dengue genome to construct a multi-epitope based subunit vaccine by utilizing immunoinformatics approach to battle against dengue infection." Scientific reports 7(**[G, AR]**

7. Alibakhshi, A., Bandehpour, M., Nafarieh, T., Gheflat, S., and Kazemi, B. (2017). "In silico analysis of immunologic regions of surface antigens (SAGs) of Toxoplasma gondii." Novelty in Biomedicine 5(3): 109-118. **[G, AR]**

8. Allen, R.B. (2017). "Rich Semantic Models and Knowledgebases for Highly-Structured Scientific Communication." arXiv preprint arXiv:1708.08423 **[G]**

9. Antunes, D.A., Rigo, M.M., Freitas, M.V., Mendes, M.F.A., Sinigaglia, M., Lizee, G., Kavraki, L.E., Selin, L.K., Cornberg, M., and Vieira, G.F. (2017). "Interpreting T-Cell Cross-reactivity through Structure: Implications for TCR-Based Cancer Immunotherapy." Frontiers in Immunology 8(**[G]**

10. Antunes, R.D.S., Paul, S., Sidney, J., Weiskopf, D., Dan, J.M., Phillips, E., Mallal, S., Crotty, S., Sette, A., and Arlehamn, C.S.L. (2017). "Definition of Human Epitopes Recognized in Tetanus Toxoid and Development of an Assay Strategy to Detect Ex Vivo Tetanus CD4(+) T Cell Responses." PloS one 12(1): **[G, AR, MA]**

11. Arnoux, F., Mariot, C., Peen, E., Lambert, N.C., Balandraud, N., Roudier, J., and Auger, I. (2017). "Peptidyl arginine deiminase immunization induces anticitrullinated protein antibodies in mice with particular MHC types." Proceedings of the National Academy of Sciences of the United States of America 114(47): E10169-E10177. **[G]**

12. Awad-Elkareem, M.A.E., Osman, S.A., Mohamed, H.A., Hassan, H.A.E., and bu-Haraz, A.H. (2017). "Prediction and Conservancy Analysis of Multiepitope Based Peptide Vaccine Against Merkel Cell Polyomavirus: An Immunoinformatics Approach." Immunome Res 13(134): 2- **[G, AR]**

13. Baidya, S., Rasel Das, M., Kabir, G., and Arifuzzaman, M. (2017). "Epitope design of L1 protein for vaccine production against Human Papilloma Virus types 16 and 18." Bioinformation 13(3): 86- **[G, AR]**

14. Bakken, T., Cowell, L., Aevermann, B.D., Novotny, M., Hodge, R., Miller, J.A., Lee, A., Chang, I., McCorrison, J., Pulendran, B., Qian, Y., Schork, N.J., Lasken, R.S., Lein, E.S., and Scheuermann, R.H. (2017). "Cell type discovery and representation in the era of high-content single cell phenotyping." Bmc Bioinformatics 18(**[G]**

15. Banjara, M., Ghosh, C., Dadas, A., Mazzone, P., and Janigro, D. (2017). "Detection of brain-directed autoantibodies in the serum of non-small cell lung cancer patients." PloS one 12(7): **[G]**

16. Barton, A., Ethier, J.F., Duvauferrier, R.., and Burgun, A. (2017). "An ontological analysis of medical Bayesian indicators of performance." Journal of Biomedical Semantics 8(1): 1- **[G]**

17. Bassani-Sternberg, M., Chong, C., Guillaume, P., Solleder, M., Pak, H., Gannon, P.O., Kandalaft, L.E., Coukos, G., and Gfeller, D. (2017). "Deciphering HLA-I motifs across HLA peptidomes improves neo-antigen predictions and identifies allostery regulating HLA specificity." Plos Computational Biology 13(8): **[G, AR]**

18. Basu, A., Sarkar, A., and Basak, P. (2017). "Epitope-based molecular docking studies of allergenic proteins with immunoglobulin protein during type I hypersensitivity reaction." JIPBS **[G]**

19. Bhalla, S., Verma, R., Kaur, H., Kumar, R., Usmani, S.S., Sharma, S., and Raghava, G.P.S. (2017). "CancerPDF: A repository of cancer-associated peptidome found in human biofluids." Scientific reports 7(**[G]**

20. Bhattacharya, R., Sivakumar, A., Tokheim, C., Guthrie, V.B., Anagnostou, V., Velculescu, V.E., and Karchin, R. (2017). "Evaluation of machine learning methods to predict peptide binding to MHC Class I proteins." bioRxiv 154757- **[G, AR]**

21. Bommana, S., Walker, E., Desclozeaux, M., Timms, P., and Polkinghorne, A. (2017). "Humoral immune response against two surface antigens of Chlamydia pecorum in vaccinated and naturally infected sheep." PloS one 12(11): **[G]**

22. Borrman, T., Cimons, J., Cosiano, M., Purcaro, M., Pierce, B.G., Baker, B.M., and Weng, Z.P. (2017). "ATLAS: A database linking binding affinities with structures for wild-type and mutant TCR-pMHC complexes." Proteins-Structure Function and Bioinformatics 85(5): 908-916. **[G]**

23. Braunlein, E. and Krackhardt, A.M. (2017). "Tools to define the melanoma-associated immunopeptidome." Immunology 152(4): 536-544. **[G, AR]**

24. Cai, N.L., Lau, A.T.Y., Yu, F.Y., Wu, D.D., Dai, L.J., Mo, H.Y., Lin, C.M., and Xu, Y.M. (2017). "Purification and characterization of a highly specific polyclonal antibody against human extracellular signal-regulated kinase 8 and its detection in lung cancer." PloS one 12(9): **[G]**

25. Ceusters, W. and Blaisure, J. A Realism-Based View on Counts in OMOP's Common Data Model. 55-62. 2017. PHEALTH 2017
Studies in Health Technology and Informatics.
Ref Type: Book, Whole **[G]**

26. Chakraborty, A.K. (2017). "A Perspective on the Role of Computational Models in Immunology." Annual Review of Immunology, Vol 35 35(403-439. **[G]**

27. Chang, T.C., Carter, R.A., Li, Y.J., Li, Y.X., Wang, H., Edmonson, M.N., Chen, X., Arnold, P., Geiger, T.L., Wu, G., Peng, J.M., Dyer, M., Downing, J.R., Green, D.R., Thomas, P.G., and Zhang, J.H. (2017). "The neoepitope landscape in pediatric cancers." Genome Medicine 9(**[G, AR]**

28. Choong, Yee Siew, Lee, Yie Vern, Soong, Jia Xin, Law, Cheh Tat, and Lim, Yee Ying. Computer-Aided Antibody Design: An Overview. Recombinant Antibodies for Infectious Diseases. 221-243. 2017. Springer.
Ref Type: Book Chapter **[G, AR]**

29. Connor, D.O., Danckert, L., Hoppe, S., Bier, F.F., and von Nickisch-Rosenegk, M. (2017). "Epitope determination of immunogenic proteins of Neisseria gonorrhoeae." PloS one 12(7): **[G]**

30. Dalkas, G.A. and Rooman, M. (2017). "SEPIa, a knowledge-driven algorithm for predicting conformational B-cell epitopes from the amino acid sequence." Bmc Bioinformatics 18(**[G, AR]**

31. Damfo, S.A., Reche, P., Gatherer, D., and Flower, D.R. (2017). "In silico design of knowledge-based Plasmodium falciparum epitope ensemble vaccines." Journal of Molecular Graphics & Modelling 78(195-205. **[G, AR]**

32. de Siqueira, Gustavo Oliveira, Canuto, S., Gonçalves, Marcos André, and Laender, Alberto HF. Automatic Hierarchical Categorization of Research Expertise Using Minimum Information. International Conference on Theory and Practice of Digital Libraries , 103-115. 2017. Springer.
Ref Type: Conference Proceeding **[G]**

33. Dey, S., Nandy, A., Basak, S.C., Nandy, P., and Das, S. (2017). "A Bioinformatics approach to designing a Zika virus vaccine." Computational Biology and Chemistry 68(143-152. **[G, AR]**

34. Dhanda, S.K., Usmani, S.S., Agrawal, P., Nagpal, G., Gautam, A., and Raghava, G.P.S. (2017). "Novel in silico tools for designing peptide-based subunit vaccines and immunotherapeutics." Briefings in bioinformatics 18(3): 467-478. [**G, AR]**

35. Degoot, A.M., Chirove, F., and Ndifon, W. (2017). "Trans-allelic model for prediction of peptide: MHC-II interactions." arXiv preprint arXiv:1712.00351 **[G, AR]**

36. Di Marco, M., Schuster, H., Backert, L., Ghosh, M., Rammensee, H.G., and Stevanovic, S. (2017). "Unveiling the Peptide Motifs of HLA-C and HLA-G from Naturally Presented Peptides and Generation of Binding Prediction Matrices." Journal of Immunology 199(8): 2639-2651. **[G, AR]**

37. Dragsted, L.O., Gao, Q., Pratico, G., Manach, C., Wishart, D.S., Scalbert, A., and Feskens, E.J.M. (2017). "Dietary and health biomarkers-time for an update." Genes and Nutrition 12(**[G]**

38. Duquesnoy, R.J. and Marrari, M. (2017). "Usefulness of the ElliPro epitope predictor program in defining the repertoire of HLA-ABC eplets." Human Immunology 78(7-8): 481-488. **[G, AR]**

39. El Bissati, K., Zhou, Y., Paulillo, S.M., Raman, S.K., Karch, C.P., Roberts, C.W., Lanar, D.E., Reed, S., Fox, C., Carter, D., Alexander, J., Sette, A., Sidney, J., Lorenzi, H., Begeman, I.J., Burkhard, P., and McLeod, R. (2017). "Protein nanovaccine confers robust immunity against Toxoplasma." Npj Vaccines 2(**[G, AR]**

40. Escalona, E., Saez, D., and Onate, A. (2017). "Immunogenicity of a Multi-Epitope DNA Vaccine Encoding Epitopes from Cu-Zn Superoxide Dismutase and Open Reading Frames of Brucella abortus in Mice." Frontiers in Immunology 8(**[G, AR]**

41. Esteban-Gil, A., Fernandez-Breis, J.T., and Boeker, M. (2017). "Analysis and visualization of disease courses in a semantically-enabled cancer registry." Journal of Biomedical Semantics 8(**[G]**

42. Facchiano, A. (2017). "Bioinformatic resources for the investigation of proteins and proteomes." Peptidomics 3(1): 1-10. **[G]**

43. Fanuel, S., Tabesh, S., Sadroddiny, E., and Kardar, G.A. (2017). "Analysis of predicted B and T-cell epitopes in Der p 23, allergen from Dermatophagoides pteronyssinus." Bioinformation 13(9): 307- **[G]**

44. Farhadi, T. and Ranjbar, M.M. (2017). "Designing and modeling of complex DNA vaccine based on MOMP of Chlamydia trachomatis: an in silico approach." Network Modeling Analysis in Health Informatics and Bioinformatics 6(1): 1- **[G]**

45. Farhadi, T. and Hashemian, S.M. (2017). "Constructing novel chimeric DNA vaccine against Salmonella enterica based on SopB and GroEL proteins: an in silico approach." Journal of Pharmaceutical Investigation 1-17.

46. Fu, Z.Y. and Lin, J. (2017). "An Overview of Bioinformatics Tools and Resources in Allergy." Food Allergens: Methods and Protocols 1592(223-245. **[G, AR]**

47. Galperin, M.Y., Fernandez-Suarez, X.M., and Rigden, D.J. (2017). "The 24th annual Nucleic Acids Research database issue: a look back and upcoming changes." Nucleic acids research 45(D1): D1-D11. **[G]**

48. Garijo, Daniel, Gil, Yolanda, and Ratnakar, Varun. The DISK Hypothesis Ontology: Capturing Hypothesis Evolution for Automated Discovery. 2017.
Ref Type: Thesis/Dissertation **[G]**

49. Gilardin, L., Delignat, S., Peyron, I., Ing, M., Lone, Y.C., Gangadharan, B., Michard, B., Kherabi, Y., Sharma, M., Pashov, A., Latouche, J.B., Hamieh, M., Toutirais, O., Loiseau, P., Galicier, L., Veyradier, A., Kaveri, S., Maillere, B., Coppo, P., and Lacroix-Desmazes, S. (2017). "The ADAMTS13(1239-1253) peptide is a dominant HLA-DR1-restricted CD4(+) T-cell epitope." Haematologica 102(11): 1833-1841. **[G, AR]**

50. Giraldo, O., Garcia, A., Lopez, F., and Corcho, O. (2017). "Using semantics for representing experimental protocols." Journal of Biomedical Semantics 8(**[G]**

51. Gistera, A., Hermansson, A., Strodthoff, D., Klement, M.L., Hedin, U., Fredrikson, G.N., Nilsson, J., Hansson, G.K., and Ketelhuth, D.F.J. (2017). "Vaccination against T-cell epitopes of native

ApoB100 reduces vascular inflammation and disease in a humanized mouse model of atherosclerosis." Journal of Internal Medicine 281(4): 383-397. **[G, AR]**

52. Gkoutos, G.V., Schofield, P.N., and Hoehndorf, R. (2017). "The anatomy of phenotype ontologies: principles, properties and applications." Briefings in bioinformatics bbx035- **[G]**

53. Gonzalez-Beltran, A.N., Campbell, J., Dunn, P., Guijarro, D., Ionescu, S., Kim, H., Lyle, J., Wiser, J., Sansone, S.A., and Rocca-Serra, P. (2017). "Data discovery with DATS: exemplar adoptions and lessons learned." Journal of the American Medical Informatics Association 25(1): 13-16. **[G]**

54. Goswami, N., Hussain, M.I., and Borah, P. (2017). "Molecular dynamics approach to probe the antigenicity of PagNGÇôan outer membrane protein of Salmonella Typhi." Journal of Biomolecular Structure and Dynamics 1-19. **[G, AR]**

55. Gourlay, L., Peri, C., Bolognesi, M., and Colombo, G. (2017). "Structure and Computation in Immunoreagent Design: From Diagnostics to Vaccines." Trends in Biotechnology 35(12): 1208-1220. **[G, AR]**

56. Griffiths, E., Dooley, D., Graham, M., Van Domselaar, G., Brinkman, F.S., and Hsiao, W.W. (2017). "Context Is Everything: Harmonization of Critical Food Microbiology Descriptors and Metadata for Improved Food Safety and Surveillance." Frontiers in Microbiology 8(1068- **[G]**

57. Grifoni, A., Angelo, M., Sidney, J., Paul, S., Peters, B., De Silva, A.D., Phillips, E., Mallal, S., Diehl, S.A., Botten, J., Boyson, J., Kirkpatrick, B.D., Whitehead, S.S., Durbin, A.P., Sette, A., and Weiskopf, D. (2017). "Patterns of Cellular Immunity Associated with Experimental Infection with rDEN2 Delta 30 (Tonga/74) Support Its Suitability as a Human Dengue Virus Challenge Strain." Journal of Virology 91(8): **[G, AR]**

58. Grimes, B.S. (2017). "The immune contexture and genomic landscape of lung adenomatous premalignancy." **[G, AR]**

59. Guillaume, P., Picaud, S., Baumgaertner, P., Montandon, N., Schmidt, J., Speiser, D.E., Coukos, G., Bassani-Sternberg, M., Fillipakopoulos, P., and Gfeller, D. (2017). "The C-terminal extension landscape of naturally presented HLA-I ligands." bioRxiv 213264- **[G, AR]**

60. Gupta, S., Mittal, P., Madhu, M.K., and Sharma, V.K. (2017). "IL17eScan: A Tool for the Identification of Peptides Inducing IL-17 Response." Frontiers in Immunology 8(**[G]**

61. Gurcan, M.N., Tomaszewski, J., Overton, J.A., Doyle, S., Ruttenberg, A., and Smith, B. (2017). "Developing the Quantitative Histopathology Image Ontology (QHIO): a case study using the hot spot detection problem." Journal of Biomedical Informatics 66(129-135. **[G]**

62. Hadrup, S.R. and Newell, E.W. (2017). "Determining T-cell specificity to understand and treat disease." Nature Biomedical Engineering 1(10): 784-795. **[G, AR]**

63. Hammerbacher, J. and Snyder, A. (2017). "Informatics for cancer immunotherapy." Annals of Oncology 28(56-73. **[G, AR]**

64. Han, Y. and Kim, D. (2017). "Deep convolutional neural networks for pan-specific peptide-MHC class I binding prediction." Bmc Bioinformatics 18(1): 585- **[G, AR]**

65. Hansen, C.S., Osterbye, T., Marcatili, P., Lund, O., Buus, S., and Nielsen, M. (2017). "ArrayPitope: Automated Analysis of Amino Acid Substitutions for Peptide Microarray-Based Antibody Epitope Mapping." PloS one 12(1): **[G, AR]**

66. Harada, N., Fukaya, S., Wada, H., Goto, R., Osada, T., Gomori, A., Ikizawa, K., Sakuragi, M., and Oda, N. (2017). "Generation of a Novel HLA Class I Transgenic Mouse Model Carrying a Knock-

in Mutation at the beta(2)-Microglobulin Locus." Journal of Immunology 198(1): 516-527. **[G, AR]**

67. Hart, G.R. (2017). "In silico vaccine design for hepatitis C: a computational platform for fighting disease." **[G, AR]**

68. He, W., Shu, J.Y., Zhang, J.A., Liu, Z.H., Xu, J.Q., Jin, X., and Wang, X.D. (2017). "Expression, purification, and renaturation of a recombinant peptide-based HIV vaccine in Escherichia coli." Canadian Journal of Microbiology 63(6): 493-501. **[G, AR]**

69. Hekmat, S., Siadat, S.D., Aghasadeghi, M.R., Sadat, S.M., Bahramali, G., Aslani, M.M., Mandavi, M., and Shahbazi, S. (2017). "From in-silico immunogenicity verification to in vitro expression of recombinant Core-NS3 fusion protein of HCV." Bratislava Medical Journal-Bratislavske Lekarske Listy 118(4): 189-195. **[G]**

70. Holay, N., Kim, Y., Lee, P., and Gujar, S. (2017). "Sharpening the edge for Precision Cancer immunotherapy: Targeting Tumor Antigens through Oncolytic vaccines." Frontiers in Immunology 8(**[G]**

71. Hossain, M.S., Azad, A., Chowdhury, P.A., and Wakayama, M. (2017). "Computational Identification and Characterization of a Promiscuous T-Cell Epitope on the Extracellular Protein 85B of Mycobacterium spp. for Peptide- Based Subunit Vaccine Design." Biomed Research International **[G, AR, MA]**

72. Hu, Y.J., You, S.N., and Ko, C.L. (2017). "Computational Ensemble Approach for Immune System Study: Conformational B-cell Epitope Prediction." EJBI 13(2): **[G, AR]**

73. Hua, C.K., Gacerez, A.T., Sentman, C.L., Ackerman, M.E., Choi, Y., and Bailey-Kellogg, C. (2017). "Computationally-driven identification of antibody epitopes." Elife 6(**[G, AR]**

74. Hua, Casey. Developing Antibody-Based Immunotherapies for the Clinic: Strategies and Tools to Translate Discoveries from Bench to Bedside. 2017. Dartmouth College.
Ref Type: Book, Whole **[G, AR]**

75. Hung, L.C. and Cheng, I.C. (2017). "Versatile carboxyl-terminus of capsid protein of porcine circovirus type 2 were recognized by monoclonal antibodies with pluripotency of binding." Molecular Immunology 85(100-110. **[G]**

76. Hunter, L.E. (2017). "Knowledge-based biomedical Data Science." Data Science Preprint): 1-7. **[G]**

77. Hyder, S.I., Ansari, J., Ramish, M.S., Yasir, M., and Fasih, T. (2017). "Emerging Role of Ontology Based Repository in Business Management Research." **[G]**

78. Idris, A.B., Mahmoud, S.M., Mohamedelamin, S., Mustafa, Y.Y., and Osman, A.A. (2017). "Immunoinformatics Predication and Modelling of a Cocktail of B-and T-cells Epitopes from Envelope Glycoprotein and Nucleocapsid Proteins of Sin Nombre Virus." Immunome Res 13(141): 2- **[G, AR]**

79. Ikram, A., Obaid, A., Awan, F.M., Hanif, R., Naz, A., Paracha, R.Z., Ali, A., and Janjua, H.A. (2017). "Identification of drug resistance and immune-driven variations in hepatitis C virus (HCV) NS3/4A, NS5A and NS5B regions reveals a new approach toward personalized medicine." Antiviral Research 137(112-124. **[G]**

80. Immanuel, C., Ramanathan, A., Balasubramaniyan, M., Khatri, V.K., Amdare, N.P., Rao, D.N., Reddy, M.V.R., and Perumal, K. (2017). "Immunoprophylaxis of multi-antigen peptide (MAP) vaccine for human lymphatic filariasis." Immunologic Research 65(3): 729-738. **[G]**

81. Isea, R. (2017). "Quantitative prediction of linear B-cell epitopes." arXiv preprint arXiv:1703.02453 **[G]**

82. Ives, C., Campia, I., Wang, R.L., Wittwehr, C., and Edwards, S. (2017). "Creating a Structured Adverse Outcome Pathway Knowledgebase via Ontology-Based Annotations." Applied In Vitro Toxicology 3(4): 298-311. **[G]**

83. Jaravine, V., Mosch, A., Raffegerst, S., Schendel, D.J., and Frishman, D. (2017). "Expitope 2.0: a tool to assess immunotherapeutic antigens for their potential cross-reactivity against naturally expressed proteins in human tissues." Bmc Cancer 17(**[G]**

84. Jia, X.M., Yang, L., Dong, M.X., Chen, S.T., Lv, L.N., Cao, D.D., Fu, J., Yang, T.T., Zhang, J., Zhang, X.L., Shang, Y.Y., Wang, G.R., Sheng, Y.J., Huang, H.R., and Chen, F. (2017). "The Bioinformatics Analysis of Comparative Genomics of Mycobacterium tuberculosis Complex (MTBC) Provides Insight into Dissimilarities between Intraspecific Groups Differingin Host Association, Virulence, and Epitope Diversity." Frontiers in Cellular and Infection Microbiology 7(**[G]**

85. Jiang, X.Y., Ringwald, M., Blake, J., and Shatkay, H. (2017). "Effective biomedical document classification for identifying publications relevant to the mouse Gene Expression Database (GXD)." Database-the Journal of Biological Databases and Curation **[G]**

86. Jimenez-Sanchez, A., Memon, D., Pourpe, S., Veeraraghavan, H., Li, Y.Y., Vargas, H.A., Gill, M.B., Park, K.J., Zivanovic, O., Konner, J., Ricca, J., Zamarin, D., Walther, T., Aghajanian, C., Wolchok, J.D., Sala, E., Merghoub, T., Snyder, A., and Miller, M.L. (2017). "Heterogeneous Tumor-Immune Microenvironments among Differentially Growing Metastases in an Ovarian Cancer Patient." Cell 170(5): 927-. **[G, AR]**

87. Judkins, John, Tay-Sontheimer, Jessica, Boyce, Richard D., and Brochhausen, Mathias. Extending the DIDEO ontology to include entities from the natural product drug interaction domain of discourse. 2017.
Ref Type: Thesis/Dissertation **[G]**

88. Kadam, K., Karbhal, R., Jayaraman, V.K., Sawant, S., and Kulkarni-Kale, U. (2017). "AllerBase: a comprehensive allergen knowledgebase." Database-the Journal of Biological Databases and Curation **[G]**

89. Kalina, J.L., Neilson, D.S., Lin, Y.Y., Hamilton, P.T., Comber, A.P., Loy, E.M.H., Sahinalp, S.C., Collins, C.C., Hach, F., and Lum, J.J. (2017). "Mutational Analysis of Gene Fusions Predicts Novel MHC Class I-Restricted T-Cell Epitopes and Immune Signatures in a Subset of Prostate Cancer." Clinical Cancer Research 23(24): 7596-7607. **[G]**

90. Kametani, Y., Katano, I., Miyamoto, A., Kikuchi, Y., Ito, R., Muguruma, Y., Tsuda, B., Habu, S., Tokuda, Y., Ando, K., and Ito, M. (2017). "NOG-hIL-4-Tg, a new humanized mouse model for producing tumor antigen-specific IgG antibody by peptide vaccination." PloS one 12(6): **[G]**

91. Kar, B., Mohapatra, A., Mohanty, J., and Sahoo, P.K. (2017). "Evaluation of ribosomal P0 peptide as a vaccine candidate against Argulus siamensis in Labeo rohita." Open Life Sciences 12(1): 99-108. **[G]**

92. Karunakaran, K.P., Yu, H., Jiang, X.Z., Chan, Q., Goldberg, M.F., Jenkins, M.K., Foster, L.J., and Brunham, R.C. (2017). "Identification of MHC-Bound Peptides from Dendritic Cells Infected with Salmonella enterica Strain SL1344: Implications for a Nontyphoidal Salmonella Vaccine." Journal of Proteome Research 16(1): 298-306. **[G]**

93. Kashyap, M., Jaiswal, V., and Farooq, U. (2017). "Prediction and analysis of promiscuous T cell-epitopes derived from the vaccine candidate antigens of Leishmania donovani binding to MHC class-II alleles using in silico approach." Infection Genetics and Evolution 53(107-115. **[G, AR]**

94. Kaufman, J. (2017). "Evolution of the MHC and the Adaptive Immune System of Jawed Vertebrates." Annual review of immunology 35(1): **[G, AR]**

95. Khan, A.M., Hu, Y., Miotto, O., Thevasagayam, N.M., Sukumaran, R., Raman, H.S.A., Brusic, V., Tan, T.W., and August, J.T. (2017). "Analysis of viral diversity for vaccine target discovery." Bmc Medical Genomics 10(4): 78- **[G, AR]**

96. Khan, N., Kumar, R., Chauhan, S., and Farooq, U. (2017). "An immunoinformatics approach to promiscuous peptide design for the Plasmodium falciparum erythrocyte membrane protein-1." Molecular Biosystems 13(10): 2160-2167. **[G, AR]**

97. Khodadoust, M.S., Olsson, N., Wagar, L.E., Haabeth, O.A.W., Chen, B.B., Swaminathan, K., Rawson, K., Liu, C.L., Steiner, D., Lund, P., Rao, S., Zhang, L.C., Marceau, C., Stehr, H., Newman, A.M., Czerwinski, D.K., Carlton, V.E.H., Moorhead, M., Faham, M., Kohrt, H.E., Carette, J., Green, M.R., Davis, M.M., Levy, R., Elias, J.E., and Alizadeh, A.A. (2017). "Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens." Nature 543(7647): 723-. **[G, AR]**

98. Koch, A.S., Brites, D., Stucki, D., Evans, J.C., Seldon, R., Heekes, A., Mulder, N., Nicol, M., Oni, T., Mizrahi, V., Warner, D.F., Parkhill, J., Gagneux, S., Martin, D.P., and Wilkinson, R.J. (2017). "The Influence of HIV on the Evolution of Mycobacterium tuberculosis." Molecular Biology and Evolution 34(7): 1654-1668. **[G]**

99. Korenkov, D., Nguyen, T.H.O., Isakova-Sivak, I., Smolonogina, T., Brown, L.E., Kedzierska, K., and Rudenko, L. (2017). "Live Attenuated Influenza Vaccines engineered to express the nucleoprotein of a recent isolate stimulate human influenza CD8+ T cells more relevant to current infections." Human Vaccines & Immunotherapeutics just-accepted): 00-00. **[G]**

100. Krallinger, M., Rabal, O., Lourenco, A., Oyarzabal, J., and Valencia, A. (2017). "Information Retrieval and Text Mining Technologies for Chemistry." Chemical Reviews 117(12): 7673-7761. **[G]**

101. Krawczyk, K., Dunbar, J., and Deane, C. M. Computational Tools for Aiding Rational Antibody Design. 399-416. 2017. COMPUTATIONAL PROTEIN DESIGN Methods in Molecular Biology.
Ref Type: Book, Whole **[G, AR]**

102. Krishna, S. (2017). "T-Cell Immunogenicity and Dysfunction in Cancer and Viral Diseases." **[G, AR, MA]**

103. Kshirsagar, M., Murugesan, K., Carbonell, J.G., and Klein-Seetharaman, J. (2017). "Multitask matrix completion for learning protein interactions across diseases." Journal of Computational Biology 24(6): 501-514 **[G]**

104. Kyeong, H.H., Choi, Y., and Kim, H.S. (2017). "GradDock: rapid simulation and tailored ranking functions for peptide-MHC Class I docking." Bioinformatics **[G, AR]**

105. Larsen, R.R. (2017). "Pathologizing Evil A Critique of Modern Psychopathy Research." **[G]**

106. Lateef, Z., Gimenez, G., Baker, E.S., and Ward, V.K. (2017). "Transcriptomic analysis of human norovirus NS1-2 protein highlights a multifunctional role in murine monocytes." Bmc Genomics 18(**[G]**

107. Lawrynowicz, Agnieszka, Potoniec, Jedrzej, Robaczyk, Michal, and Tudorache, Tania. Discovery of emerging design patterns in ontologies using tree mining. Semantic Web [Preprint], 1-28. 2017. IOS Press.
Ref Type: Unpublished Work **[G]**

108. Lee, A.J., Bhattacharya, R., Scheuermann, R.H., and Pickett, B.E. (2017). "Identification of diagnostic peptide regions that distinguish Zika virus from related mosquito-borne Flaviviruses." PloS one 12(5): **[G, AR]**

109. Lee, P. (2017). "Centralization, fragmentation, and replication in the genomic data commons." Governing Medical Knowledge Commons 46- **[G]**

110. Leonard, J.D., Gilmore, D.C., Dileepan, T., Nawrocka, W.I., Chao, J.L., Schoenbach, M.H., Jenkins, M.K., Adams, E.J., and Savage, P.A. (2017). "Identification of Natural Regulatory T Cell Epitopes Reveals Convergence on a Dominant Autoantigen." Immunity 47(1): 107-+. **[G]**

111. Leong, S.W., Lim, T.S., Ismail, A., and Choong, Y.S. (2017). "Integration of molecular dynamics simulation and hotspot residues grafting for de novo scFv design against Salmonella Typhi TolC protein." Journal of Molecular Recognition **[G]**

112. Lewis, Suzanna E. The Vision and Challenges of the Gene Ontology. The Gene Ontology Handbook. 291-302. 2017. Springer.
Ref Type: Book Chapter **[G]**

113. Li, H., Schaduangrat, N., Simeon, S., and Nantasenamat, C. (2017). "Computational study on the origin of the cancer immunotherapeutic potential of B and T cell epitope peptides." Molecular Biosystems 13(11): 2310-2322. **[G, AR]**

114. Li, L., Goedegebuure, S.P., and Gillanders, W.E. (2017). "Preclinical and clinical development of neoantigen vaccines." Annals of Oncology 28(11-17. **[G, AR]**

115. Liu, G., Li, D.L., Li, Z., Qiu, S., Li, W.H., Chao, C.C., Yang, N.B., Li, H.D., Cheng, Z., Song, X., Cheng, L., Zhang, X.Q., Wang, J., Yang, H.M., Ma, K., Hou, Y., and Li, B. (2017). "PSSMHCpan: a novel PSSM-based software for predicting class I peptide-HLA binding affinity." Gigascience 6(5): **[G, AR]**

116. Liu, Y.F., Lin, C.Y., and Hong, H.M. (2017). "In silico Design, Synthesis and Potency of an Epitope-based Vaccine Against Foot-and-mouth Disease Virus." International Journal of Pharmacology 13(2): 122-133. **[G, AR]**

117. Lohia, N. and Baranwal, M. (2017). "Immune responses to highly conserved influenza A virus matrix 1 peptides." Microbiology and Immunology 61(6): 225-231. **[G]**

118. Lu, Y.J., Chen, D.S., Hao, W.T., Xu, H.W., Zhang, Y.W., Sun, F.F., and Pan, W. (2017). "In silico characterization of Echinococcus granulosus paramyosin nucleotide sequence for the development of epitope vaccine against cystic echinococcosis." Helminthologia 54(4): 275-283. **[G, AR]**

119. Lucchese, A. (2017). "Streptococcus mutans antigen I/II and autoimmunity in cardiovascular diseases." Autoimmunity Reviews 16(5): 456-460. **[G]**

120. Lucchese, G. (2017). "From toxoplasmosis to schizophrenia via nMda dysfunction: peptide overlap between Toxoplasma gondii and N-Methyl-D-aspartate receptors as a potential Mechanistic Link." Frontiers in Psychiatry 8(**[G]**

121. Lucchese, G. and Kanduc, D. (2017). "Minimal immune determinants connect Zika virus, human Cytomegalovirus, and Toxoplasma gondii to microcephaly-related human proteins." American Journal of Reproductive Immunology 77(2): **[G]**

122. Luksza, M., Riaz, N., Makarov, V., Balachandran, V.P., Hellmann, M.D., Solovyov, A., Rizvi, N.A., Merghoub, T., Levine, A.J., Chan, T.A., Wolchok, J.D., and Greenbaum, B.D. (2017). "A neoantigen fitness model predicts tumour response to checkpoint blockade immunotherapy." Nature 551(7681): 517-+. **[G, AR]**

123. Lule, S., Colpak, A.I., Balci-Peynircioglu, B., Gursoy-Ozdemir, Y., Peker, S., Kalyoncu, U., Can, A., Tekin, N., Demiralp, D., and Dalkara, T. (2017). "Behcet Disease serum is immunoreactive to neurofilament medium which share common epitopes to bacterial HSP-65, a putative trigger." Journal of autoimmunity 84(87-96. **[G]**

124. Madhumathi, J., Prince, P.R., Rao, D.N., Karande, A.A., Reddy, M.V.R., and Kaliraj, P. (2017). "Epitope mapping of Brugia malayi ALT-2 and the development of a multi-epitope vaccine for lymphatic filariasis." Journal of Helminthology 91(1): 43-54. **[G]**

125. MAIKORE, Fatima S., SELENGE, Gantigmaa, OLAYINKA, Adebola, ABBOTT, Pamela, and Soldatova, Larisa. An Ontology for Clinical Laboratory Standard Operating Procedures. 2017.
Ref Type: Generic

126. Martinez-Arzate, S.G., Tenorio-Borroto, E., Pliego, A.B., az-Albiter, H.M., Vazquez-Chagoyan, J.C., and Gonzalez-Diaz, H. (2017). "PTML Model for Proteome Mining of B-Cell Epitopes and Theoretical-Experimental Study of Bm86 Protein Sequences from Colima, Mexico." Journal of Proteome Research 16(11): 4093-4103. **[G]**

127. Martinez-Romero, M., Jonquet, C., O'Connor, M.J., Graybeal, J., Pazos, A., and Musen, M.A. (2017). "NCBO Ontology Recommender 2.0: an enhanced approach for biomedical ontology recommendation." Journal of Biomedical Semantics 8(**[G]**

128. Marty, R., Kaabinejadian, S., Rossell, D., Slifker, M.J., van de Haar, J., Engin, H.B., de Prisco, N., Ideker, T., Hildebrand, W.H., Font-Burgada, J., and Carter, H. (2017). "MHC-I Genotype Restricts the Oncogenic Mutational Landscape." Cell 171(6): 1272-+. **[G, AR]**

129. Matiasz, N.J., Wood, J., Wang, W., Silva, A.J., and Hsu, W. (2017). "Computer-Aided Experiment Planning toward Causal Discovery in Neuroscience." Frontiers in Neuroinformatics 11(**[G]**

130. Mazor, R., Addissie, S., Jang, Y.J., Tai, C.H., Rose, J., Hakim, F., and Pastan, I. (2017). "Role of HLA-DP in the Presentation of Epitopes from the Truncated Bacterial PE38 Immunotoxin." Aaps Journal 19(1): 117-129. **[G, AR]**

131. McGee, M. (2017). "Design and Humoral Analysis of Two Epitope-Based Brucella abortus DNA Vaccines."

132. Merani, S., Lucas, M., Deshpande, P., Pfafferott, K., Chopra, A., Cooper, D., Leary, S., Luciani, F., and Gaudieri, S. (2017). "Influence of Transmitted Virus on the Host's Immune Response: A Case Study." Viral Immunology 30(7): 533-541. **[G]**

133. Miller, A., Asmann, Y., Cattaneo, L., Braggio, E., Keats, J., Auclair, D., Lonial, S., Russell, S.J., and Stewart, A.K. (2017). "High somatic mutation and neoantigen burden are correlated with decreased progression-free survival in multiple myeloma." Blood Cancer Journal 7(**[G, AR]**

134. Mishra, Ankita and Arora, Naveen. Allergenicity Assessment of Transgenic Wheat Lines In Silico. Wheat Biotechnology. 97-111. 2017. Springer.
Ref Type: Book Chapter **[G, AR]**

135. Mobbs, J.I., Illing, P.T., Dudek, N.L., Brooks, A.G., Baker, D.G., Purcell, A.W., Rossjohn, J., and Vivian, J.P. (2017). "The molecular basis for peptide repertoire selection in the human leukocyte antigen (HLA) C*06:02 molecule." Journal of Biological Chemistry 292(42): 17203-17215. **[G]**

136. Mohammed, A.A., Hashim, O., Elrahman, K.A.A., Hamdi, A., and Hassan, M.A. (2017). "Epitope-Based Peptide Vaccine Design Against Mokola Rabies Virus Glycoprotein G Utilizing In Silico Approaches." Immunome Res 13(144): 2- **[G, AR]**

137. Mottin, L., Pasche, E., Gobeill, J., de Laval, V.R., Gleizes, A., Michel, P.A., Bairoch, A., Gaudet, P., and Ruch, P. (2017). "Triage by ranking to support the curation of protein interactions." Database-the Journal of Biological Databases and Curation **[G]**

138. Muehling, L.M., Lawrence, M.G., and Woodfolk, J.A. (2017). "Pathogenic CD4(+) T cells in patients with asthma." Journal of Allergy and Clinical Immunology 140(6): 1523-1540. **[G, AR, MA]**

139. Mungall, C.J., McMurry, J.A., Kohler, S., Balhoff, J.P., Borromeo, C., Brush, M., Carbon, S., Conlin, T., Dunn, N., Engelstad, M., Foster, E., Gourdine, J.P., Jacobsen, J.O.B., Keith, D., Laraway, B., Lewis, S.E., NguyenXuan, J., Shefchek, K., Vasilevsky, N., Yuan, Z., Washington, N., Hochheiser, H., Groza, T., Smedley, D., Robinson, P.N., and Haendel, M.A. (2017). "The Monarch Initiative: an integrative data and analytic platform connecting phenotypes to genotypes across species." Nucleic acids research 45(D1): D712-D722. **[G]**

140. Murphy, J.P., Konda, P., Kowalewski, D.J., Schuster, H., Clements, D., Kim, Y., Cohen, A.M., Sharif, T., Nielsen, M., Stevanovic, S., Lee, P.W., and Gujar, S. (2017). "MHC-I Ligand Discovery Using Targeted Database Searches of Mass Spectrometry Data: Implications for T-Cell Immunotherapies." Journal of Proteome Research 16(4): 1806-1816. **[G, AR]**

141. Naeem, M.R., Ali, W., Hamad Naeem, M.A., and Abro, W.A. (2017). "A multi-level process mining framework for correlating and clustering of biomedical activities using event logs." International Journal of Advanced Computer Science and Applications 8(3): 393-401. **[G]**

142. Nagpal, G., Usmani, S.S., Dhanda, S.K., Kaur, H., Singh, S., Sharma, M., and Raghava, G.P.S. (2017). "Computer-aided designing of immunosuppressive peptides based on IL-10 inducing potential." Scientific reports 7(**[G]**

143. Nagpal, G., Chaudhary, K., Agrawal, P., and Raghava, G.P.S. (2017). "Computer-aided prediction of antigen presenting cell modulators for designing peptide-based vaccine adjuvants." bioRxiv 232025- **[G, AR]**

144. Nakamura, S., Ohmura, R., and Nakanishi, I. (2017). "An Interaction-based Approach for Affinity Prediction between Antigen Peptide and Human Leukocyte Antigen Using COMBINE Analysis." Chem-Bio Informatics Journal 17(93-102. **[G, AR]**

145. Nam, B.H., Kwak, W., Kim, Y.O., Kim, D.G., Kong, H.J., Kim, W.J., Kang, J.H., Park, J.Y., An, C.M., and Moon, J.Y. (2017). "Genome sequence of pacific abalone (Haliotis discus hannai): the first draft genome in family Haliotidae." Gigascience 6(5): 1-8. **[G, AR]**

146. Nathanson, T., Ahuja, A., Rubinsteyn, A., Aksoy, B.A., Hellmann, M.D., Miao, D., Van Allen, E., Merghoub, T., Wolchok, J.D., Snyder, A., and Hammerbacher, J. (2017). "Somatic Mutations and Neoepitope Homology in Melanomas Treated with CTLA-4 Blockade." Cancer Immunology Research 5(1): 84-91. **[G, AR]**

147. Nielsen, M., Connelley, T., and Ternette, N. (2017). "Improved Prediction of Bovine Leucocyte Antigens (BoLA) Presented Ligands by Use of Mass-Spectrometry-Determined Ligand and in Vitro Binding Data." Journal of Proteome Research **[G, AR]**

148. O'Donnell, T., Rubinsteyn, A., Bonsack, M., Riemer, A., and Hammerbacher, J. (2017). "MHCflurry: open-source class I MHC binding affinity prediction." bioRxiv 174243- **[G, AR]**

149. Oliveira, F.S., Brestelli, J., Cade, S., Zheng, J., Iodice, J., Fischer, S., Aurrecoechea, C., Kissinger, J.C., Brunk, B.P., and Stoeckert Jr, C.J. (2017). "MicrobiomeDB: a systems biology platform for integrating, mining and analyzing microbiome experiments." Nucleic acids research 46(D1): D684-D691. **[G]**

150. Olsen, L.R., Tongchusak, S., Lin, H.H., Reinherz, E.L., Brusic, V., and Zhang, G.L. (2017). "TANTIGEN: a comprehensive database of tumor T cell antigens." Cancer Immunology Immunotherapy 66(6): 731-735. **[G, AR]**

151. Ong, E., Xie, J., Ni, Z., Liu, Q., Sarntivijai, S., Lin, Y., Cooper, D., Terryn, R., Stathias, V., and Chung, C. (2017). "Ontological representation, integration, and analysis of LINCS cell line cells and their cellular responses." Bmc Bioinformatics 18(17): 556- **[G]**

152. Oom, A.L., Smith, D., and Akrami, K. (2017). "Identification of putative unique immunogenic ZIKV and DENV1-4 peptides for diagnostic cellular based tests." Scientific reports 7(**[G, AR]**

153. Osumi-Sutherland, D., Courtot, M., Balhoff, J.P., and Mungall, C. (2017). "Dead simple OWL design patterns." Journal of Biomedical Semantics 8(1): 18- **[G]**

154. Otchere, I.D., Coscolla, M., Sanchez-Buso, L., sante-Poku, A., Meehan, C., Osei-Wusu, S., Forson, A., Laryea, C., Yahayah, A.I., and Baddoo, A. (2017). "Comparative genomics of Mycobacterium africanum Lineage 5 and Lineage 6 from Ghana suggests different ecological niches." bioRxiv 202234- **[G]**

155. Pahil, S., Taneja, N., Ansari, H.R., and Raghava, G.P.S. (2017). "In silico analysis to identify vaccine candidates common to multiple serotypes of Shigella and evaluation of their immunogenicity." PloS one 12(8): e0180505- **[G]**

156. Pan, W., Chen, D.S., Lu, Y.J., Sun, F.F., Xu, H.W., Zhang, Y.W., Yan, C., Fu, L.L., Zheng, K.Y., and Tang, R.X. (2017). "Bioinformatic prediction of the epitopes of Echinococcus granulosus antigen 5." Biomedical Reports 6(2): 181-187. **[G]**

157. Papageorgiou, L. and Vlachakis, D. (2017). "Antisoma Application: A Fully Integrated V-Like Antibodies Platform." Aims Medical Science 4(4): 382-394. **[G]**

158. Parshotam, L.E. (2017). "Dynamic modelling of the processing of peptides for presentation on major histocompatibility complex class I proteins." **[G, AR]**

159. PENMAN, B.S. and GUPTA, S.U.N.E. (2017). "Detecting signatures of past pathogen selection on human HLA loci: are there needles in the haystack?" Parasitology 1-12. **[G]**

160. Picascia, S., Sidney, J., Camarca, A., Mazzarella, G., Giardullo, N., Greco, L., Auricchio, R., Auricchio, S., Troncone, R., Sette, A., and Gianfrani, C. (2017). "Gliadin-Specific CD8(+) T Cell Responses Restricted by HLA Class I A*0101 and B*0801 Molecules in Celiac Disease Patients." Journal of Immunology 198(5): 1838-1845. **[G, AR]**

161. Platteel, A.C.M., Liepe, J., Textoris-Taube, K., Keller, C., Henklein, P., Schalkwijk, H.H., Cardoso, R., Kloetzel, P.M., Mishto, M., and Sijts, A.J.A.M. (2017). "Multi-level Strategy for Identifying Proteasome-Catalyzed Spliced Epitopes Targeted by CD8(+) T Cells during Bacterial Infection." Cell Reports 20(5): 1242-1253. **[G]**

162. Popovic, B., Gibson, S., Senussi, T., Carmen, S., Kidd, S., Slidel, T., Strickland, I., Xu, J.Q., Spooner, J., Lewis, A., Hudson, N., Mackenzie, L., Keen, J., Kemp, B., Hardman, C., Hatton, D., Wilkinson, T., Vaughan, T., and Lowe, D. (2017). "Engineering the expression of an anti-interleukin-13 antibody through rational design and mutagenesis." Protein Engineering Design & Selection 30(4): 303-311. **[G]**

163. Pradhan, D., Yadav, M., Verma, R., Khan, N.S., Jena, L., and Jain, A.K. (2017). "Discovery of T-cell Driven Subunit Vaccines from Zika Virus Genome: An Immunoinformatics Approach." Interdisciplinary Sciences-Computational Life Sciences 9(4): 468-477. **[G, AR]**

164. Radauer, C. (2017). "Navigating through the Jungle of Allergens: Features and Applications of Allergen Databases." International Archives of Allergy and Immunology 173(1): 1-11. **[G, MA]**

165. Ramaiah, A., Dai, L., Contreras, D., Sinha, S., Sun, R., and Arumugaswami, V. (2017). "Comparative analysis of protein evolution in the genome of pre-epidemic and epidemic Zika virus." Infection Genetics and Evolution 51(74-85. **[G, AR]**

166. Rapp, C., Warta, R., Stamova, S., Nowrouzi, A., Geisenberger, C., Gal, Z., Roesch, S., Dettling, S., Juenger, S., Bucur, M., Jungk, C., DaoTrong, P., Ahmadi, R., Sahm, F., Reuss, D., Fermi, V., Herpel, E., Eckstein, V., Grabe, N., Schramm, C., Weigand, M.A., Debus, J., von Deimling, A., Unterberg, A., Abdollahi, A., Beckhove, P., and Herold-Mende, C. (2017). "Identification of T cell target antigens in glioblastoma stem-like cells using an integrated proteomics-based approach in patient specimens." Acta Neuropathologica 134(2): 297-316. **[G]**

167. Ren, J., Song, J.N., Ellis, J., and Li, J.Y. (2017). "Staged heterogeneity learning to identify conformational B-cell epitopes from antigen sequences." Bmc Genomics 18(**[G, AR]**

168. Roh, W. (2017). "INTEGRATIVE CANCER IMMUNOGENOMIC ANALYSIS OF SERIAL MELANOMA BIOPSIES REVEALS CORRELATES OF RESPONSE AND RESISTANCE TO SEQUENTIAL CTLA-4 AND PD-1 BLOCKADE TREATMENT." **[G]**

169. Roperto, S., Varano, M., Russo, V., Luca, R., Cagiola, M., Gaspari, M., Ceccarelli, D.M., Cuda, G., and Roperto, F. (2017). "Proteomic analysis of protein purified derivative of Mycobacterium bovis." Journal of Translational Medicine 15(**[G]**

170. Rose, N.R. (2017). "Negative selection, epitope mimicry and autoimmunity." Current Opinion in Immunology 49(51-55. **[G, AR]**

171. Roy, A., Nair, S., Sen, N., Soni, N., and Madhusudhan, M.S. (2017). "In silico methods for design of biological therapeutics." Methods **[G, AR]**

172. Rubenstein, A.B., Pethe, M.A., and Khare, S.D. (2017). "MFPred: Rapid and accurate prediction of protein-peptide recognition multispecificity using self-consistent mean field theory." Plos Computational Biology 13(6): **[G]**

173. Rubinsteyn, A., Hodes, I., Kodysh, J., and Hammerbacher, J. (2017). "Vaxrank: A Computational Tool For Designing Personalized Cancer Vaccines." bioRxiv 142919- **[G, AR]**

174. Sagan, S.A., Cruz-Herranz, A., Spencer, C.M., Ho, P.P., Steinman, L., Green, A.J., Sobel, R.A., and Zamvil, S.S. (2017). "Induction of Paralysis and Visual System Injury in Mice by T Cells Specific for Neuromyelitis Optica Autoantigen Aquaporin-4." Jove-Journal of Visualized Experiments 126): **[G]**

175. Saha, M.E. (2017). "Evolutionary Trends in Viral Pathogens within and between Outbreaks." **[G]**

176. Sanchez-Trincado, J.L., Gomez-Perosanz, M., and Reche, P.A. (2017). "Fundamentals and Methods for T- and B-Cell Epitope Prediction." Journal of Immunology Research **[G, AR]**

177. Savenkov, Vadim. Ontology for Representing Human Needs. Knowledge Engineering and Semantic Web: 8th International Conference, KESW 2017, Szczecin, Poland, November 8-10, 2017, Proceedings 786, 195. 2017. Springer.
Ref Type: Conference Proceeding **[G]**

178. Scheuermann, R.H., Sinkovits, R.S., Schenkelberg, T., and Koff, W.C. (2017). "A bioinformatics roadmap for the human vaccines project." Expert Review of Vaccines 16(6): 535-544. **[G]**

179. Schmidt, J., Guillaume, P., Dojcinovic, D., Karbach, J., Coukos, G., and Luescher, I. (2017). "In silico and cell-based analyses reveal strong divergence between prediction and observation of T-cell-recognized tumor antigen T-cell epitopes." Journal of Biological Chemistry 292(28): 11840-11849. **[G, AR]**

180. Schubert, B., de la Garza, L., Mohr, C., Walzer, M., and Kohlbacher, O. (2017). "ImmunoNodes - graphical development of complex immunoinformatics workflows." Bmc Bioinformatics 18(**[G, AR]** responses." Scientific reports 7

181. Schussek, S., Trieu, A., Apte, S.H., Sidney, J., Sette, A., and Doolan, D.L. (2017). "Novel Plasmodium antigens identified via genome-based antibody screen induce protection associated with polyfunctional T cell (**[G]**

182. Segal, Y., Dahan, S., Calabro, M., Kanduc, D., and Shoenfeld, Y. (2017). "HPV and systemic lupus erythematosus: a mosaic of potential crossreactions." Immunologic Research 65(2): 564-571. **[G]**

183. Sher, G., Zhi, D.G., and Zhang, S.J. (2017). "DRREP: deep ridge regressed epitope predictor." Bmc Genomics 18(**[G, AR]**

184. Shugay, M., Bagaev, D.V., Zvyagin, I.V., Vroomans, R.M., Crawford, J.C., Dolton, G., Komech, E.A., Sycheva, A.L., Koneva, A.E., and Egorov, E.S. (2017). "VDJdb: a curated database of T-cell receptor sequences with known antigen specificity." Nucleic acids research 46(D1): D419-D427. **[G]**

185. Skopelja-Gardner, S., Jones, J.D., and Rigby, W.F. (2017). "'NETtling' the host: Breaking of tolerance in chronic inflammation and chronic infection." Journal of autoimmunity **[G]**

186. Stec, K.F., Caputi, L., Buttigieg, P.L., D'Alelio, D., Ibarbalz, F.M., Sullivan, M.B., Chaffron, S., Bowler, C., d'Alcalá, M.R., and Iudicone, D. (2017). "Modelling plankton ecosystems in the meta-omics era. Are we ready?" Marine genomics 32(1-17. **[G]**

187. Steffen, W., Ko, F.C., Patel, J., Lyamichev, V., Albert, T.J., Benz, J., Rudolph, M.G., Bergmann, F., Streidl, T., Kratzsch, P., Boenitz-Dulat, M., Oelschlaegel, T., and Schraeml, M. (2017). "Discovery of a microbial transglutaminase enabling highly site-specific labeling of proteins." Journal of Biological Chemistry 292(38): 15622-15635. **[G]**

188. Subramanian, S., Savanur, G., and Madhavadas, S. (2017). "Passive immunization targeting the N-terminal region of phosphorylated tau (residues 68-71) improves spatial memory in okadaic acid induced tauopathy model rats." Biochemical and Biophysical Research Communications 483(1): 585-589. **[G]**

189. Sultan, H., Fesenkova, V.I., Addis, D., Fan, A.E., Kumai, T., Wu, J., Salazar, A.M., and Celis, E. (2017). "Designing therapeutic cancer vaccines by mimicking viral infections." Cancer Immunology Immunotherapy 66(2): 203-213. **[G]**

190. Sulzer, D., Alcalay, R.N., Garretti, F., Cote, L., Kanter, E., gin-Liebes, J., Liong, C., McMurtrey, C., Hildebrand, W.H., Mao, X.B., Dawson, V.L., Dawson, T.M., Oseroff, C., Pham, J., Sidney, J., Dillon, M.B., Carpenter, C., Weiskopf, D., Phillips, E., Mallal, S., Peters, B., Frazier, A., Arlehamn, C.S.L., and Sette, A. (2017). "T cells from patients with Parkinson's disease recognize alpha-synuclein peptides." Nature 546(7660): 656-+. **[G, AR]**

191. Sun, J., Li, M., Wang, Y.N., Hao, P., and Jin, X. (2017). "Elaboration of tetravalent antibody responses against dengue viruses using a subunit vaccine comprised of a single consensus dengue envelope sequence." Vaccine 35(46): 6308-6320. **[G]**

192. Sundaramurthi, J.C., Ashokkumar, M., Swaminathan, S., and Hanna, L.E. (2017). "HLA based selection of epitopes offers a potential window of opportunity for vaccine design against HIV." Vaccine 35(42): 5568-5575. **[G]**

193. Tickotsky, N., Sagiv, T., Prilusky, J., Shifrut, E., and Friedman, N. (2017). "McPAS-TCR: a manually curated catalogue of pathology-associated T cell receptor sequences." Bioinformatics 33(18): 2924-2929. **[G]**

194. Tosch, C., Bastien, B., Barraud, L., Grellier, B., Nourtier, V., Gantzer, M., Limacher, J.M., Quemeneur, E., Bendjama, K., and Preville, X. (2017). "Viral based vaccine TG4010 induces broadening of specific immune response and improves outcome in advanced NSCLC." Journal for Immunotherapy of Cancer 5(**[G]**

195. Valdez, Joshua, Rueschman, Michael, Kim, Matthew, Arabyarmohammadi, Sara, Redline, Susan, and Sahoo, Satya S. An Extensible Ontology Modeling Approach Using Post Coordinated Expressions for Semantic Provenance in Biomedical Research. OTM Confederated International Conferences" On the Move to Meaningful Internet Systems" , 337-352. 2017. Springer. Ref Type: Conference Proceeding **[G]**

196. van Hateren, A., Bailey, A., and Elliott, T. (2017). "Recent advances in Major Histocompatibility Complex (MHC) class I antigen presentation: Plastic MHC molecules and TAPBPR-mediated quality control." F1000Research 6(**[G]**

197. Vandersarren, L., Bosteels, C., Vanheerswynghels, M., Moon, J.J., Easton, A.J., Van Isterdael, G., Janssens, S., Lambrecht, B.N., and van Helden, M.J. (2017). "Epitope mapping and kinetics of CD4 T cell immunity to pneumonia virus of mice in the C57BL/6 strain." Scientific reports 7(**[G, AR]**

198. Vang, Y.S. and Xie, X. (2017). "HLA class I binding prediction via convolutional neural networks." Bioinformatics 33(17): 2658-2665. **[G, AR]**

199. Vazquez-Prieto, S., Paniagua, E., Solana, H., and Ubeira, F.M. (2017). "Complex Network Study of the Immune Epitope Database for Parasitic Organisms." Current Topics in Medicinal Chemistry 17(30): 3249-3255. **[G]**

200. Vuong, C.N., Chou, W.K., Kuttappan, V.A., Hargis, B.M., Bielke, L.R., and Berghman, L.R. (2017). "a Fast and inexpensive Protocol for empirical Verification of neutralizing epitopes in Microbial Toxins and enzymes." Frontiers in Veterinary Science 4(91- **[G]**

201. Wan, F., Hu, C.B., Ma, J.X., Gao, K., Xiang, L.X., and Shao, J.Z. (2017). "Characterization of gamma delta T Cells from Zebrafish Provides Insights into Their Important Role in Adaptive Humoral Immunity." Frontiers in Immunology 7(**[G]**

202. Wang, D.P., Chen, C., Liu, S.N., Zhou, H., Yang, K.L., Zhao, Q., Ji, X.Y., Chen, C., Xie, W., Wang, Z.F., Mi, L.Z., and Yang, H.T. (2017). "A Mutation Identified in Neonatal Microcephaly Destabilizes Zika Virus NS1 Assembly in Vitro." Scientific reports 7(**[G]**

203. Wang, J. (2017). "Logical Reasoning (Inferencing) on MicroRNA Data." Bioinformatics in MicroRNA Research 197-209. **[G]**

204. Wang, L., Li, M., Xie, J., Cao, Y., Liu, H., and He, Y. (2017). "Ontology-based systematical representation and drug class effect analysis of package insert-reported adverse events associated with cardiovascular drugs used in China." Scientific reports 7(1): 13819- **[G]**

205. Wegner, F. (2017). "Genomic studies on the impact of host/virus interaction in EBV infection using massively parallel high throughput sequencing." **[G, AR]**

206. Wu, Y.N., Wang, J.Y., Fan, S.H., Chen, R., Liu, Y.J., Zhang, J.H., Yuan, H.Y., Liang, R.Y., Zhang, N.Z., and Xia, C. (2017). "Structural Definition of Duck Major Histocompatibility Complex Class

I Molecules That Might Explain Efficient Cytotoxic T Lymphocyte Immunity to Influenza A Virus." Journal of Virology 91(14): **[G, AR]**

207. Xiao, Z.W., Ye, Z.Y., Tadwal, V.S., Shen, M.X., and Ren, E.C. (2017). "Dual non-contiguous peptide occupancy of HLA class I evoke antiviral human CD8 T cell response and form neo-epitopes with self-antigens." Scientific reports 7(**[G]**

208. Xu, J. and Jo, J. (2017). "Broad cross-reactivity of the T-cell repertoire achieves specific and sufficiently rapid target searching." arXiv preprint arXiv:1712.04633 **[G]**

209. Yan, S.K. and Wong, K.C. (2017). "Elucidating high-dimensional cancer hallmark annotation via enriched ontology." Journal of Biomedical Informatics 73(84-94. **[G]**

210. Yordanov, V., Dimitrov, I., and Doytchinova, I. (2017). "Proteochemometrics for the Prediction of Binding to the MHC Proteins." Letters in Drug Design & Discovery 14(1): 2-9. **[G, AR]**

211. Zhang, G.L., Keskin, D.B., DeCaprio, J.A., Wu, C.J., Chitkushev, L., and Brusic, V. (2017). "MCVdb: a database for knowledge discovery in Merkel cell polyomavirus with applications in T cell immunology and vaccinology." 2017 Ieee International Conference on Bioinformatics and Biomedicine (Bibm) 1483-1488. **[G, AR]**

212. Zhang, Y.H., Xing, Z.H., Liu, C.L., Wang, S.P., Huang, T., Cai, Y.D., and Kong, X.Y. (2017). "Identification of the core regulators of the HLA I-peptide binding process." Scientific reports 7(**[G, AR]**

213. Zvi, A., Rotem, S., Zauberman, A., Elia, U., Aftalion, M., Bar-Haim, E., Mamroud, E., and Cohen, O. (2017). "Novel CTL epitopes identified through a Y. pestis proteome-wide analysis in the search for vaccine candidates against plague." Vaccine 35(44): 5995-6006. **[G, AR]**

3.2.2 Analysis Resource

1. Abdelbagi, M., Hassan, T., Shihabeldin, M., Bashir, S., and Ahmed, E. (2017). "Immunoinformatics Prediction of Peptide-Based Vaccine Against African Horse Sickness Virus." Immunome Res 13(135): 2- **[AR]**

2. Acevedo, C.A.T., Valente, B.M., Burle-Caldas, G.A., Galvao, B., Santiago, H.D., Arantes, R.M.E., Junqueira, C., Gazzinelli, R.T., Roffe, E., and Teixeira, S.M.R. (2017). "Down Modulation of Host Immune Response by Amino Acid Repeats Present in a Trypanosoma cruzi Ribosomal Antigen." Frontiers in Microbiology 8(**[AR]**

3. Adalsteinsson, V.A., Ha, G., Freeman, S.S., Choudhury, A.D., Stover, D.G., Parsons, H.A., Gydush, G., Reed, S.C., Rotem, D., Rhoades, J., Loginov, D., Livitz, D., Rosebrock, D., Leshchiner, I., Kim, J., Stewart, C., Rosenberg, M., Francis, J.M., Zhang, C.Z., Cohen, O., Oh, C., Ding, H.M., Polak, P., Lloyd, M., Mahmud, S., Helvie, K., Merrill, M.S., Santiago, R.A., O'Connor, E.P., Jeong, S.H., Leeson, R., Barry, R.M., Kramkowski, J.F., Zhang, Z.W., Polacek, L., Lohr, J.G., Schleicher, M., Lipscomb, E., Saltzman, A., Oliver, N.M., Marini, L., Waks, A.G., Harshman, L.C., Tolaney, S.M., Van Allen, E.M., Winer, E.P., Lin, N.U., Nakabayashi, M., Taplin, M.E., Johannessen, C.M., Garraway, L.A., Golub, T.R., Boehm, J.S., Wagle, N., Getz, G., Love, J.C., and Meyerson, M. (2017). "Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors." Nature Communications 8(**[AR]**

4. Adhikari, U.K. and Rahman, M.M. (2017). "Overlapping CD8+and CD4+T-cell epitopes identification for the progression of epitope-based peptide vaccine from nucleocapsid and glycoprotein of emerging Rift Valley fever virus using immunoinformatics approach." Infection Genetics and Evolution 56(75-91. **[AR]**

5. Agallou, M., Margaroni, M., Athanasiou, E., Toubanaki, D.K., Kontonikola, K., Karidi, K., Kammona, O., Kiparissides, C., and Karagouni, E. (2017). "Identification of BALB/c Immune Markers Correlated with a Partial Protection to Leishmania infantum after Vaccination with a Rationally Designed Multi-epitope Cysteine Protease A Peptide-Based Nanovaccine." Plos Neglected Tropical Diseases 11(1): **[AR]**

6. Ahmed, S.S. and Steinman, L. (2017). "Narcolepsy and influenza vaccination-induced autoimmunity." Annals of Translational Medicine 5(1): **[AR]**

7. AlShamaileh, H. and Veedu, R.N. (2017). "Next-Generation Nucleic Acid Aptamers with Two-Base-Modified Nucleotides Have Improved Binding Affinity and Potency." Chembiochem 18(16): 1565-1567. **[AR]**

8. Alvey, C. (2017). "Engineered Marrow Macrophages For Cancer Therapy: Engorgement, Accumulation, Differentiation, And Acquired Immunity." **[AR]**

9. Amit, A., Dikhit, M.R., Mahantesh, V., Chaudhary, R., Singh, A.K., Singh, A., Singh, S.K., Das, V.N.R., Pandey, K., Ali, V., Narayan, S., Sahoo, G.C., Das, P., and Bimal, S. (2017). "Immunomodulation mediated through Leishmania donovani protein disulfide isomerase by eliciting CD8+T-cell in cured visceral leishmaniasis subjects and identification of its possible HLA class-1 restricted T-cell epitopes." Journal of Biomolecular Structure & Dynamics 35(1): 128-140. **[AR]**

10. Amit, A., Dikhit, M.R., Singh, A.K., Venkateshwaran, T., Das, V.N.R., Das, P., and Bimal, S. (2017). "Immuno-informatics based approaches to identify CD8+ T cell epitopes within the Leishmania donovani 3-ectonucleotidase in cured visceral leishmaniasis subjects." Microbes and Infection 19(6): 358-369. **[AR]**

11. Anagnostou, V., Smith, K.N., Forde, P.M., Niknafs, N., Bhattacharya, R., White, J., Zhang, T., Adleff, V., Phallen, J., Wali, N., Hruban, C., Guthrie, V.B., Rodgers, K., Naidoo, J., Kang, H., Sharfman, W., Georgiades, C., Verde, F., Illei, P., Li, Q.K., Gabrielson, E., Brock, M.V., Zahnow, C.A., Baylin, S.B., Scharpf, R.B., Brahmer, J.R., Karchin, R., Pardoll, D.M., and Velculescu, V.E. (2017). "Evolution of Neoantigen Landscape during Immune Checkpoint Blockade in Non-Small Cell Lung Cancer." Cancer Discovery 7(3): 264-276. **[AR]**

12. Angelo, M.A., Grifoni, A., O'Rourke, P.H., Sidney, J., Paul, S., Peters, B., De Silva, A.D., Phillips, E., Mallal, S., Diehl, S.A., Kirkpatrick, B.D., Whitehead, S.S., Durbin, A.P., Sette, A., and Weiskopf, D. (2017). "Human CD4(+) T Cell Responses to an Attenuated Tetravalent Dengue Vaccine Parallel Those Induced by Natural Infection in Magnitude, HLA Restriction, and Antigen Specificity." Journal of Virology 91(5): **[AR]**

13. Asgari, S., Ebrahim-Habibi, A., Mahdavi, M., Choopani, M., and Mirzahoseini, H. (2017). "Therapeutic protein deimmunization by T-cell epitope removal: antigen-specific immune responses in vitro and in vivo." Apmis 125(6): 544-552. **[AR]**

14. Athanasiou, E., Agallou, M., Tastsoglou, S., Kammona, O., Hatzigeorgiou, A., Kiparissides, C., and Karagouni, E. (2017). "A Poly(Lactic-co-Glycolic) Acid Nanovaccine Based on Chimeric Peptides from Different Leishmania infantum Proteins Induces Dendritic Cells Maturation and Promotes Peptide-Specific IFN gamma-Producing CD8(+) T Cells Essential for the Protection against Experimental Visceral Leishmaniasis." Frontiers in Immunology 8(**[AR]**

15. Attallah, C., Aguilar, M.F., Garay, A.S., Hetrera, F.E., Etcheverrigaray, M., Oggero, M., and Rodrigues, D.E. (2017). "An unusual cysteine V(L)87 affects the antibody fragment conformations without interfering with the disulfide bond formation." Molecular Immunology 90(143-149. **[AR]**

16. Ayres, C.M., Riley, T.P., Corcelli, S.A., and Baker, B.M. (2017). "Modeling Sequence-Dependent Peptide Fluctuations in Immunologic Recognition." Journal of Chemical Information and Modeling 57(8): 1990-1998. **[AR]**

17. Backert, L., Kowalewski, D.J., Walz, S., Schuster, H., Berlin, C., Neidert, M.C., Schemionek, M., Brummendorf, T.H., Vucinic, V., Niederwieser, D., Kanz, L., Salih, H.R., Kohlbacher, O., Weisel, K., Rammensee, H.G., Stevanovic, S., and Walz, J.S. (2017). "A meta-analysis of HLA peptidome composition in different hematological entities: entity-specific dividing lines and "panleukemia" antigens." Oncotarget 8(27): 43915-43924. **[AR]**

18. Badawi, M.M., Ahmed, S.A., Elgelani, M.A., Alnourain, T.H., Mabrouk, M.H., and SidAhmed, A.S.A. (2017). "Identification and immune recognition of viral epitopes of West Nile Virus envelope glycoprotein and their potentials of acting as peptide vaccine." Saudi Journal of Biological Sciences **[AR]**

19. Bais, P., Namburi, S., Gatti, D.M., Zhang, X.Y., and Chuang, J.H. (2017). "CloudNeo: a cloud pipeline for identifying patient-specific tumor neoantigens." Bioinformatics 33(19): 3110-3112. **[AR]**

20. Baldauf, M.C., Gerke, J.S., Kirschner, A., Blaeschke, F., Effenberger, M., Schober, K., Rubio, R.A., Kanaseki, T., Kiran, M.M., and Dallmayer, M. (2017). "Systematic identification of cancer-specific MHC-binding peptides with RAVEN." bioRxiv 193276 **[AR]**

21. Banas, B., Boger, C.A., Luckhoff, G., Kruger, B., Barabas, S., Batzilla, J., Schemmerer, M., Kostler, J., Bendfeldt, H., Rascle, A., Wagner, R., Deml, L., Leicht, J., and Kramer, B.K. (2017). "Validation of T-Track (R) CMV to assess the functionality of cytomegalovirus-reactive cell-mediated immunity in hemodialysis patients." Bmc Immunology 18(**[AR]**

22. Banerjee, S., Sen Gupta, P.S., and Bandyopadhyay, K. (2017). "Insight into SNPs and epitopes of E protein of newly emerged genotype-I isolates of JEV from Midnapur, West Bengal, India." Bmc Immunology 18(**[AR, MA]**

23. Barnea, E., Kadosh, D.M., Haimovich, Y., Satumtira, N., Dorris, M.L., Nguyen, M.T., Hammer, R.E., Tran, T.M., Colbert, R.A., Taurog, J.D., and Admon, A. (2017). "The Human Leukocyte Antigen (HLA)-B27 Peptidome in Vivo, in Spondyloarthritis-susceptible HLA-B27 Transgenic Rats and the Effect of Erap1 Deletion." Molecular & Cellular Proteomics 16(4): 642-662. **[AR]**

24. Bavaro, T., Tengattini, S., Piubelli, L., Mangione, F., Bernardini, R., Monzillo, V., Calarota, S., Marone, P., Amicosante, M., Pollegioni, L., Temporini, C., and Terreni, M. (2017). "Glycosylation

of Recombinant Antigenic Proteins from Mycobacterium tuberculosis: In Silico Prediction of Protein Epitopes and Ex Vivo Biological Evaluation of New Semi-Synthetic Glycoconjugates." Molecules 22(7): **[AR]**

25. Bazmara, H., Rasooli, I., Jahangiri, A., Sefid, F., Astaneh, S.D.A., and Payandeh, Z. (2017). "Antigenic Properties of Iron Regulated Proteins in Acinetobacter baumannii: An In Silico Approach." International Journal of Peptide Research and Therapeutics 1-9. **[AR]**

26. Bentzen, A.K. and Hadrup, S.R. (2017). "Evolution of MHC-based technologies used for detection of antigen-responsive T cells." Cancer Immunology Immunotherapy 66(5): 657-666. **[AR]**

27. Bergmann, T., Lindvall, M., Moore, E., Moore, E., Sidney, J., Miller, D., Tallmadge, R.L., Myers, P.T., Malaker, S.A., Shabanowitz, J., Osterrieder, N., Peters, B., Hunt, D.F., Antczak, D.F., and Sette, A. (2017). "Peptide-binding motifs of two common equine class I MHC molecules in Thoroughbred horses." Immunogenetics 69(5): 351-358. **[AR]**

28. Bergmann, T. (2017). "Determination of quantitative peptide-binding motifs of four common equine MHC class I alleles, and identification of an equine herpesvirus type 1-derived cytotoxic T lymphocyte epitope." **[AR]**

29. Bethune, M.T. and Joglekar, A.V. (2017). "Personalized T cell-mediated cancer immunotherapy: progress and challenges." Current opinion in biotechnology 48(142-152. **[AR]**

30. Bhardwaj, A., Nayan, V., Sharma, P., Kumar, S., Pal, Y., and Singh, J. (2017). "Molecular characterization, modeling, in silico analysis of equine pituitary gonadotropin alpha subunit and docking interaction studies with ganirelix." In silico pharmacology 5(1): 5- **[AR]**

31. Bi, W.Y.L.D., Greenwald, N.F., Abedalthagafi, M., Wala, J., Gibson, W.J., Agarwalla, P.K., Horowitz, P., Schumacher, S.E., Esaulova, E., Mei, Y., Chevalier, A., Ducar, M.A., Thorner, A.R., van Hummelen, P., Stemmer-Rachamimov, A.O., Artyomov, M., Al-Mefty, O., Dunn, G.P., Santagata, S., Dunn, I.F., and Beroukhim, R. (2017). "Genomic landscape of high-grade meningiomas." Npj Genomic Medicine 2(**[AR]**

32. Bianchi, F., Textor, J., and van den Bogaart, G. (2017). "Transmembrane Helices Are an Overlooked Source of Major Histocompatibility Complex Class I Epitopes." Frontiers in Immunology 8(**[AR]**

33. Binder, H., Hopp, L., Schweiger, M.R., Hoffmann, S., Juhling, F., Kerick, M., Timmermann, B., Siebert, S., Grimm, C., Nersisyan, L., Arakelyan, A., Herberg, M., Buske, P., Loeffler-Wirth, H., Rosolowski, M., Engel, C., Przybilla, J., Peifer, M., Friedrichs, N., Moeslein, G., Odenthal, M., Hussong, M., Peters, S., Holzapfel, S., Nattermann, J., Hueneburg, R., Schmiegel, W., Royer-Pokora, B., Aretz, S., Kloth, M., Kloor, M., Buettner, R., Galle, J., and Loeffler, M. (2017). "Genomic and transcriptomic heterogeneity of colorectal tumours arising in Lynch syndrome." Journal of Pathology 243(2): 242-254. **[AR]**

34. Bjerregaard, A.M., Nielsen, M., Hadrup, S.R., Szallasi, Z., and Eklund, A.C. (2017). "MuPeXI: prediction of neo-epitopes from tumor sequencing data." Cancer Immunology Immunotherapy 66(9): 1123-1130. **[AR]**

35. Bjerregaard, A.M., Nielsen, M., Jurtz, V., Barra, C.M., Hadrup, S.R., Szallasi, Z., and Eklund, A.C. (2017). "An Analysis of Natural T Cell Responses to Predicted Tumor Neoepitopes." Frontiers in Immunology 8(**[AR]**

36. Blatnik, R. (2017). "Development of mass spectrometry methodology for direct identification of viral epitopes from MHC I molecules." **[AR]**

37. Brocks, D., Schmidt, C.R., Daskalakis, M., Jang, H.S., Shah, N.M., Li, D.F., Li, J., Zhang, B., Hou, Y.R., Laudato, S., Lipka, D.B., Schott, J., Bierhoff, H., Assenov, Y., Helf, M., Ressnerova, A., Islam, M.S., Lindroth, A.M., Haas, S., Essers, M., Imbusch, C.D., Brors, B., Oehme, I., Witt, O., Lubbert, M., Mallm, J.P., Rippe, K., Will, R., Weichenhan, D., Stoecklin, G., Gerhauser, C., Oakes, C.C., Wang, T., and Plass, C. (2017). "DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats." Nature Genetics 49(7): 1052-+. **[AR]**

38. Bruder, J.T., Chen, P., Ekberg, G., Smith, E.C., Lazarski, C.A., Myers, B.A., Bolton, J., Sedegah, M., Villasante, E., Richie, T.L., King, C.R., Aguiar, J.C., Doolan, D.L., and Brough, D.E. (2017). "Profiling the Targets of Protective CD8(+) T Cell Responses to Infection." Molecular Therapy-Methods & Clinical Development 7(20-31. **[AR]**

39. Byström, S. (2017). "Affinity assays for profiling disease-associated proteins in human plasma." **[AR]**

40. Cai, W.Y., Qiu, C.L., Zhang, H.Y., Chen, X.Y., Zhang, X., Meng, Q.Y., and Wei, J. (2017). "Detection of circulating natural antibodies to inflammatory cytokines in type-2 diabetes and clinical significance." Journal of Inflammation-London 14(**[AR]**

41. Calcedo, R., Somanathan, S., Qin, Q.Y., Betts, M.R., Rech, A.J., Vonderheide, R.H., Mueller, C., Flotte, T.R., and Wilson, J.M. (2017). "Class I-restricted T-cell responses to a polymorphic peptide in a gene therapy clinical trial for alpha-1-antitrypsin deficiency." Proceedings of the National Academy of Sciences of the United States of America 114(7): 1655-1659. **[AR]**

42. Capasso, C., Magarkar, A., Cervera-Carascon, V., Fusciello, M., Feolaf, S., Muller, M., Garofalo, M., Kuryk, L., Tahtinen, S., Pastore, L., Bunker, A., and Cerullo, V. (2017). "A novel in silico framework to improve MHC-I epitopes and break the tolerance to melanoma." Oncoimmunology 6(9): **[AR]**

43. Capietto, A.H., Jhunjhunwala, S., and Delamarre, L. (2017). "Characterizing neoantigens for personalized cancer immunotherapy." Current Opinion in Immunology 46(58-65. **[AR]**

44. Carignano, H.A., Beribe, M.J., Caffaro, M.E., Amadio, A., Nani, J.P., Gutierrez, G., Alvarez, I., Trono, K., Miretti, M.M., and Poli, M.A. (2017). "BOLA-DRB3 gene polymorphisms influence bovine leukaemia virus infection levels in Holstein and Holstein x Jersey crossbreed dairy cattle." Animal Genetics 48(4): 420-430. **[AR]**

45. Carretero, F.J., Del Campo, A., Zinchenko, S., Garrido, F., and Aptsiauri, N. (2017). "Recovery of HLA-A2 and Beta2-microglobulin Expression in Tumor Cells Using Viral Vectors." J Cancer Sci Ther 9(622-629. **[AR]**

46. Chahal, J.S., Fang, T., Woodham, A.W., Khan, O.F., Ling, J.J., Anderson, D.G., and Ploegh, H.L. (2017). "An RNA nanoparticle vaccine against Zika virus elicits antibody and CD8+T cell responses in a mouse model." Scientific Reports 7(**[AR]**

47. Chan, K.H., Lee, W.H., Zhuo, S.M., and Ni, M. (2017). "Harnessing supramolecular peptide nanotechnology in biomedical applications." International Journal of Nanomedicine 12(1171-1182. **[AR]**

48. Charoentong, P., Finotello, F., Angelova, M., Mayer, C., Efremova, M., Rieder, D., Hackl, H., and Trajanoski, Z. (2017). "Pan-cancer Immunogenomic Analyses Reveal Genotype-Immunophenotype Relationships and Predictors of Response to Checkpoint Blockade." Cell Reports 18(1): 248-262. **[AR]**

49. Chaudhuri, R. and Ramachandran, S. (2017). "Immunoinformatics as a Tool for New Antifungal Vaccines." Vaccines for Invasive Fungal Infections: Methods and Protocols 31-43. **[AR]**

50. Chaves, L.B., Perce-da-Silva, D.D., Rodrigues-da-Silva, R.N., da Silva, J.H.M., Cassiano, G.C., Machado, R.L.D., Pratt-Riccio, L.R., Banic, D.M., and Lima, J.D. (2017). "Plasmodium vivax Cell Traversal Protein for Ookinetes and Sporozoites (PvCelTOS) gene sequence and potential epitopes are highly conserved among isolates from different regions of Brazilian Amazon." Plos Neglected Tropical Diseases 11(2): **[AR]**

51. Chin, C.F., Lai, J.Y., Choong, Y.S., Anthony, A.A., Ismail, A., and Lim, T.S. (2017). "Delineation of B-cell Epitopes of Salmonella enterica serovar Typhi Hemolysin E: Potential antibody therapeutic target." Scientific Reports 7(**[AR]**

52. Chiuppesi, F., Kaltcheva, T., Meng, Z., Barry, P.A., Diamond, D.J., and Wussow, F. (2017). "Identification of a Continuous Neutralizing Epitope within UL128 of Human Cytomegalovirus." Journal of Virology 91(6): **[AR]**

53. Contreras, M., Alberdi, P., Mateos-Hernandez, L., de Mera, I.G.F., Garcia-Perez, A.L., Vancova, M., Villar, M., Ayllon, N., Cabezas-Cruz, A., Valdes, J.J., Stuen, S., Gortazar, C., and de la Fuente, J. (2017). "Anaplasma phagocytophilum MSP4 and HSP70 Proteins Are Involved in Interactions with Host Cells during Pathogen Infection." Frontiers in Cellular and Infection Microbiology 7(**[AR]**

54. Correa-Fiz, F., Galofre-Mila, N., Costa-Hurtado, M., and Aragon, V. (2017). "Identification of a surface epitope specific of virulent strains of Haemophilus parasuis." Veterinary Microbiology 198(116-120. **[AR]**

55. Costa, J., Marani, M.M., Grazina, L., Villa, C., Meira, L., Oliveira, M.B.P.P., Leite, J.R.S.A., and Mafra, I. (2017). "Peptide selection and antibody generation for the prospective immunorecognition of Cry1Ab16 protein of transgenic maize." Food Chemistry 231(340-347. **[AR]**

56. Cui, M.J. (2017). "The Prediction and Function of Neoantigen in Oncobiology." Proceedings of the 2017 International Conference on Material Science, Energy and Environmental Engineering (Mseee 2017) 125(174-179. **[AR]**

57. Curtidor, H., Reyes, C., Bermudez, A., Vanegas, M., Varela, Y., and Patarroyo, M.E. (2017). "Conserved Binding Regions Provide the Clue for Peptide-Based Vaccine Development: A Chemical Perspective." Molecules 22(12): **[AR]**

58. Dalin, M.G., Katabi, N., Persson, M., Lee, K.W., Makarov, V., Desrichard, A., Walsh, L.A., West, L., Nadeem, Z., Ramaswami, D., Havel, J.J., Kuo, F., Chadalavada, K., Nanjangud, G.J., Ganly, I., Riaz, N., Ho, A.L., Antonescu, C.R., Ghossein, R., Stenman, G., Chan, T.A., and Morris, L.G.T. (2017). "Multi-dimensional genomic analysis of myoepithelial carcinoma identifies prevalent oncogenic gene fusions." Nature Communications 8(**[AR]**

59. Dangi, M., Singh, B., and Chhillar, A.K. (2017). "Reverse Vaccinology to Computationally Screen Antigenic Epitopes as Potential Vaccine Candidates from Clostridium botulinum Strain Hall A." Current Bioinformatics 12(4): 349-360. **[AR]**

60. Das, K. (2017). "Generation of a transplantable murine tumor model expressing the human breast cancer associated tumor antigen NY-BR-1 in HLA-DRB1* 0401-transgenic mice." **[AR]**

61. Dash, R., Das, R., Junaid, M., Akash, M.F.C., Islam, A., and Hosen, S.Z. (2017). "In silico-based vaccine design against Ebola virus glycoprotein." Advances and Applications in Bioinformatics and Chemistry: AABC 10(11- **[AR]**

62. de la Cruz-Merino, L., Chiesa, M., Caballero, R., Rojo, F., Palazon, N., Carrasco, F.H., and Sanchez-Margalet, V. (2017). "Breast Cancer Immunology and Immunotherapy: Current Status and Future Perspectives." International Review of Cell and Molecular Biology, Vol 331 331(1-53. **[AR]**

63. Del Tordello, E., Rappuoli, R., and Delany, I. Reverse Vaccinology: Exploiting Genomes for Vaccine Design. Human Vaccines. 65-86. 2017. Elsevier.
Ref Type: Book Chapter **[AR, MA]**

64. Deringer, J.R., Forero-Becerra, E.G., Ueti, M.W., Turse, J.E., Futse, J.E., Noh, S.M., Palmer, G.H., and Brown, W.C. (2017). "Identification of a T-Cell Epitope That Is Globally Conserved among Outer Membrane Proteins (OMPs) OMP7, OMP8, and OMP9 of Anaplasma marginale Strains and with OMP7 from the A. marginale subsp centrale Vaccine Strain." Clinical and Vaccine Immunology 24(1): **[AR]**

65. Di Marco, M., Peper, J.K., and Rammensee, H.G. (2017). "Identification of Immunogenic Epitopes by MS/MS." Cancer Journal 23(2): 102-107. **[AR]**

66. Dikhit, M.R., Kumar, A., Das, S., Dehury, B., Rout, A.K., Jamal, F., Sahoo, G.C., Topno, R.K., Pandey, K., Das, V.N.R., Bimal, S., and Das, P. (2017). "Identification of Potential MHC Class-II-Restricted Epitopes Derived from Leishmania donovani Antigens by Reverse Vaccinology and Evaluation of Their CD4+T-cell Responsiveness against Visceral Leishmaniasis." Frontiers in Immunology 8(**[AR]**

67. Dikhit, M.R., Amit, A., Singh, A.K., Kumar, A., Mansuri, R., Sinha, S., Topno, R.K., Mishra, R., Das, V.N.R., Pandey, K., Sahoo, G.C., Ali, V., Bimal, S., and Das, P. (2017). "Vaccine potential of HLA-A2 epitopes from Leishmania Cysteine Protease Type III (CPC)." Parasite Immunology 39(9): **[AR]**

68. Dimayuga, P.C., Zhao, X.N., Yano, J., Lio, W.M., Zhou, J.C., Mihailovic, P.M., Cercek, B., Shah, P.K., and Chyu, K.Y. (2017). "Identification of apoB-100 Peptide-Specific CD8+T Cells in Atherosclerosis." Journal of the American Heart Association 6(7): **[AR]**

69. Donaldson, B.C. (2017). "Immunomodulation and Vaccination with RHDV VLP." **[AR]**

70. Dong, S.Y., Wang, P., Zhao, P., and Chen, M.N. (2017). "Direct Loading of iTEP-Delivered CTL Epitope onto MHC Class I Complexes on the Dendritic Cell Surface." Molecular Pharmaceutics 14(10): 3312-3321. **[AR]**

71. Du, Y.S., Zhang, T.H., Dai, L., Zheng, X.J., Gorin, A.M., Oishi, J., Wu, T.T., Yoshizawa, J.M., Li, X.M., Yang, O.O., Martinez-Maza, O., Detels, R., and Sun, R. (2017). "Effects of Mutations on Replicative Fitness and Major Histocompatibility Complex Class I Binding Affinity Are Among the Determinants Underlying Cytotoxic-T-Lymphocyte Escape of HIV-1 Gag Epitopes." Mbio 8(6): **[AR]**

72. Duffy, E.B., Drake, J.R., and Harton, J.A. (2017). "Evolving Insights for MHC Class II Antigen Processing and Presentation in Health and Disease." Current Pharmacology Reports 3(5): 213-220. **[AR]**

73. Dulberger, C.L., McMurtrey, C.P., Holzemer, A., Neu, K.E., Liu, V., Steinbach, A.M., Garcia-Beltran, W.F., Sulak, M., Jabri, B., Lynch, V.J., Altfeld, M., Hildebrand, W.H., and Adams, E.J. (2017). "Human Leukocyte Antigen F Presents Peptides and Regulates Immunity through Interactions with NK Cell Receptors." Immunity 46(6): 1018-+. **[AR]**

74. Eccleston, R.C., Coveney, P.V., and Dalchau, N. (2017). "Host genotype and time dependent antigen presentation of viral peptides: predictions from theory." Scientific Reports 7(**[AR]**

75. Eccleston, R.C., Wan, S.Z., Dalchau, N., and Coveney, P.V. (2017). "The Role of Multiscale Protein Dynamics in Antigen Presentation and T Lymphocyte Recognition." Frontiers in Immunology 8(**[AR]**

76. Eckhardt, C. L., van Velzen, A. S., Hart, D. P., Voorberg, J., and Fijnvandraat, K. Towards a rationale for inhibitor development in nonsevere hemophilia A. Inhibitor Development in Nonsevere Hemophilia A , 185. 2017.
Ref Type: Thesis/Dissertation **[AR]**

77. Efremova, M., Finotello, F., Rieder, D., and Trajanoski, Z. (2017). "Neoantigens Generated by Individual Mutations and Their Role in Cancer Immunity and Immunotherapy." Frontiers in Immunology 8(**[AR]**

78. Efremova, M., Klepsch, V., Charoentong, P., Finotello, F., Rieder, D., Hackl, H., Hermann-Kleiter, N., Loewer, M., Baier, G., and Krogsdam, A. (2017). "Targeting the PD-1/PD-L1 pathway potentiates immunoediting and changes the dynamics of neutral evolution in a mouse model of colorectal cancer." bioRxiv 099747**- [AR]**

79. EL-Manzalawy, Y., Dobbs, D., and Honavar, V. G. In Silico Prediction of Linear B-Cell Epitopes on Proteins. 255-264. 2017. PREDICTION OF PROTEIN SECONDARY STRUCTURE Methods in Molecular Biology.
Ref Type: Book, Whole **[AR]**

80. Elemans, M., Boelen, L., Rasmussen, M., Buus, S., and Asquith, B. (2017). "HIV-1 adaptation to NK cell-mediated immune pressure." Plos Pathogens 13(6): **[AR]**

81. Ellis, A., Balgeman, A., Rodgers, M., Updike, C., Tomko, J., Maiello, P., Scanga, C.A., and O'Connor, S.L. (2017). "Characterization of T Cells Specific for CFP-10 and ESAT-6 in Mycobacterium tuberculosis-Infected Mauritian Cynomolgus Macaques." Infection and Immunity 85(4): **[AR]**

82. Engmark, M., Lomonte, B., Gutierrez, J.M., Laustsen, A.H., De Masi, F., Andersen, M.R., and Lund, O. (2017). "Cross-recognition of a pit viper (Crotalinae) polyspecific antivenom explored through high-density peptide microarray epitope mapping." Plos Neglected Tropical Diseases 11(7): **[AR]**

83. Ernst, Joel D. Antigenic Variation and Immune Escape in the MTBC. Strain Variation in the Mycobacterium tuberculosis Complex: Its Role in Biology, Epidemiology and Control. 171-190. 2017. Springer.
    Ref Type: Book Chapter **[AR]**

84. Faisal, A.R.M., Imtiaz, S.H., Zerin, T., Rahman, T., and Shekhar, H.U. (2017). "Computer aided epitope design as a peptide vaccine component against Lassa virus." Bioinformation 13(12): 417- **[AR]**

85. Fattahian, Y., Riahi-Madvar, A., Mirzaee, R., Asadikaram, G., and Rahbar, M.R. (2017). "In silico locating the immune-reactive segments of Lepidium draba peroxidase and designing a less immune-reactive enzyme derivative." Computational Biology and Chemistry 70(21-30. **[AR]**

86. Ferdosi, S.R. (2017). "Genome-Driven Targeted Cancer Therapy." **[AR]**

87. Finkel, Y., Stern-Ginossar, N., and Schwartz, M. (2017). "Viral Short ORFs and Their Possible Functions." Proteomics **[AR]**

88. Floe, A., Loppke, C., Hilberg, O., Wejse, C., Brix, L., and Jacobsen, K. (2017). "Development of an epitope panel for consistent identification of antigen-specific T-cells in humans." Immunology 152(2): 298-307. **[AR]**

89. Fontal, A. Neural Networks for Subcellular Localization Prediction." **[AR]**

90. Freire, M.C., Pol-Fachin, L.ü., Coêlho, D.F., Viana, I.F., Magalhães, T., Cordeiro, M.T., Fischer, N., Loeffler, F.F., Jaenisch, T., and Franca, R.F. (2017). "Mapping Putative B-Cell Zika Virus NS1 Epitopes Provides Molecular Basis for Anti-NS1 Antibody Discrimination between Zika and Dengue Viruses." ACS Omega 2(7): 3913-3920. **[AR]**

91. Fugmann, T., Sofron, A., Ritz, D., Bootz, F., and Neri, D. (2017). "The MHC Class II Immunopeptidome of Lymph Nodes in Health and in Chemically Induced Colitis." Journal of Immunology 198(3): 1357-1364. **[AR]**

92. Gall, V.A., Philips, A.V., Qiao, N., Clise-Dwyer, K., Perakis, A.A., Zhang, M., Clifton, G.T., Sukhumalchandra, P., Ma, Q., Reddy, S.M., Yu, D.H., Molldrem, J.J., Peoples, G.E., Alatrash, G., and Mittendorf, E.A. (2017). "Trastuzumab Increases HER2 Uptake and Cross-Presentation by Dendritic Cells." Cancer Research 77(19): 5374-5383. **[AR]**

93. Gawande, B.N., Rohlloff, J.C., Carter, J.D., von Carlowitz, I., Zhang, C., Schneider, D.J., and Janjic, N. (2017). "Selection of DNA aptamers with two modified bases." Proceedings of the National Academy of Sciences of the United States of America 114(11): 2898-2903. **[AR]**

94. Gell, G., Kovacs, K., Veres, G., Korponay-Szabo, I.R., and Juhasz, A. (2017). "Characterization of globulin storage proteins of a low prolamin cereal species in relation to celiac disease." Scientific Reports 7(**[AR]**

95. George, S., Miao, D., Demetri, G.D., Adeegbe, D., Rodig, S.J., Shukla, S., Lipschitz, M., min-Mansour, A., Raut, C.P., Carter, S.L., Hammerman, P., Freeman, G.J., Wu, C.J., Ott, P.A., Wong, K.K., and Van Allen, E.M. (2017). "Loss of PTEN Is Associated with Resistance to Anti-PD-1 Checkpoint Blockade Therapy in Metastatic Uterine Leiomyosarcoma." Immunity 46(2): 197-204. **[AR]**

96. Germano, G., Lamba, S., Rospo, G., Barault, L., Magri, A., Maione, F., Russo, M., Crisafulli, G., Bartolini, A., Lerda, G., Siravegna, G., Mussolin, B., Frapolli, R., Montone, M., Morano, F., de Braud, F., mirouchene-Angelozzi, N., Marsoni, S., D'Incalci, M., Orlandi, A., Giraudo, E., Sartore-Bianchi, A., Siena, S., Pietrantonio, F., Di Nicolantonio, F., and Bardelli, A. (2017). "Inactivation of DNA repair triggers neoantigen generation and impairs tumour growth." Nature 552(7683): 116-+. **[AR]**

97. Glaire, Mark A. and Church, David N. Hypermutated Colorectal Cancer and Neoantigen Load. Immunotherapy for Gastrointestinal Cancer. 187-215. 2017. Springer.
Ref Type: Book Chapter **[AR]**

98. Glanville, J., Huang, H., Nau, A., Hatton, O., Wagar, L.E., Rubelt, F., Ji, X.H., Han, A., Krams, S.M., Pettus, C., Haas, N., Arlehamn, C.S.L., Sette, A., Boyd, S.D., Scriba, T.J., Martinez, O.M., and Davis, M.M. (2017). "Identifying specificity groups in the T cell receptor repertoire." Nature 547(7661): 94-+. **[AR]**

99. Gokemeijer, J., Jawa, V., and Mitra-Kaushik, S. (2017). "How Close Are We to Profiling Immunogenicity Risk Using In Silico Algorithms and In Vitro Methods?: an Industry Perspective." Aaps Journal 19(6): 1587-1592. **[AR, MA]**

100. Golshani, M., Rafati, S., Nejati-Moheimani, M., Pourabdi, S., Arsang, A., and Bouzari, S. (2017). "Protein/Protein, DNA/DNA and DNA/Protein based vaccination strategies using truncated Omp2b against Brucella infection in BALB/c Mice." International Journal of Medical Microbiology 307(4-5): 249-256. **[AR]**

101. Golshani, M., Oloomi, M., and Bouzari, S. (2017). "In silico analysis of Shiga toxins (Stxs) to identify new potential vaccine targets for Shiga toxin-producing Escherichia coli." In silico pharmacology 5(1): 2- **[AR]**

102. Gonzalez, R., Suarez, C.F., Bohorquez, H.J., Patarroyo, M.A., and Patarroyo, M.E. (2017). "Semi-empirical quantum evaluation of peptide - MHC class II binding." Chemical Physics Letters 668(29-34. **[AR]**

103. Gori, A., Bolognesi, M., Colombo, G., and Gourlay, L.J. (2017). "Structural Vaccinology for Melioidosis Vaccine Design and Immunodiagnostics." Current Tropical Medicine Reports 4(3): 103-110. **[AR]**

104. Grassmann, A.A., Kremer, F.S., dos Santos, J.C., Souza, J.D., Pinto, L.D., and Mcbride, A.J.A. (2017). "Discovery of novel leptospirosis Vaccine candidates Using reverse and structural Vaccinology." Frontiers in Immunology 8(**[AR]**

105. Gray, L.A., D'Antoine, H.A., Tong, S.Y.C., McKinnon, M., Bessarab, D., Brown, N., Remenyi, B., Steer, A., Syn, G., Blackwell, J.M., Inouye, M., and Carapetis, J.R. (2017). "Genome-Wide Analysis of Genetic Risk Factors for Rheumatic Heart Disease in Aboriginal Australians Provides Support for Pathogenic Molecular Mimicry." Journal of Infectious Diseases 216(11): 1460-1470. **[AR]**

106. GREENSHIELDS-WATSON, A.L. (2017). "RESOLVING THE ‘CORE’ OF INFLUENZA INFECTION."

107. Grifoni, A., Angelo, M.A., Lopez, B., O'Rourke, P.H., Sidney, J., Cerpas, C., Balmaseda, A., Silveira, C.G.T., Maestri, A., Costa, P.R., Durbin, A.P., Diehl, S.A., Phillips, E., Mallal, S., De Silva, A.D., Nchinda, G., Nkenfou, C., Collins, M.H., de Silva, A.M., Lim, M.Q., Macary, P.A., Tatullo, F., Solomon, T., Satchidanandam, V., Desai, A., Ravi, V., Coloma, J., Turtle, L., Rivino, L., Kallas, E.G., Peters, B., Harris, E., Sette, A., and Weiskopf, D. (2017). "Global Assessment of Dengue Virus-Specific CD4(+) T Cell Responses in Dengue-Endemic Areas." Frontiers in Immunology 8(**[AR]**

108. Grifoni, A., Pham, J., Sidney, J., O'Rourke, P.H., Paul, S., Peters, B., Martini, S.R., de Silva, A.D., Ricciardi, M.J., and Magnani, D.M. (2017). "Prior Dengue virus exposure shapes T cell immunity to Zika virus in humans." Journal of Virology 91(24): e01469-17. **[AR, MA]**

109. Gu, W.B., Zhou, Y.L., Tu, D.D., Zhou, Z.K., Zhu, Q.H., Chen, Y.Y., and Shu, M.A. (2017). "Identification and characterization of pro-interleukin-16 from mud crab Scylla paramamosain: The first evidence of proinflammatory cytokine in crab species." Fish & Shellfish Immunology 70(701-709. **[AR]**

110. Gupta, S., Sharma, A.K., Shastri, V., Madhu, M.K., and Sharma, V.K. (2017). "Prediction of anti-inflammatory proteins/peptides: an insilico approach." Journal of Translational Medicine 15(**[AR]**

111. Ha, N.Y., Kim, Y., Min, C.K., Kim, H.I., Yen, N.T.H., Choi, M.S., Kang, J.S., Kim, Y.S., and Cho, N.H. (2017). "Longevity of antibody and T-cell responses against outer membrane antigens of Orientia tsutsugamushi in scrub typhus patients." Emerging Microbes & Infections 6(**[AR]**

112. Haasnoot, A.J., Schilham, M.W., Kamphuis, S.S., Muller, P.C.H., Heiligenhaus, A., Foll, D., Ophoff, R.A., Minden, K., Radstake, T.R., and Den Hollander, A.I. (2017). "An Amino Acid Motif In HLA-DRB1 Distinguishes Patients With Uveitis In Juvenile Idiopathic Arthritis." bioRxiv 140954- **[AR]**

113. Hajighahramani, N., Nezafat, N., Eslami, M., Negahdaripour, M., Rahmatabadi, S.S., and Ghasemi, Y. (2017). "Immunoinformatics analysis and in silico designing of a novel multi-epitope peptide vaccine against Staphylococcus aureus." Infection Genetics and Evolution 48(83-94. **[AR]**

114. Hamze, M., Meunier, S., Karle, A., Gdoura, A., Goudet, A.l., Szely, N., Pallardy, M., Carbonnel, F., Spindeldreher, S., and Mariette, X. (2017). "characterization of cD4 T cell epitopes of infliximab and rituximab identified from healthy Donors." Frontiers in Immunology 8(500- **[AR]**

115. Hart, J., MacHugh, N.D., Sheldrake, T., Nielsen, M., and Morrison, W.I. (2017). "Identification of immediate early gene products of bovine herpes virus 1 (BHV-1) as dominant antigens recognized by CD8 T cells in immune cattle." Journal of General Virology 98(7): 1843-1854. **[AR]**

116. Hartmaier, R.J., Charo, J., Fabrizio, D., Goldberg, M.E., Albacker, L.A., Pao, W., and Chmielecki, J. (2017). "Genomic analysis of 63,220 tumors reveals insights into tumor uniqueness and targeted cancer immunotherapy strategies." Genome Medicine 9(**[AR]**

117. Hegde, N.R., Gauthami, S., Sampath Kumar, H.M., and Bayry, J. (2017). "The use of databases, data mining and immunoinformatics in vaccinology: where are we?" Expert opinion on drug discovery 1-14. **[AR, MA]**

118. Heinson, A.I., Gunawardana, Y., Moesker, B., man Hume, C.C., Vataga, E., Hall, Y., Stylianou, E., McShane, H., Williams, A., Niranjan, M., and Woelk, C.H. (2017). "Enhancing the Biological Relevance of Machine Learning Classifiers for Reverse Vaccinology." International Journal of Molecular Sciences 18(2): **[AR]**

119. Hendrickx, W., Simeone, I., Anjum, S., Mokrab, Y., Bertucci, F., Finetti, P., Curigliano, G., Seliger, B., Cerulo, L., Tomei, S., Delogu, L.G., Maccalli, C., Wang, E., Miller, L.D., Marincola, F.M., Ceccarelli, M., and Bedognetti, D. (2017). "Identification of genetic determinants of breast cancer immune phenotypes by integrative genome-scale analysis." Oncoimmunology 6(2): **[AR]**

120. Hilton, H.G., McMurtrey, C.P., Han, A.S., Djaoud, Z., Guethlein, L.A., Blokhuis, J.H., Pugh, J.L., Goyos, A., Horowitz, A., Buchli, R., Jackson, K.W., Bardet, W., Bushnell, D.A., Robinson, P.J., Mendoza, J.L., Birnbaum, M.E., Nielsen, M., Garcia, K.C., Hildebrand, W.H., and Parham, P. (2017). "The Intergenic Recombinant HLA-B*46:01 Has a Distinctive Peptidome that Includes KIR2DL3 Ligands." Cell Reports 19(7): 1394-1405. **[AR]**

121. Hu, F.J. (2017). "Utilizing Solid Phase Cloning, Surface Display And Epitope Information for Antibody Generation and Characterization." **[AR]**

122. Hu, J. and Liu, Z. (2017). "DeepMHC: Deep Convolutional Neural Networks for High-performance peptide-MHC Binding Affinity Prediction." bioRxiv 239236- **[AR]**

123. Huang, M., Huang, W.J., Wen, F., and Larson, R.G. (2017). "Efficient Estimation of Binding Free Energies between Peptides and an MHC Class II Molecule Using Coarse-Grained Molecular Dynamics Simulations with a Weighted Histogram Analysis Method." Journal of Computational Chemistry 38(23): 2007-2019. **[AR]**

124. Hyun, S.J., Sohn, H.J., Lee, H.J., Lee, S.D., Kim, S., Sohn, D.H., Hong, C.H., Choi, H., Cho, H.I., and Kim, T.G. (2017). "Comprehensive Analysis of Cytomegalovirus pp65 Antigen-Specific CD8(+) T Cell Responses According to Human Leukocyte Antigen Class I Allotypes and Intraindividual Dominance." Frontiers in Immunology 8(**[AR]**

125. Ibrahim, H.S. and Kafi, S.K. (2017). "A Computational Vaccine Designing Approached for MERS-CoV Infections." American Journal of Infectious Diseases 5(1): 4-60. **[AR]**

126. Ifeonu, O.O. (2017). "Genomic Resources for Cryptosporidium Species, Human Pathogens of Public Health Significance in Developing Countries. **[AR]**

127. Imran, S. (2017). "CURRENT SCENARIO OF VACCINE DISEASE: VISC." International Journal of Current Research **[AR]**

128. Iqbal, S. (2017). "Machine Learning based Protein Sequence to (un) Structure Mapping and Interaction Prediction." **[AR]**

129. Iqbal, Sumaiya and Hoque, Md Tamjidul. PBRpredict-Suite: A Suite to Predict Residues of Peptide-Binding Domain from Sequence using Stacked Generalization. 2017.
Ref Type: Unpublished Work **[AR]**

130. Iqbal, Sumaiya and Hoque, Md Tamjidul. Modeling Sequence Pattern of Peptide-Binding Domain Residue using Stacking. 2017.
Ref Type: Unpublished Work **[AR]**

131. Isakova-Sivak, I., Korenkov, D., Smolonogina, T., Tretiak, T., Donina, S., Rekstin, A., Naykhin, A., Shcherbik, S., Pearce, N., Chen, L.M., Bousse, T., and Rudenko, L. (2017). "Comparative studies of infectivity, immunogenicity and cross-protective efficacy of live attenuated influenza vaccines containing nucleoprotein from cold-adapted or wild-type influenza virus in a mouse model." Virology 500(209-217. **[AR]**

132. Jadid, M. A. and Habibi, M. B-cell Epitope Prediction Using Extreme Learning Machine and Particle Swarm Optimization-based Undersampling. 33-38. 2017. 2017 ARTIFICIAL INTELLIGENCE AND ROBOTICS (IRANOPEN).
Ref Type: Book, Whole **[AR]**

133. Jahn, L., Hombrink, P., Hagedoorn, R.S., Kester, M.G.D., van der Steen, D.M., Rodriguez, T., Pentcheva-Hoang, T., Ru, A.H., Schoonakker, M.P., Meeuwsen, M.H., Griffioen, M., van Veelen, P.A., Falkenburg, J.H.F., and Heemskerk, M.H.M. (2017). "TCR-based therapy for multiple myeloma and other B-cell malignancies targeting intracellular transcription factor BOB1." Blood 129(10): 1284-1295. **[AR]**

134. Jahn, L. (2017). "Exploiting HLA-alloreactivity in TCR gene therapy of B cell malignancies." **[AR]**

135. Jain, R., Singh, S., kumar Verma, S., and Jain, A. (2017). "Genome-Wide Prediction of Potential Vaccine Candidates for Campylobacter jejuni Using Reverse Vaccinology." Interdisciplinary Sciences: Computational Life Sciences 1-11. **[AR]**

136. Janahi, E.M., Dhasmana, A., Srivastava, V., Sarangi, A.N., Raza, S., Arif, J.M., Bhatt, M.L.B., Lohani, M., Areeshi, M.Y., Saxena, A.M., and Haque, S. (2017). "In Silico Cd4+, Cd8+T-Cell and B-Cell Immunity Associated Immunogenic Epitope Prediction and Hla Distribution Analysis of Zika Virus." Excli Journal 16(63-72. **[AR]**

137. Jeong, K., Sao, P., Park, M.J., Lee, H., Kim, S.H., Rhee, J.H., and Lee, S.E. (2017). "Development of a Novel Subunit Vaccine Targeting Fusobacterium nucleatum FomA Porin Based on In Silico Analysis." International Journal of Oral Biology 42(2): 63-70. **[AR]**

138. Jin, J., Hjerrild, K.A., Silk, S.E., Brown, R.E., Labbe, G.M., Marshall, J.M., Wright, K.E., Bezemer, S., Clemmensen, S.B., Biswas, S., Li, Y.Y., El-Turabi, A., Douglas, A.D., Hermans, P., Detmers, F.J., de Jongh, W.A., Higgins, M.K., Ashfield, R., and Draper, S.J. (2017). "Accelerating the

clinical development of protein-based vaccines for malaria by efficient purification using a four amino acid C-terminal 'C-tag'." International Journal for Parasitology 47(7): 435-446. **[AR]**

139. Johanns, T.M., Bowman-Kirigin, J.A., Liu, C., and Dunn, G.P. (2017). "Targeting Neoantigens in Glioblastoma: An Overview of Cancer Immunogenomics and Translational Implications." Neurosurgery 64(CN_suppl_1): 165-176. **[AR]**

140. Johnson, A.J., Kennedy, S.C., Arlehamn, C.S.L., Goldberg, M.F., Saini, N.K., Xu, J.Y., Paul, S., Hegde, S.S., Blanchard, J.S., Chan, J., Jacobs, W.R., Sette, A., and Porcelli, S.A. (2017). "Identification of Mycobacterial RplJ/L10 and RpsA/S1 Proteins as Novel Targets for CD4(+) T Cells." Infection and Immunity 85(4): **[AR, MA]**

141. Josephs, T.M., Grant, E.J., and Gras, S. (2017). "Molecular challenges imposed by MHC-I restricted long epitopes on T cell immunity." Biological Chemistry 398(9): 1027-1036. **[AR]**

142. Jucaud, V. (2017). "The Immunogenicity of HLA Class II Mismatches: The Predicted Presentation of Nonself Allo-HLA-Derived Peptide by the HLA-DR Phenotype of the Recipient Is Associated with the Formation of DSA." Journal of Immunology Research **[AR]**

143. K+ñser, T., Renois, F., Wilson, H.L., Cnudde, T., Gerdts, V., Dillon, J.A., Jungersen, G., Agerholm, J.S., and Meurens, F. (2017). "Contribution of the swine model in the study of human sexually transmitted infections." Infection, Genetics and Evolution **[AR]**

144. Kaba, S.A., Karch, C.P., Seth, L., Ferlez, K.M., Storme, C.K., Pesavento, D.M., Laughlin, P.Y., Bergmann-Leitner, E.S., Burkhard, P., and Lanar, D.E. (2017). "Self-assembling protein nanoparticles with built-in flagellin domains increases protective efficacy of a Plasmodium falciparum based vaccine." Vaccine **[AR]**

145. Kadirvel, P. and Anishetty, S. (2017). "Potential role of salt-bridges in the hinge-like movement of apicomplexa specific β-hairpin of Plasmodium and Toxoplasma profilins: A molecular dynamics simulation study." Journal of Cellular Biochemistry **[AR]**

146. Kakimi, K., Karasaki, T., Matsushita, H., and Sugie, T. (2017). "Advances in personalized cancer immunotherapy." Breast Cancer 24(1): 16-24. **[AR]**

147. Karasaki, T., Nagayama, K., Kuwano, H., Nitadori, J., Sato, M., Anraku, M., Hosoi, A., Matsushita, H., Takazawa, M., Ohara, O., Nakajima, J., and Kakimi, K. (2017). "Prediction and prioritization of neoantigens: integration of RNA sequencing data with whole-exome sequencing." Cancer Science 108(2): 170-177. **[AR]**

148. Karasaki, T., Nagayama, K., Kuwano, H., Nitadori, J., Sato, M., Anraku, M., Hosoi, A., Matsushita, H., Morishita, Y., Kashiwabara, K., Takazawa, M., Ohara, O., Kakimi, K., and Nakajima, J. (2017). "An Immunogram for the Cancer-Immunity Cycle: Towards Personalized Immunotherapy of Lung Cancer." Journal of Thoracic Oncology 12(5): 791-803. **[AR]**

149. Karch, C.P., Doll, T.A.P.F., Paulillo, S.M., Nebie, I., Lanar, D.E., Corradin, G., and Burkhard, P. (2017). "The use of a P. falciparum specific coiled-coil domain to construct a self-assembling protein nanoparticle vaccine to prevent malaria." Journal of Nanobiotechnology 15(**[AR]**

150. Karkhah, A., Saadi, M., and Nouri, H.R. (2017). "In silico analyses of heat shock protein 60 and calreticulin to designing a novel vaccine shifting immune response toward T helper 2 in atherosclerosis." Computational Biology and Chemistry 67(244-254. **[AR]**

151. Kato, T., Park, J.H., Kiyotani, K., Ikeda, Y., Miyoshi, Y., and Nakamura, Y. (2017). "Integrated analysis of somatic mutations and immune microenvironment of multiple regions in breast cancers." Oncotarget 8(37): 62029-62038. **[AR]**

152. Kaufman, Jim. A New View of How MHC Class I Molecules Fight Disease: Generalists and Specialists. Evolutionary Biology: Self/Nonself Evolution, Species and Complex Traits Evolution, Methods and Concepts. 3-25. 2017. Springer.
Ref Type: Book Chapter **[AR]**

153. KAUSHIK, V.I.K.A. and SINGH, J.O.G.I. (2017). "BIOINFORMATICS TOOLS FOR CONFORMATIONAL B-CELL AND T-CELL EPITOPE PREDICTION: POTENTIAL VACCINE CANDIDATE." International Journal of Pharma and Bio Sciences **[AR]**

154. Kaushik, V., Singh, B., and Singh, J. (2017). "Bioinformatics techniques used in Hepatitis C virus research." Journal of Pure and Applied Microbiology 11(2): 921-933. **[AR]**

155. Kazemi, R., Amani, J., Akhavian, A., Mousavi, A., and Salmanian, A.H. (2017). "Design and analysis of trivalent chimeric vaccine candidate against three enterotoxigenic bacteria: an in-silico approach." Minerva Biotecnologica 29(2): 62-75. **[AR]**

156. Khan, F., Srivastava, V., and Kumar, A. (2017). "Epitope Based Peptide Prediction from Proteome of Enterotoxigenic E. coli." International Journal of Peptide Research and Therapeutics 1-14. **[AR]**

157. Khatoon, N., Pandey, R.K., and Prajapati, V.K. (2017). "Exploring Leishmania secretory proteins to design B and T cell multi-epitope subunit vaccine using immunoinformatics approach." Scientific Reports 7(**[AR]**

158. Kim, T.J., Lee, S.T., Moon, J., Sunwoo, J.S., Byun, J.I., Lim, J.A., Shin, Y.W., Jun, J.S., Lee, H.S., Lee, W.J., Yang, A.R., Choi, Y., Park, K.I., Jung, K.H., Jung, K.Y., Kim, M., Lee, S.K., and Chu, K. (2017). "Anti-LGI1 encephalitis is associated with unique HLA subtypes." Annals of Neurology 81(2): 183-192. **[AR]**

159. King, E.A. (2017). "Bayesian inference of virus evolutionary models from next-generation sequencing data." **[AR]**

160. Kiyotani, K., Park, J.H., Inoue, H., Husain, A., Olugbile, S., Zewde, M., Nakamura, Y., and Vigneswaran, W.T. (2017). "Integrated analysis of somatic mutations and immune microenvironment in malignant pleural mesothelioma." Oncoimmunology 6(2): **[AR]**

161. Kizhedath, A., Wilkinson, S., and Glassey, J. (2017). "Applicability of predictive toxicology methods for monoclonal antibody therapeutics: status Quo and scope." Archives of Toxicology 91(4): 1595-1612. **[AR]**

162. Klima, C., Cameron, A., Javed, M.A., Alexander, T., Zaheer, R., Munns, K., and McAllister, T.A. (2017). "Genomic approaches to characterizing and reducing antimicrobial resistance in beef cattle production systems." Canadian Journal of Animal Science 97(3): 347-364. **[AR]**

163. Koblischke, M., Mackroth, M.S., Schwaiger, J., Fae, I., Fischer, G., Stiasny, K., Heinz, F.X., and Aberle, J.H. (2017). "Protein structure shapes immunodominance in the CD4 T cell response to yellow fever vaccination." Scientific Reports 7(**[AR]**

164. Kochin, V., Kanaseki, T., Tokita, S., Miyamoto, S., Shionoya, Y., Kikuchi, Y., Morooka, D., Hirohashi, Y., Tsukahara, T., Watanabe, K., Toji, S., Kokai, Y., Sato, N., and Torigoe, T. (2017). "HLA-A24 ligandome analysis of colon and lung cancer cells identifies a novel cancer-testis antigen and a neoantigen that elicits specific and strong CTL responses." Oncoimmunology 6(4): **[AR]**

165. Konstantinou, G.N. (2017). "T-Cell Epitope Prediction." Food Allergens: Methods and Protocols 1592(211-222. **[AR]**

166. Kordbacheh, E., Nazarian, S., and Amerian, M. (2017). "In Silico Analysis of a Multi-subunit Immunogen, Targeting Virulence Factors of Enterohemorrhagic Escherichia coli." Journal of Applied Biotechnology Reports 4(2): 593-602. **[AR]**

167. Kornum, B.R., Burgdorf, K.S., Holm, A., Ullum, H., Jennum, P., and Knudsen, S. (2017). "Absence of autoreactive CD4(+) T-cells targeting HLA-DQA1(star)01:02/DQB1(star)06:02 restricted hypocretin/orexin epitopes in narcolepsy type 1 when detected by EliSpot." Journal of Neuroimmunology 309(7-11. **[AR]**

168. Koutsoni, O.S., Routsias, J.G., Kyriazis, I.D., Barhoumi, M., Guizani, I., Tsakris, A., and Dotsika, E. (2017). "In silico analysis and in vitro evaluation of immunogenic and immunomodulatory properties of promiscuous peptides derived from Leishmania infantum eukaryotic initiation factor." Bioorganic & medicinal chemistry 25(21): 5904-5916. **[AR]**

169. Kropf Correia, F. (2017). "Molecular characterization of T-cell activation Rho-GTPase activating protein." **[AR]**

170. Kumai, T., Fan, A., Harabuchi, Y., and Celis, E. (2017). "Cancer immunotherapy: moving forward with peptide T cell vaccines." Current Opinion in Immunology 47(57-63. **[AR]**

171. Kurniyati, K., Kelly, J.F., Vinogradov, E., Robotham, A., Tu, Y., Wang, J., Liu, J., Logan, S.M., and Li, C. (2017). "A novel glycan modifies the flagellar filament proteins of the oral bacterium Treponema denticola." Molecular Microbiology 103(1): 67-85. **[AR]**

172. Lachmann, N., Niemann, M., Reinke, P., Budde, K., Schmidt, D., Halleck, F., Pruss, A., Schonemann, C., Spierings, E., and Staeck, O. (2017). "Donor-Recipient Matching Based on Predicted Indirectly Recognizable HLA Epitopes Independently Predicts the Incidence of De Novo Donor-Specific HLA Antibodies Following Renal Transplantation." American Journal of Transplantation 17(12): 3076-3086. **[AR]**

173. Lai, J.Y., Choo, J.A.L., Tan, W.J., Too, C.T., Oo, M.Z., Suter, M.A., Mustafa, F.B., Srinivasan, N., Chan, C.E.Z., Lim, A.G.X., Zhong, Y.J., Chan, S.H., Hanson, B.J., Gascoigne, N.R.J., and Macary, P.A. (2017). "TCR-like antibodies mediate complement and antibody-dependent cellular cytotoxicity against Epstein-Barr virus-transformed B lymphoblastoid cells expressing different HLA-A*02 microvariants." Scientific Reports 7(**[AR]**

174. Lamberth, K., Reedtz-Runge, S.L., Simon, J., Klementyeva, K., Pandey, G.S., Padkjaer, S.B., Pascal, V., Leon, I.R., Gudme, C.N., Buus, S., and Sauna, Z.E. (2017). "Post hoc assessment of the immunogenicity of bioengineered factor VIIa demonstrates the use of preclinical tools." Science Translational Medicine 9(372): **[AR]**

175. Lamberth, Kasper, Weldingh, Karin Nana, Ehrenforth, Silke, Chéhadé, Mette Ribel, and Østergaard, Henrik. Immunogenicity Lessons Learned from the Clinical Development of Vatreptacog Alfa, A Recombinant Activated Factor VII Analog, in Hemophilia with Inhibitors. Protein Therapeutics. 123-160. 2017. Springer.
Ref Type: Book Chapter **[AR]**

176. Landry, S.J., Moss, D.L., Cui, D., Ferrie, R.P., Fullerton, M.L., Wells, E.A., Yang, L., Zhou, N.N., Dougherty, T., and Mettu, R.R. (2017). "Structural Basis for CD4+T Cell Epitope Dominance in Arbo-Flavivirus Envelope Proteins: A Meta-Analysis." Viral Immunology 30(7): 479-489. **[AR]**

177. Lau, Q.T., Igawa, T., Minei, R., Kosch, T.A., and Satta, Y. (2017). "Transcriptome analyses of immune tissues from three Japanese frogs (genus Rana) reveals their utility in characterizing major histocompatibility complex class II." Bmc Genomics 18(**[AR]**

178. Lee, K.H., Song, Y., O'Sullivan, M., Pereira, G., Loh, R., and Zhang, G.C. (2017). "The Implications of DNA Methylation on Food Allergy." International Archives of Allergy and Immunology 173(4): 183-192. **[AR]**

179. Leem, J., de Oliveira, S.H.P., Krawczyk, K., and Deane, C.M. (2017). "STCRDab: the structural T-cell receptor database." Nucleic acids research 46(D1): D406-D412. **[AR]**

180. Li, H.L., Gu, X.H., Li, B.J., Chen, X., Lin, H.R., and Xia, J.H. (2017). "Characterization and functional analysis of hypoxia-inducible factor HIF1 alpha and its inhibitor HIF1 alpha n in tilapia." Plos One 12(3): **[AR]**

181. Li, X. (2017). "Emerging role of mutations in epigenetic regulators including MLL2 derived from The Cancer Genome Atlas for cervical cancer." Bmc Cancer 17(**[AR]**

182. Li, X., Huang, H.L., Guan, Y.F., Gong, Y.H., He, C.Y., Yi, X., Qi, M., and Chen, Z.Y. (2017). "Whole-exome sequencing predicted cancer epitope trees of 23 early cervical cancers in Chinese women." Cancer Medicine 6(1): 207-219. **[AR]**

183. Lim, S.I., Kim, Y.K., Lim, J.A., Han, S.H., Hyun, H.S., Kim, K.S., Hyun, B.H., Kim, J.J., Cho, I.S., Song, J.Y., Choi, S.H., Kim, S.H., and An, D.J. (2017). "Antigenic characterization of classical swine fever virus YC11WB isolates from wild boar." Journal of Veterinary Science 18(2): 201-207. **[AR]**

184. Lin, J. and Alcocer, M. Overview of the Commonly Used Methods for Food Allergens. 1-9. 2017. FOOD ALLERGENS: METHODS AND PROTOCOLS
Methods in Molecular Biology.
Ref Type: Book, Whole **[AR]**

185. Lin, Y.Q., Min, X.P., Li, L.L., Yu, H., Ge, S.X., Zhang, J., and Xia, N.S. (2017). "Using a Machine-Learning Approach to Predict Discontinuous Antibody-Specific B-Cell Epitopes." Current Bioinformatics 12(5): 406-415. **[AR]**

186. Liu, D., Abbosh, P., Keliher, D., Reardon, B., Miao, D., Mouw, K., Weiner-Taylor, A., Wankowicz, S., Han, G., Teo, M.Y., Cipolla, C., Kim, J., Iyer, G., Al-Ahmadie, H., Dulaimi, E., Chen, D.Y.T., Alpaugh, R.K., Hoffman-Censits, J., Garraway, L.A., Getz, G., Carter, S.L., Bellmunt, J., Plimack, E.R., Rosenberg, J.E., and Van Allen, E.M. (2017). "Mutational patterns in chemotherapy resistant muscle-invasive bladder cancer." Nature Communications 8(**[AR]**

187. Liu, X.S. and Mardis, E.R. (2017). "Applications of Immunogenomics to Cancer." Cell 168(4): 600-612. **[AR]**

188. Lorenz, F.K.M., Ellinger, C., Kieback, E., Wilde, S., Lietz, M., Schendel, D.J., and Uckert, W. (2017). "Unbiased Identification of T-Cell Receptors Targeting Immunodominant Peptide-MHC Complexes for T-Cell Receptor Immunotherapy." Human Gene Therapy 28(12): 1158-1168. **[AR]**

189. Lourbopoulos, A., Deraos, G., Matsoukas, M.T., Touloumi, O., Giannakopoulou, A., Kalbacher, H., Grigoriadi, N., Apostolopoulos, V., and Matsoukas, J. (2017). "Cyclic MOG(35-55) ameliorates clinical and neuropathological features of experimental autoimmune encephalomyelitis." Bioorganic & medicinal chemistry 25(15): 4163-4174. **[AR]**

190. Ma, P.F., Fu, Y.J., Cai, M.C., Yan, Y., Jing, Y., Zhang, S.Z., Chen, M.J., Wu, J., Shen, Y., Zhu, L., Chen, H.Z., Gao, W.Q., Wang, M.Z., Gu, Z.Y., Bivona, T.G., Zhao, X.J., and Zhuang, G.L. (2017). "Simultaneous evolutionary expansion and constraint of genomic heterogeneity in multifocal lung cancer." Nature Communications 8(**[AR]**

191. Madonia, A., Melchiorri, C., Bonamano, S., Marcelli, M., Bulfon, C., Castiglione, F., Galeotti, M., Volpatti, D., Mosca, F., Tiscar, P.G., and Romano, N. (2017). "Computational modeling of immune system of the fish for a more effective vaccination in aquaculture." Bioinformatics 33(19): 3065-3071. **[AR]**

192. Maggi, M., Mittelman, S.D., Parmentier, J.H., Colombo, G., Meli, M., Whitmire, J.M., Merrell, D.S., Whitelegge, J., and Scotti, C. (2017). "A protease-resistant Escherichia coli asparaginase with outstanding stability and enhanced anti-leukaemic activity in vitro." Scientific Reports 7(**[AR]**

193. Mahendru, S., Roy, K., and Kukreti, S. (2017). "Peptide biomarkers: exploring the diagnostic aspect." Current Protein and Peptide Science 18(9): 914-919. **[AR]**

194. Malekshahi, Z.V., Rajabibazl, M., Ebrahimizadeh, W., Amani, J., and Negahdari, B. (2017). "Designing a Chimeric Vaccine Against Colorectal Cancer." International Journal of Cancer Management 10(12): **[AR]**

195. María, Ribas-Aparicio Rosa, Arturo, Castelán-Vega Juan, Alicia, Jiménez-Alberto, Paulina, Monterrubio-López Gloria, and Gerardo, Aparicio-Ozores. The Impact of Bioinformatics on Vaccine Design and Development. Vaccines. 2017. InTech.
Ref Type: Book Chapter **[AR]**

196. Mardis, E.R. (2017). "Neoantigen Discovery in Human Cancers." Cancer Journal 23(2): 97-101. **[AR]**

197. Maritan, M., Cozzi, R., Lo Surdo, P., Veggi, D., Bottomley, M.J., and Malito, E. (2017). "Crystal structures of human Fabs targeting the Bexsero meningococcal vaccine antigen NHBA." Acta Crystallographica Section F-Structural Biology Communications 73(305-314. **[AR]**

198. Maritan, M. (2017). "Structural characterization of the human immune response to the meningococcal vaccine antigen NHBA." **[AR]**

199. Martínez-Bravo, M.a.J., Sánchez, B., Acevedo, M.a.J., Pérez-Simón, J.A., Núñez-Roldán, A., and Aguilera, I. (2017). "De novo recipient-specific Glutathione S-transferase T1 antibody development after HLA-identical hematopoietic cell transplantation." Transplant immunology **[AR]**

200. Martin, P.J., Levine, D.M., Storer, B.E., Warren, E.H., Zheng, X.W., Nelson, S.C., Smith, A.G., Mortensen, B.K., and Hansen, J.A. (2017). "Genome-wide minor histocompatibility matching as related to the risk of graft-versus-host disease." Blood 129(6): 791-798. **[AR]**

201. Martinez-Martinez, L., Lleixa, M.C., Boera-Carnicero, G., Cortese, A., Devaux, J., Siles, A., Rajabally, Y., Martinez-Pineiro, A., Carvajal, A., Pardo, J., Delmont, E., Attarian, S., az-Manera, J., Callegari, I., Marchioni, E., Franciotta, D., Benedetti, L., Lauria, G., Martin, O.D.L., Juarez, C., Illa, I., and Querol, L. (2017). "Anti-NF155 chronic inflammatory demyelinating polyradiculoneuropathy strongly associates to HLA-DRB15." Journal of Neuroinflammation 14(**[AR]**

202. Martinez-Murillo, P., Tran, K., Guenaga, J., Lindgren, G., Adori, M., Feng, Y., Phad, G.E., Bernat, N.V., Bale, S., Ingale, J., Dubrovskaya, V., O'Dell, S., Pramanik, L., Spangberg, M., Corcoran, M., Lore, K., Mascola, J.R., Wyatt, R.T., and Hedestam, G.B.K. (2017). "Particulate Array of Well-Ordered HIV Clade C Env Trimers Elicits Neutralizing Antibodies that Display a Unique V2 Cap Approach." Immunity 46(5): 804-. **[AR]**

203. Maruyama, S.R., Garcia, G.R., Teixeira, F.R., Brandao, L.G., Anderson, J.M., Ribeiro, J.M.C., Valenzuela, J.G., Horackova, J., Verissimo, C.J., Katiki, L.M., Banin, T.M., Zangirolamo, A.F., Gardinassi, L.G., Ferreira, B.R., and de Miranda-Santos, I.K.F. (2017). "Mining a differential sialotranscriptome of Rhipicephalus microplus guides antigen discovery to formulate a vaccine that reduces tick infestations." Parasites & Vectors 10(**[AR]**

204. Masilamani, M., Pascal, M., and Sampson, H.A. (2017). "T-Cell Proliferation Assay: Determination of Immunodominant T-Cell Epitopes of Food Allergens." Food Allergens: Methods and Protocols 1592(189-198. **[AR]**

205. Mathebula, E.M., Faber, F.E., van Wyngaardt, W., van Schalkwyk, A., Pretorius, A., and Fehrsen, J. (2017). "B-cell epitopes of African horse sickness virus serotype 4 recognised by immune horse sera." Onderstepoort Journal of Veterinary Research 84(1): **[AR]**

206. Mazzaferro, C. (2017). "Predicting Protein Binding Affinity With Word Embeddings And Recurrent Neural Networks." bioRxiv 128223- **[AR]**

207. McCurry, D. (2017). "Tumor Associated Antigens Harbor Readily Defined and Universally Immunogenic Regions Relevant For Cancer Immunotherapy." **[AR]**

208. McGranahan, N., Rosenthal, R., Hiley, C.T., Rowan, A.J., Watkins, T.B.K., Wilson, G.A., Birkbak, N.J., Veeriah, S., Van Loo, P., Herrero, J., and Swanton, C. (2017). "Allele-Specific HLA Loss and Immune Escape in Lung Cancer Evolution." Cell 171(6): 1259-. **[AR]**

209. Mclean, R.T., Wilson, P., St Clair, D., Mustard, C.J., and Wei, J. (2017). "Differential antibody responses to gliadin-derived indigestible peptides in patients with schizophrenia." Translational Psychiatry 7(**[AR]**

210. Meier, J.P. (2017). "CD8+ T cell epitope-enriched HIV-1-Gag antigens with preserved structure and function." **[AR]**

211. Mehla, K. and Ramana, J. (2017). "Surface proteome mining for identification of potential vaccine candidates against Campylobacter jejuni: an in silico approach." Functional & integrative genomics 17(1): 27-37. **[AR]**

212. Mehrizi, A.A., Torabi, F., Zakeri, S., and Djadid, N.D. (2017). "Limited genetic diversity in the global Plasmodium vivax Cell traversal protein of Ookinetes and Sporozoites (CelTOS) sequences; implications for PvCelTOS-based vaccine development." Infection Genetics and Evolution 53(239-247. **[AR]**

213. Merhavi-Shoham, E., Itzhaki, O., Markel, G., Schachter, J., and Besser, M.J. (2017). "Adoptive Cell Therapy for Metastatic Melanoma." Cancer Journal 23(1): 48-53. **[AR]**

214. Meysman, P., De Neuter, N., Bartholomeus, E., Elias, G., Van den Bergh, J., Emonds, M.P., Haasnoot, G.W., Heynderickx, S., Wens, J., and Michels, N.R. (2017). "Increased herpes zoster risk associated with poor HLA-A immediate early 62 protein (IE62) affinity." Immunogenetics 1-10. **[AR]**

215. Miller, N.J., Church, C.D., Dong, L.C., Crispin, D., Fitzgibbon, M.P., Lachance, K., Jing, L.C., Shinohara, M., Gavvovidis, I., Willimsky, G., McIntosh, M., Blankenstein, T., Koelle, D.M., and Nghiem, P. (2017). "Tumor-Infiltrating Merkel Cell Polyomavirus-Specific T Cells Are Diverse and Associated with Improved Patient Survival." Cancer Immunology Research 5(2): 137-147. **[AR]**

216. Muller, M., Gfeller, D., Coukos, G., and Bassani-Sternberg, M. (2017). "'Hotspots' of antigen presentation revealed by Human Leukocyte antigen Ligandomics for neoantigen prioritization." Frontiers in Immunology 8(**[AR]**

217. Mumtaz, S., Nabney, I.T., and Flower, D.R. (2017). "Scrutinizing human MHC polymorphism: Supertype analysis using Poisson-Boltzmann electrostatics and clustering." Journal of Molecular Graphics & Modelling 77(130-136. **[AR]**

218. Murray, S.E., Nesterenko, P.A., Vanarsdall, A.L., Munks, M.W., Smart, S.M., Veziroglu, E.M., Sagario, L.C., Lee, R., Claas, F.H., and Doxiadis, I.I. (2017). "Fibroblast-adapted human CMV vaccines elicit predominantly conventional CD8 T cell responses in humans." Journal of Experimental Medicine 214(7): 1889-1899. **[AR]**

219. Mytych, D.T., Hock, M.B., Kroenke, M., Jawa, V., Kaliyaperumal, A., and Zhou, Y.C. (2017). "A Proposal to Redefine Clinical Immunogenicity Assessment." Aaps Journal 19(3): 599-602. **[AR]**

220. Naduvile Veedu, R. and AlShamaileh, H. (2017). "Next generation nucleic acid aptamers with two base modified nucleotides improve the binding affinity and potency." Chembiochem **[AR]**

221. Naiyer, M.M., Cassidy, S.A., Magri, A., Cowton, V., Chen, K., Mansour, S., Kranidioti, C., Mbiribindi, B., Rettman, P., and Harris, S. (2017). "KIR2DS2 recognizes conserved peptides derived from viral helicases in the context of HLA-C." Science immunology 2(15): **[AR]**

222. Negahdaripour, M., Eslami, M., Nezafat, N., Hajighahramani, N., Ghoshoon, M.B., Shoolian, E., Dehshahri, A., Erfani, N., Morowvat, M.H., and Ghasemi, Y. (2017). "A novel HPV prophylactic peptide vaccine, designed by immunoinformatics and structural vaccinology approaches." Infection Genetics and Evolution 54(402-416. **[AR]**

223. Negi, S.S. and Braun, W. (2017). "Cross-React: a new structural bioinformatics method for predicting allergen cross-reactivity." Bioinformatics 33(7): 1014-1020. **[AR]**

224. Nelde, A., Walz, J.S., Kowalewski, D.J., Schuster, H., Wolz, O.O., Peper, J.K., Gloria, Y.C., Langerak, A.W., Muggen, A.F., Claus, R., Bonzheim, I., Fend, F., Salih, H.R., Kanz, L., Rammensee, H.G., Stevanovic, S., and Weber, A.N.R. (2017). "HLA class I-restricted MYD88 L265P-derived peptides as specific targets for lymphoma immunotherapy." Oncoimmunology 6(3): **[AR]**

225. Nezafat, N., Eslami, M., Negahdaripour, M., Rahbar, M.R., and Ghasemi, Y. (2017). "Designing an efficient multi-epitope oral vaccine against Helicobacter pylori using immunoinformatics and structural vaccinology approaches." Molecular Biosystems 13(4): 699-713. **[AR]**

226. Ng, A.W.T., Poon, S.L., Huang, M.N., Lim, J.Q., Boot, A., Yu, W., Suzuki, Y., Thangaraju, S., Ng, C.C.Y., Tan, P., Pang, S.T., Huang, H.Y., Yu, M.C., Lee, P.H., Hsieh, S.Y., Chang, A.Y., Teh, B.T., and Rozen, S.G. (2017). "Aristolochic acids and their derivatives are widely implicated in liver cancers in Taiwan and throughout Asia." Science Translational Medicine 9(412): **[AR]**

227. Ngo, H.M., Zhou, Y., Lorenzi, H., Wang, K., Kim, T.K., Zhou, Y., El Bissati, K., Mui, E., Fraczek, L., Rajagopala, S.V., Roberts, C.W., Henriquez, F.L., Montpetit, A., Blackwell, J.M., Jamieson, S.E., Wheeler, K., Begeman, I.J., Naranjo-Galvis, C., liey-Rodriguez, N., Davis, R.G., Soroceanu, L., Cobbs, C., Steindler, D.A., Boyer, K., Noble, A.G., Swisher, C.N., Heydemann, P.T., Rabiah, P., Withers, S., Soteropoulos, P., Hood, L., and McLeod, R. (2017). "Toxoplasma Modulates Signature Pathways of Human Epilepsy, Neurodegeneration & Cancer." Scientific Reports 7(**[AR]**

228. Ngono, A.E., Vizcarra, E.A., Tang, W.W., Sheets, N., Joo, Y., Kim, K., Gorman, M.J., Diamond, M.S., and Shresta, S. (2017). "Mapping and Role of the CD8(+) T Cell Response During Primary Zika Virus Infection in Mice." Cell Host & Microbe 21(1): 35-46. **[AR]**

229. Nguyen, M.N., Pradhan, M.R., Verma, C., and Zhong, P.Y. (2017). "The interfacial character of antibody paratopes: analysis of antibody-antigen structures." Bioinformatics 33(19): 2971-2976. **[AR]**

230. Nielsen, J.S., Chang, A.R., Wick, D.A., Sedgwick, C.G., Zong, Z.S., Mungall, A.J., Martin, S.D., Kinloch, N.N., Ott-Langer, S., Brumme, Z.L., Treon, S.P., Connors, J.M., Gascoyne, R.D., Webb, J.R., Berry, B.R., Morin, R.D., Macpherson, N., and Nelson, B.H. (2017). "Mapping the human T

cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma." Oncoimmunology 6(7): **[AR]**

231. Noguchi, T., Ward, J.P., Gubin, M.M., Arthur, C.D., Lee, S.H., Hundal, J., Selby, M.J., Graziano, R.F., Mardis, E.R., Korman, A.J., and Schreiber, R.D. (2017). "Temporally Distinct PD-L1 Expression by Tumor and Host Cells Contributes to Immune Escape." Cancer Immunology Research 5(2): 106-117. **[AR]**

232. Nowak, E.C., Lines, J.L., Varn, F.S., Deng, J., Sarde, A., Mabaera, R., Kuta, A., Le Mercier, I., Cheng, C., and Noelle, R.J. (2017). "Immunoregulatory functions of VISTA." Immunological Reviews 276(1): 66-79. **[AR]**

233. Oany, A.R., Pervin, T., Mia, M., Hossain, M., Shahnaij, M., Mahmud, S., and Kibria, K.M.K. (2017). "Vaccinomics Approach for Designing Potential Peptide Vaccine by Targeting Shigella spp. Serine Protease Autotransporter Subfamily Protein SigA." Journal of Immunology Research **[AR]**

234. Ogishi, M. and Yotsuyanagi, H. (2017). "TCR-peptide contact profile determines immunogenicity in pathogen/tumor-derived MHC-I epitopes." bioRxiv 155317-

235. Opuni, K.F.M., Solomon, S., Metzen, F., Frommholz, D., and Koy, C. (2017). "In silico Epitope Mapping of Glucose-6-Phosphate Isomerase: A Rheumatoid Arthritis Autoantigen." J Proteomics Bioinform 10(60-72. **[AR]**

236. Oseroff, C., Christensen, L.H., Westernberg, L., Pham, J., Lane, J., Paul, S., Greenbaum, J., Stranzl, T., Lund, G., Hoof, I., Holm, J., Wurtzen, P.A., Meno, K.H., Frazier, A., Schulten, V., Andersen, P.S., Peters, B., and Sette, A. (2017). "Immunoproteomic analysis of house dust mite antigens reveals distinct classes of dominant T cell antigens according to function and serological reactivity." Clinical and Experimental Allergy 47(4): 577-592. **[AR]**

237. Ostroumov, D., Fekete-Drimusz, N., Saborowski, M., K++hnel, F., and Woller, N. (2017). "CD4 and CD8 T lymphocyte interplay in controlling tumor growth." Cellular and Molecular Life Sciences 1-25. **[AR]**

238. Ott, P.A., Hu, Z.T., Keskin, D.B., Shukla, S.A., Sun, J., Bozym, D.J., Zhang, W.D., Luoma, A., Giobbie-Hurder, A., Peter, L., Chen, C., Olive, O., Carter, T.A., Li, S.Q., Lieb, D.J., Eisenhaure, T., Gjini, E., Stevens, J., Lane, W.J., Javeri, I., Nellaiappan, K., Salazar, A.M., Daley, H., Seaman, M., Buchbinder, E.I., Yoon, C.H., Harden, M., Lennon, N., Gabriel, S., Rodig, S.J., Barouch, D.H., Aster, J.C., Getz, G., Wucherpfennig, K., Neuberg, D., Ritz, J., Lander, E.S., Fritsch, E.F., Hacohen, N., and Wu, C.J. (2017). "An immunogenic personal neoantigen vaccine for patients with melanoma." Nature 547(7662): 217-+. **[AR]**

239. Özcan, M. (2017). "Models for Immune Response and Immune Evasion in MSI Cancer and Lynch Syndrome." **[AR]**

240. Pahari, S., Chatterjee, D., Negi, S., Kaur, J., Singh, B., and Agrewala, J.N. (2017). "Morbid Sequences Suggest Molecular Mimicry between Microbial Peptides and Self-Antigens: A Possibility of Inciting Autoimmunity." Frontiers in Microbiology 8(**[AR]**

241. Palanisamy, N. and Lennerstrand, J. (2017). "Computational Prediction of Usutu Virus E Protein B Cell and T Cell Epitopes for Potential Vaccine Development." Scandinavian Journal of Immunology 85(5): 350-364. **[AR]**

242. Palaschak, B., Marsic, D., Herzog, R.W., Zolotukhin, S., and Markusic, D.M. (2017). "An Immune-Competent Murine Model to Study Elimination of AAV-Transduced Hepatocytes by Capsid-Specific CD8(+) T Cells." Molecular Therapy-Methods & Clinical Development 5(142-152. **[AR]**

243. Panda, S.K. and Mahapatra, R.K. (2017). "In-silico screening, identification and validation of a novel vaccine candidate in the fight against Plasmodium falciparum." Parasitology Research 116(4): 1293-1305. **[AR]**

244. Pang, P., Zhang, F.B., Jia, B., Li, M., Hu, J.W., Ji, P., Zheng, R.J., Ding, J.B., and Zhang, Y.X. (2017). "Bioinformatics analysis of T-and B-combined epitopes of OMP31 protein of Brucella melitensis in Xinjiang, China." International Journal of Clinical and Experimental Medicine 10(9): 13320-13330. **[AR]**

245. Paquin-Proulx, D., Leal, F.E., Silveira, C.G.T., Maestri, A., Brockmeyer, C., Kitchen, S.M., Cabido, V.D., Kallas, E.G., and Nixon, D.F. (2017). "T-Cell responses in individuals infected with Zika virus and in those vaccinated against dengue virus." Pathogens & immunity 2(2): 274- **[AR]**

246. Pardy, R.D., Rajah, M.M., Condotta, S.A., Taylor, N.G., Sagan, S.M., and Richer, M.J. (2017). "Analysis of the T Cell Response to Zika Virus and Identification of a Novel CD8(+) T Cell Epitope in Immunocompetent Mice." Plos Pathogens 13(2): **[AR]**

247. Parida, R. and Samanta, L. (2017). "In silico analysis of candidate proteins sharing homology with Streptococcus agalactiae proteins and their role in male infertility." Systems Biology in Reproductive Medicine 63(1): 15-28. **[AR]**

248. Parker, A. and Kaufman, J. (2017). "What chickens might tell us about the MHC class II system." Current Opinion in Immunology 46(23-29. **[AR]**

249. Payandeh, Z., Rajabibazl, M., Mortazavi, Y., and Rahimpour, A. (2017). "In Silico Analysis for Determination and Validation of Human CD20 Antigen 3D Structure." International Journal of Peptide Research and Therapeutics 1-13. **[AR]**

250. Perez-Martinez, A.P., Ong, E., Zhang, L.X., Marrs, C.F., He, Y.Q., and Yang, Z.H. (2017). "Conservation in gene encoding Mycobacterium tuberculosis antigen Rv2660 and a high predicted population coverage of H56 multistage vaccine in South Africa." Infection Genetics and Evolution 55(244-250. **[AR, MA]**

251. Peters, H.L., Tripathi, S.C., Kerros, C., Katayama, H., Garber, H.R., St John, L.S., Federico, L., Meraz, I.M., Roth, J.A., Sepesi, B., Majidi, M., Ruisaard, K., Clise-Dwyer, K., Roszik, J., Gibbons, D.L., Heymach, J.V., Swisher, S.G., Bernatchez, C., Alatrash, G., Hanash, S., and Molldrem, J.J. (2017). "Serine Proteases Enhance Immunogenic Antigen Presentation on Lung Cancer Cells." Cancer Immunology Research 5(4): 319-329. **[AR]**

252. Petrone, L., Vanini, V., Amicosante, M., Corpolongo, A., Morales, G., Ludovisi, A., Ippolito, G., Pozio, E., Teggi, A., and Goletti, D. (2017). "AT-cell diagnostic test for cystic echinococcosis based on Antigen B peptides." Parasite Immunology 39(12): **[AR]**

253. Peyron, I., Hartholt, R.B., Pedró-Cos, L., van Alphen, F., ten Brinke, A., Lardy, N., Meijer, A.B., and Voorberg, J. (2017). "Comparative profiling of HLA-DR and HLA-DQ associated factor VIII peptides presented by monocyte-derived dendritic cells." Haematologica haematol-2017. **[AR]**

254. Pfeifer, C.R., Alvey, C.M., Irianto, J., and Discher, D.E. (2017). "Genome variation across cancers scales with tissue stiffness - An invasion-mutation mechanism and implications for immune cell infiltration." Current opinion in systems biology 2(103-114. **[AR]**

255. Pickering, H. (2017). "Identification of Chlamydia trachomatis Immune Targets through Immunological and Population-Genomic Screens and Elucidation of Potential Roles in Bacterial Pathogenesis." **[AR]**

256. Poortahmasebi, V., Poorebrahim, M., Ghaziasadi, A., Abazari, M.F., Mozhgani, S.H., Aleagha, M.N., Shahbazi, F., and Alavian, S.M. (2017). "Analysis of Antigenic and Conformational Changes in Hepatitis B Surface Antigen (HBsAg) Identified in Iranian Patients with Chronic Hepatitis B." Hepatitis Monthly 17(9): **[AR]**

257. Premlal, A.L.R. (2017). "Building a Pipeline for Personalized Cancer Vaccine Design." **[AR]**

258. Probst, P., Kopp, J., Oxenius, A., Colombo, M.P., Ritz, D., Fugmann, T., and Neri, D. (2017). "Sarcoma Eradication by Doxorubicin and Targeted TNF Relies upon CD8(+) T-cell Recognition of a Retroviral Antigen." Cancer Research 77(13): 3644-3654. **[AR]**

259. Pymm, P., Illing, P.T., Ramarathinam, S.H., O'Connor, G.M., Hughes, V.A., Hitchen, C., Price, D.A., Ho, B.K., McVicar, D.W., Brooks, A.G., Purcell, A.W., Rossjohn, J., and Vivian, J.P. (2017). "MHC-I peptides get out of the groove and enable a novel mechanism of HIV-1 escape." Nature Structural & Molecular Biology 24(4): 387-+. **[AR]**

260. Qamra, A., Xing, M.J., Padmanabhan, N., Kwok, J.J.T., Zhang, S.L., Xu, C., Leong, Y.S., Lim, A.P.L., Tang, Q.Q., Ooi, W.F., Lin, J.S., Nandi, T., Yao, X.S., Ong, X.W., Lee, M., Tay, S.T., Keng, A.T.L., Santoso, E.G., Ng, C.C.Y., Ng, A., Jusakul, A., Smoot, D., Ashktorab, H., Rha, S.Y., Yeoh, K.G., Yong, W.P., Chow, P.K.H., Chan, W.H., Ong, H.S., Soo, K.C., Kim, K.M., Wong, W.K., Rozen, S.G., Teh, B., Kappei, D., Lee, J., Connolly, J., and Tan, P. (2017). "Epigenomic Promoter Alterations Amplify Gene Isoform and Immunogenic Diversity in Gastric Adenocarcinoma." Cancer Discovery 7(6): 630-651. **[AR]**

261. Qin, Y., Ekmekcioglu, S., Forget, M.A., Szekvolgyi, L., Hwu, P., Grimm, E.A., Jazaeri, A.A., and Roszik, J. (2017). "Cervical Cancer Neoantigen Landscape and Immune Activity is Associated with Human Papillomavirus Master Regulator." Frontiers in Immunology 8(**[AR]**

262. Qiu, X.T., Duvvuri, V.R., Gubbay, J.B., Webby, R.J., Kayali, G., and Bahl, J. (2017). "Lineage-specific epitope profiles for HPAI H5 pre-pandemic vaccine selection and evaluation." Influenza and Other Respiratory Viruses 11(5): 445-456. **[AR, MA]**

263. Rönnberg, B., Vapalahti, O., Goeijenbier, M., Reusken, C., Gustafsson, Â, Blomberg, J., and Lundkvist, Â. (2017). "Serogrouping and seroepidemiology of North European hantaviruses using

a novel broadly targeted synthetic nucleoprotein antigen array." Infection ecology & epidemiology 7(1): 1350086- **[AR]**

264. Rahman, T. (2017). "Modelling for selecting vaccines against antigenically variable viruses." **[AR]**

265. Ramadhani, A.N., Nofitasari, A., Puspitarini, S., Priyandoko, D., Rohman, M.S., and Lukitasari, M. (2017). "The V279F polymorphism might change protein character and immunogenicity in Lp-PLA2 protein." Egyptian Journal of Medical Human Genetics **[AR]**

266. Ramasamy, R., Joseph, B., and Whittall, T. (2017). "Potential molecular mimicry between the human endogenous retrovirus W family envelope proteins and myelin proteins in multiple sclerosis." Immunology Letters 183(79-85. **[AR]**

267. Raoufi, E., Akrami, H., Khansarinejad, B., and Abtahi, H. (2017). "Expression and Antigenic Evaluation of Helicobacter pylori UreB Fragment." Jundishapur Journal of Microbiology 10(5): **[AR]**

268. Reeves, P.M., Paul, S.R., Sluder, A.E., Brauns, T.A., and Poznansky, M.C. (2017). "Q-vaxcelerate: A distributed development approach for a new Coxiella burnetii vaccine." Human Vaccines & Immunotherapeutics 13(12): 2977-2981. **[AR]**

269. Reuben, A., Gittelman, R., Gao, J.J., Zhang, J.X., Yusko, E.C., Wu, C.J., Emerson, R., Zhang, J.H., Tipton, C., Li, J., Quek, K., Gopalakrishnan, V., Chen, R.Z., Vence, L.M., Cascone, T., Vignali, M., Fujimoto, J., Rodriguez-Canales, J., Parra, E.R., Little, L.D., Gumbs, C., Forget, M.A., Federico, L., Haymaker, C., Behrens, C., Benzeno, S., Bernatchez, C., Sepesi, B., Gibbons, D.L., Wargo, J.A., William, W.N., Swisher, S., Heymach, J.V., Robins, H., Lee, J.J., Sharma, P., Allison, J.P., Futreal, P.A., Wistuba, I.I., and Zhang, J.J. (2017). "TCR Repertoire Intratumor Heterogeneity in Localized Lung Adenocarcinomas: An Association with Predicted Neoantigen Heterogeneity and Postsurgical Recurrence." Cancer Discovery 7(10): 1088-1097. **[AR]**

270. Reyes, C., Moreno-Vranich, A., and Patarroyo, M.E. (2017). "The role of pi-interactions and hydrogen bonds in fully protective synthetic malaria vaccine development." Biochemical and Biophysical Research Communications 484(3): 501-507. **[AR]**

271. Reyes, C., Rojas-Luna, R., za-Conde, J., Tabares, L., Patarroyo, M.A., and Patarroyo, M.E. (2017). "Critical role of HLA-DR beta* binding peptides' peripheral flanking residues in fully-protective malaria vaccine development." Biochemical and Biophysical Research Communications 489(3): 339-345. **[AR]**

272. Ricciardi, M.J., Magnani, D.M., Grifoni, A., Kwon, Y.C., Gutman, M.J., Grubaugh, N.D., Gangavarapu, K., Sharkey, M., Silveira, C.G.T., Bailey, V.K., Pedreno-Lopez, N., Gonzalez-Nieto, L., Maxwell, H.S., Domingues, A., Martins, M.A., Pham, J., Weiskopf, D., Altman, J., Kallas, E.G., Andersen, K.G., Stevenson, M., Lichtenberger, P., Choe, H., Whitehead, S.S., Sette, A., and Watkins, D.I. (2017). "Ontogeny of the B- and T-cell response in a primary Zika virus infection of a dengue-naive individual during the 2016 outbreak in Miami, FL." Plos Neglected Tropical Diseases 11(12): **[AR]**

273. Ritz, D., Gloger, A., Neri, D., and Fugmann, T. (2017). "Purification of soluble HLA class I complexes from human serum or plasma deliver high quality immuno peptidomes required for biomarker discovery." Proteomics 17(1-2): **[AR]**

274. Robertson, A.G., Kim, J., Al-Ahmadie, H., Bellmunt, J., Guo, G.W., Cherniack, A.D., Hinoue, T., Laird, P.W., Hoadley, K.A., Akbani, R., Castro, M.A.A., Gibb, E.A., Kanchi, R.S., Gordenin, D.A., Shukla, S.A., Sanchez-Vega, F., Hansel, D.E., Czerniak, B.A., Reuter, V.E., Su, X.P., Carvalho, B.D., Chagas, V.S., Mungall, K.L., Sadeghi, S., Pedamallu, C.S., Lu, Y.L., Klimczak, L.J., Zhang, J.X., Choo, C., Ojesina, A.I., Bullman, S., Leraas, K.M., Lichtenberg, T.M., Wu, C.J., Schultz, N., Getz, G., Meyerson, M., Mills, G.B., McConkey, D.J., Weinstein, J.N., Kwiatkowski, D.J., and Lerner, S.P. (2017). "Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer." Cell 171(3): 540-. **[AR]**

275. Roh, W., Chen, P.L., Reuben, A., Spencer, C.N., Prieto, P.A., Miller, J.P., Gopalakrishnan, V., Wang, F., Cooper, Z.A., Reddy, S.M., Gumbs, C., Little, L., Chang, Q., Chen, W.S., Wani, K., De Macedo, M.P., Chen, E., ustin-Breneman, J.L., Jiang, H., Roszik, J., Tetzlaff, M.T., Davies, M.A., Gershenwald, J.E., Tawbi, H., Lazar, A.J., Hwu, P., Hwu, W.J., Diab, A., Glitza, I.C., Patel, S.P., Woodman, S.E., Amaria, R.N., Prieto, V.G., Hu, J.H., Sharma, P., Allison, J.P., Chin, L., Zhang, J.H., Wargo, J.A., and Futreal, P.A. (2017). "Integrated molecular analysis of tumor biopsies on sequential CTLA-4 and PD-1 blockade reveals markers of response and resistance." Science Translational Medicine 9(379): **[AR]**

276. Rosenberg, A.S. and Sauna, Z.E. (2017). "Immunogenicity assessment during the development of protein therapeutics." Journal of Pharmacy and Pharmacology **[AR]**

277. Rubinsteyn, A., Kodysh, J., Hodes, I., Mondet, S., Aksoy, B.A., Finnigan, J.P., Bhardwaj, N., and Hammerbacher, J. (2017). "Computational pipeline for the PGV-001 neoantigen vaccine trial." bioRxiv 174516- **[AR]**

278. Sade-Feldman, M., Jiao, Y.X.J., Chen, J.H., Rooney, M.S., Barzily-Rokni, M., Eliane, J.P., Bjorgaard, S.L., Hammond, M.R., Vitzthum, H., Blackmon, S.M., Frederick, D.T., Hazar-Rethinam, M., Nadres, B.A., Van Seventer, E.E., Shukla, S.A., Yizhak, K., Ray, J.P., Rosebrock, D., Livitz, D., Adalsteinsson, V., Getz, G., Duncan, L.M., Li, B., Corcoran, R.B., Lawrence, D.P., Stemmer-Rachamimov, A., Boland, G.M., Landau, D.A., Flaherty, K.T., Sullivan, R.J., and Hacohen, N. (2017). "Resistance to checkpoint blockade therapy through inactivation of antigen presentation." Nature Communications 8(**[AR]**

279. Sahin, U., Derhovanessian, E., Miller, M., Kloke, B.P., Simon, P., Lower, M., Bukur, V., Tadmor, A.D., Luxemburger, U., Schrors, B., Omokoko, T., Vormehr, M., Albrecht, C., Paruzynski, A., Kuhn, A.N., Buck, J., Heesch, S., Katharina, H., Muller, F., Ortseifer, I., Vogler, I., Godehardt, E., Attig, S., Rae, R., Breitkreuz, A., Tolliver, C., Suchan, M., Martic, G., Hohberger, A., Sorn, P., Diekmann, J., Ciesla, J., Waksmann, O., Burck, A.K., Witt, M., Zillgen, M., Rothermel, A., Kasemann, B., Langer, D., Bolte, S., Diken, M., Kreiter, S., Nemecek, R., Gebhardt, C., Grabbe, S., Holler, C., Utikal, J., Huber, C., Loquai, C., and Tureci, O. (2017). "Personalized RNA mutanome vaccines mobilize poly-specific therapeutic immunity against cancer." Nature 547(7662): 222-+. **[AR]**

280. Salvat, R.S., Verma, D., Parker, A.S., Kirsch, J.R., Brooks, S.A., Bailey-Kellogg, C., and Griswold, K.E. (2017). "Computationally optimized deimmunization libraries yield highly mutated enzymes

with low immunogenicity and enhanced activity." Proceedings of the National Academy of Sciences of the United States of America 114(26): E5085-E5093. **[AR]**

281. Sankar, S., Ramamurthy, M., Nandagopal, B., and Sridharan, G. (2017). "T-cell epitopes predicted from the Nucleocapsid protein of Sin Nombre virus restricted to 30 HLA alleles common to the North American population." Bioinformation 13(3): 94- **[AR]**

282. Scholz, E.M., Marcilla, M., Daura, X., Arribas-Layton, D., James, E.A., and Alvarez, I. (2017). "Human leukocyte Antigen (HLA)-DRB1*15:01 and HLA-DRB5*01:01 Present Complementary Peptide Repertoires." Frontiers in Immunology 8(**[AR]**

283. Schon, C., Sothilingam, V., Muhlfriedel, R., Garrido, M.G., Beck, S.C., Tanimoto, N., Wissinger, B., Paquet-Durand, F., Biel, M., Michalakis, S., and Seeliger, M.W. (2017). "Gene Therapy Successfully Delays Degeneration in a Mouse Model of PDE6A-Linked Retinitis Pigmentosa (RP43)." Human Gene Therapy 28(12): 1180-1188. **[AR]**

284. Schone, D., Hrycak, C.P., Windmann, S., Lapuente, D., Dittmer, U., Tenbusch, M., and Bayer, W. (2017). "Immunodominance of Adenovirus-Derived CD8(+) T Cell Epitopes Interferes with the Induction of Transgene-Specific Immunity in Adenovirus-Based Immunization." Journal of Virology 91(20): **[AR]**

285. Schrama, D., Ritter, C., and Becker, J.C. (2017). "T cell receptor repertoire usage in cancer as a surrogate marker for immune responses." Seminars in Immunopathology 39(3): 255-268. **[AR]**

286. Schrors, B., Lubcke, S., Lennerz, V., Fatho, M., Bicker, A., Wolfel, C., Derigs, P., Hankeln, T., Schadendorf, D., Paschen, A., and Wolfel, T. (2017). "HLA class I loss in metachronous metastases prevents continuous T cell recognition of mutated neoantigens in a human melanoma model." Oncotarget 8(17): 28312-28327. **[AR]**

287. Schulten, V. . Strategies to Study T Cells and T Cell Targets in Allergic Disease. Allergen. 2017. InTech.
Ref Type: Book Chapter **[AR]**

288. Scriba, T.J., Carpenter, C., Pro, S.C., Sidney, J., Musvosvi, M., Rozot, V., Seumois, G., Rosales, S.L., Vijayanand, P., Goletti, D., Makgotlho, E., Hanekom, W., Hatherill, M., Peters, B., Sette, A., and Arlehamn, C.S.L. (2017). "Differential Recognition of Mycobacterium tuberculosis-Specific Epitopes as a Function of Tuberculosis Disease History." American Journal of Respiratory and Critical Care Medicine 196(6): 772-781. **[AR]**

289. Seliktar-Ofir, S., Merhavi-Shoham, E., Itzhaki, O., Yunger, S., Markel, G., Schachter, J., and Besser, M.J. (2017). "Selection of Shared and Neoantigen-Reactive T Cells for Adoptive Cell Therapy Based on CD137 Separation." Frontiers in Immunology 8(**[AR]**

290. Selot, R., Arumugam, S., Mary, B., Cheemadan, S., and Jayandharan, G.R. (2017). "Optimized AAV rh.10 Vectors That Partially Evade Neutralizing Antibodies during Hepatic Gene Transfer." Frontiers in Pharmacology 8(**[AR]**

291. Shukla, S.A., Howitt, B.E., Wu, C.J., and Konstantinopoulos, P.A. (2017). "Predicted neoantigen load in non-hypermutated endometrial cancers: Correlation with outcome and tumor-specific genomic alterations." Gynecologic Oncology Reports 19(42-45. **[AR]**

292. Singer, M. and Frischknecht, F. (2017). "Time for Genome Editing: Next Generation Attenuated Malaria Parasites." Trends in Parasitology 33(3): 202-213. **[AR]**

293. Singh, N.K., Riley, T.P., Baker, S.C.B., Borrman, T., Weng, Z.P., and Baker, B.M. (2017). "Emerging Concepts in TCR Specificity: Rationalizing and (Maybe) Predicting Outcomes." Journal of Immunology 199(7): 2203-2213. **[AR]**

294. Singh, S.P., Srivastava, D., and Mishra, B.N. (2017). "Genome-wide identification of novel vaccine candidates for Plasmodium falciparum malaria using integrative bioinformatics approaches." 3 Biotech 7(**[AR]**

295. Skevaki, C., Hudemann, C., Matrosovich, M., Möbs, C., Paul, S., Wachtendorf, A., Alhamwe, B.A., Potaczek, D.P., Hagner, S., and Gemsa, D. (2017). "Influenza-derived peptides cross-react with allergens and provide asthma protection." Journal of Allergy and Clinical Immunology **[AR]**

296. Solihah, B., Winarko, E., Afiahayati, Hartati, S., and Wibowo, M.E. (2017). "A Systematic Review: B-Cell Conformational Epitope Prediction from Epitope Characteristics View." 2017 3Rd International Conference on Science and Technology - Computer (Icst) 93-98. **[AR]**

297. Sommermeyer, D., Hill, T., Shamah, S.M., Salter, A.I., Chen, Y., Mohler, K.M., and Riddell, S.R. (2017). "Fully human CD19-specific chimeric antigen receptors for T-cell therapy." Leukemia 31(10): 2191-2199. **[AR]**

298. Song, P.X., He, S.Y., Zhou, A.H., Lv, G., Guo, J.J., Zhou, J., Han, Y.L., Zhou, H.Y., Hao, Z., and Cong, H. (2017). "Vaccination with toxofilin DNA in combination with an alummonophosphoryl lipid A mixed adjuvant induces significant protective immunity against Toxoplasma gondii." Bmc Infectious Diseases 17(**[AR]**

299. Sorensen, M.R., Ilsoe, M., Strube, M.L., Bishop, R., Erbs, G., Hartmann, S.B., and Jungersen, G. (2017). "Sequence-Based Genotyping of Expressed Swine Leukocyte Antigen Class I Alleles by Next-Generation Sequencing Reveal Novel Swine Leukocyte Antigen Class I Haplotupes and Alleles in Belgian Danish, and Kenyan Fattening Pigs and Gottingen Minipigs." Frontiers in Immunology 8(**[AR]**

300. Speir, M., Authier-Hall, A., Brooks, C.R., Farrand, K.J., Compton, B.J., Anderson, R.J., Heiser, A., Osmond, T.L., Tang, C.W., Berzofsky, J.A., Terabe, M., Painter, G.F., Hermans, I.F., and Weinkove, R. (2017). "Glycolipid-peptide conjugate vaccines enhance CD8(+) T cell responses against human viral proteins." Scientific Reports 7(**[AR]**

301. Speir, M., Hermans, I.F., and Weinkove, R. (2017). "Engaging Natural Killer T Cells as 'Universal Helpers' for Vaccination." Drugs 77(1): 1-15. **[AR]**

302. Sritrakul, T., Nitipan, S., Wajjwalku, W., La-Ard, A., Suphatpahirapol, C., Petkarnjanapong, W., Ongphiphadhanakul, B., and Prapong, S. (2017). "Leptospira borgpetersenii hybrid leucine-rich

repeat protein: Cloning and expression, immunogenic identification and molecular docking evaluation." Journal of Microbiological Methods 142(52-62. **[AR]**

303. Stepniewska-Dziubinska, M.M., Zielenkiewicz, P., and Siedlecki, P. Development and evaluation of a deep learning model for protein-ligand binding affinity prediction." **[AR]**

304. Stevanović, S., Pasetto, A., Helman, S.R., Gartner, J.J., Prickett, T.D., Howie, B., Robins, H.S., Robbins, P.F., Klebanoff, C.A., and Rosenberg, S.A. (2017). "Landscape of immunogenic tumor antigens in successful immunotherapy of virally induced epithelial cancer." Science 356(6334): 200-205. **[AR]**

305. Suarez, C.F., Pabon, L., Barrera, A., za-Conde, J., Patarroyo, M.A., and Patarroyo, M.E. (2017). "Structural analysis of owl monkey MHC-DR shows that fully-protective malaria vaccine components can be readily used in humans." Biochemical and Biophysical Research Communications 491(4): 1062-1069. **[AR]**

306. Sveen, A., Johannessen, B., Tengs, T., Danielsen, S.A., Eilertsen, I.A., Lind, G.E., Berg, K.C.G., Leithe, E., Meza-Zepeda, L.A., Domingo, E., Myklebost, O., Kerr, D., Tomlinson, I., Nesbakken, A., Skotheim, R.I., and Lothe, R.A. (2017). "Multilevel genomics of colorectal cancers with microsatellite instability-clinical impact of JAK1 mutations and consensus molecular subtype 1." Genome Medicine 9(**[AR]**

307. Sypek, M., Kausman, J., Holt, S., and Hughes, P. (2017). "HLA Epitope Matching in Kidney Transplantation: An Overview for the General Nephrologist." American Journal of Kidney Diseases **[AR]**

308. Tagliamonte, Maria, Tornesello, Maria Lina, Buonaguro, Franco M., and Buonaguro, Luigi. Vaccine Approaches in Hepatocellular Carcinoma. Immunotherapy of Hepatocellular Carcinoma. 1-17. 2017. Springer.
Ref Type: Book Chapter **[AR]**

309. Taherzadeh, G., Zhou, Y., Liew, A.W.-C., and Yang, Y. (2017). "Structure-based prediction of protein-peptide binding regions using Random Forest." Bioinformatics **[AR]**

310. Tahmoorespur, M., Nazifi, N., and Pirkhezranian, Z. (2017). "In Silico Prediction of B-Cell and T-Cell Epitopes of Protective Antigen of Bacillus anthracis in Development of Vaccines Against Anthrax." Iranian Journal of Applied Animal Science 7(**[AR]**

311. Tang, S. and Madhavan, S. (2017). "neoantigenR: An annotation based pipeline for tumor neoantigen identification from sequencing data." bioRxiv 171843- **[AR]**

312. Tappeiner, E., Finotello, F., Charoentong, P., Mayer, C., Rieder, D., and Trajanoski, Z. (2017). "TIminer: NGS data mining pipeline for cancer immunology and immunotherapy." Bioinformatics 33(19): 3140-3141. **[AR]**

313. Tauber, Alfred I. Immunity: the evolution of an idea. 2017. Oxford University Press.
Ref Type: Book, Whole **[AR]**

314. Taylor, D.W., Bobbili, N., Khadka, V.S., Quakyi, I.A., and Leke, R.G.F. (2017). "Individuals living in a malaria-endemic area of Cameroon do not have an acquired antibody response to Plasmodium falciparum histidine-rich protein 2." Malaria Journal 16(**[AR]**

315. Tian, Y., Babor, M., Lane, J., Schulten, V., Patil, V.S., Seumois, G., Rosales, S.L., Fu, Z., Picarda, G., Burel, J., Zapardiel-Gonzalo, J., Tennekoon, R.N., De Silva, A.D., Premawansa, S., Premawansa, G., Wijewickrama, A., Greenbaum, J.A., Vijayanand, P., Weiskopf, D., Sette, A., and Peters, B. (2017). "Unique phenotypes and clonal expansions of human CD4 effector memory T cells re-expressing CD45RA." Nature Communications 8(**[AR]**

316. Tipu, H.N., Ahmed, D., and Gardezi, S.A.H. (2017). "In silico identification of epitopes from house cat and dog proteins as peptide immunotherapy candidates based on human leukocyte antigen binding affinity." Iranian journal of veterinary research 18(1): 56- **[AR]**

317. Tosi, A., la Santa, S., Cappuzzello, E., Marotta, C., Walerich, D., Del Sal, G., Zanovello, P., Sommaggio, R., and Rosato, A. (2017). "Identification of a HLA-A*0201-restricted immunogenic epitope from the universal tumor antigen DEPDC1." Oncoimmunology 6(8): **[AR]**

318. Tourani, M., Karkhah, A., and Najafi, A. (2017). "Development of an. epitope-based vaccine inhibiting immune cells rolling and migration against atherosclerosis using in silico approaches." Computational Biology and Chemistry 70(156-163. **[AR]**

319. Tsutsui, R., Tsukagoshi, H., Nagasawa, K., Takahashi, M., Matsushima, Y., Ryo, A., Kuroda, M., Takami, H., and Kimura, H. (2017). "Genetic analyses of the fusion protein genes in human parainfluenza virus types 1 and 3 among patients with acute respiratory infections in Eastern Japan from 2011 to 2015." Journal of medical microbiology 66(2): 160-168. **[AR]**

320. Tu, X.N., Li, S., Zhao, L.J., Xiao, R., Wang, X.L., and Zhu, F. (2017). "Human leukemia antigen-A*0201-restricted epitopes of human endogenous retrovirus W family envelope (HERV-W env) induce strong cytotoxic T lymphocyte responses." Virologica Sinica 32(4): 280-289. **[AR]**

321. Tumiotto, C., Riviere, L., Bellecave, P., Recordon-Pinson, P., Vilain-Parce, A., Guidicelli, G.L., and Fleury, H. (2017). "Sanger and Next-Generation Sequencing data for characterization of CTL epitopes in archived HIV-1 proviral DNA." Plos One 12(9): **[AR]**

322. Turajlic, S., Litchfield, K., Xu, H., Rosenthal, R., McGranahan, N., Reading, J.L., Wong, Y.N.S., Rowan, A., Kanu, N., Al Bakir, M., Chambers, T., Salgado, R., Savas, P., Loi, S., Birkbak, N.J., Sansregret, L., Gore, M., Larkin, J., Quezada, S.A., and Swanton, C. (2017). "Insertion-and-deletion-derived tumour-specific neoantigens and the immunogenic phenotype: a pan-cancer analysis." Lancet Oncology 18(8): 1009-1021. **[AR]**

323. Turtle, L., Tatullo, F., Bali, T., Ravi, V., Soni, M., Chan, S., Chib, S., Venkataswamy, M.M., Fadnis, P., Yaich, M., Fernandez, S., Klenerman, P., Satchidanandam, V., and Solomon, T. (2017). "Cellular Immune Responses to Live Attenuated Japanese Encephalitis (JE) Vaccine SA14-14-2 in Adults in a JE/Dengue Co-Endemic Area." Plos Neglected Tropical Diseases 11(1): **[AR]**

324. URGE HURRISA, B.E.K.S. (2017). "SEROTYPING AND MOLECULAR CHARACTERIZATION OF FMD VIRUS ISOLATED FROM OUTBREAK CASES IN SELECTED REGION AND ADDIS ABABA, ETHIOPIA." **[AR]**

325. Van den Driessche, G. and Fourches, D. (2017). "Adverse drug reactions triggered by the common HLA-B*57:01 variant: a molecular docking study." Journal of cheminformatics 9(**[AR]**

326. van der Kant, R., Karow-Zwick, A.R., Van Durme, J., Blech, M., Gallardo, R., Seeliger, D., Assfalg, K., Baatsen, P., Compernolle, G., Gils, A., Studts, J.M., Schulz, P., Garidel, P., Schymkowitz, J., and Rousseau, F. (2017). "Prediction and Reduction of the Aggregation of Monoclonal Antibodies." Journal of Molecular Biology 429(8): 1244-1261. **[AR]**

327. Vijayamahantesh, Amit, A., Dikhit, M.R., Singh, A.K., Venkateshwaran, T., Das, V.N.R., Das, P., and Bimal, S. (2017). "Immuno-infoimatics based approaches to identify CD8+T cell epitopes within the Leishmania donovani 3-ectonucleotidase in cured visceral leishmaniasis subjects." Microbes and Infection 19(6): 358-369. **[AR]**

328. Vitiello, A. and Zanetti, M. (2017). "Neoantigen prediction and the need for validation." Nature Biotechnology 35(9): 815-817. **[AR]**

329. Vivek-Ananth, R.P., Mohanraj, K., Vandanashree, M., Jhingran, A., Craig, J.P., and Samal, A. (2017). "Comparative systems analysis of the secretome of the opportunistic pathogen Aspergillus fumigatus and other Aspergillus species." bioRxiv 230953- **[AR]**

330. Wagih, O. (2017). "ggseqlogo: a versatile R package for drawing sequence logos." Bioinformatics 33(22): 3645-3647. **[AR]**

331. Waheed, Y., Safi, S.Z., Najmi, M.H., Aziz, H., and Imran, M. (2017). "Prediction of promiscuous T cell epitopes in RNA dependent RNA polymerase of Chikungunya virus." Asian Pacific Journal of Tropical Medicine 10(8): 825-829. **[AR]**

332. Wai, C.Y., Leung, N.Y., Leung, P.S., and Chu, K.H. (2017). "Immunotherapy of Food Allergy: a Comprehensive Review." Clinical reviews in allergy & immunology 1-19. **[AR]**

333. Wang, L., Winnewisser, J., Federle, C., Jessberger, G., Nave, K.A., Werner, H.B., Kyewski, B., Klein, L., and Hinterberger, M. (2017). "Epitope-Specific Tolerance Modes Differentially Specify Susceptibility to Proteolipid Protein-Induced Experimental Autoimmune Encephalomyelitis." Frontiers in Immunology 8(**[AR]**

334. Wang, M., Zhu, D., Zhu, J., Nussinov, R., and Ma, B. (2017). "Local and global anatomy of antibody-protein antigen recognition." Journal of Molecular Recognition **[AR]**

335. Wang, X.Y., Zhou, D.F., Wang, G.H., Huang, L.B., Zheng, Q.K., Li, C.G., and Cheng, Z.Q. (2017). "A novel multi-variant epitope ensemble vaccine against avian leukosis virus subgroup J." Vaccine 35(48): 6685-6690. **[AR]**

336. Wang, X., Ren, Z., Sun, Q., Wan, X., Sun, Y., Hua, Y., Fu, M., Shao, N., Du, Y., and Zhang, Q. (2017). "Evaluation and Comparison of Newly Built Linear B-Cell Epitope Predic-tion Software from a Users' Perspective." Current Bioinformatics **[AR]**

337. Wang, Y., Singh, N.K., Spear, T.T., Hellman, L.M., Piepenbrink, K.H., McMahan, R.H., Rosen, H.R., Vander Kooi, C.W., Nishimura, M., and Baker, B.M. (2017). "How an alloreactive T-cell receptor achieves peptide and MHC specificity." Proceedings of the National Academy of Sciences of the United States of America 114(24): E4792-E4801. **[AR]**

338. Warnecke, A., Musunuri, S., N'diaye, M., Sandalova, T., Achour, A., Bergquist, J., and Harris, R.A. (2017). "Nitration of MOG diminishes its encephalitogenicity depending on MHC haplotype." Journal of Neuroimmunology 303(1-12. **[AR]**

339. Wayengera, M., Mwebaza, I., Welishe, J., Nakimuli, C., Kateete, D.P., Wampande, E., Kirimunda, S., Bayigga, L., Musubika, C., and Babirye, P. (2017). "Sero-diagnosis of active Mycobacterium tuberculosis disease among HIV co-infected persons using thymidylate kinase based antigen and antibody capture enzyme immuno-assays." Mycobacterial diseases: tuberculosis & leprosy 7(2): **[AR]**

340. Wayengera, M., Mwebaza, I., Welishe, J., Bayiyana, A., Kateete, D.P., Wampande, E., Kirimunda, S., Kigozi, E., Katabazi, F., and Musubika, C. (2017). "Immuno-diagnosis of Mycobacterium tuberculosis in sputum, and reduction of timelines for its positive cultures to within 3 h by pathogen-specific thymidylate kinase expression assays." BMC research notes 10(1): 368- **[AR]**

341. Weitzner, B.D., Jeliazkov, J.R., Lyskov, S., Marze, N., Kuroda, D., Frick, R., dolf-Bryfogle, J., Biswas, N., Dunbrack, R.L., and Gray, J.J. (2017). "Modeling and docking of antibody structures with Rosetta." Nature Protocols 12(2): 401-416. **[AR]**

342. Welner, S., Nielsen, M., Rasmussen, M., Buus, S., Jungersen, G., and Larsen, L.E. (2017). "Prediction and in vitro verification of potential CTL epitopes conserved among PRRSV-2 strains." Immunogenetics 69(10): 689-702. **[AR]**

343. Wieczorek, M., Abualrous, E.T., Sticht, J., varo-Benito, M., Stolzenberg, S., Noe, F., and Freund, C. (2017). "Major Histocompatibility Complex (MHC) Class I and MHC Class II Proteins: Conformational Plasticity in Antigen Presentation." Frontiers in Immunology 8(**[AR]**

344. Wienzek-Lischka, S., Konig, I.R., Papenkort, E.M., Hackstein, H., Santoso, S., Sachs, U.J., and Bein, G. (2017). "HLA-DRB3*01:01 is a predictor of immunization against human platelet antigen-1a but not of the severity of fetal and neonatal alloimmune thrombocytopenia." Transfusion 57(3): 533-540. **[AR]**

345. Xia, J., Zhang, Y., Zhao, H.H., Wang, J., Gao, X.R., Chen, J.P., Fu, B., Shen, Y.Q., Miao, F.Q., Zhang, J.Q., and Teng, G.J. (2017). "Non-Invasive Monitoring of CNS MHC-I Molecules in Ischemic Stroke Mice." Theranostics 7(11): 2837-2848. **[AR]**

346. Xie, J., Zeng, X., Lu, D.F., Liu, Z.X., and Wang, J. (2017). "MHC2NNZ: A novel peptide binding prediction approach for HLA DQ molecules." Modern Physics Letters B 31(19-21): **[AR]**

347. Yang, M., Haase, C., Viljanen, J., Xu, B.Z., Ge, C.R., Kihlberg, J., and Holmdahl, R. (2017). "Cutting Edge: Processing of Oxidized Peptides in Macrophages Regulates T Cell Activation and Development of Autoimmune Arthritis." Journal of Immunology 199(12): 3937-3942. **[AR]**

348. Yarchoan, M., Johnson, B.A., Lutz, E.R., Laheru, D.A., and Jaffee, E.M. (2017). "Targeting neoantigens to augment antitumour immunity." Nature Reviews Cancer 17(4): 209-222. **[AR]**

349. Yin, X., Jing, Y., Cai, M.C., Ma, P.F., Zhang, Y., Xu, C., Zhang, M.Y., Di, W., and Zhuang, G.L. (2017). "Clonality, Heterogeneity, and Evolution of Synchronous Bilateral Ovarian Cancer." Cancer Research 77(23): 6551-6561. **[AR]**

350. Yokota, R., Kaminaga, Y., and Kobayashi, T.J. (2017). "Quantification of Inter-Sample Differences in T-Cell Receptor Repertoires Using Sequence-Based Information." Frontiers in Immunology 8(**[AR]**

351. Yoshida, M., Ishioka, Y., Ozawa, T., Okuyama, H., Iguchi, M., Ota, T., Ito, T., Nagira, M., Morita, A., Tanaka, H., Naito, H., Kidoya, H., and Takakura, N. (2017). "Soluble HLA-associated peptide from PSF1 has a cancer vaccine potency." Scientific Reports 7(**[AR]**

352. Yu, W., Wang, L., Wang, M., Liu, S., Li, W., Wang, X., Li, X., Yu, S., Yao, D., Ma, J., Yu, L., Chen, J., Feng, Z., and Cui, Y. (2017). "Identification and characterization of CD4(+) T cell epitopes on manganese transport protein C of Staphylococcus aureus." Microbial Pathogenesis 112(30-37. **[AR]**

353. Yurina, V., Raras, T.Y.M., Rudijanto, A., Lyrawati, D., and Handono, K. (2017). "Design and construction of DNA vaccine expressing lectin-like oxidize-LDL receptor-1 (LOX-1) as atherosclerosis vaccine candidate." Journal of Biotech Research [ISSN: 1944-3285] 8(103-112. **[AR]**

354. Zandian, A., Forsstrom, B., Haggmark-Manberg, A., Schwenk, J.M., Uhlen, M., Nilsson, P., and Ayoglu, B. (2017). "Whole-Proteome Peptide Microarrays for Profiling Autoantibody Repertoires within Multiple Sclerosis and Narcolepsy." Journal of proteome research 16(3): 1300-1314. **[AR]**

355. Zandian, A. (2017). "Array-based Autoantibody Profiling and Epitope Mapping." **[AR]**

356. ZHang, T., Li, H., Lan, X., ZHang, C.H., Yang, Z.H., Cao, W., Fen, N., Liu, Y., Yan, Y., and Ma, X. (2017). "The bioinformatics analyses reveal novel antigen epitopes in major outer membrane protein of Chlamydia trachomatis." Indian journal of medical microbiology 35(4): 522- **[AR]**

357. Zhang, X.L., Kim, S., Hundal, J., Herndon, J.M., Li, S.Q., Petti, A.A., Soysal, S.D., Li, L.J., McLellan, M.D., Hoog, J., Primeau, T., Myers, N., Vickery, T.L., Sturmoski, M., Hagemann, I.S., Miller, C.A., Ellis, M.J., Mardis, E.R., Hansen, T., Fleming, T.P., Goedegebuure, S.P., and Gillanders, W.E. (2017). "Breast Cancer Neoantigens Can Induce CD8(+) T-Cell Responses and Antitumor Immunity." Cancer Immunology Research 5(7): 516-523. **[AR]**

358. Zhao, J.W., Yan, M., Shi, G., Zhang, S.L., and Ming, L. (2017). "In silico identification of cytotoxic T lymphocyte epitopes encoded by RD5 region of Mycobacterium tuberculosis." Journal of Infection in Developing Countries 11(10): 806-+. **[AR]**

359. Zheng, J.F., Huang, Q.N., Huang, R.L., Deng, F.Y., Yue, X.Y., Yin, J.P., Zhao, W.J., Chen, Y., Wen, L.F., Zhou, J., Huang, R.D., Riemekasten, G., Liu, Z.G., Petersen, F., and Yu, X.H. (2017). "B Cells Are Indispensable for a Novel Mouse Model of Primary Sjogren's Syndrome." Frontiers in Immunology 8(**[AR]**

360. Zheng, J.Z., Lin, X.F., Wang, X.Y., Zheng, L.Y., Lan, S.S., Jin, S.S., Ou, Z.F., and Wu, J.M. (2017). "In Silico Analysis of Epitope-Based Vaccine Candidates against Hepatitis B Virus Polymerase Protein." Viruses-Basel 9(5): **[AR]**

361. Zhou, W.Q., Duan, Z.W., Yang, B., and Xiao, C.L. (2017). "The effective regulation of pro- and anti-inflammatory cytokines induced by combination of PA-MSHA and BPIFB1 in initiation of innate immune responses." Open Medicine 12(1): 299-307. **[AR]**

362. Zhou, Z., Lyu, X.Z., Wu, J.C., Yang, X.Y., Wu, S.S., Zhou, J., Gu, X., Su, Z.X., and Chen, S.Q. (2017). "TSNAD: an integrated software for cancer somatic mutation and tumour-specific neoantigen detection." Royal Society Open Science 4(4): **[AR]**

363. Zia, Q., Azhar, A., Ahmad, S., Afsar, M., Hasan, Z., Owais, M., Alam, M., Akbar, S., Ganash, M., Ashraf, G.M., Zubair, S., and Aliev, G. (2017). "PeMtb: A Database of MHC Antigenic Peptide of Mycobacterium tuberculosis." Current Pharmaceutical Biotechnology 18(8): 648-652. **[AR]**

3.2.3 Epitope Meta-Analyses

1. Arevalo, M.T., Li, J.W., az-Arevalo, D., Chen, Y.P., Navarro, A., Wu, L.H., Yan, Y.Y., and Zeng, M.T. (2017). "A dual purpose universal influenza vaccine candidate confers protective immunity against anthrax." Immunology 150(3): 276-289. **[MA]**
2. Arslan, A. and van Noort, V. (2017). "Evolutionary conservation of Ebola virus proteins predicts important functions at residue level." Bioinformatics 33(2): 151-154. **[MA]**

3. Brault, A.C., Domi, A., McDonald, E.M., Talmi-Frank, D., McCurley, N., Basu, R., Robinson, H.L., Hellerstein, M., Duggal, N.K., and Bowen, R.A. (2017). "A Zika vaccine targeting NS1 protein protects immunocompetent adult mice in a lethal challenge model." Scientific reports 7(1): 14769- **[MA]**

4. Culshaw, A., Mongkolsapaya, J., and Screaton, G.R. (2017). "The immunopathology of dengue and Zika virus infections." Current opinion in immunology 48(1-6. **[MA]**

5. Ellis, J.A., Gow, S.P., Lee, L.B., Lacoste, S., and Ball, E.C. (2017). "Comparative efficacy of intranasal and injectable vaccines in stimulating Bordetella bronchiseptica-reactive anamnestic antibody responses in household dogs." Canadian Veterinary Journal-Revue Veterinaire Canadienne 58(8): 809-815. **[MA]**

6. Esteves, E., Rosa, N., Correia, M.J., Arrais, J.P., and Barros, M. (2017). "New Targets for Zika Virus Determined by Human-Viral Interactomic: A Bioinformatics Approach." BioMed Research International 2017(**[MA]**

7. Fulton, B.O., Sachs, D., Schwarz, M.C., Palese, P., and Evans, M.J. (2017). "Transposon mutagenesis of the Zika virus genome highlights regions essential for RNA replication and restricted for immune evasion." Journal of virology 91(15): e00698-17. **[MA]**
8. González-González, E., Alvarez, M.M.s., Márquez-Ipiña, A.R., Trujillo-de Santiago, G., Rodríguez-Martínez, L.M., Annabi, N., and Khademhosseini, A. (2017). "Anti-Ebola therapies based on monoclonal antibodies: current state and challenges ahead." Critical reviews in biotechnology 37(1): 53-68. **[MA]**

9. Gu, X.X., Plotkin, S.A., Edwards, K.M., Sette, A., Mills, K.H.G., Levy, O., Sant, A.J., Mo, A., Alexander, W., Lu, K.T., and Taylor, C.E. (2017). "Waning Immunity and Microbial Vaccines-

Workshop of the National Institute of Allergy and Infectious Diseases." Clinical and Vaccine Immunology 24(7): **[MA]**

10. In't Veld, R.H., Da Silva, C.G., Kaijzel, E.L., Chan, A.B., and Cruz, L.J. (2017). "The Potential of Nano-Vehicle Mediated Therapy in Vasculitis and Multiple Sclerosis." Current Pharmaceutical Design 23(13): 1985-1992. **[MA]**

11. Javed, F., Manzoor, K.N., Ali, M., Haq, I.U., Khan, A.A., Zaib, A., and Manzoor, S. (2017). "Zika virus: what we need to know?" Journal of basic microbiology **[MA]**

12. Jiang, Y., Liu, H., Wang, X., Xiao, S., Li, M., Li, G., Zhao, L., Zhao, X., Dou, X., and Wan, K. (2017). "Genetic diversity of immune-related antigens in Region of Difference 2 of Mycobacterium tuberculosis strains." Tuberculosis 104(1-7. **[MA]**

13. Kuzmenko, Y.V., Starodubova, E.S., Shevtsova, A.S., Chernokhaeva, L.L., Latanova, A.A., Preobrazhenskaia, O.V., Timofeev, A.V., Karganova, G.G., and Karpov, V.L. (2017). "Intracellular degradation and localization of NS1 of tick-borne encephalitis virus affect its protective properties." Journal of General Virology 98(1): 50-55. **[MA]**

14. Lapuente, D. (2017). "Evaluation of IL-1beta and IL-18 as genetic adjuvants in adenoviral immunizations against influenza A viruses." **[MA]**

15. Lewinsohn, D.A., Swarbrick, G.M., Park, B., Cansler, M.E., Null, M.D., Toren, K.G., Baseke, J., Zalwango, S., Mayanja-Kizza, H., and Malone, L.L. (2017). "Comprehensive definition of human immunodominant CD8 antigens in tuberculosis." NPJ vaccines 2(1): 8- **[MA]**

16. Liang, F., Lindgren, G., Lin, A., Thompson, E.A., Ols, S., Rohss, J., John, S., Hassett, K., Yuzhakov, O., Bahl, K., Brito, L.A., Salter, H., Ciaramella, G., and Lore, K. (2017). "Efficient Targeting and Activation of Antigen Presenting Cells In Vivo after Modified mRNA Vaccine Administration in Rhesus Macaques." Molecular Therapy 25(12): 2635-2647. **[MA]**

17. Lima, N.S., Rolland, M., Modjarrad, K., and Trautmann, L. (2017). "T Cell Immunity and Zika Virus Vaccine Development." Trends in immunology 38(8): 594-605. **[MA]**

18. Lutynska, A., Golos, A., Augustynowicz, E., and Orzechowska, B. (2017). "Vaccinomics and adversomics as new trends in vaccinology." Postepy Higieny I Medycyny Doswiadczalnej 71(1240-1253. **[MA]**

19. Lv, J., Ren, Z.Y., Zhang, Y.Y., Liu, Y.E., Gao, J., Yao, K., Feng, D., Li, Z.Y., Feng, X., Liu, Y.X., and Jia, N. (2017). "Study on age-dependent pre-existing 2009 pandemic influenza virus T and B cell responses from Chinese population." Bmc Infectious Diseases 17(**[MA]**

20. Mahakapuge, T.A.N. (2017). "Adjuvant-mediated manipulation of immune memory resilience." **[MA]**

21. Mieves, J.F., Wittke, K., Freitag, H., Volk, H.D., Scheibenbogen, C., and Hanitsch, L.G. (2017). "Influenza Vaccination in Patients with Common Variable Immunodeficiency (CVID)." Current Allergy and Asthma Reports 17(11): **[MA]**

22. Moreira-Soto, A., Soto-Garita, C., and Corrales-Aguilar, E. (2017). "Neotropical primary bat cell lines show restricted dengue virus replication." Comparative Immunology Microbiology and Infectious Diseases 50(101-105. **[MA]**

23. Mueller, G.A. (2017). "Contributions and Future Directions for Structural Biology in the Study of Allergens." International Archives of Allergy and Immunology 174(2): 57-66. **[MA]**

24. Munjal, A., Khandia, R., Dhama, K., Sachan, S., Karthik, K., Tiwari, R., Malik, Y.S., Kumar, D., Singh, R.K., and Iqbal, H. (2017). "Advances in developing therapies to combat Zika virus: current knowledge and future perspectives." Frontiers in microbiology 8(1469- **[MA]**

25. Muraro, E., Merlo, A., Martorelli, D., Cangemi, M., Santa, S.D., Dolcetti, R., and Rosato, A. (2017). "Fighting viral infections and virus-Driven Tumors with Cytotoxic CD4(+) T Cells." Frontiers in Immunology 8(**[MA]**

26. Panina, A.A., Dement'yeva, I.G., Aliev, T.K., Toporova, V.A., Bokov, M.N., Pozdnyakova, L.P., Shemchukova, O.B., Dolgikh, D.A., Sveshnikov, P.G., and Kirpichnikov, M.P. (2017). "Chimeric fab fragments of antibodies to recombinant Ebola virus glycoprotein." Russian Journal of Bioorganic Chemistry 43(4): 409-420. **[MA]**

27. Payyappilly, R.J., Karunakaran, U., and Adilat, D. (2017). "Dimorphism in response of sexes to dengue infection modifying course and outcome of disease." Journal of International Medicine and Dentistry 4(2): 47-55. **[MA]**

28. Priyamvada, L., Hudson, W., Ahmed, R., and Wrammert, J. (2017). "Humoral cross-reactivity between Zika and dengue viruses: implications for protection and pathology." Emerging Microbes & Infections 6(**[MA]**

29. Reiber, H. (2017). "Polyspecific antibodies without persisting antigen in multiple sclerosis, neurolupus and Guillain-Barre syndrome: immune network connectivity in chronic diseases." Arquivos de Neuro-Psiquiatria 75(8): 580-588. **[MA]**

30. Reiber, H. (2017). "Chronic Diseases with Delayed Onset After Vaccinations and Infections. A Complex Systems Approach to Pathology and Therapy." Journal of Archives in Military Medicine In Pre): **[MA]**

31. Ripoll, D.R., Mitchell, D.A., Dupuy, L.C., Wallqvist, A., Schmaljohn, C., and Chaudhury, S. (2017). "Combinatorial peptide-based epitope mapping from Ebola virus DNA vaccines and infections reveals residue-level determinants of antibody binding." Human vaccines & immunotherapeutics 13(12): 2953-2966. **[MA]**

32. Savic, M., Dembinski, J.L., Laake, I., Hungnes, O., Cox, R., Oftung, F., Trogstad, L., and Mjaaland, S. (2017). "Distinct T and NK cell populations may serve as immune correlates of protection against symptomatic pandemic influenza A(H1N1) virus infection during pregnancy." Plos One 12(11): **[MA]**

33. Schotsaert, M. and Garcia-Sastre, A. (2017). "Inactivated influenza virus vaccines: the future of TIV and QIV." Current Opinion in Virology 23(102-106. **[MA]**

34. Seth, L., Ferlez, K.M.B., Kaba, S.A., Musser, D.M., Emadi, S., Matyas, G.R., Beck, Z., Alving, C.R., Burkhard, P., and Lanar, D.E. (2017). "Development of a self-assembling protein nanoparticle vaccine targeting Plasmodium falciparum Circumsporozoite Protein delivered in three Army Liposome Formulation adjuvants." Vaccine 35(41): 5448-5454. **[MA]**

35. Sharma, S., Malmeström, C., Lindberg, C., Meisel, S., Schön, K., Verolin, T., and Lycke, N.Y. (2017). "A sensitive method for detecting peptide-specific CD4+ T cell responses in peripheral blood from patients with Myasthenia gravis." Frontiers in Immunology 8(1370- **[MA]**

36. Skogberg, G., Jackson, S., and Âstrand, A. (2017). "Mechanisms of tolerance and potential therapeutic interventions in Alopecia Areata." Pharmacology & therapeutics **[MA]**

37. Slon Campos, J.L. (2017). "Evaluation of a Tetravalent DNA Vaccine against Dengue: Integrating Biochemical Studies on Dengue Virus Envelope Protein to a Domain-Based Antigen Design." **[MA]**

38. Sun, H., Han, X., Yan, X., Xu, J., Huang, Q., Meng, F., Zhang, H., and Li, S. (2017). "A novel mimovirus encoding ChgA$_{10\text{-}19}$ peptide with PD-L1 induces T cell tolerance and ameliorates the severity of diabetes." Cellular immunology 320(56-61. **[MA]**

39. Vazquez-Prieto, S., Paniagua, E., Solana, H., Ubeira, F.M., and Gonzalez-Diaz, H. (2017). "A study of the Immune Epitope Database for some fungi species using network topological indices." Molecular Diversity 21(3): 713-718. **[MA]**

40. Wada, Y., Nithichanon, A., Nobusawa, E., Moise, L., Martin, W.D., Yamamoto, N., Terahara, K., Hagiwara, H., Odagiri, T., Tashiro, M., Lertmemongkolchai, G., Takeyama, H., De Groot, A.S., Ato, M., and Takahashi, Y. (2017). "A humanized mouse model identifies key amino acids for low immunogenicity of H7N9 vaccines." Scientific reports 7(**[MA]**

41. Wahid, B., Ali, A., Rafique, S., and Idrees, M. (2017). "Current status of therapeutic and vaccine approaches against Zika virus." European journal of internal medicine 44(12-18. **[MA]**

42. Weltman, J.K. (2017). "Exclusive and Common Subsets of Zika Virus Polyprotein Mutants." J Med Microb Diagn 6(256): 2161-0703. **[MA]**

43. Yan, A.W. (2017). "Influenza viral dynamics models to explore the roles of innate and adaptive immunity." **[MA]**

44. Yan, A.W.C., Cao, P.X., Heffernan, J.M., McVernon, J., Quinn, K.M., La Gruta, N.L., Laurie, K.L., and Mccaw, J.M. (2017). "Modelling cross-reactivity and memory in the cellular adaptive immune response to influenza infection in the host." Journal of Theoretical Biology 413(34-49. **[MA]**

45. Zuanazzi, D., Arts, E.J., Jorge, P.K., Mulyar, Y., Gibson, R., Xiao, Y., Bringel dos Santos, M., Machado, M.A.A., and Siqueira, W.L. (2017). "Postnatal identification of Zika virus peptides from saliva." Journal of dental research 96(10): 1078-1084. **[MA]**

3.2.4 Informal In-Text

1. Abdollahi, A., Mansouri, S., Amani, J., Fasihi-Ramandi, M., and Moradi, M. (2017). "Development and immunereactivity evaluation of a chimeric recombinant protein encoding Brucella antigen: In silico to in vitro."
2. Ajitha, M. (2017). "Novel Algorithms to Predict the Structure and Functions of Uncharacterized Proteins."
3. Al Asari, M.A.M., Giasuddin, M., Mahmud, M.S., Akter, S., Islam, E., Samad, M.A., Karim, M.R., and Dey, S.K. (2017). "In silico analysis of VP1 gene for prediction of peptide vaccine against three serotypes (O, A & Asia1) of Foot & Mouth Disease Virus circulating in Bangladesh." Imperial Journal of Interdisciplinary Research 3(10):
4. Alam, J., Koh, J.H., Kwok, S.K., Park, S.H., Park, K., and Choi, Y. (2017). "Functional Epitopes for Ant-Aquaporin 5 Antibodies in Sjogren Syndrome." Journal of dental research 96(12): 1414-1421.
5. Alibakhshi, A., Bandehpour, M., and Kazemi, B. (2017). "Cloning, expression and purification of a polytopic antigen comprising of surface antigens of Toxoplasma gondii." Iranian journal of microbiology 9(4): 251-
6. Amigo, L., Sanchón, J., Cruz, A., Picariello, G., Recio, I., and Miralles, B. Identification of digestion resistant casein domains after in vitro gastrointestinal digestion followed by the incorporation of the intestinal brush border membrane peptidases. 2017.
   Ref Type: Conference Proceeding
7. Arun, T.R., Rana, R., Rekha, V., and Sabarinath, T. (2017). "In silico identification of diagnostic candidates from predicted lipoproteome of Mycoplasma mycoides subsp. capri." Adv.Anim.Vet.Sci 5(10): 419-424.
8. Badenes, Carlos, Denaux, Ronald, De Vos, Martine, Garijo, Daniel, Gomez-Perez, Jose Manuel, Lawrynowicz, Agnieszka, Lisena, Pasquale, Palma, Raul, Troncy, Raphaël, and Vila, Daniel. K-CAP2017 Satellites: Workshops and Tutorials. Proceedings of the Knowledge Capture Conference , 1e. 2017. ACM.
   Ref Type: Conference Proceeding
9. Balachandran, V.P., Łuksza, M., Zhao, J.N., Makarov, V., Moral, J.A., Remark, R., Herbst, B., Askan, G., Bhanot, U., and Senbabaoglu, Y. (2017). "Identification of unique neoantigen qualities in long-term survivors of pancreatic cancer." Nature 551(7681):
10. Benci, J.L. (2017). "Tumor Interferon Signaling Initiates And Sustains A Multigenic Resistance Program To Immune Checkpoint Blockade."
11. Bhattacharya, Arnav, Roy, Vijay Laxmi, Das, Subrata, Das, Chitrarpita, Mukherjee, Tanima, and Biswas, N. MUTATIONAL LANDSCAPE OF CYTOKINE GENES ACROSS MAJOR TUMOUR TYPES IDENTIFIES NEW TARGETS. NGBT conference; Oct , 02-04. 2017.
   Ref Type: Conference Proceeding
12. Bobes, R.l.J., Navarrete-Perea, J., Ochoa-Leyva, A., Anaya, V.c.H., Hernández, M., Cervantes-Torres, J., Estrada, K., Sánchez-Lopez, F., Soberón, X., and Rosas, G. (2017). "Experimental and

theoretical approaches to investigate the immunogenicity of Taenia solium-derived KE7 antigen." Infection and immunity 85(12): e00395-17.

13. Borthwick, N., Lin, Z., Akahoshi, T., Llano, A., Silva-Arrieta, S., Ahmed, T., Dorrell, L., Brander, C., Murakoshi, H., and Takiguchi, M. (2017). "Novel, in-natural-infection subdominant HIV-1 CD8+ T-cell epitopes revealed in human recipients of conserved-region T-cell vaccines." PloS one 12(4): e0176418-

14. Borzi, M.M., Silva, K.R., Montassier, M.d.F.S., Fernando, F.S., Tamanine, M.d.L.F., dos Santos, R.M., de Oliveira, E.S., Mariguela, V.C., Lopes, P.D., and Reischak, D. (2017). "Development and application of an enzyme-linked immunosorbent assay (ELISA) using a soluble recombinant nucleoprotein for the detection of antibodies to avian influenza virus." African Journal of Microbiology Research 11(18): 697-704.

15. Bräunlein, E. and Krackhardt, A.M. (2017). "Identification and Characterization of neoantigens As well As Respective immune Responses in Cancer Patients." Frontiers in immunology 8(1702-

16. Brito, R.C., Guimarães, F.G., Velloso, J.P., Corrêa-Oliveira, R., Ruiz, J.C., Reis, A.B., and Resende, D.M. (2017). "Immunoinformatics features linked to Leishmania vaccine development: Data integration of experimental and in silico studies." International journal of molecular sciences 18(2): 371-

17. Buragohain, L., Nanda, T., Ghosh, A., Ghosh, M., Kumar, R., Kumar, S., Gupta, S.S., Bharali, A., Mohanty, A.K., and Singh, I. (2017). "Identification of serum protein markers for early diagnosis of pregnancy in buffalo." Animal Science Journal 88(8): 1189-1197.

18. Camacho-Nuez, M., Hernández-Silva, D.J., Castañeda-Ortiz, E.J., Paredes-Martínez, M.a.E., Rocha-Martínez, M.K., Alvarez-Sánchez, M.a.E., Mercado-Curiel, R.F., guilar-Tipacamu, G., and Mosqueda, J. (2017). "Hap2, a novel gene in Babesia bigemina is expressed in tick stages, and specific antibodies block zygote formation." Parasites & vectors 10(1): 568-

19. Candido-Ferreira, I.L., Kronenberger, T., Sayegh, R.S.R., Batista, I.d.F.C., and da Silva Junior, P.I. (2017). "evidence of an antimicrobial Peptide signature encrypted in hecT e3 Ubiquitin ligases." Frontiers in immunology 7(664-

20. Carrillo, E., Fernandez, L., Ibarra-Meneses, A.V., Santos, M.L., Nico, D., de Luca, P.M., Correa, C.B., de Almeida, R.P., Moreno, J., and Palatnik-de-Sousa, C.B. (2017). "F1 Domain of the Leishmania (Leishmania) donovani Nucleoside Hydrolase Promotes a Th1 Response in Leishmania (Leishmania) infantum Cured Patients and in Asymptomatic Individuals Living in an Endemic Area of Leishmaniasis." Frontiers in immunology 8(750-

21. Carvalho, A.M.R., Costa, L.E., Salles, B.C., Santos, T.s.T., Ramos, F.F., Lima, M.P., Chávez-Fumagalli, M.A., Silvestre, B.T., Portela, S., and Roatt, B.M. (2017). "An ELISA immunoassay employing a conserved Leishmania hypothetical protein for the serodiagnosis of visceral and tegumentary leishmaniasis in dogs and humans." Cellular immunology 318(42-48.

22. Chandramohan, V., Bryant, J.D., Piao, H., Keir, S.T., Lipp, E.S., Lefaivre, M., Perkinson, K., Bigner, D.D., Gromeier, M., and McLendon, R.E. (2017). "Validation of an Immunohistochemistry

Assay for Detection of CD155, the Poliovirus Receptor, in Malignant Gliomas." Archives of pathology & laboratory medicine 141(12): 1697-1704.

23. Chang, J., Eggenhuizen, P., O'Sullivan, K.M., Alikhan, M.A., Holdsworth, S.R., Ooi, J.D., and Kitching, A.R. (2017). "CD8+ T cells effect glomerular injury in experimental anti-myeloperoxidase GN." Journal of the American Society of Nephrology 28(1): 47-55.

24. Chee, J., Robinson, B.W., Holt, R.A., and Creaney, J. (2017). "Immunotherapy for Lung Malignancies: From Gene Sequencing to Novel Therapies." Chest 151(4): 891-897.

25. Chen, L., Anthony, A., Oveissi, S., Huang, M., Zanker, D., Xiao, K., Wu, C., Zou, Q., and Chen, W. (2017). "Broad-Based CD4+ T Cell Responses to Influenza A Virus in a Healthy Individual Who Lacks Typical Immunodominance Hierarchy." Frontiers in immunology 8(375-

26. Chen, T., Jiang, H., Sun, H., Xie, Z., Ren, P., Zhao, L., Dong, H., Shi, M., Lv, Z., and Wu, Z. (2017). "Sequence analysis and characterization of pyruvate kinase from Clonorchis sinensis, a 53.1-kDa homopentamer, implicated immune protective efficacy against clonorchiasis." Parasites & vectors 10(1): 557-

27. Chenzhang, Y., Wen, Q., Ding, X., Cao, M., Chen, Z., Mu, X., and Wang, T. (2017). "Identification of the impact on T-and B-cell epitopes of human papillomavirus type-16 E6 and E7 variant in Southwest China." Immunology letters 181(26-30.

28. Choi, J., Kim, M.G., Oh, Y.K., and Kim, Y.B. (2017). "Progress of Middle East respiratory syndrome coronavirus vaccines: a patent review." Expert opinion on therapeutic patents 27(6): 721-731.

29. Clancy-Thompson, E., Chen, G.Z., Tyler, P.M., Servos, M.M., Barisa, M., Brennan, P.J., Ploegh, H.L., and Dougan, S.K. (2017). "Monoclonal invariant NKT (iNKT) cell mice reveal a role for both tissue of origin and the TCR in development of iNKT functional subsets." The Journal of Immunology 199(1): 159-171.

30. Cooke, B. (2017). "Expression of Influenza nucleoprotein in microalgal chloroplasts. Application for generation of edible vaccines."

31. Cooper, M. and Lummas, S. (2017). "Antibodies for Immunochemistry." Immunohistochemistry and Immunocytochemistry: Essential Methods

32. Cordero, O.J., Varela-Calviño, R.n., López-González, T., Grujic, M., Juranic, Z., Mouriño, C., Hernández-Rodríguez, Í., Rodríguez-López, M., de la Iglesia, B.A., and Pego-Reigosa, J.M.a. (2017). "Anti-CD26 autoantibodies are involved in rheumatoid arthritis and show potential clinical interest." Clinical biochemistry 50(16-17): 903-910.

33. Cunha-Neto, E., Rosa, D.S., Harris, P.E., Olson, T., Morrow, A., Ciotlos, S., Herst, C.V., and Rubsamen, R.M. (2017). "an approach for a synthetic CtL Vaccine design against Zika Flavivirus Using Class i and Class ii epitopes identified by Computer Modeling." Frontiers in immunology 8(640-

34. Dagadu, G.P. (2017). "Molecular Characterization and Phylogenetic Analysis of Contagious ecthyma Virus in Goats."

35. De Angelis, E., Pilolli, R., Bavaro, S.L., and Monaci, L. (2017). "Insight into the gastro-duodenal digestion resistance of soybean proteins and potential implications for residual immunogenicity." Food & function 8(4): 1599-1610.

36. de Oliveira, N.R., Jorge, S.+., Gomes, C.K., Rizzi, C., Pacce, V.D., Collares, T.F., Monte, L.G., and Dellagostin, O.A.n. (2017). "A novel chimeric protein composed of recombinant Mycoplasma hyopneumoniae antigens as a vaccine candidate evaluated in mice." Veterinary microbiology 201(146-153.

37. Dehghani, B., Ghasabi, F., Hashempoor, T., Joulaei, H., Hasanshahi, Z., Halaji, M., Chatrabnous, N., Mousavi, Z., and Moayedi, J. (2017). "Functional and structural characterization of Ebola virus glycoprotein (1976-2015) - An in silico study." International Journal of Biomathematics 10(08): 1750108-

38. Dewi, I.P. (2017). "B-CELL EPITOPE PREDICTION of Mycobacterium tuberculosis Ag85A ANTIGEN." UNEJ e-Proceeding 108-111.

39. Do Nascimento, N.M. (2017). "The Ro/SSA Complex in Systemic Lupus Erythematosus Patients."

40. Dong, H.T., Jitrakorn, S., Kayansamruaj, P., Pirarat, N., Rodkhum, C., Rattanarojpong, T., Senapin, S., and Saksmerprome, V. (2017). "Infectious spleen and kidney necrosis disease (ISKND) outbreaks in farmed barramundi (Lates calcarifer) in Vietnam." Fish & shellfish immunology 68(65-73.

41. dos Santos Franco, L., Vidal, P.O., and Amorim, J.H. (2017). "In silico design of a Zika virus non-structural protein 5 aiming vaccine protection against zika and dengue in different human populations." Journal of biomedical science 24(1): 88-

42. Dunachie, S.J., Jenjaroen, K., Reynolds, C.J., Quigley, K.J., Sergeant, R., Sumonwiriya, M., Chaichana, P., Chumseng, S., Ariyaprasert, P., and Lassaux, P. (2017). "Infection with Burkholderia pseudomalleiGÇôimmune correlates of survival in acute melioidosis." Scientific reports 7(1): 12143-

43. Ehsan, M., Gao, W., Gadahi, J.A., Lu, M., Liu, X., Wang, Y., Yan, R., Xu, L., Song, X., and Li, X. (2017). "Arginine kinase from Haemonchus contortus decreased the proliferation and increased the apoptosis of goat PBMCs in vitro." Parasites & vectors 10(1): 311-

44. Eltahla, A.A., Leung, P., Pirozyan, M.R., Rodrigo, C., Grebely, J., Applegate, T., Maher, L., Luciani, F., Lloyd, A.R., and Bull, R.A. (2017). "Dynamic evolution of hepatitis C virus resistance-associated substitutions in the absence of antiviral treatment." Scientific reports 7(41719-

45. Esposito, S. and Longo, M.R. (2017). "Guillain-Barré syndrome." Autoimmunity reviews 16(1): 96-101.

46. Ettinger, Ruth A., Liberman, Joseph A., Gunasekera, Devi, James, Eddie A., Thompson, Arthur R., and Pratt, Kathleen P. FVIII Proteins with a Modified Immunodominant T-Cell Epitope Exhibit Reduced Immunogenicity and Normal Procoagulant Activity. 2017. Am Soc Hematology. Ref Type: Generic

47. Fabian, K.P. (2017). "Tumor Blood Vessel-Associated Antigens as Targets for Cancer Immunotherapy."

48. Fan, S., Cai, H., Xu, X., Feng, M., Wang, L., Liao, Y., Zhang, Y., He, Z., Yang, F., and Yu, W. (2017). "The characteristics of herpes simplex virus type 1 infection in rhesus macaques and the associated pathological features." Viruses 9(2): 26-

49. Filskov, J., Mikkelsen, M., Hansen, P.R., Christensen, J.P., Thomsen, A.R., Andersen, P., Bukh, J., and Agger, E.M. (2017). "Broadening CD4+ and CD8+ T cell responses against hepatitis C virus by vaccination with NS3 overlapping peptide panels in cross-priming liposomes." Journal of virology 91(14): e00130-17.

50. Flores-Ramirez, G., Danchenko, M., Quevedo-Díaz, M., and Skultety, L. (2017). "Reliable tool for detection of novel Coxiella burnetii antigens, using immobilized human polyclonal antibodies." Journal of Chromatography B 1047(84-91.

51. Forrest, C.P.G. (2017). "Cytotoxic T lymphocyte immunodominance to Epstein-Barr virus infection."

52. Fujii, K., Miyahara, Y., Harada, N., Muraoka, D., Komura, M., Yamaguchi, R., Yagita, H., Nakamura, J., Sugino, S., and Okumura, S. (2017). "Identification of an immunogenic neo-epitope encoded by mouse sarcoma using CXCR3 ligand mRNAs as sensors." OncoImmunology 6(5): e1306617-

53. Furman, D. (2017). "Systems Biology of T Cells." Cancer Immunotherapy Principles and Practice 71-

54. Gonzalo-Asensio, J., Marinova, D., Martin, C., and Aguilo, N. (2017). "MTBVAC: Attenuating the human pathogen of tuberculosis towards a promising vaccine against the TB epidemic." Frontiers in immunology 8(1803-

55. Gulbahce, N., Magbanua, M.J., Chin, R., Agarwal, M.R., Luo, X., Liu, J., Hayden, D.M., Mao, Q., Ciotlos, S., and Li, Z. (2017). "Quantitative whole genome sequencing of circulating tumor cells enables personalized combination therapy of metastatic cancer." Cancer research 77(16): 4530-4541.

56. Guo, L., Yin, R., Xu, G., Gong, X., Chang, Z., Hong, D., Liu, H., Ding, S., Han, X., and Li, Y. (2017). "Immunologic properties and therapeutic efficacy of a multivalent epitopeGÇÉbased vaccine against four Helicobacter pylori adhesins (urease, Lpp20, HpaA, and CagL) in Mongolian gerbils." Helicobacter 22(6):

57. Guo, L., Yang, H., Tang, F., Yin, R., Liu, H., Gong, X., Wei, J., Zhang, Y., Xu, G., and Liu, K. (2017). "Oral immunization with a multivalent epitope-based vaccine, based on NAP, Urease, HSP60, and HpaA, provides therapeutic effect on H. pylori infection in mongolian gerbils." Frontiers in cellular and infection microbiology 7(349-

58. Gupta, S., Santra, L., Naskar, S., Maurya, S.K., Rana, M., Ghosh, J., and Dhara, S.K. (2017). "Heterologous expression of porcine elongase 6 (ELOVL6) gene in a human cell line." The Indian journal of medical research 145(4): 563-

59. Gutiérrez, A.H., Rapp-Gabrielson, V.J., Terry, F.E., Loving, C.L., Moise, L., Martin, W.D., and De Groot, A.S. (2017). "T-cell epitope content comparison (EpiCC) of swine H1 influenza A virus hemagglutinin." Influenza and other respiratory viruses 11(6): 531-542.

60. Høglund, R.A., Lossius, A., Johansen, J.N., Homan, J., Benth, J.J.J., Robins, H., Bogen, B., Bremel, R.D., and Holmøy, T. (2017). "In Silico Prediction analysis of idiotope-Driven T-B cell collaboration in Multiple sclerosis." Frontiers in immunology 8(1255-

61. Hadpech, S., Nangola, S., Chupradit, K., Fanhchaksai, K., Furnon, W., Urvoas, A., Valerio-Lepiniec, M., Minard, P., Boulanger, P., and Hong, S.S. (2017). "Alpha-helicoidal HEAT-like Repeat Proteins αRep) Selected as Interactors of HIV-1 Nucleocapsid Negatively Interfere with Viral Genome Packaging and Virus Maturation." Scientific reports 7(1): 16335-

62. Hall, C.E., Koparde, V.N., Jameson-Lee, M., Elnasseh, A.G., Scalora, A.F., Kobulnicky, D.J., Serrano, M.G., Roberts, C.H., Buck, G.A., and Neale, M.C. (2017). "Sequence homology between HLA-bound cytomegalovirus and human peptides: A potential trigger for alloreactivity." PloS one 12(8): e0178763-

63. Han, Y., Zhou, A., Lu, G., Zhao, G., Sha, W., Wang, L., Guo, J., Zhou, J., Zhou, H., and Cong, H. (2017). "DNA Vaccines Encoding Toxoplasma gondii Cathepsin C 1 Induce Protection against Toxoplasmosis in Mice." The Korean journal of parasitology 55(5): 505-

64. Han, Y., Zhou, A., Lu, G., Zhao, G., Wang, L., Guo, J., Song, P., Zhou, J., Zhou, H., and Cong, H. (2017). "Protection via a ROM4 DNA vaccine and peptide against Toxoplasma gondii in BALB/c mice." BMC infectious diseases 17(1): 59-

65. Hanrahan, C. (2017). "Investigation of the Actin-nucleator Spire in Controlling the Morphology of Neuronal Dendrites."

66. Hasan, M.S. (2017). "Comparative genomics of schistosomes: identifying parasites specific genes, drug and vaccine targets."

67. Hashemi-Moghaddam, H., Zavareh, S., Karimpour, S., and Madanchi, H. (2017). "Evaluation of molecularly imprinted polymer based on HER2 epitope for targeted drug delivery in ovarian cancer mouse model." Reactive and Functional Polymers 121(82-90.

68. Heidenreich, F., Rücker-Braun, E., Walz, J.S., Eugster, A., Kühn, D., Dietz, S., Nelde, A., Tunger, A., Wehner, R., and Link, C.S. (2017). "Mass spectrometry-based identification of a naturally presented receptor tyrosine kinase-like orphan receptor 1-derived epitope recognized by CD8+ cytotoxic T cells." haematologica 102(11): e460-e464.

69. Heinson, A.I. (2017). "Bioinformatics approaches to vaccine design for bacterial pathogens."

70. Hoh, K.E. and Swaminathan, V. (2017). "In silico identification and characterization of putative kuruma prawn (Marsupenaeus japonicus) allergens." Indian Journal of Allergy, Asthma and Immunology 31(2): 87-

71. Huang, H., Li, S., Zhang, Y., Han, X., Jia, B., Liu, H., Liu, D., Tan, S., Wang, Q., and Bi, Y. (2017). "CD8+ T cell immune response in immunocompetent mice during Zika virus infection." Journal of virology 91(22): e00900-e00917.

72. Inderberg, E.M., Wälchli, S.+., Myhre, M.R., Trachsel, S., Almåsbak, H., Kvalheim, G., and Gaudernack, G. (2017). "T cell therapy targeting a public neoantigen in microsatellite instable colon cancer reduces in vivo tumor growth." OncoImmunology 6(4): e1302631-

73. Itani, F.R. (2017). "Infection with neuroantigen-encoding Listeria: induction of CD8 T cell responses and suppression of demyelinating disease."

74. Jagadesh, A., Salam, A.A.A., Zadeh, V.R., Krishnan, A., and Arunkumar, G. (2017). "Molecular characterization of neuraminidase genes of influenza A (H3N2) viruses circulating in Southwest India from 2009 to 2013." Archives of virology 162(7): 1887-1902.

75. Jahangiri, A., Rasooli, I., Owlia, P., Fooladi, A.A.I., and Salimian, J. (2017). "In silico design of an immunogen against Acinetobacter baumannii based on a novel model for native structure of outer membrane protein A." Microbial pathogenesis 105(201-210.

76. Jakubczak, A., Kowalczyk, M., Kostro, K., and Jezewska-Witkowska, G. (2017). "Comparative molecular analysis of strains of the Aleutian Disease Virus isolated from farmed and wild mink." strain 3(4-

77. Jamal, F., Dikhit, M.R., Singh, M.K., Shivam, P., Kumari, S., Pushpanjali, S., Dubey, A.K., Kumar, P., Narayan, S., and Gupta, A.K. (2017). "Identification of B-cell Epitope of Leishmania donovani and its application in diagnosis of visceral leishmaniasis." Journal of Biomolecular Structure and Dynamics 35(16): 3569-3580.

78. Jeibouei, S., Bandehpour, M., Kazemi, B., and Haghighi, A. (2017). "Designing a DNA Vaccine-based Leishmania major Polytope (Preliminary Report)." Iranian journal of parasitology 12(3): 441-

79. Joshi, M. and Datta, M. (2017). "Comprehensive molecular and clinical databases and repositories of influenza." Int.J.Pharm.Tech.Biotech 4(1): 20-28.

80. Kalaiselvan, S., Sankar, S., Ramamurthy, M., Ghosh, A.R., Nandagopal, B., and Sridharan, G. (2017). "Prediction of B cell epitopes among hantavirus strains causing hemorragic fever with renal syndrome." Journal of cellular biochemistry 118(5): 1182-1188.

81. Kaushik, V., Sharma, N., and Singh, J. (2017). "In silico identification of vaccine candidate from various screening methods against hepatitis C virus." International Journal of Bioinformatics Research and Applications 13(3): 301-312.

82. Kelly, A. and Trowsdale, J. (2017). "Introduction: MHC/KIR and governance of specificity." Immunogenetics 69(8-9): 481-488.

83. Keshtvarz, M., Salimian, J., Yaseri, M., Bathaie, S.Z., Rezaie, E., Aliramezani, A., Norouzbabaei, Z., Amani, J., and Douraghi, M. (2017). "Bioinformatic prediction and experimental validation of a PE38-based recombinant immunotoxin targeting the Fn14 receptor in cancer cells." Immunotherapy 9(5): 387-400.

84. Khan, S., Oosterhuis, K., Wunderlich, K., Bunnik, E.M., Bhaggoe, M., Boedhoe, S., Karia, S., Steenbergen, R.D., Bosch, L., and Serroyen, J. (2017). "Development of a replication-deficient adenoviral vector-based vaccine candidate for the interception of HPV16- and HPV18-induced infections and disease." International journal of cancer 141(2): 393-404.

85. Khanna, D. and Rana, P.S. (2017). "Multilevel ensemble model for prediction of IgA and IgG antibodies." Immunology letters 184(51-60.

86. Krysan, Kostyantyn. Molecular and Cellular Determinants of Malignant Transformation in Pulmonary Premalignancy. 2017. University of California, Los Angeles LOS ANGELES United States.
Ref Type: Report

87. Krysan, K., Tran, L., Grimes, B., Walser, T., Park, S., Gregory, F., Lee, J., Wallace, W.D., and Dubinett, S. (2017). "Neoepitopes and Immune Contexture in Pulmonary Premalignancy." Journal of Thoracic Oncology 12(8): S1545-S1546.

88. Lara, L.J., Peconick, A.P., Fassani, É, Júnior, A.M.P., Chalfun, P.R.B., Raymundo, D.L., Barçante, T.A., and Barçante, J.d. (2017). "Predicted philogeny, secondary conformational structure, and epitope antigenicity of immunological sequences in poultry." Genetics and molecular research: GMR 16(2):

89. Lebozec, Kristell, Jandrot-Perrus, Martine, Avenard, Gilles, Favre-Bulle, Olivier, and Billiald, Philippe. Design, development and characterization of ACT017, a humanized Fab that blocks platelet's glycoprotein VI function without causing bleeding risks. MAbs 9[6], 945-958. 2017. Taylor & Francis.
Ref Type: Conference Proceeding

90. Lempereur, L., Larcombe, S.D., Durrani, Z., Karagenc, T., Bilgic, H.B., Bakirci, S., Hacilarlioglu, S., Kinnaird, J., Thompson, J., and Weir, W. (2017). "Identification of candidate transmission-blocking antigen genes in Theileria annulata and related vector-borne apicomplexan parasites." BMC genomics 18(1): 438-

91. Li, F., Kang, H., Li, J., Zhang, D., Zhang, Y., Dannenberg, A.M., Liu, X., Niu, H., Ma, L., and Tang, R. (2017). "Subunit vaccines consisting of antigens from dormant and replicating bacteria show promising therapeutic effect against Mycobacterium bovis BCG latent infection." Scandinavian journal of immunology

92. Lima, M.P.d., Pégo, P.N., Silva, G.d.V.F.F., and De Simone, S.G. (2017). "Identification of targeted epitopes of yellow fever virus based on homology with other species of flavivirus."

93. Liu, H., Shen, W., Shu, J., Kou, Z., and Jin, X. (2017). "A novel polyepitope vaccine elicited HIV peptide specific CD4+ T cell responses in HLA-A2/DRB1 transgenic mice." PloS one 12(9): e0184207-

94. Liu, S.A., Stanfield, B.A., Chouljenko, V.N., Naidu, S., Langohr, I., Del Piero, F., Ferracone, J., Roy, A.A., and Kousoulas, K.G. (2017). "Intramuscular immunization of mice with the live-attenuated herpes simplex virus 1 vaccine strain VC2 expressing equine herpesvirus 1 (EHV-1) glycoprotein D generates anti-EHV-1 immune responses in mice." Journal of virology 91(12): e02445-16.

95. Liu, X., Chen, C., Chen, C., Marslin, G., Ding, R., and Wu, S. (2017). "Construction and evaluation of a novel triple cell epitopebased polypeptide vaccine against cow mastitis induced by Staphylococcus aureus, Escherichia coli and Streptococcus." Tropical Journal of Pharmaceutical Research 16(10): 2477-2486.

96. Liu, X., Chen, C., Chen, C., Ding, R., and Marslin, G. (2017). "Construction of a Recombinant OmpC Dominant Epitope-Based Vaccine Against Escherichia coli and Evaluation of Its Immunogenicity and Protective Immunity." Jundishapur Journal of Microbiology 10(11):

97. Lorente, E., Barriga, A., García-Arriaza, J., Lemonnier, F.A., Esteban, M., and López, D. (2017). "Complex antigen presentation pathway for an HLA-A* 0201-restricted epitope from Chikungunya 6K protein." PLOS Neglected Tropical Diseases 11(10): e0006036-

98. Lu, G., Zhou, J., Zhou, A., Han, Y., Guo, J., Song, P., Zhou, H., Cong, H., Hou, M., and Wang, L. (2017). "SAG5B and SAG5C combined vaccine protects mice against Toxoplasma gondii infection." Parasitology international 66(5): 596-602.

99. Lu, T. and Zhang, W. (2017). "Identifying Immuno-Dominant and Neutralizing Epitopes from K88 Fimbriae of Enterotoxigenic Escherichia coli (ETEC)." Kansas Agricultural Experiment Station Research Reports 3(7): 54-

100. Lu, Y.C., Zheng, Z., Robbins, P.F., Tran, E., Prickett, T.D., Gartner, J.J., Li, Y.F., Ray, S., Franco, Z., and Bliskovsky, V. (2017). "An Efficient Single-Cell RNA-Seq Approach to Identify Neoantigen-Specific T Cell Receptors." Molecular Therapy

101. Mahdavi, M., Moreau, V., and Kheirollahi, M. (2017). "Identification of B and T cell epitope based peptide vaccine from IGF-1 receptor in breast cancer." Journal of Molecular Graphics and Modelling 75(316-321.

102. Mahlokozera, T., Vellimana, A.K., Li, T., Mao, D.D., Zohny, Z.S., Kim, D.H., Tran, D.D., Marcus, D.S., Fouke, S.J., and Campian, J.L. (2017). "Biological and therapeutic implications of multisector sequencing in newly diagnosed glioblastomas." Neuro-oncology

103. Maidana, S.S., Craig, P.O., Craig, M.a.I., Ludwig, L., Mauroy, A., Thiry, E., and Romera, S.A. (2017). "Evidence of natural interspecific recombinant viruses between bovine alphaherpesviruses 1 and 5." Virus research 242(122-130.

104. Majee, S.B. and Biswas, G.R. (2017). "Computational methods in preformulation study for pharmaceutical solid dosage forms of therapeutic proteins." Physical Sciences Reviews 2(6):

105. Mameli, G., Erre, G.L., Caggiu, E., Mura, S., Cossu, D., Bo, M., Cadoni, M.L., Piras, A., Mundula, N., and Colombo, E. (2017). "Identification of a HERV-K env surface peptide highly recognized in Rheumatoid Arthritis (RA) patients: a cross-sectional case-control study." Clinical & Experimental Immunology 189(1): 127-131.

106. Manee, M.M., Alharbi, S.N., Algarni, A.T., Alghamdi, W.M., Altammami, M.A., Alkhrayef, M.N., and Alnafjan, B.M. (2017). "Molecular cloning, bioinformatics analysis, and expression of small heat shock protein beta-1 from Camelus dromedarius, Arabian camel." PloS one 12(12): e0189905-

107. Marín-López, A., Calvo-Pinilla, E., Barriales, D., Lorenzo, G., Benavente, J., Brun, A., Martínez-Costas, J.M., and Ortego, J. (2017). "Microspheres-prime/rMVA-boost vaccination enhances humoral and cellular immune response in IFNAR (-/-) mice conferring protection against serotypes 1 and 4 of bluetongue virus." Antiviral research 142(55-62.

108. Mard-Soltani, M., Rasaee, M.J., Sheikhi, A., and Hedayati, M. (2017). "Eliciting an antibody response against a recombinant TSH containing fusion protein." Journal of Immunoassay and Immunochemistry 38(3): 257-270.

109. Martínez-Bravo, M.a.J., Sánchez, B., Sousa, J.M., Acevedo, M.a.J., Gómez-Bravo, M.A., Núñez-Roldán, A., and Aguilera, I. (2017). "T-cell allorecognition of donor glutathione S-transferase T1 in plasma cell-rich rejection." World journal of hepatology 9(27): 1115-

110. Matsushita, H., Hasegawa, K., Oda, K., Yamamoto, S., Nishijima, A., Imai, Y., Asada, K., Ikeda, Y., Karasaki, T., and Fujiwara, K. (2017). "The frequency of neoantigens per somatic mutation rather than overall mutational load or number of predicted neoantigens per se is a prognostic factor in ovarian clear cell carcinoma." OncoImmunology 6(8): e1338996-

111. Mazor, R., Crown, D., Addissie, S., Jang, Y., Kaplan, G., and Pastan, I. (2017). "Elimination of murine and human T-cell epitopes in recombinant immunotoxin eliminates neutralizing and anti-drug antibodies in vivo." Cellular & molecular immunology 14(5): 432-

112. McElroy, A.K., Akondy, R.S., Harmon, J.R., Ellebedy, A.H., Cannon, D., Klena, J.D., Sidney, J., Sette, A., Mehta, A.K., and Kraft, C.S. (2017). "A case of human Lassa virus infection with robust acute T-cell activation and long-term virus-specific T-cell responses." The Journal of infectious diseases 215(12): 1862-1872.

113. McMurtrey, C., Harriff, M.J., Swarbrick, G.M., Duncan, A., Cansler, M., Null, M., Bardet, W., Jackson, K.W., Lewinsohn, D.A., and Hildebrand, W. (2017). "T cell recognition of Mycobacterium tuberculosis peptides presented by HLA-E derived from infected human cells." PloS one 12(11): e0188288-

114. Miho, E. (2017). "Discovering Fundamental Principles of Antibody Repertoires by Large-Scale Systems and Network Analysis."

115. Miles, S., Navatta, M., Dematteis, S., and Mourglia-Ettlin, G. (2017). "Identification of universal diagnostic peptide candidates for neglected tropical diseases caused by cestodes through the integration of multi-genome-wide analyses and immunoinformatic predictions." Infection, Genetics and Evolution 54(338-346.

116. Miller, C.A., Dahiya, S., Li, T., Fulton, R., Smyth, M.D., Dunn, G.P., Rubin, J.B., and Mardis, E.R. (2017). "Temporal and Clonal Progression in a Pediatric Ependymoma Patient Through Multiple Treatments." bioRxiv 115923-

117. Mistry, J. and Flower, D.R. (2017). "Designing Epitope Ensemble Vaccines against TB by Selection: Prioritizing Antigens using Predicted Immunogenicity." Bioinformation 13(7): 220-

118. Mitchell, D.A., Dupuy, L.C., Sanchez-Lockhart, M., Palacios, G., Back, J.W., Shimanovskaya, K., Chaudhury, S., Ripoll, D.R., Wallqvist, A., and Schmaljohn, C.S. (2017). "Epitope mapping of Ebola virus dominant and subdominant glycoprotein epitopes facilitates construction of an epitope-based DNA vaccine able to focus the antibody response in mice." Human vaccines & immunotherapeutics 13(12): 2883-2893.

119. Moazami-goodarzi, M., Fotouhi-Ardakani, R., and Afgar, A. (2017). "Insilco new aspects of peptide-based vaccine designing for human papilloma virus infection." International Journal of Bioinformatics Research and Applications 13(3): 223-241.

120. Mondal, R.K., Khatun, M., Banerjee, P., Ghosh, A., Sarkar, S., Santra, A., Das, K., Chowdhury, A., Banerjee, S., and Datta, S. (2017). "Synergistic impact of mutations in Hepatitis B Virus genome contribute to its occult phenotype in chronic Hepatitis C Virus carriers." Scientific reports 7(1): 9653-

121. Monsalve, D.M., Pacheco, Y., costa-Ampudia, Y., Rodr+¡guez, Y., Ram+¡rez-Santana, C., and Anaya, J.M. (2017). "Zika virus and autoimmunity. One-step forward." Autoimmunity reviews

122. Moradi, J., Tabrizi, M., Izad, M., Mosavari, N., and Feizabadi, M.M. (2017). "Designing a Novel Multi-epitope DNA-Based Vaccine Against Tuberculosis: In Silico Approach." Jundishapur Journal of Microbiology 10(3):

123. Morfopoulou, S., Mee, E.T., Connaughton, S.M., Brown, J.R., Gilmour, K., Duprex, W.P., Ferguson, D., Hubank, M., Hutchinson, C., and Kaliakatsos, M. (2017). "Deep sequencing reveals persistence of cell-associated mumps vaccine virus in chronic encephalitis." Acta neuropathologica 133(1): 139-147.

124. Nadugala, M.N., Jeewandara, C., Malavige, G.N., Premaratne, P.H., and Goonasekara, C.L. (2017). "Natural antibody responses to the capsid protein in sera of Dengue infected patients from Sri Lanka." PloS one 12(6): e0178009-

125. Naeem, A. and Waheed, Y. (2017). "Sequence analysis of hepatitis C virus nonstructural protein 3-4A serine protease and prediction of conserved B and T cell epitopes." Biomedical reports 7(6): 563-566.

126. Nandy, A. and Basak, S.C. (2017). "Viral epidemics and vaccine preparedness." J Mol Pathol Epidemiol 2(S1-

127. Nandy, A. (2017). "Characterization of Zika and Other Human Infecting Flavivirus Envelope Proteins and Determination of Common Conserved Epitope Regions." EC Microbiology 8(29-46.

128. Nelson, C.W., Narechania, A., Burk, R.D., Schiffman, M., Cullen, M., Boland, J.F., Chen, Z., Wentzensen, N., Yang, Q., and Mitchell, J. (2017). "Divergence of HPV16 variants reflects loci undergoing inter-host positive selection, potentially immunologic selection." PeerJ PrePrints

129. Nunes-Silva, V., Frantz, Stefan, and Ramos, Gustavo Campos. Lymphocytes at the heart of wound healing. The Immunology of Cardiovascular Homeostasis and Pathology. 225-250. 2017. Springer.
Ref Type: Book Chapter

130. Nunes, D.S., Gonzaga, H.T., Ribeiro, V.S., Cunha-Júnior, J.P., and Costa-Cruz, J.M. (2017). "Usefulness of gel filtration fraction as potential biomarker for neurocysticercosis in serum: towards a new diagnostic tool." Parasitology 144(4): 426-435.

131. Nyhalah, D.J., Dobgima, G.S., and Titanji, V.P. (2017). "Enhanced acquired antibodies to a chimeric Plasmodium falciparum antigen; UB05-09 is associated with protective immunity against malaria." Parasite immunology

132. Oh, M.W. and Yoo, H.S. (2017). "In-silico prediction and modeling of ApxA exotoxins of Actinobacillus pleuropneumoniae: ApxIA,-IIA,-IIIA and-IVA." PeerJ PrePrints

133. Pérez-Gamarra, S., Hattara, L., Batra, G., Saviranta, P., and Lamminmäki, U. (2017). "Array-in-well binding assay for multiparameter screening of phage displayed antibodies." Methods 116(43-50.

134. Pérez, P.S., Di Lello, F.A., Mullen, E.G., Galdame, O.A., Livellara, B.I., Gadano, A.C., Campos, R.H., and Flichman, D.M. (2017). "Compartmentalization of hepatitis C virus variants in patients with hepatocellular carcinoma." Molecular carcinogenesis 56(2): 371-380.

135. Palmieri, N., Shrestha, A., Ruttkowski, B.., Beck, T., Vogl, C., Tomley, F., Blake, D.P., and Joachim, A. (2017). "The genome of the protozoan parasite Cystoisospora suis and a reverse vaccinology approach to identify vaccine candidates." International journal for parasitology 47(4): 189-202.

136. Pan, J., Zhang, Q., Sei, S., Shoemaker, R.H., Lubet, R.A., Wang, Y., and You, M. (2017). "Immunoprevention of KRAS-driven lung adenocarcinoma by a multipeptide vaccine." Oncotarget 8(47): 82689-

137. Panina, A.A., Dementieva, I.G., Aliev, T.K., Toporova, V.A., Balabashin, D.S., Bokov, M.N., Pozdnyakova, L.P., Shchemchukova, O.B., Dolgikh, D.A., and Sveshnikov, P.G. (2017). "Recombinant Antibodies to the Ebola Virus Glycoprotein." Acta naturae 9(4): 84-

138. Park, B.K., Gautam, A., Maharjan, S., Lee, S.I., Lee, Y., and Kwon, H.J. (2017). "Production of Anti-c-Myc Monoclonal Antibody Inhibiting DNA Binding of c-Myc and Max Dimer by Epitope Peptide-CpG-DNA-Liposome Complex Without Carriers." International Journal of Peptide Research and Therapeutics 1-8.

139. Pashova, S., Schneider, C., von Gunten, S., and Pashov, A. (2017). "Antibody repertoire profiling with mimotope arrays." Human vaccines & immunotherapeutics 13(2): 314-322.

140. Patiño-Galindo, J.. and González-Candelas, F. (2017). "Comparative analysis of variation and selection in the HCV genome." Infection, Genetics and Evolution 49(104-110.

141. Pianta, A., Arvikar, S.L., Strle, K., Drouin, E.E., Wang, Q., Costello, C.E., and Steere, A.C. (2017). "Two rheumatoid arthritisGÇôspecific autoantigens correlate microbial immunity with autoimmune responses in joints." The Journal of clinical investigation 127(8): 2946-2956.

142. Pinal-Fernandez, I., Ferrer-Fabregas, B., Trallero-Araguas, E., Balada, E., Martínez, M.A., Milisenda, J.C.s., Aparicio-Español, G., Labrador-Horrillo, M., Garcia-Patos, V., and Grau-Junyent, J.M. (2017). "Tumour TIF1 mutations and loss of heterozygosity related to cancer-associated myositis." Rheumatology

143. Poorebrahim, M., Asghari, M., Abazari, M.F., Askari, H., Sadeghi, S., Taheri-Kafrani, A., Nasr-Esfahani, M.H., Ghoraeian, P., Aleagha, M.N., and Arab, S.S. (2017). "Immunomodulatory effects of a rationally designed peptide mimetic of human IFNβ in EAE model of multiple sclerosis." Progress in Neuro-Psychopharmacology and Biological Psychiatry

144. Pourseif, M.M., Moghaddam, G., Naghili, B., Saeedi, N., Parvizpour, S., Nematollahi, A., and Omidi, Y. (2017). "A novel in silico minigene vaccine based on CD4+ T-helper and B-cell epitopes

of EG95 isolates for vaccination against cystic echinococcosis." Computational biology and chemistry

145. Prandi, B., Tedeschi, T., Folloni, S., Galaverna, G., and Sforza, S. (2017). "Peptides from gluten digestion: A comparison between old and modern wheat varieties." Food research international 91(92-102.

146. Prechl, J.. (2017). "A generalized quantitative antibody homeostasis model: antigen saturation, natural antibodies and a quantitative antibody network." Clinical & translational immunology 6(2):

147. Presley, C., Han, L., O'leary, J., Chao, H., Shamas, T., Kerin, A., Rose, M., and Gross, C. (2017). "Concurrent Care and Aggressive End-of-Life Lung Cancer Care." Journal of Thoracic Oncology 12(8): S1545-

148. Prisilla, A., Prathiviraj, R., and Chellapandi, P. (2017). "Molecular Evolutionary Constraints that Determine the Avirulence State of Clostridium botulinum C2 Toxin." Journal of molecular evolution 84(4): 174-186.

149. Puzzo, F., Colella, P., Biferi, M.G., Bali, D., Paulk, N.K., Vidal, P., Collaud, F., Simon-Sola, M., Charles, S., and Hardet, R. (2017). "Rescue of Pompe disease in mice by AAV-mediated liver delivery of secretable acid α-glucosidase." Science translational medicine 9(418): eaam6375-

150. Ríos-Huerta, R., Monreal-Escalante, E., Govea-Alonso, D.O., Angulo, C., and Rosales-Mendoza, S. (2017). "Expression of an immunogenic LTB-based chimeric protein targeting Zaire ebolavirus epitopes from GP1 in plant cells." Plant cell reports 36(2): 355-365.

151. Rahmawati, I.L., Rantam, F.A., and Tyasningsih, W. (2017). "Amino Acid Analysis of Fusion (F) Gene and Prediction of Epitope B-Cell Newcastle Disease Surabaya Isolate As Vaccine Candidate." KnE Life Sciences 3(6): 316-326.

152. Rajeswari, P. Raja, Raju, S Viswanadha, Ashour, Amira S., and Dey, Nilanjan. Insilico Approach for Epitope Prediction toward Novel Vaccine Delivery System Design. Feature Detectors and Motion Detection in Video Processing. 256-266. 2017. IGI Global.
Ref Type: Book Chapter

153. Ramirez-Valdez, Andrei, Blobel, Nicolas J., Ishizuka, Andrew S., Pan, Jenny, Vodnala, Suman, Restifo, Nicholas P., Lynn, Geoffrey M., and Seder, Robert A. Peptide-based polymer Toll-Like Receptor 7/8 agonist nanoparticles increase the breadth of anti-tumor CD8 T cell immunity. 2017. Am Assoc Immnol.
Ref Type: Generic

154. Ratner, D., Orning, M.P., and Lien, E. (2017). "Bacterial secretion systems and regulation of inflammasome activation." Journal of leukocyte biology 101(1): 165-181.

155. Raveendran, S., Fecek, R.J., Brown, M.C., Fabian, K.L.P., and Taylor, J.L. (2017). "HSP90 Inhibition Enhances the Anti-Tumor Efficacy of Combination Chemo Immunotherapy Targeting DNA Repair Proteins." MOJ Immunol 6(1): 00181-

156. Reddy, V., Desai, A., Krishna, S.S., and Vasanthapuram, R. (2017). "Molecular mimicry between chikungunya virus and host components: a possible mechanism for the arthritic manifestations." PLOS Neglected Tropical Diseases 11(1): e0005238-

157. Rezaee, M.A., Rasaee, M.J., and Mohammadnejad, J. (2017). "Selection of specific inhibitor peptides in enzyme-linked immunosorbent assay (ELISA) of cardiac troponin I using immuno-dominant epitopes as competitor." Journal of Immunoassay and Immunochemistry 38(1): 72-81.

158. Ritvo, P.G., Chaara, W., El Soufi, K., Bonnet, B., Six, A., Mariotti-Ferrandiz, E., and Klatzmann, D. (2017). "High-resolution repertoire analysis of Tfr and Tfh cells reveals unexpectedly high diversities indicating a bystander activation of follicular T cells." bioRxiv 231977-

159. Rivino, L. and Lim, M.Q. (2017). "CD4+ and CD8+ T-cell immunity to Dengue - lessons for the study of Zika virus." Immunology 150(2): 146-154.

160. Rocha, L.B., Alves, R.P.d.S., Caetano, B.A., Pereira, L.R., Mitsunari, T., Amorim, J.H., Polatto, J.M., Botosso, V.F., Gallina, N.M.F., and Palacios, R. (2017). "Epitope Sequences in Dengue Virus NS1 Protein Identified by Monoclonal Antibodies." Antibodies 6(4): 14-

161. Rosales-Mendoza, S., Nieto-Gómez, R., and Angulo, C. (2017). "A perspective on the development of plant-made vaccines in the fight against Ebola virus." Frontiers in immunology 8(252-

162. Roschitzki, B. and LeibundGut-Landmann, S. (2017). "Identification of Fungal T Cell Epitopes by Mass Spectrometry-Based Proteomics." Vaccines for Invasive Fungal Infections: Methods and Protocols 65-74.

163. Ruibal, P. (2017). "Relationship Between HLA and T Cell Responses to Ebola Virus.”

164. Saadi, M., Karkhah, A., and Nouri, H.R. (2017). "Development of a multi-epitope peptide vaccine inducing robust T cell responses against brucellosis using immunoinformatics based approaches." Infection, Genetics and Evolution 51(227-234.

165. Saeed, A.F., Wang, R., Ling, S., and Wang, S. (2017). "Antibody engineering for pursuing a healthier future." Frontiers in microbiology 8(495-

166. Sankar, S., Ramamurthy, M., Nandagopal, B., and Sridharan, G. (2017). "In Silico Validation of D7 Salivary Protein-derived B-and T-cell Epitopes of Aedes aegypti as Potential Vaccine to Prevent Transmission of Flaviviruses and Togaviruses to Humans." Bioinformation 13(11): 366-

167. Scarborough, H., Little, N., Johnson, L., and DeGregori, J. (2017). "Context-Dependent Oncogenic Adaptation in the Genesis of Lung Cancer." Journal of Thoracic Oncology 12(8): S1545-

168. Schwelberger, H.G., Feurle, J., and Houen, G. (2017). "Mapping of the binding sites of human histamine N-methyltransferase (HNMT) monoclonal antibodies." Inflammation Research 66(11): 1021-1029.

169. Schwelberger, H.G., Feurle, J., and Houen, G. (2017). "Monoclonal antibodies for human and porcine histamine N-methyltransferase (HMT) facilitate protein expression and localization studies." Inflammation Research 66(1): 67-77.

170. Selvaa Kumar, C. and Dokhale, S. (2017). "IDENTIFICATION OF METALLOPROTEASES LIKE DOMAIN IN TRITICUM AESTIVUM α/β GLIADIN PROTEIN FROM BIOINFORMATICS PERSPECTIVE: A HYPOTHESIS."

171. Shabgah, A.G., Navashenaq, J.G., Seyedzadeh, M.H., Moghadasi, S.H., Shokri, F., Razavi, S.A., and Kardar, G.A. (2017). "Effects of Viral Peptide Presentation on CD4+ T Cell Responses to MHC Class II-Restricted Tumor Peptides." International Journal of Cancer Management 10(6):

172. Shah, Priyanka, Paul, Kiran V., Manoharan, Malini, Chaudhuri, Amitabha, and Gupta, Ravi. A novel algorithm to identify TCR-binding somatic mutations from human cancers. 2017. AACR.
Ref Type: Generic

173. Sharma, P., Sharma, P., Mishra, S., and Kumar, A. (2017). "Analysis of Promiscuous T cell Epitopes for Vaccine Development Against West Nile Virus Using Bioinformatics Approaches." International Journal of Peptide Research and Therapeutics 1-11.

174. Sharma, P., Srivastav, S., Mishra, S., and Kumar, A. (2017). "Sequence and structure based binding prediction study of HLA class I and cTAP binding peptides for Japanese encephalitis vaccine development." International Journal of Peptide Research and Therapeutics 23(2): 269-279.

175. Skepper, J. and Powell, J. (2017). "Ultrastructural Immunochemistry." Immunohistochemistry and Immunocytochemistry: Essential Methods

176. Srivastava, U., Singh, S., Gautam, B., Yadav, P., Yadav, M., Thomas, G., and Singh, G. (2017). "Linear epitope prediction in HPV type 16 E7 antigen and their docked interaction with human TMEM 50A structural model." Bioinformation 13(5): 122-

177. Stewart, Geoffrey A. and Robinson, Clive. Indoor and Outdoor Allergens and Pollutants. Middleton's Allergy Essentials. 73-116. 2017. Elsevier.
Ref Type: Book Chapter

178. Subhasree, C.R., Priya, R.S.K., Diwakar, M., Subramaniam, S., and Shyama, S. (2017). "REVIEW ON COMPARATIVE GENOMICS FOR MYCOBACTERIUM TUBERCULOSIS STRAINS." INTERNATIONAL JOURNAL OF PHARMACEUTICAL SCIENCES AND RESEARCH 8(12): 5022-5042.

179. Sunderland, K.S., Yang, M., and Mao, C. (2017). "Phage-Enabled Nanomedicine: From Probes to Therapeutics in Precision Medicine." Angewandte Chemie International Edition 56(8): 1964-1992.

180. Syrstad, Meghan. Reagents and Tools to Identify Epizootic Hemorrhagic Disease Virus-2. 2017. South Dakota State University.
Ref Type: Book, Whole

181. Talukdar, S., Bayan, U., and Saikia, K.K. (2017). "In silico identification of vaccine candidates against Klebsiella oxytoca." Computational biology and chemistry 69(48-54.

182. Tan, S., Zhang, S., Wu, B., Zhao, Y., Zhang, W., Han, M., Wu, Y., Shi, G., Liu, Y., and Yan, J. (2017). "Hemagglutinin-specific CD4+ T-cell responses following 2009-pH1N1 inactivated split-vaccine inoculation in humans." Vaccine 35(42): 5644-5652.

183. Taylor, A., Gavin, H., Shih, J., Zhang, X., Campbell, J., Andrew, C., and Meyerson, M. (2017). "Genome Engineering to Generate Models of Chromosome Arm-Level Aneuploidies in Lung Cancer." Journal of Thoracic Oncology 12(8): S1545-

184. Thammakorn, S. “Epitope and T-cell Reactivity Prediction Using Machine Learning Approaches.” 2017.
Ref Type: Thesis/Dissertation

185. Todorova, K., Metodiev, M.V., Metodieva, G., Mincheff, M., Fernández, N., and Hayrabedyan, S. (2017). "Micro-RNA-204 Participates in TMPRSS2/ERG Regulation and Androgen Receptor Reprogramming in Prostate Cancer." Hormones and Cancer 8(1): 28-48.

186. Todorova, R. (2017). "PEPTIDE-BASED IMMUNOTHERAPY IN SARCOMA." Comptes rendus de l’Académie bulgare des Sciences 70(12):

187. Trier, Nicole H. and Houen, Gunnar. Peptide Antibodies in Clinical Laboratory Diagnostics. Advances in clinical chemistry. 81, 43-96. 2017. Elsevier.
Ref Type: Book Chapter

188. Tuppurainen, E.S.M., Venter, E.H., Shisler, J.L., Gari, G., Mekonnen, G.A., Juleff, N., Lyons, N.A., De Clercq, K., Upton, C., and Bowden, T.R. (2017). "Capripoxvirus diseases: current status and opportunities for control." Transboundary and emerging diseases 64(3): 729-745.

189. Vance, D.J., Tremblay, J.M., Rong, Y., Angalakurthi, S.K., Volkin, D.B., Middaugh, C.R., Weis, D.D., Shoemaker, C.B., and Mantis, N.J. (2017). "High-resolution epitope positioning of a large collection of neutralizing and nonneutralizing single-domain antibodies on the enzymatic and binding subunits of ricin toxin." Clinical and Vaccine Immunology 24(12): e00236-17.

190. Vidya, J., Sajitha, S., Ushasree, M.V., Sindhu, R., Binod, P., Madhavan, A., and Pandey, A. (2017). "Genetic and metabolic engineering approaches for the production and delivery of L-asparaginases: An overview." Bioresource technology 245(1775-1781.

191. Wada, S., Yada, E., Ohtake, J., and Sasada, T. (2017). "Personalized peptide vaccines for cancer therapy: current progress and state of the art." Expert Review of Precision Medicine and Drug Development 2(6): 371-381.

192. Wadood, A., Mehmood, A., Khan, H., Ilyas, M., Ahmad, A., Alarjah, M., and bu-Izneid, T. (2017). "Epitopes based drug design for dengue virus envelope protein: A computational approach." Computational biology and chemistry 71(152-160.

193. Wang, L., Hao, C., Deng, Y., Liu, Y., Hu, S., Peng, Y., He, M., Fu, J., Liu, M., and Chen, J. (2017). "Screening epitopes on systemic lupus erythematosus autoantigens with a peptide array." Oncotarget 8(49): 85559-

194. Wang, P., Xiong, X., Jiao, J., Yang, X., Jiang, Y., Wen, B., and Gong, W. (2017). "Th1 epitope peptides induce protective immunity against Rickettsia rickettsii infection in C3H/HeN mice." Vaccine 35(51): 7204-7212.

195. Wang, X.X., Chen, X., Li, Y.Q., Xiao, T.Y., Jiang, Y., Li, M.C., Liu, H.C., and Wan, K.L. (2017). "Identification and evaluation of T cell epitopes of Rv0585c from Mycobacterium tuberculosis." Zhonghua liu xing bing xue za zhi= Zhonghua liuxingbingxue zazhi 38(5): 665-669.

196. Wang, X., Chen, S., Xu, Y., Zheng, H., Xiao, T., Li, Y., Chen, X., Huang, M., Zhang, H., and Fang, X. (2017). "Identification and evaluation of the novel immunodominant antigen Rv2351c from Mycobacterium tuberculosis." Emerging microbes & infections 6(6): e48-

197. Weber, L.K., Palermo, A., Kügler, J., Armant, O., Isse, A., Rentschler, S., Jaenisch, T., Hubbuch, J.., Dübel, S., and Nesterov-Mueller, A. (2017). "Single amino acid fingerprinting of the human antibody repertoire with high density peptide arrays." Journal of immunological methods 443(45-54.

198. Wen, J., Tang, W.W., Sheets, N., Ellisonyurin, J., Sette, A., Kim, K., and Shresta, S. (2017). "Identification of Zika virus epitopes reveals immunodominant and protective roles for dengue virus cross-reactive CD8+ T cells." Nature microbiology 2(6): 17036-

199. Yadav, G., Rao, R., Raj, U., and Varadwaj, P.K. (2017). "Computational modeling and analysis of prominent T-cell epitopes for assisting in designing vaccine of ZIKA virus." Journal of Applied Pharmaceutical Science Vol 7(08): 116-122.

200. Yagnik, B., Sharma, D., Padh, H., and Desai, P. (2017). "Immunization with r-Lactococcus lactis expressing outer membrane protein A of Shigella dysenteriae type-1: evaluation of oral and intranasal route of administration." Journal of applied microbiology 122(2): 493-505.

201. Yan, G., Wang, X., Chen, Z., Wu, X., Pan, J., Huang, Y., Wan, G., and Yang, Z. (2017). "In-silico ADME Studies for New Drug Discovery: From Chemical Compounds to Chinese Herbal Medicines." Current drug metabolism 18(6): 535-539.

202. Yordanov, V., Dimitrov, I., and Doytchinova, I. (2017). "Proteochemometrics-based Prediction of Peptide Binding to HLA-DP Proteins." Journal of chemical information and modeling

203. You, X., Li, R., Wan, K., Liu, L., Xie, X., Zhao, L., Wu, N., Deng, X., Wang, L., and Zeng, Y. (2017). "Evaluation of Rv0220, Rv2958c, Rv2994 and Rv3347c of Mycobacterium tuberculosis for serodiagnosis of tuberculosis." Microbial biotechnology 10(3): 604-611.

204. Yuan, Y., Kos, F.J., He, T.F., Yin, H.H., Li, M., Hardwick, N., Zurcher, K., Schmolze, D., Lee, P., and Pillai, R.K. (2017). "Complete regression of cutaneous metastases with systemic immune response in a patient with triple negative breast cancer receiving p53MVA vaccine with pembrolizumab." OncoImmunology 6(12): e1363138-

205. Zamanzadeh, Z., Ataei, M., Nabavi, S.M., Ahangari, G., Sadeghi, M., and Sanati, M.H. (2017). "In Silico Perspectives on the Prediction of the PLP’s Epitopes involved in Multiple Sclerosis." Iranian journal of biotechnology 15(1): 10-

206. Zare, A., Pourfathollah, A.A., Pourpak, Z., Szebeni, J., Ghaffari, S.M.R., and Kardar, G.A. (2017). "Peptide-based Vaccines Derived from Fc+¦RI Beta Subunit Can Reduce Allergic Response in Mice Model." Iranian Journal of Allergy, Asthma and Immunology 16(4): 289-

207. Zarei, M., Mosayebi, G., Khansarinejad, B., and Abtahi, H. (2017). "Antigenic and immunogenic evaluation of Helicobacter pylori FlaA epitopes." Iranian journal of basic medical sciences 20(8): 920-

208. Zhang, C., Hua, R., Cui, Y., Wang, S., Yan, H., Li, D., Zhang, Y., Tu, Z., Hao, P., and Chen, X. (2017). "Comprehensive mapping of antigen specific T cell responses in hepatitis C virus infected patients with or without spontaneous viral clearance." PloS one 12(2): e0171217-

209. Zhang, C., Iqbal, J., and Gómez-Duarte, O.G. (2017). "Murine immunization with CS21 pili or LngA major subunit of enterotoxigenic Escherichia coli (ETEC) elicits systemic and mucosal immune responses and inhibits ETEC gut colonization." Veterinary microbiology 202(90-100.

210. Zhang, W., He, H., Zang, M., Wu, Q., Zhao, H., Lu, L.l., Ma, P., Zheng, H., Wang, N., and Zhang, Y. (2017). "Genetic features of aflatoxin-associated hepatocellular carcinoma." Gastroenterology 153(1): 249-262.

211. Zhang, X., Sharma, P.K., Goedegebuure, S.P., and Gillanders, W.E. (2017). "Personalized cancer vaccines: Targeting the cancer mutanome." Vaccine 35(7): 1094-1100.

212. Zhang, Y., Kurupati, R., Liu, L., Zhou, X.Y., Zhang, G., Hudaihed, A., Filisio, F., Giles-Davis, W., Xu, X., and Karakousis, G.C. (2017). "Enhancing CD8+ T cell fatty acid catabolism within a metabolically challenging tumor microenvironment increases the efficacy of melanoma immunotherapy." Cancer cell 32(3): 377-391.

213. Zhao, G., Song, X., Kong, X., Zhang, N., Qu, S., Zhu, W., Yang, Y., and Wang, Q. (2017). "Immunization with Toxoplasma gondii aspartic protease 3 increases survival time of infected mice." Acta tropica 171(17-23.

214. Zhao, Y., Zhang, S., Naren, G., and Qin, G. (2017). "The Immunoreactive Protein was Produced During Absorption of Glycinin or its Hydrolysate in IPEC-J2." International Journal of Food Engineering 13(9):

215. Zheng, J., Huang, Q., Huang, R., Deng, F., Yue, X., Chen, Y., Yin, J., Huang, R., Riemekasten, G., and Liu, Z. (2017). "B cells are indispensible for a novel mouse model of primary Sj+¦grenGÇÖs syndrome." Frontiers in immunology 8(1384-

216. Zheng, W., Liu, F., He, Y., Liu, Q., Humphreys, G.B., Tsuboi, T., Fan, Q., Luo, E., Cao, Y., and Cui, L. (2017). "Functional characterization of Plasmodium berghei PSOP25 during ookinete development and as a malaria transmission-blocking vaccine candidate." Parasites & vectors 10(1): 8-

217. Zhou, J. and Wang, L. (2017). "SAG4 DNA and Peptide Vaccination Provides Partial Protection against T. gondii Infection in BALB/c Mice." Frontiers in microbiology 8(1733-

218. Zhou, J., Lu, G., Wang, L., Zhou, A.H., Han, Y.L., Guo, J.J., Song, P.X., Zhou, H.Y., Cong, H., and Hou, M. (2017). "Structuraland antigenic analysis of a new Rhoptry Pseudokinase Gene (ROP54) in Toxoplasma gondii." Acta parasitologica 62(3): 513-519.

219. Zhou, T.C., Li, X., Li, L., Li, X.F., Zhang, L., and Wei, J. (2017). "Evolution of full-length genomes of HBV quasispecies in sera of patients with a coexistence of HBsAg and anti-HBs antibodies." Scientific reports 7(1): 661-

Zolkind, P., Dunn, G.P., Lin, T., Griffith, M., Griffith, O.L., and Uppaluri, R. (2017). "Neoantigens in immunotherapy and personalized vaccines: Implications for head and neck squamous cell carcinoma." Oral oncology 71(169-176.

4 References

Andreatta M, Karosiene E, Rasmussen M, Stryhn A, Buus S, Nielsen M. Accurate pan-specific prediction of peptide-MHC class II binding affinity with improved binding core identification. Immunogenetics. 2015 Nov;67(11-12):641-50. doi: 10.1007/s00251-015-0873-y. Epub 2015 Sep 29. PubMed PMID: 26416257; PubMed Central PMCID: PMC4637192.

Andreatta M, Nielsen M. Gapped sequence alignment using artificial neural networks: application to the MHC class I system. Bioinformatics. 2016 Feb 15;32(4):511-7. doi: 10.1093/bioinformatics/btv639. Epub 2015 Oct 29. PubMed PMID: 26515819.

Bui HH, Sidney J, Peters B, Sathiamurthy M, Sinichi A, Purton KA, Mothe BR, Chisari FV, Watkins DI, Sette A. Automated generation and evaluation of specific MHC binding predictive tools: ARB matrix applications. Immunogenetics. 2005 Jun;57(5):304-14. Epub 2005 May 3.

Bui HH, Sidney J, Dinh K, Southwood S, Newman MJ, Sette A. Predicting population coverage of T-cell epitope-based diagnostics and vaccines. BMC Bioinformatics. 2006 Mar 17;7(1):153. PMID: 16545123

Bui HH, Sidney J, Li W, Fusseder N, Sette A. Development of an epitope conservancy analysis tool to facilitate the design of epitope-based diagnostics and vaccines. BMC Bioinformatics. 2007 Sep 26;8(1):361. PMID: 17897458

Calis JJ, Maybeno M, Greenbaum JA, Weiskopf D, De Silva AD, Sette A, Keşmir C, Peters B. Properties of MHC class I presented peptides that enhance immunogenicity. PLoS Comput Biol. 2013 Oct;9(10):e1003266. doi:10.1371/journal.pcbi.1003266. Epub 2013 Oct 24. PubMed PMID: 24204222; PubMed Central PMCID: PMC3808449.

Chou P, Fasman G. Prediction of the secondary structure of proteins from their amino acid sequence. Adv Enzymol Relat Areas Mol Biol. 1978:45–148. PMID: 364941

Emini E, Hughes J, Perlow D, Boger J. Induction of hepatitis A virus-neutralizing antibody by a virus specific synthetic peptide. J Virol. 1985;55:836–839. PMID: 2991600

Giguère S, Drouin A, Lacoste A, Marchand M, Corbeil J, Laviolette F. MHC-NP: predicting peptides naturally processed by the MHC. J Immunol Methods. 2013 Dec 31;400-401:30-6. doi: 10.1016/j.jim.2013.10.003. Epub 2013 Oct 18. PubMed PMID: 24144535.

González-Galarza FF, Takeshita LY, Santos EJ, Kempson F, Maia MH, da Silva AL, Teles e Silva AL, Ghattaoraya GS, Alfirevic A, Jones AR, Middleton D. Allele frequency net 2015 update: new features for HLA epitopes, KIR and disease and HLA adverse drug reaction associations. Nucleic Acids Res. 2015 Jan;43(Database issue):D784-8. doi: 10.1093/nar/gku1166. Epub 2014 Nov 20. PubMed PMID: 25414323; PubMed Central PMCID: PMC4383964

Haste Andersen P, Nielsen M, Lund O. Prediction of residues in discontinuous B-cell epitopes using protein 3D structures. Protein Sci. 2006 Nov;15(11):2558-67. Epub 2006 Sep 25. PMID: 17001032

Hoof I, Peters B, Sidney J, Pedersen LE, Sette A, Lund O, Buus S, Nielsen M, NetMHCpan, a method for MHC class I binding prediction beyond humans. Immunogenetics. 2009 Jan;61(1):1-13. PMID: 19002680

Jespersen MC, Peters B, Nielsen M, Marcatili P. BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes. Nucleic Acids Res. 2017 May 2. doi: 10.1093/nar/gkx346. [Epub ahead of print] PubMed PMID: 28472356.

Karosiene E, Lundegaard C, Lund O and Nielsen M. 2012. NetMHCcons: a consensus method for the major histocompatibility complex class I predictions. *Immunogenetics* **64(3)**:177-186. PMID: 22009319

Karplus PA, Schulz GE. Prediction of chain flexibility in proteins. Naturwissenschaften. 1985. 72:212-213.

Keşmir C, Nussbaum AK, Schild H, Detours V, Brunak S. Prediction of proteasome cleavage motifs by neural networks. Protein Eng. 2002 Apr;15(4):287-96. PMID: 11983929

Kim Y, Ponomarenko J, Zhu Z, Tamang D, Wang P, Greenbaum J, Lundegaard C, Sette A, Lund O, Bourne PE, Nielsen M, Peters B. Immune epitope database analysis resource. Nucleic Acids Res. 2012 Jul;40(Web Server issue):W525-30. doi: 10.1093/nar/gks438. Epub 2012 May 18. PubMed PMID: 22610854; PubMed Central PMCID: PMC3394288

Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B. Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. BMC Bioinformatics. 2014 Jul 14;15:241. doi: 10.1186/1471-2105-15-241. PubMed PMID: 25017736; PubMed Central PMCID: PMC4111843

Kim Y, Sidney J, Pinilla C, Sette A, Peters B. Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior. BMC Bioinformatics. 2009 Nov 30;10:394. PMID: 19948066

Kolaskar AS, Tongaonkar PC. A semi-empirical method for prediction of antigenic determinants on protein antigens. FEBS Lett. 1990 Dec 10;276(1-2):172-4. PMID: 1702393

Kringelum JV, Lundegaard C, Lund O, Nielsen M. Reliable B cell epitope predictions: impacts of method development and improved benchmarking. PLoS Comput Biol. 2012;8(12):e1002829. doi: 10.1371/journal.pcbi.1002829. Epub 2012 Dec 27. PubMed PMID: 23300419; PubMed Central PMCID: PMC3531324.

Kringelum JV, Nielsen M, Padkjær SB, Lund O. Structural analysis of B-cell epitopes in antibody:protein complexes. Mol Immunol. 2013 Jan;53(1-2):24-34. doi: 10.1016/j.molimm.2012.06.001. Epub 2012 Jul 10. PubMed PMID: 22784991; PubMed Central PMCID: PMC3461403

Larsen JE, Lund O, Nielsen M. Improved method for predicting linear B-cell epitopes. Immunome Res. 2006 Apr 24;2:2. PMID: 16635264

Larsen MV, Lundegaard C, Lamberth K, Buus S, Brunak S, Lund O, Nielsen M. An integrative approach to CTL epitope prediction: a combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions. Eur J Immunol. 2005 Aug;35(8):2295-303. PMID: 15997466

Liang S, Zheng D, Standley DM, Yao B, Zacharias M, Zhang C. EPSVR and EPMeta: prediction of antigenic epitopes using support vector regression and multiple server results. BMC Bioinformatics. 2010 Jul 16;11:381. doi: 10.1186/1471-2105-11-381. PubMed PMID: 20637083; PubMed Central PMCID: PMC2910724.

Marcatili P, Rosi A, Tramontano A., 2008. PIGS: automatic prediction of antibody structures. Bioinformatics 24(17):1953-4. PMID: 18641403

Moutaftsi M, Peters B, Pasquetto V, Tscharke DC, Sidney J, Bui HH, Grey H, Sette A. A consensus epitope prediction approach identifies the breadth of murine T(CD8+)-cell responses to vaccinia virus. Nat Biotechnol. 2006 Jul;24(7):817-9. PMID: 16767078

Nielsen M, Andreatta M. NNAlign: a platform to construct and evaluate artificial neural network models of receptor-ligand interactions. Nucleic Acids Res. 2017 Apr 12. doi: 10.1093/nar/gkx276. [Epub ahead of print] PubMed PMID: 28407117.

Nielsen M, Andreatta M. NetMHCpan-3.0; improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length datasets. Genome Med. 2016 Mar

30;8(1):33. doi: 10.1186/s13073-016-0288-x. PubMed PMID: 27029192; PubMed Central PMCID: PMC4812631.

Nielsen M, Lundegaard C, Blicher T, Peters B, Sette A, Justesen S, Buus S, and Lund O. 2008. Quantitative predictions of peptide binding to any HLA-DR molecule of known sequence: NetMHCIIpan. PLoS Comput Biol.4(7)e1000107. PMID: 18604266

Nielsen M, Lundegaard C, Lund O. Prediction of MHC class II binding affinity using SMM-align, a novel stabilization matrix alignment method. BMC Bioinformatics. 2007 Jul 4;8:238. PMID: 17608956

Nielsen M, Lundegaard C, Worning P, Lauemoller SL, Lamberth K, Buus S, Brunak S, Lund O., Reliable prediction of T-cell epitopes using neural networks with novel sequence representations, Protein Sci. 2003 May;12(5):1007-17

Parker J, Guo D, Hodges R. New hydrophilicity scale derived from High-Performance Liquid Chromatography peptide retention data: correlation of predicted surface residues with antigenicity and X-ray-derived accessible sites. Biochemistry. 1986;25:5425–5432. PMID: 2430611

Paul S, Arlehamn CSL, Schulten V, Westernberg L, Sidney J, Peters B, Sette A. Experimental validation of the RATE tool for inferring HLA restrictions of T cell epitopes. BMC Immunol. 2017 Jun 21;18(Suppl 1):20. doi: 10.1186/s12865-017-0204-1. PubMed PMID: 28681704.

Paul S, Dillon MB, Lindestam Arlehamn CS, Huang H, Davis MM, McKinney DM, Scriba TJ, Sidney J, Peters B, Sette A. A population response analysis approach to assign class II HLA-epitope restrictions. J Immunol. 2015 Jun 15;194(12):6164-76. doi: 10.4049/jimmunol.1403074. Epub 2015 May 6. PubMed PMID: 25948811; PubMed Central PMCID: PMC4458389.

Paul S, Sidney J, Sette A, Peters B. TepiTool: A Pipeline for Computational Prediction of T Cell Epitope Candidates. Curr Protoc Immunol. 2016 Aug 1;114:18.19.1-18.19.24. doi: 10.1002/cpim.12. PubMed PMID: 27479659; PubMed Central PMCID: PMC4981331.

Peters B, Sidney J, Bourne P, Bui HH, Buus S, Doh G, Fleri W, Kronenberg M, Kubo R, Lund O, Nemazee D, Ponomarenko JV, Sathiamurthy M, Schoenberger S, Stewart S, Surko P, Way S, Wilson S, Sette A. The immune epitope database and analysis resource: from vision to blueprint. PLoS Biol. 2005 Mar;3(3):e91. PMID: 15760272.

Peters B, Sette A., "Generating quantitative models describing the sequence specificity of biological processes with the stabilized matrix method." BMC Bioinformatics 2005 May 31;6(1):132

Peters B, Bulik S, Tampe R, Van Endert PM, Holzhutter HG. Identifying MHC class I epitopes by predicting the TAP transport efficiency of epitope precursors. J Immunol. 2003 Aug 15;171(4):1741-9.

Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. BMC Struct Biol. 2007 Oct 2;7(1):64. PMID: 17910770

Ponomarenko J, H. H. Bui, W. Li, N. Fusseder, P. E. Bourne, A. Sette, B. Peters. (2008). “ElliPro: a new structure-based tool for the prediction of antibody epitopes.” BMC Bioinformatics, 9(514). PMID: 19055730

Rasmussen M, Fenoy E, Harndahl M, Kristensen AB, Nielsen IK, Nielsen M, Buus S. Pan-Specific Prediction of Peptide-MHC Class I Complex Stability, a Correlate of T Cell Immunogenicity. J Immunol. 2016 Aug 15;197(4):1517-24. doi: 10.4049/jimmunol.1600582. Epub 2016 Jul 8. PubMed PMID: 27402703; PubMed Central PMCID: PMC4976001.

Rubinstein ND, Mayrose I, Martz E, Pupko T. Epitopia: a web-server for predicting B-cell epitopes. BMC Bioinformatics. 2009 Sep 14;10:287. doi: 10.1186/1471-2105-10-287. PubMed PMID: 19751513; PubMed Central PMCID: PMC2751785.

Sidney J, Assarsson E, Moore C, Ngo S, Pinilla C, Sette A, Peters B. Quantitative peptide binding motifs for 19 human and mouse MHC class I molecules derived using positional scanning combinatorial peptide libraries. Immunome Res. 2008 Jan 25;4:2. PMID: 18221540

Stranzl T, Larsen MV, Lundegaard C, Nielsen M. NetCTLpan: pan-specific MHC class I pathway epitope predictions. Immunogenetics. 2010 Jun;62(6):357-68. Epub 2010 Apr 9. PubMed PMID: 20379710; PubMed Central PMCID: PMC2875469

Sturniolo T, Bono E, Ding J, Raddrizzani L, Tuereci O, Sahin U, Braxenthaler M, Gallazzi F, Protti MP, Sinigaglia F, Hammer J. Generation of tissue-specific and promiscuous HLA ligand databases using DNA microarrays and virtual HLA class II matrices. Nat Biotechnol. 1999 Jun;17(6):555-61. PMID: 10385319

Tenzer S, Peters B, Bulik S, Schoor O, Lemmel C, Schatz MM, Kloetzel PM, Rammensee HG, Schild H, Holzhutter HG. Modeling the MHC class I pathway by combining predictions of proteasomal cleavage, TAP transport and MHC class I binding. Cell Mol Life Sci. 2005 May;62(9):1025-37.

Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M. Automated benchmarking of peptide-MHC class I binding predictions. Bioinformatics. 2015 Jul 1;31(13):2174-81. doi: 10.1093/bioinformatics/btv123. Epub 2015 Feb 25. PubMed PMID: 25717196; PubMed Central PMCID: PMC4481849.

Vita R, Overton JA, Greenbaum JA, Ponomarenko J, Clark JD, Cantrell JR, Wheeler DK, Gabbard JL, Hix D, Sette A, Peters B. The immune epitope database (IEDB) 3.0. Nucleic Acids Res. 2014 Oct 9. pii: gku938. [Epub ahead of print] PubMed PMID: 25300482.

Wang, P., J. Sidney, C. Dow, B. Mothe, A. Sette, B. Peters. (2008). "A Systematic Assessment of MHC Class II Peptide Binding Predictions and Evaluation of a Consensus Approach." PLoS Computational Biology **4**(4). PMID: 18389056

Wang P, Sidney J, Kim Y, Sette A, Lund O, Nielsen M, Peters B. 2010. Peptide binding predictions for HLA DR, DP and DQ molecules. BMC Bioinformatics. 11:568

Zhang H, Lund O, Nielsen M. The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: Application to MHC-peptide binding. Bioinformatics. 2009 Mar 17. PMID: 19297351