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Immune Epitope Database and Analysis Program

2013 Annual IEDB Compendium

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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 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 ninth Annual Compendium of the Immune Epitope Database and Analysis Resource consists of three sections. The first section contains a list of the antibody and T cell epitope information in the database as of 8 January 2014. The second section describes the features of the IEDB 2.12 website and the Analysis Resource 2.11. The third section lists the scientific publications in 2013 for which the IEDB played a contributory role.

Since the publication of last year's 2012 Annual Compendium, the quantity of data available in the IEDB has increased significantly with the addition of over 1000 fully curated references. The curation of peptidic and non-peptidic epitope data relating to all infectious diseases, including NIAID Category A, B, and C priority pathogens and NIAID Emerging and Re-emerging infectious diseases, 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 2012, 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 2012 and 2013. Of the 2966 species/strains listed, 156 were added in 2013. 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 2013" indicates with an "X" if epitopes for the species/strain was added to the IEDB in 2013. 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-12", "T-12", "B-13", and "T-13" indicate the cumulative number of distinct B cell and T cell epitopes in the database at the end of 2012 and 2013, respectively. The two rightmost columns display the differences in the B and T cell epitope counts from 2012 to 2013. The changes in B and T cell epitope counts are shown in red. In 2013, the number of B cell epitopes increased by 1,887 from 30,643 to 32,530, and the number of T cell epitopes increased by 10,801 from 64,719 to 75,520.

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

NEW 2013	ORGAN-ISM ID	SPECIES/STRAIN	B-12	T-12	B-13	T-13	Δ B	Δ T
X	3816	Abrus precatorius			1		1	
	5755	Acanthamoeba castellanii	14	3	14	3		
	4026	Acer pseudoplatanus	1		1			
	2147	Acholeplasma	1		1			
	264635	Acholeplasma granularum	1		1			
	2148	Acholeplasma laidlawii		2		2		
	351607	Acidothermus cellulolyticus 11B		1		1		
	470	Acinetobacter baumannii		1		1		
X	400667	Acinetobacter baumannii ATCC 17978			10	13	10	13
	471	Acinetobacter calcoaceticus		1		1		
	29430	Acinetobacter haemolyticus	1		1			
	10001530	Acinetobacter haemolyticus strain 57	1		1			
	10001531	Acinetobacter haemolyticus strain 61	1		1			
	10001503	Acinetobacter lwoffii F78	1		1			
	62977	Acinetobacter sp. ADP1		1		1		
	7902	Acipenser gueldenstaedtii	1		1			
	228399	Actinobacillus pleuropneumoniae serovar 1 str. 4074	2	1	2	1		
	416269	Actinobacillus pleuropneumoniae serovar 5b str. L20		1		1		
	209841	Actinobacillus pleuropneumoniae serovar 7	1		1			
	272636	Adeno-associated virus		18		18		
	10804	Adeno-associated virus - 2	21	66	42	67	21	1
X	82300	Adeno-associated virus - 5			9		9	
	202813	Adeno-associated virus - 8	1	7	17	7	16	
X	235455	Adeno-associated virus 9			9		9	
	10508	Adenoviridae	3	2	3	7		5
	7160	Aedes albopictus	7		7			
	4494	Aegilops markgrafii		1		1		
	37682	Aegilops tauschii		1		1		
	6100	Aequorea victoria	1		3		2	
	105751	Aeromonas bestiarum		1		1		
	645	Aeromonas salmonicida	59		59			
	29491	Aeromonas salmonicida subsp. salmonicida		1		1		
	56636	Aeropyrum pernix	3		3			
	272557	Aeropyrum pernix K1		2		2		
	117204	African horse sickness virus 3	21		21			
	36421	African horse sickness virus 4	28		28			
	10497	African swine fever virus	1		1			
	10498	African swine fever virus BA71V	46		46			
	85777	Agelas mauritiana		1		1		
	714	Aggregatibacter actinomycetemcomitans	1	4	1	4		
	10001628	Aggregatibacter actinomycetemcomitans serotype b str. Y4	1		1			
	358	Agrobacterium tumefaciens		1		1		
	10000828	Ajellomyces dermatitidis ATCC 60636		2		2		
	65690	AK7 murine leukemia virus		1		1		
	11791	AKR (endogenous) murine leukemia virus		7		8		1
	511	Alcaligenes faecalis	3	1	3	1		
	512	Alcaligenes sp.		1		1		
	10783	Aleutian mink disease parvovirus (STRAIN G)	3		3			
	28314	Aleutian mink disease virus	1		1			
	172148	Alkhumra hemorrhagic fever virus		4		4		

NEW 2013	ORGAN-ISM ID	SPECIES/STRAIN	B-12	T-12	B-13	T-13	Δ B	Δ T
	3517	Alnus glutinosa		17		17		
	9502	Alouatta caraya	1		1			
	333754	Alphapapillomavirus 10	4		4			
X	333766	Alphapapillomavirus 13				1		1
	337043	Alphapapillomavirus 4		1		1		
	337042	Alphapapillomavirus 7	9		9			
	5599	Alternaria alternata	5	36	5	36		
	314275	Alteromonas macleodii str. 'Deep ecotype'		1		1		
	261202	Alto Paraguay hantavirus		3		3		
	45218	Amapari virus		3		3		
	4212	Ambrosia artemisiifolia	4	32	4	32		
	4215	Ambrosia artemisiifolia var. elatior	9	12	9	12		
	4214	Ambrosia trifida		10		10		
	86782	Amur virus		35		35		
	170955	Amur virus Solovey/AP63/1999		2		2		
	171929	Anacardium occidentale	52		63		11	
	4615	Ananas comosus	3		3			
	769	Anaplasma centrale		1		1		
	770	Anaplasma marginale	17	14	17	14		
	10000760	Anaplasma marginale South Idaho		2		2		
	320483	Anaplasma marginale str. Florida	19	61	19	61		
	234826	Anaplasma marginale str. St. Maries	16	22	16	22		
	212042	Anaplasma phagocytophilum str. HZ	21		21			
	10001573	Anatid herpesvirus 1 Clone-03	1		1			
	46607	Andes virus	2	77	2	77		
	10000553	Andes virus CHI-7913	53		53			
	6858	Androctonus australis	9		9			
	70175	Androctonus australis hector	23		24		1	
	6860	Androctonus mauritanicus mauritanicus	1		1			
	334426	Angiostrongylus costaricensis	1	1	1	1		
	6269	Anisakis simplex	8		8			
	155017	Anogeissus	1		1			
	7165	Anopheles gambiae		1		1		
	8845	Anser cygnoides	2		2			
	29661	Anthoxanthum odoratum		3		3		
	9505	Aotus trivirgatus	1		1			
	7460	Apis mellifera	14	99	14	99		
	7469	Apis mellifera ligustica		1		1		
	4045	Apium graveolens		14		14		
X	63363	Aquifex aeolicus			2		2	
	224324	Aquifex aeolicus VF5		3		3		
	3702	Arabidopsis thaliana	2	4	2	4		
	201444	Aracatuba virus		5		5		
	3818	Arachis hypogaea	386	54	386	157		103
	308159	Araucaria virus		3		3		
	10000980	Arcanobacterium pyogenes Strain 42	4		4			
	224325	Archaeoglobus fulgidus DSM 4304		1		1		
	11618	Arenavirus		2		2		
	3704	Armoracia rusticana	5		5			
	6661	Artemia franciscana	2		2			
	4220	Artemisia vulgaris	1	68	1	68		
	29320	Arthrobacter nicotinovorans	1		1			

NEW 2013	ORGAN-ISM ID	SPECIES/STRAIN	B-12	T-12	B-13	T-13	Δ B	Δ T
	290399	Arthrobacter sp. FB24		1		1		
	6253	Ascaris suum	1	1	1	1		
	746128	Aspergillus fumigatus	126	50	126	85		35
	451804	Aspergillus fumigatus A1163		13		13		
	330879	Aspergillus fumigatus Af293		18		18		
	5061	Aspergillus niger		1		1		
	5067	Aspergillus parasiticus		1		1		
	5064	Aspergillus restrictus	1		1			
	33178	Aspergillus terreus	2		2			
	9509	Ateles geoffroyi		1		1		
	9510	Ateles paniscus	1		1			
	9511	Ateles sp.	1		1			
	287752	Aurantimonas manganoxydans SI85-9A1		1		1		
	46015	Autographa californica nucleopolyhedrovirus		1		1		
	4497	Avena nuda		1		1		
	4498	Avena sativa		4		4		
	11861	Avian erythroblastosis virus	1		1			
	172851	Avian hepatitis E virus	15		15			
	11127	Avian infectious bronchitis virus (strain M41)	4	3	4	3		
	231428	Avian infectious bronchitis virus (strain Vic S)	11	8	11	8		
	10001967	Avian leukosis virus isolate CAUHM01	1		1			
X	10001965	Avian leukosis virus strain NX0101			1		1	
	38171	Avian reovirus strain S1133	2		5		3	
	195700	Avian rotavirus PO-13	6		6			
	354	Azotobacter vinelandii		2		2		
	322710	Azotobacter vinelandii DJ		1		1		
	5866	Babesia bigemina		3		3		
	5865	Babesia bovis	3	8	3	8		
	10001459	Babesia bovis Argentina R1A	4		4			
	10000382	Babesia bovis Mexico	1	4	1	4		
	10000383	Babesia bovis Mexico Mo7	1	33	1	33		
	5872	Babesia equi	8		8			
	5868	Babesia microti	2		2			
	120505	Baboon cytomegalovirus		1		1		
	196403	Baboon endogenous virus	1	1	1	1		
	11764	Baboon endogenous virus strain M7	1		1			
	1390	Bacillus amyloliquefaciens	18	2	18	2		
	1392	Bacillus anthracis	252	199	398	199	146	
	486619	Bacillus anthracis str. A0193		1		1		
	592021	Bacillus anthracis str. A0248		1		1		
	486623	Bacillus anthracis str. A0389		4		4		
	486621	Bacillus anthracis str. A0442		1		1		
	486620	Bacillus anthracis str. A0465		5		5		
	486624	Bacillus anthracis str. A0488		81		81		
	191218	Bacillus anthracis str. A2012		28		28		
	198094	Bacillus anthracis str. Ames		1		1		
	261594	Bacillus anthracis str. 'Ames Ancestor'		1		1		
	568206	Bacillus anthracis str. CDC 684		2		2		
	260799	Bacillus anthracis str. Sterne	5	3	5	3		
	10000291	Bacillus anthracis str. Sterne 34F2	1		1			
	405536	Bacillus anthracis str. Tsiankovskii-I		1		1		
	1396	Bacillus cereus	1	4	1	4		

NEW 2013	ORGAN-ISM ID	SPECIES/STRAIN	B-12	T-12	B-13	T-13	Δ B	Δ T
	572264	Bacillus cereus 03BB102		1		1		
	451709	Bacillus cereus 03BB108		8		8		
	405533	Bacillus cereus AH1134		3		3		
	222523	Bacillus cereus ATCC 10987		1		1		
	226900	Bacillus cereus ATCC 14579		2		2		
	526977	Bacillus cereus ATCC 4342		1		1		
	405532	Bacillus cereus B4264		1		1		
	347495	Bacillus cereus F837/76		1		1		
	269801	Bacillus cereus G9241		34		34		
	405531	Bacillus cereus G9842		1		1		
	451708	Bacillus cereus H3081.97		12		12		
	451707	Bacillus cereus NVH0597-99		7		7		
	405917	Bacillus cereus W		1		1		
	441769	Bacillus coahuilensis m4-4		1		1		
	315749	Bacillus cytotoxicus NVH 391-98		2		2		
	1467	Bacillus lentus		1		1		
	1402	Bacillus licheniformis		10		10		
	1404	Bacillus megaterium		1		1		
	313627	Bacillus sp. NRRL B-14911		1		1		
	1423	Bacillus subtilis	2	4	2	4		
	224308	Bacillus subtilis subsp. subtilis str. 168		1		1		
	535026	Bacillus subtilis subsp. subtilis str. NCIB 3610		1		1		
	1428	Bacillus thuringiensis	5		5			
	527019	Bacillus thuringiensis IBL 200		1		1		
	339854	Bacillus thuringiensis serovar israelensis ATCC 35646		6		6		
	29339	Bacillus thuringiensis serovar kurstaki	3		3			
	527029	Bacillus thuringiensis serovar pondicheriensis BGSC 4BA1		1		1		
	1435	Bacillus thuringiensis serovar san diego		2		2		
	527026	Bacillus thuringiensis serovar sotto str. T04001		1		1		
	527024	Bacillus thuringiensis serovar tochigiensis BGSC 4Y1		1		1		
	412694	Bacillus thuringiensis str. Al Hakam		9		9		
	315730	Bacillus weihenstephanensis KBAB4		4		4		
	2	Bacteria	11		11			
	12040	Barley yellow dwarf virus-PAV	1		1			
	283166	Bartonella henselae str. Houston-1		1		1		
X	349344	Bat SARS CoV Rp3/2004				1		1
	37962	Bayou virus	1		1			
	12260	Bean pod mottle virus	2		2			
	31715	Bean-pod mottle virus (strain Kentucky G7)	9	1	9	1		
	31721	Beet necrotic yellow vein virus	10		10			
	12161	Beet yellows virus	5		5			
	3645	Bertholletia excelsa	7	24	7	24		
	161934	Beta vulgaris	5		5			
	3505	Betula pendula	44	355	70	357	26	2
	10629	BK polyomavirus		52		52		
	10001761	BK polyomavirus strain Dunlop		1		1		
	65743	Blackcurrant reversion virus	2		2			
	6973	Blattella germanica	20	56	20	56		
	40697	Blomia tropicalis	19		19			
	40051	Bluetongue virus	7		7			
	10904	Bluetongue virus (serotype 1 / isolate Australia)	7		7			
	10900	Bluetongue virus (serotype 10 / American isolate)	3		3			

NEW 2013	ORGANISM ID	SPECIES/STRAIN	B-12	T-12	B-13	T-13	Δ B	Δ T
	33717	Bluetongue virus (serotype 13 / isolate USA)	2		2			
	33718	Bluetongue virus (serotype 17 / isolate USA)	4		4			
	35327	Bluetongue virus 1	3		4		1	
	10906	Bluetongue virus 10	3		3			
	35329	Bluetongue virus 11	6		6			
	35330	Bluetongue virus 13	1		1			
X	45029	Bluetongue virus 16			3		3	
X	10002028	Bluetongue virus 16 Beatrice Hill/1987			2		2	
X	10002006	Bluetongue virus 16 BN96/16			2		2	
X	10002027	Bluetongue virus 16 Kumamoto/1985			2		2	
	10903	Bluetongue virus 17	4		4			
	94967	Bluetongue virus 4	2		2			
	197780	Bluetongue virus 8		10	2	10	2	
	388634	Bombyx mandarina nuclear polyhedrosis virus		1		1		
	271108	Bombyx mori nucleopolyhedrovirus	2		2			
	360910	Bordetella avium 197N		1		1		
	518	Bordetella bronchiseptica		1		1		
	520	Bordetella pertussis	225	45	250	87	25	42
	257313	Bordetella pertussis Tohama I		11		11		
	12455	Borna disease virus	8	4	8	4		
	10000518	Borna disease virus Giessen strain He/80	6		6			
	29518	Borrelia afzelii	1	1	1	1		
	390236	Borrelia afzelii PKo	2		2			
	139	Borrelia burgdorferi	46	40	50	40	4	
	498740	Borrelia burgdorferi 64b		2		2		
	224326	Borrelia burgdorferi B31	99	10	99	10		
	10001091	Borrelia burgdorferi BEP4	1		1			
	10000675	Borrelia burgdorferi CA12		6		6		
	521007	Borrelia burgdorferi N40	4	3	4	3		
	445985	Borrelia burgdorferi ZS7	2	45	2	45		
	412419	Borrelia duttonii Ly	7		7			
	29519	Borrelia garinii	4	29	4	29		
	10000530	Borrelia garinii IP90	3		3			
	9913	Bos taurus	1151	386	1180	388	29	2
	8722	Bothrops asper	1		1			
X	8726	Bothrops jararacussu			13		13	
	11128	Bovine coronavirus	7		7			
X	10002018	Bovine coronavirus Kakegawa			1		1	
	12065	Bovine enterovirus strain VG-5-27	6		6			
	10000472	Bovine ephemeral fever virus BB7721	2		2			
	10320	Bovine herpesvirus 1	4	40	4	40		
	10000404	Bovine herpesvirus 1 Lam	1		1			
	263683	Bovine herpesvirus 5 strain TX89	2		2			
	79889	Bovine herpesvirus type 1.1	1		1			
	10323	Bovine herpesvirus type 1.1 (strain Cooper)	8	17	8	17		
	10324	Bovine herpesvirus type 1.1 (strain P8-2)	1		1			
	11901	Bovine leukemia virus	32	29	32	29		
	10559	Bovine papillomavirus type 1	16		16			
	10560	Bovine papillomavirus type 2	15		15			
	10562	Bovine papillomavirus type 4	10	3	10	3		
	11215	Bovine parainfluenza virus 3		1		1		
	11246	Bovine respiratory syncytial virus	2	1	3	2	1	1

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	31611	Bovine respiratory syncytial virus (strain 391-2)	3		3			
	11249	Bovine respiratory syncytial virus (strain RB94)	3		4		1	
	82823	Bovine respiratory syncytial virus strain lelystad	1		1			
	82824	Bovine respiratory syncytial virus strain snook		75	1	75	1	
	10927	Bovine rotavirus	7	1	7	1		
	36439	Bovine rotavirus strain NCDV/G6	1		1			
	10933	Bovine rotavirus strain RF	12	7	12	7		
	10934	Bovine rotavirus strain UK/G6		1		1		
	11099	Bovine viral diarrhea virus 1	1	11	1	11		
	11100	Bovine viral diarrhea virus 1-NADL	3	3	4	3	1	
	54315	Bovine viral diarrhea virus 2	1		1			
	82470	Bovine viral diarrhea virus strain Oregon C24V	5	3	5	3		
	158474	Bovine viral diarrhea virus strain Trangie Y546	1		1			
X	221918	Bovine viral diarrhea virus VEDEVAC			6		6	
	288000	Bradyrhizobium sp. BTAi1		1		1		
	3707	Brassica juncea	9		9			
	235	Brucella abortus	4	29	4	29		
	520450	Brucella abortus bv. 2 str. 86/8/59		1		1		
	575591	Brucella abortus NCTC 8038		1		1		
	430066	Brucella abortus S19		13		13		
	641140	Brucella abortus str. 2308 A		1		1		
	10001424	Brucella abortus W99	1		1			
	483179	Brucella canis ATCC 23365		6		6		
	29459	Brucella melitensis	6	63	6	63		
	359391	Brucella melitensis biovar Abortus 2308		31		31		
	224914	Brucella melitensis bv. 1 str. 16M	6	6	6	6		
	520464	Brucella melitensis bv. 1 str. Rev.1	1		1			
	236	Brucella ovis		1		1		
	10001886	Brucella ovis 020	2		2			
	10001888	Brucella ovis 63/290	1		1			
	444178	Brucella ovis ATCC 25840		7		7		
	10001887	Brucella ovis Reo 198	1		1			
	29461	Brucella suis		7		7		
	204722	Brucella suis 1330		28	1	28	1	
	470137	Brucella suis ATCC 23445		3	1	3	1	
	6279	Brugia malayi	3	5	3	5		
	6280	Brugia pahangi	1		1			
	89462	Bubalus bubalis		1		1		
	32605	Buffalopox virus		2		2		
X	565995	Bundibugyo ebolavirus			1		1	
	8616	Bungarus multicinctus	17	3	17	3		
	32008	Burkholderia	1		1			
	339670	Burkholderia ambifaria AMMD		4		4		
	331271	Burkholderia cenocepacia AU 1054		4		4		
	350702	Burkholderia cenocepacia PC184		1		1		
	292	Burkholderia cepacia	3	1	3	1		
	134537	Burkholderia fungorum	1		1			
	482957	Burkholderia lata		2		2		
	13373	Burkholderia mallei		45		45		
	243160	Burkholderia mallei ATCC 23344		38		38		
	334802	Burkholderia mallei FMH		1		1		
	320390	Burkholderia mallei GB8 horse 4		1		1		

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	334803	Burkholderia mallei JHU		2		2		
	412022	Burkholderia mallei NCTC 10229		10		10		
	320388	Burkholderia mallei SAVP1		25		25		
	28450	Burkholderia pseudomallei		1	5	1	5	
	357348	Burkholderia pseudomallei 1106a		1		1		
	441160	Burkholderia pseudomallei 14		1		1		
	320372	Burkholderia pseudomallei 1710b		3		3		
	425067	Burkholderia pseudomallei 305		2		2		
	360118	Burkholderia pseudomallei 406e		1		1		
	320373	Burkholderia pseudomallei 668		7		7		
	441158	Burkholderia pseudomallei 9		1		1		
	441159	Burkholderia pseudomallei 91		1		1		
	272560	Burkholderia pseudomallei K96243		22	3	292	3	270
	320374	Burkholderia pseudomallei S13		1		1		
	271848	Burkholderia thailandensis E264		2		2		
	269482	Burkholderia vietnamiensis G4		9		9		
	6239	Caenorhabditis elegans	1	9	1	9		
	35305	California encephalitis virus		1		1		
	9483	Callithrix jacchus		3		3		
	28873	Camelpox virus		2		2		
	203172	Camelpox virus CMS		28		28		
	203174	Camelpox virus CP1		1		1		
	203173	Camelpox virus M-96		133		133		
	306254	Campylobacter coli RM2228		3		3		
	32019	Campylobacter fetus subsp. fetus	3		3			
	197	Campylobacter jejuni	15	20	15	20		
	195099	Campylobacter jejuni RM1221		13		13		
	32022	Campylobacter jejuni subsp. jejuni	2		2			
	10000679	Campylobacter jejuni subsp. jejuni 16971.94GSH (O:41)	2		2			
	407148	Campylobacter jejuni subsp. jejuni 81116		14		14		
	354242	Campylobacter jejuni subsp. jejuni 81-176		3		3		
	482628	Campylobacter jejuni subsp. jejuni BH-01-0142		1		1		
	360112	Campylobacter jejuni subsp. jejuni HB93-13		2		2		
	192222	Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819	10	12	10	12		
X	10002003	Campylobacter jejuni subsp. jejuni serotype HS:15			1		1	
	306263	Campylobacter lari RM2100		1		1		
	28080	Campylobacter upsaliensis	3		3			
	44088	Canarypox virus		6		6		
	5476	Candida albicans	99	68	99	68		
	10000335	Candida albicans A-9 (serotype B)	1		1			
	10000337	Candida albicans KIT 1113	1		1			
	10001652	Candida albicans NIH B-792 (serotype B)	1		1			
	237561	Candida albicans SC5314		3		3		
	10000339	Candida albicans serotype A	1		1			
	300021	Candida albicans var. stellatoidea	2		2			
	10001740	Candida glabrata IFO 0622	1		1			
	5480	Candida parapsilosis	1		1			
	10001747	Candida parapsilosis M1015	1		1			
	45582	Candida saitoana	1		1			
	234267	Candidatus Solibacter usitatus Ellin6076		2		2		
	292348	Canine calicivirus (strain 48)	2		2			
	11232	Canine distemper virus	4	8	4	8		

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	11233	Canine distemper virus strain Onderstepoort	6	19	6	19		
	10788	Canine parvovirus	22	20	22	20		
	246878	Canine parvovirus 2	3		3			
	10790	Canine parvovirus strain CPV-D CORNELL 320	1		1			
	10791	Canine parvovirus strain N	47		47			
	9615	Canis lupus familiaris	6	68	6	69		1
	9925	Capra hircus	1		1			
	11660	Caprine arthritis encephalitis virus	14	1	14	1		
	11662	Caprine arthritis encephalitis virus G63	6		6			
	11661	Caprine arthritis encephalitis virus strain Cork	9		9			
	7957	Carassius auratus	3		3			
	64289	Carey Island virus		2		2		
	32201	Carya illinoinensis	19		19			
	10185	Castor fiber		1		1		
	10141	Cavia porcellus	32	72	32	73		1
	9515	Cebus apella	1		1			
	6878	Centruroides noxius	8		8			
X	9860	Cervus elaphus			2		2	
	9864	Cervus elaphus nelsoni	4		4			
	9721	Cetacea	1		1			
	13415	Chamaecyparis obtusa	1	68	1	68		
	266779	Chelativorans sp. BNC1		2		2		
	12618	Chicken anemia virus	3		3			
	37124	Chikungunya virus	3	3	5	3	2	
	10001934	Chikungunya virus Singapore/11/2008	3		3			
	10001997	Chikungunya virus strain LR2006_OPY1 IMT/Reunion Island/2006	1		1			
	310542	Chimpanzee adenovirus	2		2			
	7154	Chironomus thummi	2	3	2	3		
	7155	Chironomus thummi thummi	58	27	58	27		
	9397	Chiroptera	1		1			
	83560	Chlamydia muridarum		1		1		
	243161	Chlamydia muridarum str. Nigg		28		28		
	83558	Chlamydia pneumoniae	57	21	57	21		
	83554	Chlamydia psittaci	78	2	78	2		
	331636	Chlamydia psittaci 6BC	1		1			
	813	Chlamydia trachomatis	122	58	122	62		4
	315277	Chlamydia trachomatis A/HAR-13	6	1	6	1		
	10000858	Chlamydia trachomatis B/Jali-20/OT	2		2			
	272561	Chlamydia trachomatis D/UW-3/CX		1		1		
	10001141	Chlamydia trachomatis Serovar A	22	8	22	8		
	10000804	Chlamydia trachomatis Serovar B	47	5	47	5		
	10000763	Chlamydia trachomatis Serovar C	16	1	16	1		
	10001085	Chlamydia trachomatis Serovar D	3		3			
	10001121	Chlamydia trachomatis Serovar Da	1		1			
	10000764	Chlamydia trachomatis Serovar E	18	1	18	1		
	10000845	Chlamydia trachomatis Serovar F	3		3			
	10000765	Chlamydia trachomatis Serovar H	7		7			
	10000766	Chlamydia trachomatis Serovar I	10		10			
	10001008	Chlamydia trachomatis Serovar J	6		6			
	10000767	Chlamydia trachomatis serovar K	14		14			
	10000853	Chlamydia trachomatis Serovar L1	21	3	21	3		
	10000768	Chlamydia trachomatis Serovar L2	15	7	15	12		5

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	10000769	Chlamydia trachomatis Serovar L3	2		2			
	204428	Chlamydiae	16		16			
	83555	Chlamydophila abortus	3		3			
	10000559	Chlamydophila abortus B-577	11		11			
	115713	Chlamydophila pneumoniae CWL029		49		49		
	10000852	Chlamydophila pneumoniae Kajaani 6		7		7		
	182082	Chlamydophila pneumoniae TW-183	7		7			
	9534	Chlorocebus aethiops		3		3		
	169173	Choclo virus		2		2		
	7777	Chondrichthyes	1		1			
	544	Citrobacter	1		1			
	546	Citrobacter freundii	1		1			
	12162	Citrus tristeza virus	4		4			
	29918	Cladosporium herbarum		18		18		
	11096	Classical swine fever virus	12	3	12	3		
	358769	Classical swine fever virus - Alfort/187	70		70			
	358805	Classical swine fever virus - Alfort/Tuebingen	5		5			
	11098	Classical swine fever virus - Brescia	4		4			
	279150	Classical swine fever virus 96TD	2		2			
	10001025	Classical swine fever virus Glentorf		26		26		
	10001578	Classical swine fever virus LPC/AHRI	4		4			
	10001764	Classical swine fever virus Margarita (AJ704817)	4	1	4	1		
	10000451	Classical swine fever virus Shimen	16		16			
	36911	Clavispora lusitaniae	1		1			
X	299180	Cloning vector pRU1105				1		1
	214432	Cloning vector pscFvCA-E8VHd		1		1		
	1491	Clostridium botulinum	178	76	178	76		
	36826	Clostridium botulinum A	46		46			
	10000293	Clostridium botulinum A 1	1		1			
	10000294	Clostridium botulinum A 2	2		2			
	10000302	Clostridium botulinum A Kyoto-F	1		1			
	413999	Clostridium botulinum A str. ATCC 3502		3		3		
	441771	Clostridium botulinum A str. Hall	44		44			
	10000301	Clostridium botulinum A str. Hall hyper	3		3			
	36827	Clostridium botulinum B	29		29			
	10000295	Clostridium botulinum B 111	2		2			
	10000303	Clostridium botulinum B Lammana	1		1			
	10000305	Clostridium botulinum B Okra	3		3			
	508765	Clostridium botulinum B str. Eklund 17B		1		1		
	10000297	Clostridium botulinum C 92-13	5		5			
	10000306	Clostridium botulinum C Stockholm	2		2			
	36829	Clostridium botulinum D	2		2			
	10000296	Clostridium botulinum D 1873	2		2			
	36830	Clostridium botulinum E	3	3	3	3		
	10000299	Clostridium botulinum E Beluga	2		2			
	508767	Clostridium botulinum E3 str. Alaska E43		1		1		
	36831	Clostridium botulinum F	3		3			
	10000304	Clostridium botulinum F NCTC 10281	1		1			
	445335	Clostridium botulinum NCTC 2916		2		2		
	445338	Clostridium botulinum str. Iwanei E	6		6			
	1496	Clostridium difficile	15		22		7	
	10000307	Clostridium difficile BART'S W1	1		1			

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	10001847	Clostridium difficile BI / NAP1/ 027	1		1			
	386415	Clostridium novyi NT		2		2		
	29362	Clostridium papyrosolvens	1		1			
	1502	Clostridium perfringens	10	1	10	1		
	107819	Clostridium perfringens D	1		1			
	195102	Clostridium perfringens str. 13		1		1		
	1513	Clostridium tetani	76	236	77	240	1	4
	212717	Clostridium tetani E88		16		16		
	203119	Clostridium thermocellum ATCC 27405		1		1		
	5501	Coccidioides immitis		1		1		
	199306	Coccidioides posadasii		9		9		
	9014	Colinus virginianus	1	2	1	2		
	1005048	Collimonas fungivorans Ter331		2		2		
	8932	Columba livia		8		9		1
	314285	Congregibacter litoralis KT71		1		1		
	6491	Conus geographus	30		30			
	6492	Conus magus	2		2			
	6493	Conus striatus	11		11			
	32614	Convict Creek 107 virus	1	3	1	3		
	13451	Corylus avellana	27	53	27	53		
	1717	Corynebacterium diphtheriae	10	50	11	51	1	1
	152794	Corynebacterium efficiens		5		5		
	196164	Corynebacterium efficiens YS-314		2		2		
	1718	Corynebacterium glutamicum		22		26		4
	196627	Corynebacterium glutamicum ATCC 13032		7		7		
	306537	Corynebacterium jeikeium K411		1		1		
	10703	Corynephage beta	2		2			
	12264	Cowpea mosaic virus		1		1		
	10243	Cowpox virus		23		25		2
	265872	Cowpox virus (Brighton Red)		1		1		
	10000571	Cowpox virus (Brighton Red) White-pock		1		1		
	777	Coxiella burnetii		52		166		114
	434923	Coxiella burnetii CbuG_Q212		1		1		
	434922	Coxiella burnetii Dugway 5J108-111		6		6		
	360116	Coxiella burnetii 'MSU Goat Q177'		4		4		
	360117	Coxiella burnetii Q321		14		14		
	360115	Coxiella burnetii RSA 331		6		6		
	227377	Coxiella burnetii RSA 493		10		10		
	12066	Coxsackievirus	1		1			
	31704	Coxsackievirus A16	1		1			
	42782	Coxsackievirus A20	1		1			
	103903	Coxsackievirus B3 (strain Nancy)	13	30	13	30		
	103905	Coxsackievirus B4 (strain E2)	6	41	6	41		
	103906	Coxsackievirus B4 (strain JVB / Benschoten / New York/51)		76		76		
	10029	Cricetulus griseus	1		1			
	11593	Crimean-Congo hemorrhagic fever virus		1	1	1	1	
	368445	Crocodilepox virus		2		2		
	8732	Crotalus durissus terrificus	4		4			
	6657	Crustacea	2		2			
	5207	Cryptococcus neoformans	2	1	2	1		
	178876	Cryptococcus neoformans var. grubii	1		1			
	283643	Cryptococcus neoformans var. neoformans B-3501A	1	3	1	3		

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	10001132	Cryptococcus neoformans var. neoformans Serotype A	1		1			
	10001120	Cryptococcus neoformans var. neoformans Serotype D	1		1			
	3369	Cryptomeria japonica	41	181	43	181	2	
	237895	Cryptosporidium hominis		3		3		
	5807	Cryptosporidium parvum		28		28		
	353152	Cryptosporidium parvum Iowa II		76		76		
	220837	Cryptosporidium sp. MNJ-1		1		1		
	12305	Cucumber mosaic virus	1		1			
	117125	Cucumber mosaic virus (strain Pepo)	1		1			
	3656	Cucumis melo	13		13			
	208899	Cupixi virus		1		1		
	13469	Cupressus sempervirens		8		8		
	119219	Cupriavidus metallidurans		1		1		
	266264	Cupriavidus metallidurans CH34		2		2		
	5503	Curvularia lunata	20	10	20	10		
	301964	CY1014 virus		1		1		
	4903	Cyberlindnera jadinii	12		12			
	1004253	Cyberlindnera mrakii	1	1	1	1		
	46457	Cycloclasticus oligotrophus		1		1		
	28909	Cynodon dactylon	27	48	27	48		
	269798	Cytophaga hutchinsonii ATCC 33406		1		1		
	4509	Dactylis glomerata		7		7		
	7955	Danio rerio	1	3	1	3		
	4039	Daucus carota		1		1		
	305674	Deerpox virus W-848-83		2		2		
	243164	Dehalococcoides ethenogenes 195		1		1		
	337052	Deltapapillomavirus 4	8		8			
	12637	Dengue virus	9	47	22	420	13	373
	11053	Dengue virus 1	13	91	19	103	6	12
X	408685	Dengue virus 1 Brazil/97-11/1997				906		906
	10001582	Dengue virus 1 Mochizuki	2		4		2	
	11059	Dengue virus 1 Nauru/West Pac/1974	3		4	47	1	47
	10001945	Dengue virus 1 PVP159	1		1			
	33741	Dengue virus 1 Singapore/S275/1990		30		215		185
	11060	Dengue virus 2	89	153	91	184	2	31
	31635	Dengue virus 2 16681-PDK53	3	2	4	31	1	29
X	10002010	Dengue virus 2 D2/SG/05K4155DK1/2005				49		49
	11064	Dengue virus 2 Jamaica/1409/1983	263	11	263	1109		1098
	11062	Dengue virus 2 Malaysia M2	1		1			
	10001583	Dengue virus 2 New Guinea C	1	4	1	4		
X	408694	Dengue virus 2 Peru/IQT2913/1996				87		87
	10001635	Dengue virus 2 PL046		7		7		
	11066	Dengue virus 2 Puerto Rico/PR159-S1/1969	30		32	1	2	1
	10001768	Dengue virus 2 S-16803	10		10			
X	10001705	Dengue virus 2 strain 43			1		1	
	31634	Dengue virus 2 Thailand/16681/84	30	57	30	57		
	11065	Dengue virus 2 Thailand/NGS-C/1944	17	17	17	31		14
	11069	Dengue virus 3	19	71	22	242	3	171
X	408690	Dengue virus 3 China/80-2/1980				61		61
X	408691	Dengue virus 3 Martinique/1243/1999				763		763
	408870	Dengue virus 3 Philippines/H87/1956	8	4	8	4		
X	408693	Dengue virus 3 Singapore/8120/1995				67		67

NEW 2013	ORGAN-ISM ID	SPECIES/STRAIN	B-12	T-12	B-13	T-13	Δ B	Δ T
X	408692	Dengue virus 3 Sri Lanka/1266/2000				65		65
	10001619	Dengue virus 3 strain 16652	16		16			
	10001944	Dengue virus 3 Thailand/PaH881/1988	1		1			
	11070	Dengue virus 4	7	62	7	79		17
	10001943	Dengue virus 4 Burma/63632/1976	1		1			
	408871	Dengue virus 4 Dominica/814669/1981	1	6	1	138		132
	408686	Dengue virus 4 Philippines/H241/1956	3		4	928	1	928
X	408687	Dengue virus 4 Singapore/8976/1995				5		5
	408688	Dengue virus 4 Thailand/0348/1991		1		11		10
	10000965	Dengue virus type 1 FGA/89	2		2			
	10000440	Dengue virus type 1 Hawaii	18	10	18	10		
	10000961	Dengue virus type 1 strain 16007	14		14			
	10000442	Dengue virus type 3 CH53489		7		7		
	246753	Dengue virus vector p4(Delta30)		2		2		
	6954	Dermatophagoides farinae	16	77	16	77		
	6956	Dermatophagoides pteronyssinus	72	203	74	224	2	21
	439235	Desulfatibacillum alkenivorans AK-01		1		1		
	272564	Desulfitobacterium hafniense DCB-2		2		2		
	281689	Desulfuromonas acetoxidans DSM 684		1		1		
	11319	Dhori virus (strain Indian/1313/61)	1		1			
	44689	Dictyostelium discoideum		1		1		
X	4163	Digitalis			1		1	
	12506	Dobrava-Belgrade virus		16		16		
	7441	Dolichovespula maculata	11	20	11	20		
	292633	Dragon grouper nervous necrosis virus	20		20			
	7227	Drosophila melanogaster	3	14	3	14		
	12639	Duck hepatitis B virus	263	20	263	20		
	38767	Duvenhage virus		2		2		
	11021	Eastern equine encephalitis virus	1	1	42	1	41	
	11022	Eastern equine encephalitis virus (STRAIN VA33[TEN BROECK])		1		1		
	10000439	Eastern equine encephalitis virus SV	8		8			
	128952	Ebola virus - Mayinga, Zaire, 1976	11	13	20	13	9	
	205488	Ebola virus sp.		5		8		3
	53751	Echinacea purpurea	1		1			
	6210	Echinococcus granulosus	39		39			
	6211	Echinococcus multilocularis	6		6			
	99586	Echis ocellatus	5		5			
	33758	Echovirus		1		1		
	12643	Ectromelia virus		5		6		1
	944	Ehrlichia canis	7		7	1		1
	269484	Ehrlichia canis str. Jake	16		16			
	945	Ehrlichia chaffeensis	13	1	14	1	1	
	205920	Ehrlichia chaffeensis str. Arkansas	23		23			
	35795	Ehrlichia muris	2	3	2	3		
	779	Ehrlichia ruminantium	3		3			
	5801	Eimeria acervulina	1		1			
	5802	Eimeria tenella	6		6			
	35321	El Moro Canyon virus		2		2		
X	8005	Electrophorus electricus			3		3	
	6035	Encephalitozoon cuniculi		5		5		
	284813	Encephalitozoon cuniculi GB-M1		27		27		
	12104	Encephalomyocarditis virus		1		1		

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	370354	Entamoeba dispar SAW760		16		16		
	5759	Entamoeba histolytica	29	13	29	13		
	294381	Entamoeba histolytica HM-1:IMSS		97		97		
	10000352	Entamoeba histolytica YS-27	1		1			
	12340	Enterobacteria phage 933J	1		1			
	10730	Enterobacteria phage 933W	1		1			
	291401	Enterobacteria phage CP-1639		1		1		
	10863	Enterobacteria phage f1	1	1	1	1		
	10864	Enterobacteria phage fd	7		7			
	10710	Enterobacteria phage lambda	2	7	2	7		
	10754	Enterobacteria phage P22	5		5			
X	10847	Enterobacteria phage phiX174			1		1	
	10658	Enterobacteria phage PRD1	2		2			
	55884	Enterobacteria phage SfV		1		1		
	10665	Enterobacteria phage T4	10	20	10	20		
	10760	Enterobacteria phage T7	1		1			
	543	Enterobacteriaceae	3		3			
	12022	Enterobacterio phage MS2	1		1			
	1351	Enterococcus faecalis	2		2			
	1352	Enterococcus faecium	6		6			
	333849	Enterococcus faecium DO		1		1		
	150846	Enterovirus 5865/sin/000009	2		2			
	39054	Enterovirus A71	12	1	12	1		
	138950	Enterovirus C	6	3	6	3		
	12064	Enterovirus E	13		13			
	31330	Ephydatia fluviatilis		1		1		
	82830	Epstein-barr virus strain ag876	1	1	1	1		
	10326	Equid herpesvirus 1	5		7		2	
	10000525	Equid herpesvirus 2 16V	1		1			
	10000526	Equid herpesvirus 2 5FN	1		1			
	10000524	Equid herpesvirus 2 691	1		1			
	10000391	Equid herpesvirus 2 ER32	1		1			
	10000527	Equid herpesvirus 2 FIN60	1		1			
	10331	Equid herpesvirus 4	5		6		1	
	10000405	Equid herpesvirus 4 TH20	2		2			
	82831	Equid herpesvirus type 2 strain 86/87	1		1			
	11047	Equine arteritis virus	2		2			
X	299386	Equine arteritis virus Bucyrus			2		2	
	11665	Equine infectious anemia virus	91	109	91	109		
	11670	Equine infectious anemia virus (CLONE 1369)		1		1		
	11671	Equine infectious anemia virus (STRAIN WSU5)		16		16		
	10000499	Equine infectious anemia virus PV		2		2		
	10000835	Equine rhinitis A virus 393/76	4		4			
	650131	Equine rhinitis B virus 1 strain P1436/71	6		6			
	10001929	Equine rhinitis B virus 2 strain 313/75	5		5			
	10001930	Equine rhinitis B virus 3 isolate 2225AS	5		5			
	9796	Equus caballus	8	44	8	44		
	9798	Equus przewalskii		1		1		
	562	Escherichia coli	198	103	199	103	1	
	10001633	Escherichia coli 055:B5	3		3			
	358709	Escherichia coli 101-1		5		5		
	10001145	Escherichia coli 1471	2		2			

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	10000727	Escherichia coli 180/C3	1		1			
	362663	Escherichia coli 536		59		59		
	525281	Escherichia coli 83972		3		3		
	405955	Escherichia coli APEC O1		7		7		
	481805	Escherichia coli ATCC 8739		1		1		
	37762	Escherichia coli B	1	1	1	1		
	10000728	Escherichia coli B B/r CM6		1		1		
	344601	Escherichia coli B171		11		11		
	550676	Escherichia coli B185		1		1		
	340184	Escherichia coli B7A		5		5		
	199310	Escherichia coli CFT073	1	1	1	1		
	340186	Escherichia coli E110019		1		1		
	340185	Escherichia coli E22		11		11		
	331111	Escherichia coli E24377A		31		31		
	316401	Escherichia coli ETEC H10407	64	31	64	31		
	340197	Escherichia coli F11		12		12		
	10001528	Escherichia coli F515	1		1			
X	10001463	Escherichia coli F576			1		1	
	331112	Escherichia coli HS		8		8		
	585034	Escherichia coli IAI1	3		3			
	10001502	Escherichia coli J-5	1		1			
	10001753	Escherichia coli K1		1		1		
	83333	Escherichia coli K-12	13	16	19	17	6	1
	679206	Escherichia coli MS 119-7		1		1		
	679205	Escherichia coli MS 124-1		1		1		
	10001659	Escherichia coli O125	1		1			
	168807	Escherichia coli O127:H6	1		1			
	83334	Escherichia coli O157:H7		103	1	103	1	
	478005	Escherichia coli O157:H7 str. EC4486		1		1		
	478006	Escherichia coli O157:H7 str. EC4501		2		2		
	478008	Escherichia coli O157:H7 str. EC869		14		14		
	155864	Escherichia coli O157:H7 str. EDL933	2	19	2	19		
	386585	Escherichia coli O157:H7 str. Sakai		13		13		
	10000733	Escherichia coli O5:K4:H4	1		1			
	244320	Escherichia coli O55:H7		1		1		
	217992	Escherichia coli O6		7		7		
X	10002022	Escherichia coli O6 O6:K15:H31				1		1
	10000734	Escherichia coli O65:K-:H-	1		1			
	316385	Escherichia coli str. K-12 substr. DH10B		2		2		
	511145	Escherichia coli str. K-12 substr. MG1655		26		26		
	316407	Escherichia coli str. K-12 substr. W3110		1		1		
	364106	Escherichia coli UTI89		2		2		
	3039	Euglena gracilis	1		1			
	2759	Eukaryota	1		1			
	34828	Eulemur mongoz	1		1			
	6958	Euroglyphus maynei		10		10		
	3617	Fagopyrum esculentum	40		40			
	62330	Fagopyrum tataricum	5		5			
	6690	Farfantepenaeus aztecus	51		51			
	46835	Fasciola gigantica	2		2			
	6192	Fasciola hepatica	254	11	254	11		
	11978	Feline calicivirus	4		4			

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	11981	Feline calicivirus (STRAIN F9)	2		2			
	11980	Feline calicivirus (STRAIN JAPANESE F4)	6		6			
	12663	Feline coronavirus		1		1		
	11673	Feline immunodeficiency virus		28		28		
	11674	Feline immunodeficiency virus (isolate Petaluma)	2	3	2	3		
	45409	Feline immunodeficiency virus (isolate wo)	3		3			
	36372	Feline immunodeficiency virus (strain UK8)		1		1		
	33734	Feline infectious peritonitis virus (strain 79-1146)	10	7	10	7		
	10001624	Feline infectious peritonitis virus (strain KU-2)	14	27	14	27		
	11769	Feline leukemia virus strain A/Glasgow-1	6		6			
	10001130	Feline leukemia virus subtype A	2		2			
	10786	Feline panleukopenia virus		4		4		
	9685	Felis catus	32	93	32	93		
	4606	Festuca arundinacea	1		1			
	156586	Flavobacteria bacterium BBFL7		1		1		
	12110	Foot-and-mouth disease virus	24	4	24	4		
	12111	Foot-and-mouth disease virus - type A		2		2		
	10000991	Foot-and-mouth disease virus - type A (strain A22 Iraq)	5	1	5	1		
	10000989	Foot-and-mouth disease virus - type A (strain A22)	8	6	8	6		
	110195	Foot-and-mouth disease virus - type Asia 1	8	3	9	3	1	
X	10002020	Foot-and-mouth disease virus - type Asia 1 Nepal 29/97			4		4	
	10000995	Foot-and-mouth disease virus - type Asia 1 Pakistan	1		1			
	10001946	Foot-and-mouth disease virus - type Asia 1 YS/CHA/05	1		2		1	
	12116	Foot-and-mouth disease virus - type C	6	26	6	26		
	12118	Foot-and-mouth disease virus - type O	25	4	30	5	5	1
	10000801	Foot-and-mouth disease virus - type O (O/SKR/2002)	1		1			
	10001118	Foot-and-mouth disease virus - type O (strain HKN/14/82)	2		2			
	10000856	Foot-and-mouth disease virus - type O isolate O/UKG/35/2001		14		14		
	10001642	Foot-and-mouth disease virus - type O Wuppertal/FRG/82		1		1		
	10000992	Foot-and-mouth disease virus - type SAT 1 (Strain Bot 1/68)	1		1			
	35292	Foot-and-mouth disease virus - type SAT 2	1	1	1	1		
	10000993	Foot-and-mouth disease virus - type SAT 2 (Strain Ken 3/57)	1		1			
	10001000	Foot-and-mouth disease virus - type SAT 2 (strain Rho 1/48)	4		4			
	12123	Foot-and-mouth disease virus - type SAT 3		1		1		
	10000994	Foot-and-mouth disease virus - type SAT 3 (Strain Bec 1/65)	1		1			
	12112	Foot-and-mouth disease virus (strain A10-61)	8		8			
	12114	Foot-and-mouth disease virus (strain A12)	21		21			
	12115	Foot-and-mouth disease virus (strain A24 Cruzeiro)	17	4	17	9		5
	12113	Foot-and-mouth disease virus (strain A5)	3		3			
	12120	Foot-and-mouth disease virus (strain C1-Santa Pau)	1		1			
	12117	Foot-and-mouth disease virus (strain C3 Indaial)	2		2			
	73482	Foot-and-mouth disease virus (strain O1)	18	1	18	1		
	10000820	Foot-and-mouth disease virus (strain O1) (O/Taiwan/1/97)	1		1			
	10000964	Foot-and-mouth disease virus (strain O1) (O1 Brugge)	2		2			
	10000516	Foot-and-mouth disease virus (strain O1) (O1 Campos)	18	18	18	18		
	10000513	Foot-and-mouth disease virus (strain O1) (O1 Kaufbeuren)	41	8	42	8	1	
X	10000806	Foot-and-mouth disease virus (strain O1) (O1 Manisa)			1		1	
	10000514	Foot-and-mouth disease virus (strain O1) (O1BFS 1860)	9		9			
	10000515	Foot-and-mouth disease virus (strain O1) (O1BFS)	5		5			
	10000556	Foot-and-mouth disease virus (strain O1) Kaufbeuren	42	12	43	12	1	
X	10001102	Foot-and-mouth disease virus (strain O1) O/UKG/11/2001			1	1	1	1
	161727	Foot-and-mouth disease virus A10/Holland	11	14	11	14		

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	12121	Foot-and-mouth disease virus C1	1		1			
	10000840	Foot-and-mouth disease virus C1 Brescia It/64	2		2			
	10000986	Foot-and-mouth disease virus C1 CS30	1		1			
	10000836	Foot-and-mouth disease virus C1 CS8	22	24	22	24		
	46290	Foot-and-mouth disease virus C3	4	1	4	1		
	10001039	Foot-and-mouth disease virus C3 (strain Resendne-Br/55)	1		1			
	244367	Foot-and-mouth disease virus C-S8c1	12	17	15	17	3	
	31621	Four Corners hantavirus	2	5	2	5		
	10261	Fowlpox virus		7		7		
	10263	Fowlpox virus isolate HP-438/Munich		1		1		
	401614	Francisella novicida U112		1		1		
	263	Francisella tularensis		7	3	7	3	
	351581	Francisella tularensis subsp. holarctica FSC200		1		1		
	458234	Francisella tularensis subsp. holarctica FTNF002-00		1		1		
	376619	Francisella tularensis subsp. holarctica LVS	2	291	2	291		
	393011	Francisella tularensis subsp. holarctica OSU18		5		5		
	119856	Francisella tularensis subsp. tularensis		5		5		
	430557	Francisella tularensis subsp. tularensis FSC033		27		27		
	393115	Francisella tularensis subsp. tularensis FSC198		50		50		
	177416	Francisella tularensis subsp. tularensis SCHU S4		90		90		
	418136	Francisella tularensis subsp. tularensis WY96-3418		1		1		
	298653	Frankia sp. EAN1pec		2		2		
	38873	Fraxinus excelsior		3		3		
	11795	Friend murine leukemia virus	6	25	6	26		1
	209882	Fusobacterium nucleatum subsp. vincentii ATCC 49256		1		1		
X	8049	Gadus morhua			30		30	
	8053	Gadus morhua callarias	10		10			
	7137	Galleria mellonella	1		1			
	9031	Gallus gallus	257	178	259	187	2	9
	373098	Gambierdiscus toxicus	6		6			
	11824	Gardner-Arnstein feline leukemia oncovirus B	13		13			
	54290	GB virus C	16		16			
	471223	Geobacillus sp. WCH70		2		2		
	1422	Geobacillus stearothermophilus	1	1	2	1	1	
	5741	Giardia intestinalis		8		8		
	598745	Giardia intestinalis ATCC 50581		5		5		
	184922	Giardia lamblia ATCC 50803		239		239		
X	37546	Glossina morsitans morsitans			2		2	
	28448	Gluconacetobacter xylinus		1		1		
	3847	Glycine max	71	2	97	2	26	
X	61466	Gnathostoma binucleatum			10		10	
	38251	Goose parvovirus	7		7			
	9593	Gorilla gorilla		1		1		
	9595	Gorilla gorilla gorilla		5		5		
	55951	Grapevine leafroll-associated virus 3	1		1			
	35288	Grapevine virus A	19		19			
	45219	Guanarito virus		838		840		2
	10001616	Guanarito virus strain INH-95551		1		1		
	114727	H1N1 subtype	9	25	9	25		
	10000477	H1N1 subtype Influenza A virus (A/Netherlands/306/00 (H1N1))		1		1		
	10001225	H1N1 subtype Influenza A/Oklahoma/7485/01		5		5		
X	36420	H1N1 swine influenza virus				12		12

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	10001315	H1N1 swine influenza virus (A/swine/Korea/S10/2004(H1N1))		3		3		
	10001316	H1N1 swine influenza virus (A/swine/Korea/S175/2004(H1N1))		1		1		
	119210	H3N2 subtype	2	19	2	19		
	10001157	H3N2 subtype Influenza A virus (A/Hong Kong(H3N2))		15		15		
	102793	H5N1 subtype	14	31	16	31	2	
X	102796	H9N2 subtype			1		1	
	10001317	H9N2 subtype Influenza A virus (A/swine/Korea/S81/2004(H9N2))		1		1		
	10001318	H9N2 subtype Influenza A virus (A/swine/Korea/S83/2004(H9N2))		2		2		
	6289	Haemonchus contortus	1		1			
	197575	Haemophilus aegyptius	1		1			
	730	Haemophilus ducreyi	3	1	3	1		
	233412	Haemophilus ducreyi 35000HP	1		1			
	727	Haemophilus influenzae	24	64	24	64		
	374927	Haemophilus influenzae 22.1-21		1		1		
	375177	Haemophilus influenzae 3655		1		1		
	521004	Haemophilus influenzae 6P18H1		1		1		
	10001055	Haemophilus influenzae 6U	2		2			
	521005	Haemophilus influenzae 7P49H1		2		2		
	281310	Haemophilus influenzae 86-028NP	1		1			
	10001056	Haemophilus influenzae ATCC 9795	2		2			
	10001053	Haemophilus influenzae MinnA	9		9			
	10000833	Haemophilus influenzae NTHi 1128	6		6			
	10001042	Haemophilus influenzae NTHi 1479	12	4	12	4		
	10000807	Haemophilus influenzae NTHi UC19	2	2	2	2		
	374928	Haemophilus influenzae PittAA		2		2		
	374931	Haemophilus influenzae PittGG		1		1		
	374932	Haemophilus influenzae PittHH	1		1			
	262727	Haemophilus influenzae R2846		3		3		
	262728	Haemophilus influenzae R2866		1		1		
	375432	Haemophilus influenzae R3021		3		3		
	71421	Haemophilus influenzae Rd KW20		1		1		
	10000860	Haemophilus influenzae Serotype B	17	9	17	9		
	10001155	Haemophilus influenzae strain 1479	2		2			
	10001150	Haemophilus influenzae Strain Eagan	58		58			
	10001523	Haemophilus influenzae strain I-69 Rd-/b+	4		4			
	10001520	Haemophilus influenzae strain RM7004	1		1			
	10001149	Haemophilus influenzae Subtype 1H	23		23			
	10000861	Haemophilus influenzae Variant d1	18		18			
	10690	Haemophilus phage HP1		1		1		
	205914	Haemophilus somnus 129PT		1		1		
	228400	Haemophilus somnus 2336	1		1			
	6454	Haliotis rufescens	1		1			
	10626	Hamster polyomavirus	11		11			
	11599	Hantaan virus	2	45	2	50		5
	11602	Hantaan virus 76-118	13	22	13	22		
	370830	Hantaan virus Q32		4		4		
	470918	Hantaanvirus CGHu1		1		1		
	458678	Hantaanvirus CGRn93P8		2		2		
	11598	Hantavirus		5		5		
	74942	Hantavirus CRF355		1		1		
	42358	Hantavirus Monongahela-3		5		5		
	279233	Hantavirus Z37		2		2		

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	13557	Hapalemur griseus		1		1		
X	489455	HBV genotype A			1		1	
	489460	HBV genotype B	1		1			
	489466	HBV genotype C	3		4		1	
	489483	HBV genotype D	1		1	1		1
	4232	Helianthus annuus	18		18			
	32025	Helicobacter hepaticus		1		1		
	235279	Helicobacter hepaticus ATCC 51449	2		2			
	210	Helicobacter pylori	37	4	38	11	1	7
	85962	Helicobacter pylori 26695	13	6	13	10		4
	10001667	Helicobacter pylori 487	1		1			
	10001794	Helicobacter pylori B128 Gerbil-adapted variant 7.13	1		1			
	563041	Helicobacter pylori G27	2		2			
	10000718	Helicobacter pylori J223	2		2			
	85963	Helicobacter pylori J99		53		53		
X	637383	Helicobacter pylori NCTC 11639				2		2
	570508	Helicobacter pylori P12		2		2		
	102617	Helicobacter pylori SS1	1		1			
	10000720	Helicobacter pylori UA948	2		2			
	10000721	Helicobacter pylori UA955	1		1			
	6339	Heligmosomoides polygyrus	3		3			
	6536	Helix pomatia	1		1			
	63330	Hendra virus	7		7			
	12092	Hepatitis A virus	23	22	23	22		
	10407	Hepatitis B virus	247	480	260	599	13	119
	31512	Hepatitis B virus adr/mutant		1		1		
	10409	Hepatitis B virus adr4		11		11		
	10410	Hepatitis B virus adw/991	2	2	2	2		
	10412	Hepatitis B virus adw/Indonesia/PIDW420		2		2		
	10415	Hepatitis B virus adw/Okinawa/PODW282		4		4		
	45410	Hepatitis B virus adw4/Brazil/isolate w4b		6		6		
	10411	Hepatitis B virus alpha1		15		16		1
	489469	Hepatitis B virus ayw/China/Tibet127/2002	1		1			
X	490133	Hepatitis B virus ayw/France/Tiollais/1979				2		2
	391647	Hepatitis B virus ayw2	6		6			
	391646	Hepatitis B virus ayw3	1		1			
	391650	Hepatitis B virus ayw4	1		1			
	10414	Hepatitis B virus LSH/chimpanzee		2		2		
	10001156	Hepatitis B virus subtype AD	3	3	3	3		
	106820	Hepatitis B virus subtype adr	23	25	23	25		
	106821	Hepatitis B virus subtype adw	17	60	17	60		
	10408	Hepatitis B virus subtype adw2	71	60	71	60		
	10419	Hepatitis B virus subtype adyw		35		35		
	10000436	Hepatitis B virus subtype AY	7		7			
	10000437	Hepatitis B virus subtype AYR		1		1		
	10418	Hepatitis B virus subtype ayw	57	165	57	166		1
	11103	Hepatitis C virus	643	865	647	966	4	101
	11104	Hepatitis C virus (isolate 1)	37	223	37	223		
	356391	Hepatitis C virus (isolate 6a33)		5		5		
	356413	Hepatitis C virus (isolate BEBE1)		10		10		
	11105	Hepatitis C virus (isolate BK)	3	43	3	43		
	333284	Hepatitis C virus (isolate Con1)	4	3	4	3		

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	356419	Hepatitis C virus (isolate EUH1480)		4		4		
	329389	Hepatitis C virus (isolate Glasgow)	3	1	3	1		
	11108	Hepatitis C virus (isolate H)	128	81	129	81	1	
	63746	Hepatitis C virus (isolate H77)	85	207	87	207	2	
	356410	Hepatitis C virus (isolate HC-G9)	2	1	2	1		
	11110	Hepatitis C virus (isolate HCT18)	1		1			
	356416	Hepatitis C virus (isolate HCV-K3a/650)		14		14		
	31644	Hepatitis C virus (isolate HCV-KF)	1	1	1	1		
	356386	Hepatitis C virus (isolate India)		1		1		
	11116	Hepatitis C virus (isolate Japanese)	6	18	6	18		
	356417	Hepatitis C virus (isolate JK049)		5		5		
	356415	Hepatitis C virus (isolate NZL1)	1	1	1	1		
	31645	Hepatitis C virus (isolate Taiwan)	3	19	3	19		
	356421	Hepatitis C virus (isolate Th580)		4		4		
	357355	Hepatitis C virus (isolate Tr Kj)		3		3		
	356424	Hepatitis C virus (isolate VN004)		1		1		
	41856	Hepatitis C virus genotype 1	2	60	2	60		
	40271	Hepatitis C virus genotype 2	41	6	41	6		
	356114	Hepatitis C virus genotype 3	121	13	121	13		
	33745	Hepatitis C virus genotype 4		2		2		
	33746	Hepatitis C virus genotype 5		2		2		
	42182	Hepatitis C virus genotype 6		7		7		
	421877	Hepatitis C virus isolate HC-J1	3	26	3	26		
	11113	Hepatitis C virus isolate HC-J6	7	2	7	2		
	11115	Hepatitis C virus isolate HC-J8	2	1	2	1		
	356411	Hepatitis C virus JFH-1	6	1	6	1		
	31646	Hepatitis C virus subtype 1a	195	358	195	365		7
	10000453	Hepatitis C virus subtype 1a (isolate Gla)	5		5			
	10000455	Hepatitis C virus subtype 1a 1/910		17		17		
	10000457	Hepatitis C virus subtype 1a Chiron Corp.	1	1	1	1		
	31647	Hepatitis C virus subtype 1b	530	222	539	230	9	8
	10000456	Hepatitis C virus subtype 1b AD78	71		71			
	10000968	Hepatitis C virus subtype 1b isolate BE-11	3		3			
	10000460	Hepatitis C virus subtype 1b JK1	13		13			
	31649	Hepatitis C virus subtype 2a	80	23	80	23		
	31650	Hepatitis C virus subtype 2b	101	3	101	3		
	356426	Hepatitis C virus subtype 3a	8	53	8	76		23
	42792	Hepatitis C virus subtype 3g	1		1			
	31653	Hepatitis C virus subtype 4a	1	1	1	1		
	31654	Hepatitis C virus subtype 5a	1	1	1	1		
	31655	Hepatitis C virus subtype 6a		1		1		
	12475	Hepatitis delta virus	48	7	48	7		
	10000523	Hepatitis delta virus TW2667		5		5		
	12461	Hepatitis E virus	133	27	133	27		
	31767	Hepatitis E virus (strain Burma)	160		160			
	31768	Hepatitis E virus (strain Mexico)	31		31			
	10000519	Hepatitis E virus China Xinjiang	1		1			
	10000520	Hepatitis E virus SAR-55	1	6	1	6		
	39113	Hepatitis GB virus B		4		4		
	28300	Heron hepatitis B virus		1		1		
	10299	Herpes simplex virus (type 1 / strain 17)	44	30	44	30		
	10301	Herpes simplex virus (type 1 / strain Angelotti)		1		1		

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	10304	Herpes simplex virus (type 1 / strain F)	17	5	17	5		
	10303	Herpes simplex virus (type 1 / strain HFEM)	2		2			
	10308	Herpes simplex virus (type 1 / strain Patton)	3		3			
	10309	Herpes simplex virus (type 1 / strain SC16)	6	2	6	2		
	126283	Herpes simplex virus unknown type		1		1		
	10292	Herpesviridae		33		33		
	49011	Hesperocyparis arizonica	2	6	2	6		
	3981	Hevea brasiliensis	169	43	169	43		
X	471721	HIV-1 CRF01_AE			1		1	
	388799	HIV-1 group O	1		1			
	505184	HIV-1 M:A	5		6	1	1	1
	505185	HIV-1 M:B	1		3	1	2	1
	11685	HIV-1 M:B_ARV2/SF2		43		43		
	11706	HIV-1 M:B_HXB2R	11	12	11	12		
	11696	HIV-1 M:B_MN	9	21	9	21		
	505186	HIV-1 M:C	5		6		1	
	327105	HIV-1 O_ANT70	1		1			
	11583	HoJo virus		1		1		
	29679	Holcus lanatus	14		14			
	9606	Homo sapiens	5774	10878	6165	11108	391	230
	397342	Horsepox virus		6		6		
X	10533	Human adenovirus 1				1		1
X	10541	Human adenovirus 11				12		12
	343462	Human adenovirus 11p	7		7			
	28282	Human adenovirus 12	10	2	10	2		
	46921	Human adenovirus 13	1		1			
	28276	Human adenovirus 15	1		1			
	10515	Human adenovirus 2	28	5	28	6		1
	45659	Human adenovirus 3	20	1	25	1	5	
X	10529	Human adenovirus 31				1		1
	28284	Human adenovirus 40	2	1	2	1		
	46941	Human adenovirus 46	1		1			
	28285	Human adenovirus 5	22	173	22	173		
	31545	Human adenovirus 8	1		1	1		1
X	129875	Human adenovirus A				1		1
	10001392	Human adenovirus B strain Harbin04B	5		5			
	129951	Human adenovirus C	1	3	1	3		
	130309	Human adenovirus F	1		1			
	158465	Human calicivirus Hu/NLV/GII/MD145-12/1987/US	1		1			
	11137	Human coronavirus 229E		2		2		
	31631	Human coronavirus OC43		1		1		
X	10002015	Human coxsackievirus A16 shzh05-1			92		92	
	12067	Human coxsackievirus A9	30		30			
	12071	Human coxsackievirus B1	12		12			
	82639	Human coxsackievirus B2	1		1			
	12072	Human coxsackievirus B3	7	15	7	15		
	10001213	Human coxsackievirus B3 (strain RK)	1		1			
	12073	Human coxsackievirus B4	17	50	17	50		
	11827	Human endogenous retrovirus	1	1	1	1		
	64382	Human Endogenous Retrovirus IDDMK1,2-22	3		3			
	45617	Human endogenous retrovirus K	12		12			
	69153	Human enterovirus 71 (strain BRCR)	1		1			

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	10001902	Human enterovirus 71 NUH0083/SIN/08	3		4		1	
	10000548	Human enterovirus 71 Subgenogroup C2	18		19		1	
X	10000549	Human enterovirus 71 Subgenogroup C4			1		1	
	208726	Human hepatitis A virus	4		4			
	12098	Human hepatitis A virus Hu/Australia/HM175/1976	86	80	86	80		
	10298	Human herpesvirus 1	141	142	141	142		
	10000394	Human herpesvirus 1 103/65	1		1			
	10000396	Human herpesvirus 1 McIntyre		1		1		
	10000398	Human herpesvirus 1 NS	1		1			
	10306	Human herpesvirus 1 strain KOS	17	4	17	4		
	10310	Human herpesvirus 2	96	188	96	188		
	10312	Human herpesvirus 2 strain 186		1		1		
	10313	Human herpesvirus 2 strain 333	2	5	2	5		
	10315	Human herpesvirus 2 strain HG52		31		31		
	10335	Human herpesvirus 3	9	79	9	81		2
	10000406	Human herpesvirus 3 H-551	26	15	26	15		
	10338	Human herpesvirus 3 strain Dumas		28		28		
	10376	Human herpesvirus 4	126	349	132	364	6	15
	10377	Human herpesvirus 4 (strain B95-8)	68	264	68	267		3
X	10378	Human herpesvirus 4 (strain RAJI)			1		1	
	10000420	Human herpesvirus 4 BL74		1		1		
	10000421	Human herpesvirus 4 CKL		10		10		
	10000424	Human herpesvirus 4 GD1		1		1		
	36352	Human herpesvirus 4 type 1	4	12	4	13		1
	12509	Human herpesvirus 4 type 2	2	5	2	6		1
	10000427	Human herpesvirus 4 type A		5		5		
	10359	Human herpesvirus 5	83	474	83	489		15
	10360	Human herpesvirus 5 strain AD169	28	360	29	361	1	1
	10363	Human herpesvirus 5 strain Towne	5	24	5	24		
	10368	Human herpesvirus 6	2	22	2	25		3
	10369	Human herpesvirus 6 (strain GS)	2		2			
	10370	Human herpesvirus 6 (strain Uganda-1102)	1	2	1	2		
	36351	Human herpesvirus 6 strain Z29	1	13	1	13		
	32603	Human herpesvirus 6A		6	1	6	1	
	32604	Human herpesvirus 6B	1	2	1	2		
	10000535	Human herpesvirus 6B HST	1		1			
	10372	Human herpesvirus 7	2	2	2	2		
	57278	Human herpesvirus 7 strain JI		1		1		
	37296	Human herpesvirus 8	26	482	26	482		
	12721	Human immunodeficiency virus	1	11	1	11		
	11676	Human immunodeficiency virus 1	57	286	88	355	31	69
	10000500	Human immunodeficiency virus 1 IIIB	1	2	1	2		
	11709	Human immunodeficiency virus 2		6	1	6	1	
	11682	Human immunodeficiency virus type 1 (BH5 ISOLATE)		1		1		
	11686	Human immunodeficiency virus type 1 (BRU ISOLATE)	1	3	1	4		1
	11687	Human immunodeficiency virus type 1 (CDC-451 ISOLATE)		3		3		
	11679	Human immunodeficiency virus type 1 (CLONE 12)		6		6		
	11689	Human immunodeficiency virus type 1 (ELI ISOLATE)		6		6		
	362651	Human immunodeficiency virus type 1 (isolate YU2)	5	21	8	21	3	
	11694	Human immunodeficiency virus type 1 (JH3 ISOLATE)		3		3		
	11688	Human immunodeficiency virus type 1 (JRCSF ISOLATE)		35		35		
	11697	Human immunodeficiency virus type 1 (MAL ISOLATE)		7		7		

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	11704	Human immunodeficiency virus type 1 (MFA ISOLATE)		2		2		
	11695	Human immunodeficiency virus type 1 (NDK ISOLATE)		8		8		
	11698	Human immunodeficiency virus type 1 (NEW YORK-5 ISOLATE)	1	1	1	1		
	11699	Human immunodeficiency virus type 1 (OYI ISOLATE)		3		3		
	11701	Human immunodeficiency virus type 1 (RF/HAT ISOLATE)	1	19	1	19		
	11691	Human immunodeficiency virus type 1 (SF162 ISOLATE)	2	1	2	1		
	11690	Human immunodeficiency virus type 1 (SF33 ISOLATE)		2		2		
	11703	Human immunodeficiency virus type 1 (STRAIN UGANDAN / ISOLATE U455)		14		14		
	31678	Human immunodeficiency virus type 1 (WMJ1 isolate)		15		15		
	11705	Human immunodeficiency virus type 1 (WMJ2 ISOLATE)		1		1		
	11683	Human immunodeficiency virus type 1 (Z2/CDC-Z34 ISOLATE)		1		1		
	11678	Human immunodeficiency virus type 1 BH10	2	19	2	19		
	11714	Human immunodeficiency virus type 2 (ISOLATE BEN)		7		7		
	11715	Human immunodeficiency virus type 2 (ISOLATE CAM2)		1		1		
	11713	Human immunodeficiency virus type 2 (ISOLATE D194)		1		1		
	11716	Human immunodeficiency virus type 2 (ISOLATE D205,7)		1		1		
	11717	Human immunodeficiency virus type 2 (ISOLATE GHANA-1)		5		5		
	73484	Human immunodeficiency virus type 2 (isolate KR)		2		2		
	11718	Human immunodeficiency virus type 2 (ISOLATE SBLISY)		2		2		
	162145	Human metapneumovirus	8	119	8	121		2
	10566	Human papillomavirus	4	2	4	2		
	10580	Human papillomavirus type 11	9	40	9	40		
	10573	Human papillomavirus type 13	1	1	1	1		
	333760	Human papillomavirus type 16	311	359	323	372	12	13
	333761	Human papillomavirus type 18	22	81	23	81	1	
	10583	Human papillomavirus type 1a	7	13	8	13	1	
	333751	Human papillomavirus type 2		7		7		
	333762	Human papillomavirus type 26		1		1		
X	37111	Human papillomavirus type 28				1		1
	37112	Human papillomavirus type 29		1		1		
	10614	Human papillomavirus type 3		3		3		
	10585	Human papillomavirus type 31	8	6	8	6		
	333763	Human papillomavirus type 32	1	1	1	1		
	10586	Human papillomavirus type 33	5	8	5	9		1
	10587	Human papillomavirus type 35		1		1		
	10588	Human papillomavirus type 39		1		1		
	10617	Human papillomavirus type 4		4		4		
	10615	Human papillomavirus type 40	1	1	1	1		
	10592	Human papillomavirus type 44		1		1		
	10593	Human papillomavirus type 45		5		5		
X	333923	Human papillomavirus type 5			1		1	
	10595	Human papillomavirus type 51		1		1		
	10618	Human papillomavirus type 52		33		33		
	333765	Human papillomavirus type 53		1		1		
	10596	Human papillomavirus type 56		3		3		
	10598	Human papillomavirus type 58	1	32	1	32		
	37115	Human papillomavirus type 59		1		1		
	31552	Human papillomavirus type 6	11	4	12	4	1	
	45240	Human papillomavirus type 68		1		1		
X	37121	Human papillomavirus type 69				1		1
	10600	Human papillomavirus type 6b	11	25	11	25		

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	10620	Human papillomavirus type 7	1	3	1	3		
	51033	Human papillomavirus type 73		1		1		
	36412	Human parainfluenza 1 virus (strains A1426 / 86-315 / 62M-753)		1		1		
	11217	Human parainfluenza 3 virus (strain NIH 47885)	8		8			
	11212	Human parainfluenza virus 2	10		10			
	11214	Human parainfluenza virus 2 (strain Toshiba)	3		3			
	11216	Human parainfluenza virus 3	2		2			
	12063	Human parechovirus 1	5		5			
	289365	Human parvovirus 4		3		3		
	10798	Human parvovirus B19	93	44	93	44		
	10000438	Human parvovirus B19 genotype 1	1		1			
	12080	Human poliovirus 1	6	1	6	1		
	12081	Human poliovirus 1 Mahoney	47	31	47	31		
	12082	Human poliovirus 1 strain Sabin	7		7			
	10001028	Human poliovirus 2 (strain MEF-1)	1		1			
	10001040	Human poliovirus 2 (strain Sabin)	2	7	2	7		
	12086	Human poliovirus 3	5	2	5	2		
	270338	Human poliovirus 3 strain Sabin	80	1	80	1		
	11250	Human respiratory syncytial virus	21	186	21	186		
	11255	Human respiratory syncytial virus (strain RSB6190)	6		6			
	11256	Human respiratory syncytial virus (strain RSB6256)	10		10			
	11252	Human respiratory syncytial virus (strain RSB642)	1		1			
	11251	Human respiratory syncytial virus (subgroup B / strain 18537)	2	1	2	1		
	208893	Human respiratory syncytial virus A	1	3	1	3		
	10000960	Human respiratory syncytial virus A Mon/3/88	6		6			
	11260	Human respiratory syncytial virus A strain Long	120	16	120	16		
	10001456	Human respiratory syncytial virus A strain RGH	1		1			
	11259	Human respiratory syncytial virus A2	52	114	54	115	2	1
	79692	Human respiratory syncytial virus B1	1	25	1	25		
	410078	Human respiratory syncytial virus S2	1		1			
	12134	Human rhinovirus 1A		19		19		
	10000987	Human rhinovirus 2 Vienna	5		5			
	12130	Human rhinovirus A2	11		11			
	12132	Human rhinovirus A89	3		3			
	12131	Human rhinovirus B14	14		14			
	10950	Human rotavirus (SEROTYPE 2 / STRAIN DS1)	1		1			
	31569	Human rotavirus (serotype 2 / strain RV-5)	1		1			
	10941	Human rotavirus A	13	2	13	74		72
	10960	Human rotavirus G4 strain St. Thomas 3	6	1	6	1		
	374507	Human rotavirus G9 isolate F45	7		7			
	10001215	Human rotavirus G9 WI61	1		1			
	408599	Human rotavirus G9P[8]	1		1			
	94432	Human rotavirus MP409	1	1	1	1		
	10952	Human rotavirus strain KU	9		9			
	10957	Human rotavirus strain P	1	4	1	4		
	10958	Human rotavirus strain RRV	1		1			
	10962	Human rotavirus strain WA	10	7	10	7		
	11927	Human T-cell lymphotrophic virus type 1 (Caribbean isolate)		5		5		
	10001004	Human T-cell lymphotrophic virus type 1 (Caribbean isolate) (Strain HS35)	1		1			
	11928	Human T-cell lymphotrophic virus type 1 (isolate MT-2)	1		1			
	11926	Human T-cell lymphotrophic virus type 1 (strain ATK)	30	118	30	118		

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	39015	Human T-cell lymphotropic virus type 1 (african isolate)		2		2		
	11908	Human T-lymphotropic virus 1	234	276	234	277		1
	11909	Human T-lymphotropic virus 2	63	2	63	2		
	11120	Infectious bronchitis virus	5		7		2	
	10000825	Infectious bronchitis virus Avian strain D207	11		11			
	10001431	Infectious bronchitis virus CK/CH/LDL/97I	1		1			
	633557	Infectious bronchitis virus CK/CH/LHLJ/04V	1		1			
	10995	Infectious bursal disease virus	10		10			
	10997	Infectious bursal disease virus 002-73/AUS	1		1			
X	10996	Infectious bursal disease virus 52/70				10		10
	31560	Infectious bursal disease virus E	1		1			
	11290	Infectious hematopoietic necrosis virus	8		8			
	11002	Infectious pancreatic necrosis virus	1		1			
	11320	Influenza A virus	53	333	62	473	9	140
	229051	Influenza A virus (A/81/HO)		3		3		
	387139	Influenza A virus (A/Aichi/2/1968(H3N2))	11	10	11	10		
	203129	Influenza A virus (A/Aichi/2/1994(H3N2))		1		1		
	553345	Influenza A virus (A/Aichi/72/2007(H3N2))	1		1			
	385576	Influenza A virus (A/Alaska/6/1977(H3N2))		1		1		
	383602	Influenza A virus (A/Anas acuta/Primorje/695/1976(H2N3))		10		10		
	370810	Influenza A virus (A/Anhui/1/2005(H5N1))	2		3		1	
	370811	Influenza A virus (A/Anhui/2/2005(H5N1))	1		1			
	464314	Influenza A virus (A/Anhui/T2/2006(H5N1))	1		1			
	384498	Influenza A virus (A/Ann Arbor/6/1960(H2N2))	1	181	1	181		
	947939	Influenza A virus (A/aquatic bird/Korea/w44/2005(H7N3))		1		1		
	62446	Influenza A virus (A/Argentina/3779/94(H3N2))		1		1		
X	642794	Influenza A virus (A/Auckland/1/2009(H1N1))				1		1
	444793	Influenza A virus (A/Auckland/590/2000(H1N1))		1		1		
	359921	Influenza A virus (A/Australian shelduck/Western Australia/1756/1983(H15N2))	1		1			
	385630	Influenza A virus (A/Bangkok/1/1979(H3N2))	2	4	2	4		
	223931	Influenza A virus (A/Bangkok/10/1983(H1N1))		1		1		
X	388041	Influenza A virus (A/bar-headed goose/Qinghai/1A/2005(H5N1))			1		1	
	336238	Influenza A virus (A/Bar-headed Goose/Qinghai/61/05(H5N1))		8		8		
	647096	Influenza A virus (A/Beijing/01/2009(H1N1))		21		21		
	384500	Influenza A virus (A/Beijing/11/1956(H1N1))		22		22		
	518922	Influenza A virus (A/Beijing/262/1995(H1N1))	1		1			
	380950	Influenza A virus (A/Beijing/32/1992(H3N2))		54		54		
	648856	Influenza A virus (A/Beijing/501/2009(H1N1))	1		1			
	304883	Influenza A virus (A/Belfast/53582/2004(H3N?))		2		2		
	1086859	Influenza A virus (A/Bilthoven/4791/1981(H3N2))		3		3		
	336092	Influenza A virus (A/black-headed goose/Qinghai/1/2005(H5N1))	2		2			
	88776	Influenza A virus (A/Brevig Mission/1/1918(H1N1))	1		1	1		1
	504904	Influenza A virus (A/Brisbane/59/2007(H1N1))		12		12		
	385587	Influenza A virus (A/budgerigar/Hokkaido/1/1977(H4N6))		4		4		
	641501	Influenza A virus (A/California/04/2009(H1N1))	57	72	60	93	3	21
	641809	Influenza A virus (A/California/07/2009(H1N1))	1	6	3	8	2	2
X	425557	Influenza A virus (A/California/10/1978(H1N1))				1		1
	352963	Influenza A virus (A/California/7/2004(H3N2))		1		1		
	387191	Influenza A virus (A/camel/Mongolia/1982(H1N1))		8		8		
	402518	Influenza A virus (A/Canada/rv504/2004(H7N3))	1		1			
	205946	Influenza A virus (A/Chicken/Beijing/1/95(H9N2))		1		1		

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	404137	Influenza A virus (A/chicken/Beijing/nl/2002(H9N2))		1		1		
	36418	Influenza A virus (A/chicken/Brescia/1902(H7N7))		1		1		
	342137	Influenza A virus (A/chicken/CA/375TR/2002(H6N2))		1		1		
	196462	Influenza A virus (A/chicken/California/1002a/00(H6N2))	1	1	1	1		
	11384	Influenza A virus (A/chicken/FPV/Weybridge(H7N7))		1		1		
	329593	Influenza A virus (A/chicken/Fujian/25/00(H9N2))		5		5		
	197579	Influenza A virus (A/Chicken/Guangdong/11/97(H9N2))		1		1		
	407418	Influenza A virus (A/chicken/Guiyang/2147/2005(H5N1))		1		1		
	435359	Influenza A virus (A/chicken/Hebei/706/2005(H5N1))		1		1		
	357205	Influenza A virus (A/chicken/Hong Kong/3123.1/2002(H5N1))		1		1		
	97353	Influenza A virus (A/Chicken/Hong Kong/739/94(H9N2))		1		1		
	97348	Influenza A virus (A/Chicken/Hong Kong/G23/97(H9N2))		1		1		
	292039	Influenza A virus (A/chicken/HongKong/SF1/03(H9N2))	1		1			
	292045	Influenza A virus (A/chicken/HongKong/YU427/03(H9N2))	1		1			
X	932622	Influenza A virus (A/chicken/Huadong/4/2008(H5N1))			1		1	
	404150	Influenza A virus (A/chicken/Hubei/wk/1997(H5N1))		2		2		
	404155	Influenza A virus (A/chicken/Hunan/fg/2004(H5N1))		2		2		
	680729	Influenza A virus (A/chicken/Italy/1067/1999(H7N1))		17		17		
	447133	Influenza A virus (A/chicken/Japan/1925(H7N7))	1		1			
	404163	Influenza A virus (A/chicken/Jilin/hg/2002(H5N1))		1		1		
	300750	Influenza A virus (A/chicken/Korea/S1/2003(H9N2))		1		1		
	342221	Influenza A virus (A/chicken/Korea/S4/2003(H9N2))		1		1		
	298713	Influenza A virus (A/chicken/Korea/SNU0091/00(H9N2))		1		1		
	298716	Influenza A virus (A/chicken/Korea/SNU1035C/00(H9N2))		1		1		
X	376721	Influenza A virus (A/chicken/Kurgan/05/2005(H5N1))			1		1	
	680739	Influenza A virus (A/chicken/Mexico/37821-771/1996(H5N2))		1		1		
	270490	Influenza A virus (A/chicken/Nakorn-Patom/Thailand/CU-K3/2004(H5N1))		1		1		
	215862	Influenza A virus (A/Chicken/Nanchang/2-220/2001(H3N6))		1		1		
	404573	Influenza A virus (A/chicken/Netherlands/03010132/03(H7N7))	1		1			
	89169	Influenza A virus (A/Chicken/Pennsylvania/13552-1/98 (H7N2NSB))	1		1			
	385617	Influenza A virus (A/chicken/Pennsylvania/1370/1983(H5N2))	1		1			
	392810	Influenza A virus (A/chicken/Rostock/8/1934(H7N1))	2	4	2	4		
	402527	Influenza A virus (A/chicken/Scotland/1959(H5N1))		1		1		
	197585	Influenza A virus (A/chicken/Shandong/6/96(H9N2))	1		1			
	183741	Influenza A virus (A/Chicken/Shanghai/F/98(H9N2))	1		1			
X	404408	Influenza A virus (A/chicken/Shanxi/2/2006(H5N1))			1		1	
X	371214	Influenza A virus (A/chicken/Taiwan/0329/01(H6N1))			5		5	
X	449656	Influenza A virus (A/chicken/Taiwan/2838V/00(H6N1))			14		14	
	264510	Influenza A virus (A/chicken/Thailand/LV1NF/2004(H5N1))		1		1		
	393548	Influenza A virus (A/chicken/Tula/Russia/Oct-5/2005(H5N1))		1		1		
	768647	Influenza A virus (A/chicken/Uchal/8286/2006(H9N2))		1		1		
	768646	Influenza A virus (A/chicken/Uchal/8293/2006(H9N2))		1		1		
	299730	Influenza A virus (A/chicken/Viet Nam/AG-010/2004(H5N1))		1		1		
	380836	Influenza A virus (A/chicken/Vietnam/5/2003(H5N1))		1		1		
	365129	Influenza A virus (A/chicken/Vietnam/DT171/2004(H5N1))		1		1		
	380985	Influenza A virus (A/Chile/1/1983(H1N1))		1		1		
	62541	Influenza A virus (A/Christchurch/2/1988(H3N2))		1		1		
	514193	Influenza A virus (A/CHU/2-524/2005(H3N2))		2		2		
	284168	Influenza A virus (A/Ck/HK/2133.1/2003(H5N1))		1		1		
	354235	Influenza A virus (A/Ck/HK/CSW161/2003(H9N2))		1		1		
	284195	Influenza A virus (A/Ck/YN/115/2004(H5N1))		1		1		

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	107493	Influenza A virus (A/Cordoba/3278/96(H3N2))		1		1		
	320306	Influenza A virus (A/crested eagle/Belgium/01/2004(H5N1))	2		2			
	291592	Influenza A virus (A/crow/Kyoto/53/2004(H5N1))	1		1			
	504697	Influenza A virus (A/Cygnus olor/Czech Republic/10732/07(H5N1))		1		1		
	385583	Influenza A virus (A/Denver/1957(H1N1))		2		2		
	284202	Influenza A virus (A/Dk/ST/5048/2001(H3N8))	1		1			
	88297	Influenza A virus (A/duck/Bavaria/1/1977 (H1N1))		2		2		
	658578	Influenza A virus (A/duck/Beijing/MG0617/2005(H9N2))		1		1		
	383550	Influenza A virus (A/duck/England/1/1956(H11N6))		1		1		
	274829	Influenza A virus (A/duck/Fujian/17/2001(H5N1))		1		1		
	365078	Influenza A virus (A/duck/Guangxi/1586/2004(H5N1))		1		1		
	365080	Influenza A virus (A/duck/Guangxi/1793/2004(H5N1))		1		1		
	395841	Influenza A virus (A/duck/Hokkaido/1130/01(H1N1))		1		1		
	249372	Influenza A virus (A/duck/Hokkaido/13/00(H9N2))	2		2			
	387207	Influenza A virus (A/duck/Hokkaido/8/1980(H3N8))		6		6		
	183783	Influenza A virus (A/duck/Hong Kong/3096/99(H6N2))		1		1		
	176672	Influenza A virus (A/Duck/Hong Kong/ww461/2000(H5N1))		1		1		
	384946	Influenza A virus (A/duck/Hungary/1/1970(H6N2))		1		1		
	370813	Influenza A virus (A/duck/IT/701/2005(H10N7))		1		1		
	311169	Influenza A virus (A/duck/Korea/S10/03(H3N2))		1		1		
	441962	Influenza A virus (A/duck/Mongolia/47/2001(H7N1))		3		3		
	353253	Influenza A virus (A/duck/Novosibirsk/56/2005(H5N1))	6	2	6	2		
X	352034	Influenza A virus (A/duck/Potsdam/1402-6/1986(H5N2))			1		1	
	210656	Influenza A virus (A/Duck/Shantou/1881/00(H9N2))		1		1		
	210659	Influenza A virus (A/Duck/Shantou/2088/01(H9N2))		1		1		
	210663	Influenza A virus (A/Duck/Shantou/2134/00(H9N2))		1		1		
	210655	Influenza A virus (A/Duck/Shantou/2144/00(H9N2))		1		1		
X	447188	Influenza A virus (A/duck/Tasmania/277/2007(H7N2))			1		1	
	385580	Influenza A virus (A/duck/Ukraine/1/1963(H3N8))	3		3			
	380842	Influenza A virus (A/duck/Vietnam/15/2003(H5N1))		1		1		
	496036	Influenza A virus (A/duck/Vietnam/37/2007(H5N1))		1		1		
	279797	Influenza A virus (A/egret/Hong Kong/757.3/2002(H5N1))		3		3		
	421901	Influenza A virus (A/Egypt/0636-NAMRU3/2007(H5N1))	2	1	2	1		
	418868	Influenza A virus (A/Egypt/14724-NAMRU3/2006(H5N1))	1		1			
	562988	Influenza A virus (A/Egypt/2289-NAMRU3/2008(H5N1))	1		1			
	562992	Influenza A virus (A/Egypt/3300-NAMRU3/2008(H5N1))	1		1			
	192549	Influenza A virus (A/Egypt/96/2002(H1N2))		1		1		
	380284	Influenza A virus (A/England/268/1996(H7N7))	1		1			
	380210	Influenza A virus (A/England/333/1980(H1N1))	1	1	1	1		
	198059	Influenza A virus (A/England/627/01(H1N2))		2		2		
	573797	Influenza A virus (A/England/654/2007(H1N1))		1		1		
	387147	Influenza A virus (A/England/878/1969(H3N2))	1	2	1	2		
	137578	Influenza A virus (A/England/939/69 x A/PR/8/34)		2		2		
	135661	Influenza A virus (A/environment/Hong Kong/437-10/99 (H5N1))		1		1		
	680789	Influenza A virus (A/environment/Viet Nam/1203/2004(H5N1))	1		1			
	387213	Influenza A virus (A/equine/Alaska/1/1991(H3N8))		1		1		
	475493	Influenza A virus (A/equine/California/8560/2002(H3N8))		2		2		
	385585	Influenza A virus (A/equine/Jilin/1/1989(H3N8))	1		1			
	380340	Influenza A virus (A/equine/London/1416/1973(H7N7))	1		1			
	336794	Influenza A virus (A/equine/Massachussetts/213/2003(H3N8))		1		1		
	387223	Influenza A virus (A/equine/Miami/1963(H3N8))	5		5			

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	336800	Influenza A virus (A/equine/New York/1/1999(H3N8))		3		3		
	225089	Influenza A virus (A/equine/NewMarket/D64/79(H3N8))		1		1		
	380339	Influenza A virus (A/equine/Tennessee/5/1986(H3N8))		1		1		
	578079	Influenza A virus (A/ferret/Maryland/P10-UMD/2008(H9N2))		1		1		
	207401	Influenza A virus (A/finch/Canada/NS1301/2001(H3N8))		2		2		
	367120	Influenza A virus (A/Fort Monmouth/1/1947(H1N1))	1		1			
	380282	Influenza A virus (A/Fort Monmouth/1/1947-mouse adapted(H1N1))		24		24		
	260806	Influenza A virus (A/FPV/Dutch/1927(H7N7))	1		1			
	107558	Influenza A virus (A/France/75/97(H3N2))		1		1		
X	293090	Influenza A virus (A/Fujian/411/2002(H3N2))				1		1
	62549	Influenza A virus (A/Fukuoka/C29/1985(H3N2))	5		5			
	354228	Influenza A virus (A/Gf/HK/SSP607/2003(H9N2))		1		1		
	93838	Influenza A virus (A/goose/Guangdong/1/1996(H5N1))		5		5		
	165512	Influenza A virus (A/goose/Guangdong/3/1997(H5N1))	3	1	3	1		
	182781	Influenza A virus (A/Goose/Hong Kong/385.3/2000(H5N1))		1		1		
	680799	Influenza A virus (A/goose/Hong Kong/437-6/1999(H5N1))		1		1		
	680803	Influenza A virus (A/goose/Hong Kong/739.2/2002(H5N1))		1		1		
	380330	Influenza A virus (A/goose/Hong Kong/8/1976(H1N1))		2		2		
	402464	Influenza A virus (A/gray teal/Australia/2/1979(H4N4))		1		1		
	1041990	Influenza A virus (A/Guangdong/15/2007(H3N2))	3		3			
	387239	Influenza A virus (A/gull/Delaware/475/1986(H2N2))		1		1		
	384499	Influenza A virus (A/gull/Maryland/704/1977(H13N6))		1		1		
	387156	Influenza A virus (A/Harbin/1/1988(H1N2))		11		11		
	303316	Influenza A virus (A/Hatay/2004/(H5N1))	3		3			
	380951	Influenza A virus (A/Hebei/19/1995(H3N2))	1		1			
	387243	Influenza A virus (A/herring gull/DE/677/1988(H2N8))		1		1		
	462695	Influenza A virus (A/Hiroshima/52/2005(H3))	2		2			
	223947	Influenza A virus (A/Hokkaido/20/89(H3N2))		2		2		
X	645724	Influenza A virus (A/Hong Kong/01/2009(H1N1))			3		3	
	506350	Influenza A virus (A/Hong Kong/1/1968(H3N2))	2	2	7	2	5	
	130760	Influenza A virus (A/Hong Kong/1073/99(H9N2))	1	25	1	25		
	130761	Influenza A virus (A/Hong Kong/1074/99(H9N2))	2	1	2	1		
	164326	Influenza A virus (A/Hong Kong/1131/1998(H1N1))	1	1	1	1		
	162326	Influenza A virus (A/Hong Kong/1143/99(H3N2))	1		1			
	130763	Influenza A virus (A/Hong Kong/156/97(H5N1))	2	26	2	26		
	231851	Influenza A virus (A/Hong Kong/1774/99(H3N2))		1		1		
	317652	Influenza A virus (A/Hong Kong/2/68(H3N2))		4		4		
	657165	Influenza A virus (A/Hong Kong/213/03)	2	2	2	2		
	432070	Influenza A virus (A/Hong Kong/213/2003(H5N1))	1	4	1	4		
	155218	Influenza A virus (A/Hong Kong/482/97(H5N1))	7	1	7	1		
	88104	Influenza A virus (A/Hong Kong/483/1997(H5N1))	2	10	3	10	1	
	680692	Influenza A virus (A/Hong Kong/485/1997(H5N1))	1	1	1	1		
	155222	Influenza A virus (A/Hong Kong/488/97(H5N1))		1		1		
	155225	Influenza A virus (A/Hong Kong/507/97(H5N1))		5		5		
	155226	Influenza A virus (A/Hong Kong/514/97(H5N1))		2		2		
	155227	Influenza A virus (A/Hong Kong/516/97(H5N1))		2		2		
	88103	Influenza A virus (A/Hong Kong/532/1997(H5N1))		1		1		
	155220	Influenza A virus (A/Hong Kong/542/97(H5N1))	1		1			
	446023	Influenza A virus (A/Hong Kong/68(H3N2))	1		1			
	499286	Influenza A virus (A/Hong Kong/CUHK13527/2003(H3N2))		1		1		
X	1081253	Influenza A virus (A/Indiana/08/2011(H3N2))				6		6

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	400788	Influenza A virus (A/Indonesia/5/2005(H5N1))	1	2	1	2		
	468968	Influenza A virus (A/Indonesia/560H/2006(H5N1))	1		1			
	421472	Influenza A virus (A/Indonesia/CDC1032N/2007(H5N1))	1		1			
	400810	Influenza A virus (A/Indonesia/CDC594/2006(H5N1))	1		1			
	400828	Influenza A virus (A/Indonesia/CDC669/2006(H5N1))	2		2			
	400830	Influenza A virus (A/Indonesia/CDC699/2006(H5N1))	2		2			
	472511	Influenza A virus (A/Indonesia/TLL007/2006(H5N1))	1		1			
X	488233	Influenza A virus (A/Iran/1/1957(H2N2))				1		1
	402194	Influenza A virus (A/Istanbul/CTF/10/2004(H3N2))		1		1		
	387161	Influenza A virus (A/Japan/305/1957(H2N2))	2	28	4	29	2	1
X	382813	Influenza A virus (A/Japan/305+/1957(H2N2))			2		2	
	307819	Influenza A virus (A/Jiangsu/38/2004(H3N2))		1		1		
	203126	Influenza A virus (A/Kamata/14/91(H3N2))	1		1			
	154540	Influenza A virus (A/Kayano/57(H2N2))		1		1		
	384495	Influenza A virus (A/Kiev/59/1979(H1N1))		1		1		
	327310	Influenza A virus (A/Kinmen/645/04(H3N2))		1		1		
	225088	Influenza A virus (A/Kitakyushu/159/93(H3N2))		1		1		
	62478	Influenza A virus (A/Kitakyushu/93(H3N2))		1		1		
X	644289	Influenza A virus (A/Korea/01/2009(H1N1))			1		1	
	488241	Influenza A virus (A/Korea/426/1968(H2N2))		1		1		
	436004	Influenza A virus (A/kunke/1/71(H3N2))		1		1		
	393557	Influenza A virus (A/Leningrad/1954/1(H1N1))		4		4		
	393697	Influenza A virus (A/Liaoning/25/2000(H1N1))		1		1		
	62559	Influenza A virus (A/Los Angeles/1987(H3N2))	5		5			
	95888	Influenza A virus (A/mallard duck/PA/10218/84(H5N2))	8		8			
	282124	Influenza A virus (A/mallard/Alberta/127/00(H3N8))		1		1		
	352764	Influenza A virus (A/mallard/Alberta/202/1996(H2N5))	1		1			
	352520	Influenza A virus (A/mallard/Alberta/35/1976(H1N1))		2		2		
	352564	Influenza A virus (A/mallard/Astrakhan/263/1982(H14N5))	1		1			
	185794	Influenza A virus (A/mallard/NZ/1/97(H5N2))		1		1		
	293055	Influenza A virus (A/mallard/Ohio/556/1987(H5N9))		1		1		
	655288	Influenza A virus (A/mallard/Quebec/10969/2006(H2N3))		1		1		
	383586	Influenza A virus (A/Memphis/1/1971(H3N2))	19	11	19	11		
	378139	Influenza A virus (A/Memphis/1/1978(H1N1))		5		5		
	383577	Influenza A virus (A/Memphis/1/1990(H3N2))		1		1		
	79695	Influenza A virus (A/Memphis/1/71H-A/Bellamy/42N)		1		1		
	416730	Influenza A virus (A/Memphis/10/1996(H1N1))		1		1		
	385640	Influenza A virus (A/Memphis/102/1972(H3N2))		8		8		
X	378131	Influenza A virus (A/Memphis/13/1978(H1N1))				1		1
	383574	Influenza A virus (A/Memphis/2/1985(H3N2))	1		1			
	228928	Influenza A virus (A/Memphis/31/98(H3N2))	6		6			
X	383578	Influenza A virus (A/Memphis/4/1980(H3N2))				1		1
	383571	Influenza A virus (A/Memphis/6/1986(H3N2))	4		4			
	402938	Influenza A virus (A/Michigan/2/2003(H1N2))	1		1			
	480019	Influenza A virus (A/Moscow/10/1999(H3N2))		2		2		
	334590	Influenza A virus (A/Moscow/343/2003(H3N2))		1		1		
	389259	Influenza A virus (A/Nagasaki/N03/2005(H3N2))		1		1		
	62488	Influenza A virus (A/Nanchang/58/1993(H3N2))		1		1		
	936115	Influenza A virus (A/Netherlands/18/1994(H3N2))		1		1		
X	680693	Influenza A virus (A/Netherlands/219/2003(H7N7))			1		1	
	132884	Influenza A virus (A/Netherlands/458/98 (H3N2))		1		1		
X	643212	Influenza A virus (A/Netherlands/602/2009(H1N1))				14		14

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	132783	Influenza A virus (A/Netherlands/626/89 (H3N2))		1		1		
	132841	Influenza A virus (A/Netherlands/785e/90 (H3N2))		1		1		
	381512	Influenza A virus (A/New Caledonia/20/1999(H1N1))	3	187	3	214		27
	311695	Influenza A virus (A/New York/124/2001(H3N2))		1		1		
	311775	Influenza A virus (A/New York/205/2001(H1N1))		10		10		
	335358	Influenza A virus (A/New York/232/2004(H3N2))		110		110		
	327205	Influenza A virus (A/New York/348/2003(H1N1))		121		122		1
	335333	Influenza A virus (A/New York/384/2005(H3N2))		61		62		1
	335337	Influenza A virus (A/New York/388/2005(H3N2))		14		14		
	342508	Influenza A virus (A/New York/444/2001(H1N1))		24		24		
	364132	Influenza A virus (A/New York/504/1998(H3N2))		1		1		
	383028	Influenza A virus (A/New York/687/1995(H3N2))	1		1			
	62564	Influenza A virus (A/New_York/15/94(H3N2))		1		1		
	62496	Influenza A virus (A/New_York/17/94(H3N2))		1		1		
	370128	Influenza A virus (A/Northern Territory/60/1968(H3N2))		1		1		
	384505	Influenza A virus (A/nt/60/1968(H3N2))		67		67		
	155917	Influenza A virus (A/NWS/33HA-A/tern/Australia/G70C/75NA(H1N9))	1		1			
	382820	Influenza A virus (A/NWS/G70C(H1N9))	1		1			
	62503	Influenza A virus (A/Ohio/3/95(H3N2))		1		1		
	1163697	Influenza A virus (A/Oklahoma/309/2006(H3N2))		3	4	3	4	
	223935	Influenza A virus (A/Okuda/57(H2N2))	1	9	1	9		
	754366	Influenza A virus (A/Ontario/309862/2009(H1N1))	1		1			
X	383281	Influenza A virus (A/Otago/5/2005(H1N1))				1		1
	381513	Influenza A virus (A/Panama/2007/1999(H3N2))	10	14	10	14		
	137885	Influenza A virus (A/parakeet/Chiba/1/97(H9N2))		3		3		
	137886	Influenza A virus (A/parakeet/Narita/92A/98(H9N2))		2		2		
	11448	Influenza A virus (A/parrot/Ulster/73(H7N1))		1		1		
X	654811	Influenza A virus (A/Perth/16/2009(H3N2))			1		1	
	385624	Influenza A virus (A/Port Chalmers/1/1973(H3N2))	7	1	7	1		
	385600	Influenza A virus (A/Puerto Rico/8/1934(Cambridge)(H1N1))	1		1			
	211044	Influenza A virus (A/Puerto Rico/8/1934(H1N1))	24	418	26	422	2	4
	183764	Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))	7	88	7	88		
	89172	Influenza A virus (A/quail/Arkansas/16309-7/94 (H7N3NSA))	1		1			
	216877	Influenza A virus (A/quail/Hong Kong/FY298/00(H9N2))		4		4		
	183778	Influenza A virus (A/quail/Hong Kong/SF550/00(H6N1))		2		2		
	197589	Influenza A virus (A/Quail/Shanghai/8/96(H9N2))		1		1		
	417758	Influenza A virus (A/quail/Shantou/1475/2004(H9N2))	1		1			
	411167	Influenza A virus (A/Queensland/11/2001(H3N2))		1		1		
	286239	Influenza A virus (A/red knot/Delaware/2561/87(H10N5))		1		1		
	382828	Influenza A virus (A/RI/5-/1957(H2N2))		1		1		
	221012	Influenza A virus (A/Rio/6/69(H3N2))		1		1		
	142948	Influenza A virus (A/ruddy turnstone/Delaware/67/1998(H12N4))		1		1		
	380343	Influenza A virus (A/ruddy turnstone/New Jersey/47/1985(H4N6))		2		2		
	385616	Influenza A virus (A/ruddy turnstone/NJ/60/1985(N9))		1		1		
	192720	Influenza A virus (A/Saudi Arabia/2581/2001(H1N2))		1		1		
	192535	Influenza A virus (A/Saudi Arabia/7971/2000(H1N1))		1		1		
	384493	Influenza A virus (A/seal/Mass/1/1980(H7N7))	1	1	1	1		
	62512	Influenza A virus (A/Shangdong/5/94(H3N2))		1		1		
	380948	Influenza A virus (A/Shangdong/9/1993(H3N2))	13		13			
	383568	Influenza A virus (A/Shanghai/11/1987(H3N2))		1		1		
	1093545	Influenza A virus (A/shorebird/Delaware Bay/277/2000(H9N7))		1		1		

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	342207	Influenza A virus (A/shorebird/Delaware/141/2002(H9N9))		1		1		
	342210	Influenza A virus (A/shorebird/Delaware/275/2001(H9N7))		1		1		
	62575	Influenza A virus (A/Sichuan/2/1987(H3N2))		4		4		
	382781	Influenza A virus (A/Singapore/1/1957(H2N2))	1	30	1	30		
	742305	Influenza A virus (A/slaty-backed gull/Japan/6KS0185/2006(H4N8))		1		1		
	464623	Influenza A virus (A/Solomon Islands/3/2006(H1N1))	1		2		1	
	59375	Influenza A virus (A/South Carolina/1/1918(H1N1))	4	1	6	1	2	
	177131	Influenza A virus (A/SW/KS/13481-T/00(H1N2))		1		1		
	177128	Influenza A virus (A/SW/MN/12883/00(H1N2))		2		2		
	177188	Influenza A virus (A/SW/MN/3227/00(H1N2))		1		1		
	382842	Influenza A virus (A/swine/29/1937(H1N1))		2		2		
	336207	Influenza A virus (A/swine/Bakum/1832/00(H1N2))		3		3		
	336205	Influenza A virus (A/swine/Bakum/5/95(H1N1))		2		2		
	256045	Influenza A virus (A/swine/Chiai/77-10/2001(H3N1))		1		1		
	136474	Influenza A virus (A/Swine/Colorado/23619/99(H3N2))		1		1		
	169169	Influenza A virus (A/swine/Cotes d'Armor/1482/1999(H1N1))		1		1		
	158306	Influenza A virus (A/swine/Cotes d'Armor/800/00(H1N2))		1		1		
	1068705	Influenza A virus (A/swine/Guangdong/221/2009(H1N1))		1		1		
	522740	Influenza A virus (A/swine/Hannover/1/1981(H1N1))		6		6		
	145306	Influenza A virus (A/swine/Hong Kong/10/98(H9N2))	5		5			
	382848	Influenza A virus (A/swine/Hong Kong/126/1982(H3N2))		1		1		
	384483	Influenza A virus (A/swine/Hong Kong/127/1982(H3N2))		1		1		
	173473	Influenza A virus (A/swine/Hong Kong/2106/98(H9N2))		2		2		
	380332	Influenza A virus (A/swine/Hong Kong/273/1994(H1N1))		1		1		
	173477	Influenza A virus (A/swine/Hong Kong/3297/98(H9N2))		3		3		
	380217	Influenza A virus (A/swine/Hong Kong/4/1976(H3N2))		1		1		
	253682	Influenza A virus (A/swine/Hong Kong/5190/99(H3N2))		3		3		
	991335	Influenza A virus (A/swine/Hong Kong/71/2009(H1N1))		1		1		
	384484	Influenza A virus (A/swine/Hong Kong/81/1978(H3N2))		11		11		
	145307	Influenza A virus (A/swine/Hong Kong/9/98(H9N2))	2		2			
	253691	Influenza A virus (A/swine/Hong Kong/9840/01(H3N2))		1		1		
	306061	Influenza A virus (A/swine/IDT/Bakum1832/2000(H1N2))		1		1		
	384487	Influenza A virus (A/Swine/Indiana/1726/1988(H1N1))		2		2		
	128982	Influenza A virus (A/Swine/Indiana/9K035/99 (H1N2))		2		2		
	161502	Influenza A virus (A/swine/Italy/1509-6/97(H1N1))		12		12		
	164042	Influenza A virus (A/Swine/Italy/1513-1/98(H1N1))		1		1		
	169166	Influenza A virus (A/swine/Italy/1521/98(H1N2))		2		2		
	170342	Influenza A virus (A/swine/Italy/1654-1/99(H1N2))		1		1		
	383561	Influenza A virus (A/swine/Italy/1850/1977(H3N2))		1		1		
	383531	Influenza A virus (A/swine/Italy/2/1979(H1N1))		3		3		
	147095	Influenza A virus (A/Swine/Italy/25823/94(H3N2))		2		2		
	383566	Influenza A virus (A/swine/Italy/425/1976(H1N1))		1		1		
	383564	Influenza A virus (A/swine/Italy/547/1985(H1N1))		3		3		
	383558	Influenza A virus (A/swine/Italy/809/1989(H3N2))		1		1		
	538555	Influenza A virus (A/swine/Korea/Hongsong2/2004(H1N2))		2		2		
	300748	Influenza A virus (A/swine/Korea/S190/2004(H9N2))		3		3		
X	300749	Influenza A virus (A/swine/Korea/S452/2004(H9N2))				1		1
	187164	Influenza A virus (A/Swine/Minnesota/55551/2000(H1N2))		1		1		
	426738	Influenza A virus (A/swine/Miyagi/5/2003(H1N2))		2		2		
	186460	Influenza A virus (A/swine/New Jersey/11/1976(H1N1))	1		1			
	515581	Influenza A virus (A/swine/Ohio/24366/2007(H1N1))		1		1		

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	172149	Influenza A virus (A/swine/Quebec/192/81(H1N1))	1		1			
	83206	Influenza A virus (A/swine/Scotland/410440/94(H1N2))		3		3		
	332747	Influenza A virus (A/swine/Tennessee/25/1977(H1N1))	1		1			
	385644	Influenza A virus (A/swine/Ukkel/1/1984(H3N2))		1		1		
	82372	Influenza A virus (A/Sydney/05/97-like(H3N2))		1		1		
	587884	Influenza A virus (A/Sydney/5/1997(H3N2))	7		7			
	380213	Influenza A virus (A/Taiwan/1/1986(H1N1))		1		1		
	371082	Influenza A virus (A/Taiwan/2/2006(H1N1))		8		8		
	560463	Influenza A virus (A/Taiwan/VGHYM0325-06/2002(H3N2))		1		1		
	395842	Influenza A virus (A/tern/Australia/1/04(H2N5))		1		1		
	405050	Influenza A virus (A/tern/Australia/1402/2004(H2N5))		1		1		
	384509	Influenza A virus (A/tern/Australia/G70C/1975(H11N9))	10		10			
	384510	Influenza A virus (A/tern/South Africa/1961(H5N3))	1		1			
	641812	Influenza A virus (A/Texas/05/2009(H1N1))	1		1			
	444318	Influenza A virus (A/Texas/1/1977(H3N2))	1	14	1	14		
	414044	Influenza A virus (A/Thailand/1(KAN-1A)/2004(H5N1))	1		1			
	411157	Influenza A virus (A/Thailand/271/2005(H1N1))	1		1			
	270945	Influenza A virus (A/Thailand/4(SP-528)/2004(H5N1))		20		21		1
	427773	Influenza A virus (A/Thailand/SP83/2004(H5N1))	1		1			
	270484	Influenza A virus (A/tiger/Thailand/CU-LV/2004(H5N1))		2		2		
	322564	Influenza A virus (A/tiger/Thailand/CU-T4/04(H5N1))		6		6		
	322566	Influenza A virus (A/tiger/Thailand/CU-T6/04(H5N1))		1		1		
	225071	Influenza A virus (A/Tokyo/1566/98(H3N2))		1		1		
	342396	Influenza A virus (A/turkey/Canada-Ontario/NS-01839-1/05(H3))		1		1		
X	511839	Influenza A virus (A/turkey/England/N28/1973(H5N2))			1		1	
	380285	Influenza A virus (A/turkey/Ireland/1378/1983(H5N8))		1		1		
	402489	Influenza A virus (A/turkey/Minnesota/1200/1980(H7N3))		1		1		
	1342434	Influenza A virus (A/turkey/Minnesota/511/1978(H9N2))		2		2		
	383603	Influenza A virus (A/turkey/Minnesota/833/1980(H4N2))		1		1		
	342145	Influenza A virus (A/turkey/MN/735/79(H6N2))		2		2		
	165420	Influenza A virus (A/Turkey/MO/24093/99(H1N2))		5		5		
	533026	Influenza A virus (A/turkey/Ohio/313053/2004(H3N2))		3		3		
	293054	Influenza A virus (A/turkey/Ontario/6213/66(H5N?))	1		1			
	380301	Influenza A virus (A/turkey/Ontario/7732/1966(H5N9))	5	6	5	6		
	380299	Influenza A virus (A/turkey/Wisconsin/1968(H5N9))		1		1		
	385599	Influenza A virus (A/udorn/1972(H3N2))		1		1		
	381517	Influenza A virus (A/Udorn/307/1972(H3N2))		4		5		1
	392811	Influenza A virus (A/Udorn/8/1972(H3N2))	1		1			
	506282	Influenza A virus (A/unknown/New York/11646-5/2005(H7N2))	1		1			
	62596	Influenza A virus (A/USSR/26/1985(H3N2))		1		1		
	381516	Influenza A virus (A/USSR/90/1977(H1N1))	11		11			
	370127	Influenza A virus (A/Victoria/1968(H3N2))		1		1		
	392809	Influenza A virus (A/Victoria/3/1975(H3N2))	44	8	44	8		
	284218	Influenza A virus (A/Viet Nam/1203/2004(H5N1))	60	115	62	115	2	
	299390	Influenza A virus (A/Viet Nam/HN/2004(H5N1))		6		6		
	427890	Influenza A virus (A/Viet Nam/JP4207/2005(H5N1))	1		1			
	644788	Influenza A virus (A/Vietnam/1194/2004(H5N1))	5	4	7	4	2	
	357210	Influenza A virus (A/Vietnam/CL100/2004(H5N1))	1		1			
	357208	Influenza A virus (A/Vietnam/CL26/2004(H5N1))		78		78		
	382832	Influenza A virus (A/VM113-V1(H1N1))	1		1			
	383121	Influenza A virus (A/Waikato/7/2000(H3N2))		2		2		
	191090	Influenza A virus (A/Weiss/1943(H1N1))		1		1		

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	383152	Influenza A virus (A/Wellington/22/2001(H3N2))		1		1		
	383231	Influenza A virus (A/Wellington/8/2004(H3N2))		2		2		
	11484	Influenza A virus (A/whale/Maine/1/84(H13N9))	3		3			
	344598	Influenza A virus (A/whooper swan/Mongolia/6/05(H5N1))		1		1		
	381518	Influenza A virus (A/Wilson-Smith/1933(H1N1))		109		110		1
	380346	Influenza A virus (A/Wisconsin/3523/1988(H1N1))	2		2			
	461772	Influenza A virus (A/Wisconsin/43/2006(H3N2))	1		1			
	380978	Influenza A virus (A/Wisconsin/4755/1994(H1N1))		6		6		
	393902	Influenza A virus (A/Wisconsin/67/2005(H3N2))		4	1	5	1	1
	382835	Influenza A virus (A/WSN/1933(H1N1))	6	3	6	3		
	63106	Influenza A virus (A/Wuhan/359/1995(H3N2))	5		5			
	480024	Influenza A virus (A/Wyoming/03/2003(H3N2))		7		7		
	432094	Influenza A virus (A/Wyoming/3/2003-X-147(H3N2))		1		1		
	430417	Influenza A virus (A/Wyoming/3e5/2003(H3))	1		1			
	132504	Influenza A virus (A/X-31(H3N2))	78	173	78	173		
	380905	Influenza A virus (A/X-47(H3N2))	3	2	3	2		
	577543	Influenza A virus (A/Xinjiang/1/2006(H5N1))	4		4			
	327311	Influenza A virus (A/Yilan/515/03(H3N2))		1		1		
	255681	Influenza A virus (A/Yokohama/22/2002(H1N2))		2		2		
	11408	Influenza A virus (STRAIN A/EQUINE/NEW MARKET/76)		1		1		
	55532	Influenza A virus (strain A/SW/Quebec/1192/1986)		1		1		
	168278	Influenza A virus (swine/Finistere/127/99(H3N2))		4		4		
	41857	Influenza A virus H3N2	1	38	1	40		2
	10000865	Influenza A virus H3N2 (A/Kiev/301/94)	3		3			
	10000550	Influenza A virus H3N2 (A/Netherlands/9/03 (H3N2))		1		1		
	10000474	Influenza A virus H3N2 (A/Resvir-9 (H3N2))		10		10		
X	35322	Influenza A virus H3N8			1		1	
	415166	Influenza A virus(A/swine/Henan/2/2004(H9N2))		1		1		
	415167	Influenza A virus(A/swine/Henan/3/2004(H9N2))		2		2		
	415169	Influenza A virus(A/swine/Henan/5/2004(H9N2))		1		1		
	415172	Influenza A virus(A/swine/Henan/8/2004(H9N2))		2		2		
	415176	Influenza A virus(A/swine/Shandong/fNY/2003(H9N2))		3		3		
	415177	Influenza A virus(A/swine/Shandong/fZC/2003(H9N2))		7		7		
	11520	Influenza B virus	3	6	3	6		
	11521	Influenza B virus (B/Ann Arbor/1/1986)		3		3		
	107404	Influenza B virus (B/Beijing/184/93)		1		1		
X	604436	Influenza B virus (B/Brisbane/60/2008)			1		1	
	107406	Influenza B virus (B/Chiba/447/98)		1		1		
X	461739	Influenza B virus (B/Florida/4/2006)			1		1	
	206203	Influenza B virus (B/Hong Kong/330/2001)		23		23		
	224964	Influenza B virus (B/Johannesburg/5/99)	1		1			
	184816	Influenza B virus (B/Kadoma/122/99)	2		2			
	256080	Influenza B virus (B/Kobe/1/2003)	1		1			
	504664	Influenza B virus (B/Kobe/113/2005)	1		1			
	504666	Influenza B virus (B/Kobe/115/2005-T1)	1		1			
	503386	Influenza B virus (B/Kobe/3/2004)	1		1			
	504662	Influenza B virus (B/Kobe/39/2005)	1		1			
	504660	Influenza B virus (B/Kobe/67/2005)	1		1			
	171425	Influenza B virus (B/Kobe/87/2001)	1		1			
	107412	Influenza B virus (B/Lee/40)	5	3	5	3		
X	464417	Influenza B virus (B/Malaysia/2506/2004)			1		1	
X	289338	Influenza B virus (B/Nanchang/12/98)				1		1

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	11541	Influenza B virus (B/Oregon/5/80)	16		16			
	150127	Influenza B virus (B/Osaka/983/97-V3)	1		1			
	335812	Influenza B virus (B/Shanghai/361/2002)	1		1			
	1077587	Influenza B virus (B/Victoria/2/1987)	2	1	2	1		
	11531	Influenza B virus (STRAIN B/HONG KONG/8/73)		1		1		
	11532	Influenza B virus (STRAIN B/HT/84)		1		1		
	11552	Influenza C virus		1		1		
	11553	Influenza C virus (C/Ann Arbor/1/50)	9		9			
	9725	Inia geoffrensis		1		1		
	55635	Inula helenium		1		1		
	42097	Isla Vista virus	1	2	1	2		
	261204	Itapua hantavirus		10		10		
	6945	Ixodes scapularis	10		10			
	11072	Japanese encephalitis virus	36	53	36	53		
	10000444	Japanese encephalitis virus CH2195LA	1		1			
	10000445	Japanese encephalitis virus JaOH0566	1		1			
	11075	Japanese encephalitis virus strain JAOARS982	4	4	4	4		
	11076	Japanese encephalitis virus strain Nakayama	2	2	2	2		
	11073	Japanese encephalitis virus strain SA-14	1	1	6	1	5	
	10001648	Japanese encephalitis virus strain SA-14 -14-2	2		2			
	10001335	Japanese encephalitis virus Vellore P20778	1	1	1	1		
	10632	JC polyomavirus	1	5	1	35		30
	10001762	JC polyomavirus strain MAD1		1		1		
	16719	Juglans nigra	1		1			
	51240	Juglans regia	34		34			
	11619	Junin virus	3	871	3	871		
	10001614	Junin virus strain MC2		1		1		
	13101	Juniperus ashei	13		13			
	453927	Juniperus formosana	1		1			
	69008	Juniperus oxycedrus		3		3		
	430511	Juquitiba virus		2		2		
	122291	Kappapapillomavirus 1	2		2			
	10623	Kappapapillomavirus 2	3	7	3	7		
	156230	Karenia brevis	1		1			
	42894	Khabarovsk virus		1		1		
	10638	Kilham polyomavirus		1		1		
	573	Klebsiella pneumoniae	23	6	23	6		
	484021	Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044		1		1		
	11077	Kunjin virus	11	1	11	1		
	11078	Kunjin virus (STRAIN MRM61C)		2		2		
	11577	La Crosse virus	2	1	2	1		
	11578	La Crosse virus L74		2		2		
	8753	Lachesis muta muta	21		21			
	300015	Lactate dehydrogenase elevating virus C	1		1			
	300016	Lactate dehydrogenase elevating virus Plagemann	1		1			
	11048	Lactate dehydrogenase-elevating virus	14		14			
	219334	Lactobacillus casei subsp. casei ATCC 393	2		2			
	1585	Lactobacillus delbrueckii subsp. bulgaricus	1		1			
	10001913	Lactobacillus johnsonii JCM 1022	3		3			
	557433	Lactobacillus reuteri JCM 1112	3		3			
	1358	Lactococcus lactis		2		2		
	100641	Lactococcus lactis phage p2	2		2			

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X	35345	Lactococcus phage TP901-1			3		3	
	9519	Lagothrix lagotricha	1		1			
	61172	Laguna Negra virus		11		11		
	378830	Lake Victoria marburgvirus - Angola2005	4		6	18	2	18
	33728	Lake Victoria marburgvirus - Popp	1	14	1	14		
	35258	Lambdapapillomavirus 2		25		25		
	80365	Laminaria digitata	2		2			
	11085	Langat virus		1		1		
	136371	Lasallia papulosa	1		1			
	11620	Lassa virus	4	633	12	666	8	33
	11621	Lassa virus GA391		45		45		
	11622	Lassa virus Josiah		379		379		
	6925	Latrodectus tredecimguttatus		1		1		
	85223	Laurus nobilis		1		1		
	69245	Lechiguanas virus		5		5		
	446	Legionella pneumophila		1		1		
	272624	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	1		1			
	218308	Lehmannia valentiana	1		1			
	5658	Leishmania	1		2		1	
	5667	Leishmania aethiopica	16		16			
	5659	Leishmania amazonensis		10		10		
	5660	Leishmania braziliensis	6		6			
	420245	Leishmania braziliensis MHOM/BR/75/M2904	3		3			
	44271	Leishmania chagasi	3		3			
	5661	Leishmania donovani	15	38	15	38		
	99875	Leishmania donovani donovani	1		1			
	10000341	Leishmania donovani donovani 1S2D	1		1			
	5671	Leishmania infantum	93	1	93	1		
	435258	Leishmania infantum JPCM5	15		15			
	10000345	Leishmania infantum LEM 75	14		14			
	5664	Leishmania major	16	120	16	124		4
	347515	Leishmania major strain Friedlin	23	14	23	14		
	5665	Leishmania mexicana	2	1	2	3		2
	5679	Leishmania panamensis	3	6	3	6		
	5682	Leishmania pifanoi		20		20		
	11049	Lelystad virus	66	12	66	12		
	9447	Lemur catta	1		1			
	3864	Lens culinaris	19		19			
	36936	Lepidoglyphus destructor	5	10	5	10		
	173	Leptospira interrogans	4	4	4	4		
	44275	Leptospira interrogans serovar Copenhageni	2		2			
	267671	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	11		11			
	57678	Leptospira interrogans serovar Lai	10	10	10	10		
	189518	Leptospira interrogans serovar Lai str. 56601	1		1			
	10000814	Leptospira interrogans serovar Lai str. HY-1	1		1			
	44276	Leptospira interrogans serovar Pomona		3		3		
	10000847	Leptospira sp. Akiyami A AUT10	1		1			
	1245	Leuconostoc mesenteroides	1		1			
	6850	Limulus polyphemus		1		1		
	1642	Listeria innocua	2	3	2	3		
	1638	Listeria ivanovii	1	1	1	1		
	1639	Listeria monocytogenes	18	88	18	89		1

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	393133	Listeria monocytogenes 10403S		4		4		
	10000308	Listeria monocytogenes ATCC 35967		1		1		
	10000309	Listeria monocytogenes ATCC 43251		3		3		
	169963	Listeria monocytogenes EGD-e	5	57	5	57		
	393128	Listeria monocytogenes F6900		1		1		
	393117	Listeria monocytogenes FSL J1-194		1		1		
	393124	Listeria monocytogenes FSL N3-165		2		2		
	393126	Listeria monocytogenes FSL R2-561		1		1		
	552536	Listeria monocytogenes HCC23		2		2		
	401650	Listeria monocytogenes HPB2262		3		3		
	393130	Listeria monocytogenes J0161		4		4		
	267409	Listeria monocytogenes serotype 1/2a str. F6854		3		3		
	568819	Listeria monocytogenes serotype 4b str. CLIP 80459		4		4		
	265669	Listeria monocytogenes serotype 4b str. F2365		6		6		
	267410	Listeria monocytogenes serotype 4b str. H7858		23		23		
	386043	Listeria welshimeri serovar 6b str. SLCC5334		3		3		
	6299	Litomosoides carinii	3		3			
X	6689	Litopenaeus vannamei			118		118	
	217686	Little cherry virus 1		1		1		
	4522	Lolium perenne	36	118	36	118		
	36386	Louping ill virus (strain 31)	1		1			
X	58216	Loxosceles gaucho			1		1	
	58218	Loxosceles intermedia	1		13		12	
X	58217	Loxosceles laeta			2		2	
	11623	Lymphocytic choriomeningitis virus	3	369	3	640		271
	11624	Lymphocytic choriomeningitis virus (strain Armstrong)		1142		1142		
	10000496	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 3)		1		1		
	10000487	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 4)	1		1			
	10000497	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 5)	1		1			
	10000488	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 53b)		45		45		
	11625	Lymphocytic choriomeningitis virus (strain Pasteur)		5		5		
	11626	Lymphocytic choriomeningitis virus (strain Traub)		3		3		
	11627	Lymphocytic choriomeningitis virus (strain WE)		69		69		
	10000494	Lymphocytic choriomeningitis virus (strain WE) variant 8.7		1		1		
	10000495	Lymphocytic choriomeningitis virus (strain WE) WE CL1.2		1		1		
	10000490	Lymphocytic choriomeningitis virus A22.2b		1		1		
	10000491	Lymphocytic choriomeningitis virus Docile		2		2		
	9541	Macaca fascicularis	1	3	2	3	1	
	9544	Macaca mulatta	1	2	1	2		
	10373	Macaca mulatta cytomegalovirus		47		47		
	9548	Macaca radiata	14	1	14	1		
	10325	Macacine herpesvirus 1	1		1			
	47929	Macacine herpesvirus 3		68		68		
	45455	Macacine herpesvirus 4		18		18		
	11628	Machupo virus		784		796		12
	10001615	Machupo virus strain Carvallo		1		1		
	9322	Macropus sp.	1		1			
	431944	Magnetospirillum gryphiswaldense MSR-1		1		1		
	272627	Magnetospirillum magnetotacticum MS-1		3		3		
	76777	Malassezia sympodialis	1		1			
	3750	Malus domestica	27	1	27	38		37
	1239567	Mamastrovirus 3	2		2			

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	40674	Mammalia	2		2			
	351073	Mammalian orthoreovirus		1		1		
	7130	Manduca sexta		3		3		
	29780	Mangifera indica	1		1			
	45201	Mannheimia haemolytica serotype 1	82		82			
	221988	Mannheimia succiniciproducens MBEL55E		2		2		
	11269	Marburg marburgvirus	1	72	1	72		
	33727	Marburg virus - Musoke, Kenya, 1980	3	81	3	81		
	270374	Marinobacter sp. ELB17		1		1		
	38020	marmosets	3		3			
	11234	Measles virus	63	38	63	38		
	10000462	Measles virus CAM/RB		1		1		
X	262307	Measles virus genotype A			4		4	
X	171264	Measles virus genotype D3			1		1	
	11235	Measles virus strain Edmonston	167	210	167	210		
	70146	Measles virus strain Edmonston-B		13	2	13	2	
	70149	Measles virus strain Edmonston-Zagreb	1		1			
	11236	Measles virus strain Halle		34		34		
	132487	Measles virus strain Schwarz	1	1	1	1		
	55429	Megathura crenulata	1		1			
	9103	Meleagris gallopavo	3		3			
	152219	Menangle virus	2		2			
	12107	Mengo virus	5	13	5	13		
	493803	Merkel cell polyomavirus		2		2		
	10036	Mesocricetus auratus	31		31			
	243232	Methanocaldococcus jannaschii DSM 2661	2	1	2	1		
	187420	Methanothermobacter thermautotrophicus str. Delta H		1		1		
	420662	Methylibium petroleiphilum PM1		1		1		
	10793	Mink enteritis virus strain Abashiri	1		1			
	467144	Modified Vaccinia Ankara virus		52		52		
	11801	Moloney murine leukemia virus		5		5		
	10244	Monkeypox virus	5		5			
	13616	Monodelphis domestica	1	4	1	4		
	1000585	Montano virus	3		3			
	264732	Moorella thermoacetica ATCC 39073		1		1		
	300180	Mopeia Lassa virus reassortant 29		3		3		
	11629	Mopeia virus		12		12		
	480	Moraxella catarrhalis	10		10			
	10001556	Moraxella catarrhalis 26404	1		1			
	10001849	Moraxella catarrhalis serotype A	3		3			
	10001831	Moraxella catarrhalis serotype B	1		1			
	10001851	Moraxella catarrhalis serotype C	1		1			
	582	Morganella morganii	1		1			
	11757	Mouse mammary tumor virus		12		12		
	11161	Mumps virus	3		3			
	11169	Mumps virus strain Kilham	1		1			
	11173	Mumps virus strain SBL-1	3		3			
	334203	Mupapillomavirus 1	1	37	1	37		
	10366	Murid herpesvirus 1	2	49	2	49		
	10000411	Murid herpesvirus 1 deltaMS94.5		2		2		
	10000412	Murid herpesvirus 1 Isolate G4		1		1		
	10000413	Murid herpesvirus 1 Isolate K6		1		1		

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	33708	Murid herpesvirus 4	1	52	1	52		
	10000536	Murid herpesvirus 4 G2.4		3		3		
	10000537	Murid herpesvirus 4 WUMS		3		3		
	10530	Murine adenovirus 1	1	2	1	2		
	69156	Murine cytomegalovirus (strain K181)	2	11	2	13		2
	10367	Murine cytomegalovirus (strain Smith)		31		32		1
	10001396	Murine cytomegalovirus (strain Smith) MW97.01		5		5		
	35275	Murine endogenous retrovirus		11		11		
	11138	Murine hepatitis virus	3	31	3	31		
	12760	Murine hepatitis virus strain 4		5		5		
	11142	Murine hepatitis virus strain A59	26	4	26	4		
	11144	Murine hepatitis virus strain JHM	25	15	25	15		
	11786	Murine leukemia virus	1	12	1	13		1
	10001207	Murine leukemia virus LP-BM5		1		1		
	223997	Murine norovirus 1	2		2			
X	10002026	Murine norovirus 1 Mu/NoV/GV/MNV1/2002/USA				1		1
X	463722	Murine norovirus GV/CR6/2005/USA				1		1
	11263	Murine pneumonia virus		1		14		13
	10634	Murine polyomavirus	3	26	3	26		
	10636	Murine polyomavirus strain A2		3		3		
	28327	Murine rotavirus		3		3		
	70865	Murine rotavirus EDIM		27		27		
	11812	Murine sarcoma virus 3611	4		4			
	44561	Murine type C retrovirus		1		1		
	11079	Murray Valley encephalitis virus	21	7	21	7		
	301478	Murray valley encephalitis virus (strain MVE-1-51)	11	10	11	14		4
	10090	Mus musculus	532	2572	560	3630	28	1058
	10001019	Mus musculus B10.D2		1		1		
	10000000	Mus musculus BALB/c		2		2		
	10000055	Mus musculus DBA/2	1		1			
	10092	Mus musculus domesticus		2		2		
	57486	Mus musculus molossinus		1		1		
	4641	Musa acuminata	50	1	50	1		
	214697	Musa acuminata AAA Group	1		1			
X	37325	Muscovy duck parvovirus			4		4	
	10001918	Muscovy duck reovirus S12	2		2			
	9666	Mustela lutreola	1		1			
	1763	Mycobacterium	3	14	3	15		1
X	1198627	Mycobacterium abscessus subsp. bolletii str. GO 06				1		1
	1764	Mycobacterium avium	6	12	6	12		
	243243	Mycobacterium avium 104		10		10		
	10000313	Mycobacterium avium serovar 1	1		1			
	10000314	Mycobacterium avium serovar 2	1		1			
	10000316	Mycobacterium avium serovar 25	1		1			
	10000317	Mycobacterium avium serovar 26	1		1			
	10000318	Mycobacterium avium serovar 4	2		2			
	10000319	Mycobacterium avium serovar 8	1	1	1	1		
	10000320	Mycobacterium avium serovar 9	1		1			
	1770	Mycobacterium avium subsp. paratuberculosis	25	13	31	13	6	
	262316	Mycobacterium avium subsp. paratuberculosis K-10	3	25	3	25		
	10000328	Mycobacterium avium subsp. paratuberculosis Strain Ben		1		1		
	1765	Mycobacterium bovis	47	126	48	126	1	

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	233413	Mycobacterium bovis AF2122/97		49		49		
	10000322	Mycobacterium bovis AN5	9	28	9	28		
	33892	Mycobacterium bovis BCG	11	146	11	146		
	410289	Mycobacterium bovis BCG str. Pasteur 1173P2	1	88	1	88		
	10000323	Mycobacterium bovis T/91/1378		6		6		
	1774	Mycobacterium chelonae	1		1			
	1766	Mycobacterium fortuitum		1		1		
	144549	Mycobacterium fortuitum subsp. fortuitum		1		1		
	10000331	Mycobacterium gastri W471	1		1			
	350054	Mycobacterium gilvum PYR-GCK		4		4		
	1778	Mycobacterium gordonae	1		1			
	1767	Mycobacterium intracellulare		1		1		
	487521	Mycobacterium intracellulare ATCC 13950	1		1			
	912594	Mycobacterium iranicum		1		1		
	1768	Mycobacterium kansasii	9	13	9	13		
	557599	Mycobacterium kansasii ATCC 12478	1		1			
	1769	Mycobacterium leprae	119	404	119	404		
	272631	Mycobacterium leprae TN		3		30		27
	525368	Mycobacterium parascrofulaceum ATCC BAA-614		1		1		
	43304	Mycobacterium peregrinum	2		2			
	1771	Mycobacterium phlei		1		1		
	1783	Mycobacterium scrofulaceum	4		4			
	1772	Mycobacterium smegmatis		1		2		1
	164757	Mycobacterium sp. JLS		1		1		
	189918	Mycobacterium sp. KMS		1		1		
	164756	Mycobacterium sp. MCS		1		1		
	1773	Mycobacterium tuberculosis	491	1342	501	2007	10	665
	10000329	Mycobacterium tuberculosis 103	1		1			
	348776	Mycobacterium tuberculosis C		67		67		
	83331	Mycobacterium tuberculosis CDC1551		22		22		
	336982	Mycobacterium tuberculosis F11		13		13		
	419947	Mycobacterium tuberculosis H37Ra		57		57		
	83332	Mycobacterium tuberculosis H37Rv	53	781	56	793	3	12
	652616	Mycobacterium tuberculosis str. Erdman = ATCC 35801	15	19	15	19		
	395095	Mycobacterium tuberculosis str. Haarlem		88		88		
	182785	Mycobacterium tuberculosis subsp. tuberculosis		1		1		
	1809	Mycobacterium ulcerans		7		7		
	362242	Mycobacterium ulcerans Agy99		1		1		
	350058	Mycobacterium vanbaalenii PYR-1		1		1		
	347257	Mycoplasma agalactiae PG2	3		3			
	28903	Mycoplasma bovis	21		21			
	10001075	Mycoplasma gallisepticum strain S6	1		1			
	2097	Mycoplasma genitalium		1		1		
	243273	Mycoplasma genitalium G37	8		8			
	2099	Mycoplasma hyopneumoniae	2		2			
	295358	Mycoplasma hyopneumoniae 232	21		21			
	754503	Mycoplasma hyopneumoniae 7422	1		1			
	262722	Mycoplasma hyopneumoniae 7448	1		1			
	28227	Mycoplasma penetrans	34		34			
	2104	Mycoplasma pneumoniae	12	2	12	2		
	722438	Mycoplasma pneumoniae FH	3		3			
	272634	Mycoplasma pneumoniae M129	9		9			

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	13618	Myrmecia pilosula	2		2			
	246197	Myxococcus xanthus DK 1622		1		1		
	10273	Myxoma virus		3		3		
	8656	Naja atra	7		7			
	35670	Naja naja	3		3			
	8654	Naja nigricollis	3	2	3	2		
	8657	Naja oxiana	4		4			
	8658	Naja pallida	1	1	1	1		
	51031	Necator americanus	17		17			
	367400	Neembucu hantavirus		4		4		
	485	Neisseria gonorrhoeae	23	11	23	11		
	10001558	Neisseria gonorrhoeae 15253	1		1			
	10000863	Neisseria gonorrhoeae 4505	1		1			
	528354	Neisseria gonorrhoeae MS11	8		8			
	10001077	Neisseria gonorrhoeae SU89	1		1			
	10001078	Neisseria gonorrhoeae SU96	3		3			
	487	Neisseria meningitidis	59	22	59	23		1
	272831	Neisseria meningitidis FAM18	1		1			
	909420	Neisseria meningitidis H44/76	1		1			
	10001560	Neisseria meningitidis M982B	2		2			
	122586	Neisseria meningitidis MC58	13		17		4	
	65699	Neisseria meningitidis serogroup A	5		5			
	10001051	Neisseria meningitidis serogroup A Strain 8659	1		1			
	491	Neisseria meningitidis serogroup B	39	1	39	1		
	10000843	Neisseria meningitidis serogroup B H44/76	74	22	74	22		
	10001003	Neisseria meningitidis serogroup B CU385	2		2			
	10001050	Neisseria meningitidis serogroup B Strain 7967	1		1			
	10000979	Neisseria meningitidis serogroup B Strain 8047	4		4			
	10000972	Neisseria meningitidis serogroup B Strain B16.B6	1		1			
	10001162	Neisseria meningitidis serogroup B Strain M1239	2		2			
	10001049	Neisseria meningitidis serogroup B Strain S3446	1		1			
	135720	Neisseria meningitidis serogroup C	3		3			
	10001044	Neisseria meningitidis serogroup C MC51	1		1			
	10001783	Neisseria meningitidis serogroup C strain C11	1	1	1	1		
	10001797	Neisseria meningitidis serogroup C strain MC19	1		1			
	10001713	Neisseria meningitidis serogroup W-135	1		1			
	648194	Neisseria meningitidis serogroup Y	3		3			
	10001524	Neisseria meningitidis strain 3006	1		1			
	29176	Neospora caninum	2	17	2	17		
	572307	Neospora caninum Liverpool		1		1		
	452646	Neovison vison		1		1		
	5141	Neurospora crassa	6	3	6	3		
	11176	Newcastle disease virus	14	3	14	4		1
	11177	Newcastle disease virus (STRAIN AUSTRALIA-VICTORIA/32)	4		4			
	10001138	Newcastle disease virus (strain Eaves)	1		1			
	10001032	Newcastle disease virus (strain La Sota)	1		1			
	10001140	Newcastle disease virus (strain WA2116)	1		1			
	351071	Newcastle disease virus AF2240	1		1			
	11178	Newcastle disease virus strain Beaudette C/45	12		12			
	11180	Newcastle disease virus strain D26/76	4		4			
	11186	Newcastle disease virus strain Queensland/66	4		4			
	4100	Nicotiana benthamiana	5		5			

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	4097	Nicotiana tabacum	1		1			
	121791	Nipah virus	5		5			
	314278	Nitrococcus mobilis Nb-231		1		1		
	37329	Nocardia farcinica		1		1		
	10001484	Norovirus genogroup 1 GI.12	1		1			
	10001116	Norovirus genogroup 1 isolates 96-908	4		4			
	10000832	Norovirus genogroup 2 Camberwell 1890	1		1			
	10001606	Norovirus genogroup 2 Hu/NoV/Farmington Hills/2002/USA	1	2	1	2		
	10000829	Norovirus genogroup 2 Mexico type strain 36	3		3			
	10000560	Norovirus genogroup 3 Bo/Jena/1980/DE	1		1			
	10001485	Norovirus genogroup 3 GIII.1	1		1			
	122928	Norovirus GI	1		2		1	
	647514	Norovirus GI.1	1		1			
	647515	Norovirus GI.2	1		1			
X	647516	Norovirus GI.3				1		1
	647519	Norovirus GI.5	1		1			
	647521	Norovirus GI.7	1		1			
	122929	Norovirus GII	2		2			
	499191	Norovirus GII.1	1		1			
	747305	Norovirus GII.10	1		1			
	520963	Norovirus GII.11	1		1			
	520964	Norovirus GII.18	1		1			
	490039	Norovirus GII.2	1		1			
	489821	Norovirus GII.4	1		1	2		2
	508775	Norovirus GII.9	1		1	1		1
	524364	Norovirus Hu/1968/US		1	1	1	1	
	1182144	Norovirus Hu/GII.4/Minerva/2006/USA	2		2			
	1156983	Norovirus Hu/GII.4/Minerva/CS1258/2006/USA	1		1			
	588533	Norovirus Hu/GII/GZ-1/2008/CHN	1		1			
	150080	Norovirus isolates	1		1			
	11983	Norwalk virus	2	1	2	1		
	63737	Nostoc punctiforme PCC 73102		1		1		
	8663	Notechis scutatus	2		2			
	8996	Numida meleagris	1		1			
	4146	Olea europaea	70	19	70	19		
	42764	Oliveros virus		1		1		
	6282	Onchocerca volvulus	3	39	3	39		
	8018	Oncorhynchus keta		6		6		
	8022	Oncorhynchus mykiss	1		1			
	69247	Oran virus		2		2		
	9733	Orcinus orca		1		1		
	784	Orientia tsutsugamushi	86		86			
	10000761	Orientia tsutsugamushi Karp	1		1			
	357244	Orientia tsutsugamushi str. Boryong	2	2	2	2		
	334380	Orientia tsutsugamushi str. Ikeda		1		1		
	9258	Ornithorhynchus anatinus		1		1		
	9986	Oryctolagus cuniculus	38	7	52	7	14	
	39947	Oryza sativa Japonica Group	5	1	5	1		
	28869	Ovine respiratory syncytial virus	1		1			
	9940	Ovis aries	81	17	81	17		
	8667	Oxyuranus scutellatus scutellatus	4		4			
	9598	Pan troglodytes	7	21	7	21		

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	188763	Panine herpesvirus 2		2		2		
	3469	Papaver somniferum	1		1			
	9555	Papio anubis	1		1			
	9556	Papio cynocephalus	1		1			
	121759	Paracoccidioides brasiliensis	4	16	4	16		
	10000566	Paracoccidioides brasiliensis B339		8		8		
	502780	Paracoccidioides brasiliensis Pb18	1	1	1	1		
	266	Paracoccus denitrificans	3		3			
	318586	Paracoccus denitrificans PD1222		2		2		
	11207	Parainfluenza virus 5	1	1	1	1		
	8255	Paralichthys olivaceus	1		1			
	45222	Parana virus		1		1		
	33127	Parietaria judaica	61	2	61	2		
	13187	Parietaria officinalis	2		2			
X	147272	Paspalum notatum				16		16
	747	Pasteurella multocida		10		10		
	272843	Pasteurella multocida subsp. multocida str. Pm70		4		4		
	10000759	Pasteurella multocida X-73	2		2			
X	554	Pectobacterium carotovorum			2		2	
	1254	Pediococcus acidilactici	1		1			
	6687	Penaeus monodon	10	4	10	4		
	5076	Penicillium chrysogenum	45	19	45	19		
	5077	Penicillium citrinum	13		13			
	69248	Pergamino virus		1		1		
	6978	Periplaneta americana	9	3	9	3		
	31604	Peste-des-petits-ruminants virus	9	1	13	1	4	
	10001020	Peste-des-petits-ruminants virus (strain Nigeria 75/1)		1		1		
	28479	Phalaris aquatica		9		9		
	3885	Phaseolus vulgaris	5	1	5	1		
	9057	Phasianus colchicus colchicus	1		1			
	15957	Phleum pratense	49	769	50	769	1	
	10000463	Phocine distemper virus 2558/Han 88	5		5			
	42345	Phoenix dactylifera		3		3		
	314292	Photobacterium angustum S14		1		1		
	659	Photobacterium phosphoreum		1		1		
	72539	Physalis mottle virus	2		2			
	9755	Physeter catodon	1	29	1	30		1
	4787	Phytophthora infestans	2		2			
	11630	Pichinde virus		8		8		
	10001618	Pichinde virus strain Munchique		1		1		
	3318	Pinaceae	2		2			
	3352	Pinus taeda	4		4			
	60876	Pixuna virus		1		1		
	39414	Plantago lanceolata		2		2		
	2439	Plasmid ColB2	1		1			
	2465	Plasmid F	1		1			
	5820	Plasmodium	5	5	5	5		
	5821	Plasmodium berghei	14	44	14	49		5
	5823	Plasmodium berghei ANKA	6	5	7	8	1	3
	10000356	Plasmodium berghei NK65	2	2	2	2		
	5824	Plasmodium brasilianum	2		2			
	5825	Plasmodium chabaudi	4	4	4	4		

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	10000357	Plasmodium chabaudi adami DS	2	37	2	37		
	31271	Plasmodium chabaudi chabaudi		2		2		
	5827	Plasmodium cynomolgi	2		2			
	5833	Plasmodium falciparum	612	767	688	798	76	31
	10000358	Plasmodium falciparum 366		1		1		
	36329	Plasmodium falciparum 3D7	153	198	158	200	5	2
	57266	Plasmodium falciparum 7G8	40	50	40	50		
	10000363	Plasmodium falciparum Brazil-608	1	1	1	1		
	5835	Plasmodium falciparum CAMP/Malaysia	36	2	36	2		
	5836	Plasmodium falciparum CDC/Honduras	1		1			
	5837	Plasmodium falciparum FC27/Papua New Guinea	44	60	44	60		
	10000366	Plasmodium falciparum FCB-2	1		1			
	5838	Plasmodium falciparum FCR-3/Gambia	41		94		53	
X	10000369	Plasmodium falciparum FVO				5		5
	10000371	Plasmodium falciparum Indochina I/CDC	32		32			
X	10002007	Plasmodium falciparum isolate UAS22			4		4	
X	10002009	Plasmodium falciparum isolate UAS29			2		2	
X	10002008	Plasmodium falciparum isolate UAS31			1		1	
	5848	Plasmodium falciparum isolate WELLCOME	25	51	25	51		
	10000373	Plasmodium falciparum ItG2G1		1		1		
	5839	Plasmodium falciparum K1	18	19	18	19		
	5840	Plasmodium falciparum LE5		2		2		
	5841	Plasmodium falciparum Mad20/Papua New Guinea	8	47	8	47		
	5843	Plasmodium falciparum NF54	13	31	13	31		
	5842	Plasmodium falciparum NF7/Ghana	5		5			
	57270	Plasmodium falciparum Palo Alto/Uganda	14		38		24	
X	10002011	Plasmodium falciparum R29/IT4			1		1	
	5834	Plasmodium falciparum RO-33	8	1	8	1		
	10000375	Plasmodium falciparum RO71	1	1	1	1		
	5846	Plasmodium falciparum T4/Thailand	25		25			
	10000816	Plasmodium falciparum T9/96	1	1	1	1		
	10000376	Plasmodium falciparum UF-5	2		2			
	5857	Plasmodium fragile		3		3		
	5850	Plasmodium knowlesi	2	6	2	6		
	5851	Plasmodium knowlesi strain H	7	7	7	7		
	5852	Plasmodium knowlesi strain Nuri		3		3		
	5858	Plasmodium malariae	1		1			
	5854	Plasmodium reichenowi		3		3		
	5859	Plasmodium simium	2		2			
	5855	Plasmodium vivax	83	147	95	147	12	
	10000378	Plasmodium vivax NK		2		2		
	126793	Plasmodium vivax Sal-1	10	1	10	1		
	31273	Plasmodium vivax strain Belem	6	34	6	34		
	10000862	Plasmodium vivax VK247	1		1			
	27990	Plasmodium vivax-like sp.	2		3		1	
	5861	Plasmodium yoelii	17	38	17	38		
	73239	Plasmodium yoelii yoelii	22	30	22	30		
	352914	Plasmodium yoelii yoelii 17XNL	6	1	6	1		
	10000555	Plasmodium yoelii yoelii 265BY		1		1		
	10000381	Plasmodium yoelii yoelii YM	1	5	1	5		
	9479	Platyrrhini	1		1			
	103448	Pleistophora sp. LS		1		1		

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	703	Plesiomonas shigelloides		1		1		
	12211	Plum pox virus	1		1			
	10001100	Plum pox virus (strain W)	6		6			
	12213	Plum pox virus isolate NAT		1		1		
	4754	Pneumocystis carinii	2	1	2	1		
	263815	Pneumocystis murina	3		3			
	270473	Pneumonia virus of mice J3666		6		6		
	4545	Poa pratensis	34	31	34	31		
	365044	Polaromonas naphthalenivorans CJ2		1		1		
	12088	Poliovirus type 3 (strains P3/LEON/37 AND P3/LEON 12A[1]B)	4	15	4	15		
	80956	Pomacentrus moluccensis		1		1		
	9601	Pongo abelii		1		1		
	9600	Pongo pygmaeus		2		2		
	46221	Porcine circovirus		49		49		
	133704	Porcine circovirus 1	5		5			
	10001964	Porcine circovirus 1 strain 1/G	7		7			
	85708	Porcine circovirus 2	26		27		1	
X	10001881	Porcine circovirus 2 -A			1		1	
	10001239	Porcine circovirus strain ISU31	7		7			
	61673	Porcine endogenous retrovirus	2	11	2	11		
	194958	Porcine endogenous retrovirus A	2		2			
	194959	Porcine endogenous retrovirus B	1		1			
	28295	Porcine epidemic diarrhea virus	1		1			
	229032	Porcine epidemic diarrhea virus (strain CV777)	4		4			
X	10002000	Porcine epidemic diarrhea virus CH/SHH/06			1		1	
	10796	Porcine parvovirus	37		37			
	28344	Porcine reproductive and respiratory syndrome virus	75	12	75	34		22
	10001586	Porcine reproductive and respiratory syndrome virus 07V063	3		3			
	10001587	Porcine reproductive and respiratory syndrome virus 08V204	2		2			
	10001800	Porcine reproductive and respiratory syndrome virus HuN4	1	4	1	4		
	10001771	Porcine reproductive and respiratory syndrome virus HuN4-F112		1		1		
	10000969	Porcine respiratory and reproductive syndrome virus 111/92	9		9			
	10000529	Porcine respiratory and reproductive syndrome virus CH-1a	7	1	7	1		
	10000859	Porcine respiratory and reproductive syndrome virus JA142	1		1			
	10000864	Porcine respiratory and reproductive syndrome virus MD-001	2		2			
	10000888	Porcine respiratory and reproductive syndrome virus Olot/91	3		3			
	10919	Porcine rotavirus (STRAIN YM)	2	1	2	1		
	101350	Porcine rotavirus strain A253	2		2			
	10917	Porcine rotavirus strain Gottfried	2		2			
	53179	Porcine rubulavirus	3		3			
	11150	Porcine transmissible gastroenteritis coronavirus strain FS772/70	2		2			
	10001798	Porcine transmissible gastroenteritis coronavirus strain Pur46-MAD	4		4			
	11151	Porcine transmissible gastroenteritis coronavirus strain Purdue	14		14			
	837	Porphyromonas gingivalis	74	20	74	20		
	10001079	Porphyromonas gingivalis 381	71	55	71	55		
X	431947	Porphyromonas gingivalis ATCC 33277				4		4
	10001081	Porphyromonas gingivalis HG66	2		2			
	10001223	Porphyromonas gingivalis OMZ 409	23		23			
	1125722	Porphyromonas gingivalis W50		36		36		
	242619	Porphyromonas gingivalis W83	2		2			
	37128	Potato mop-top virus	8		8			

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	12216	Potato virus Y	1		1			
	12220	Potato virus Y strain O	6		6			
	11083	Powassan virus		2		2		
	93058	Prochlorococcus marinus str. MIT 9202	1		1			
	765103	Propionibacterium acnes HL030PA1		1		1		
	1752	Propionibacterium freudenreichii subsp. shermanii		1		1		
	11603	Prospect Hill virus	1	2	1	2		
	1224	Proteobacteria	3		3			
	583	Proteus	2		2			
	584	Proteus mirabilis	6		6			
	10001006	Proteus mirabilis CFT322	1		1			
	529507	Proteus mirabilis HI4320	1		1			
	10001498	Proteus mirabilis O23	1		1			
	10001490	Proteus mirabilis O24	1		1			
	10001491	Proteus mirabilis O29	1		1			
	10001500	Proteus mirabilis O43	1		1			
	10001499	Proteus mirabilis O6	1		1			
	102862	Proteus penneri	1		1			
	10001836	Proteus penneri 14 (O59)	2		2			
	10001837	Proteus penneri 15 (O52)	2		2			
	10001835	Proteus penneri 7 (O61)	2		2			
	10001581	Proteus penneri 8 (O67)	1		1			
	10001501	Proteus penneri ATCC 33519	1		1			
	10001489	Proteus vulgaris Strain 5/43	1		1			
	88086	Protobothrops elegans	7		7			
	88087	Protobothrops flavoviridis	3		3			
	10001514	Providencia stuartii O33	1		1			
	10001588	Providencia stuartii O4	1		1			
	300559	PRRSV VR2332	22		22			
	36596	Prunus armeniaca	4		4			
	42229	Prunus avium	3	1	3	1		
	3758	Prunus domestica	4		4			
	3755	Prunus dulcis	18		19		1	
	3760	Prunus persica	17	51	17	51		
	8671	Pseudechis porphyriacus	3		3			
	342610	Pseudoalteromonas atlantica T6c		1		1		
	286	Pseudomonas	1		1			
	287	Pseudomonas aeruginosa	74	50	74	53		3
	350704	Pseudomonas aeruginosa C3719		2		2		
	10001057	Pseudomonas aeruginosa CD4	1		1			
	10000822	Pseudomonas aeruginosa Immunotype 3	1		1			
	10000723	Pseudomonas aeruginosa Immunotype 4	4		4			
	10001058	Pseudomonas aeruginosa K122-4	1		1			
	10000817	Pseudomonas aeruginosa KB7	2		2			
	10000818	Pseudomonas aeruginosa P1	1		1			
	388272	Pseudomonas aeruginosa PACS2		4		4		
	10000725	Pseudomonas aeruginosa PAK	7	3	7	3		
	10000815	Pseudomonas aeruginosa PAO	2	2	2	2		
	208964	Pseudomonas aeruginosa PAO1	1	1	1	1		
	10001519	Pseudomonas aeruginosa serotype O11	1		1			
	208963	Pseudomonas aeruginosa UCBPP-PA14		20		20		
	237609	Pseudomonas alkylphenolia		1		1		

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	294	Pseudomonas fluorescens		4		4		
	10879	Pseudomonas phage phi6	7		7			
	303	Pseudomonas putida	1	8	1	8		
	351746	Pseudomonas putida F1		4		4		
	76869	Pseudomonas putida GB-1		1		1		
	306	Pseudomonas sp.		1		1		
	74138	Pseudomonas sp. DJ-12		1		1		
	71238	Pseudomonas sp. G-179		1		1		
	159091	Pseudomonas sp. KIE171		1		1		
	91465	Pseudomonas sp. MIS38		1		1		
	150396	Pseudomonas sp. MT-1		1		1		
	312	Pseudomonas sp. RS-16	1		1			
	192087	Pseudomonas syringae pv. atrofaciens	4		4			
	10001690	Pseudomonas syringae pv. atrofaciens str. IMV 4394	1		1			
	10001688	Pseudomonas syringae pv. atrofaciens str. IMV 7836	1		1			
	10001689	Pseudomonas syringae pv. atrofaciens str. IMV K-1025	1		1			
	129138	Pseudomonas syringae pv. morsprunorum	2		2			
	10001700	Pseudomonas syringae pv. morsprunorum str. CFBP 1650	1		1			
	10001698	Pseudomonas syringae pv. morsprunorum str. GSPB 883	1		1			
	319	Pseudomonas syringae pv. phaseolicola	1		1			
	264730	Pseudomonas syringae pv. phaseolicola 1448A		1		1		
	10001697	Pseudomonas syringae pv. phaseolicola str. IMV 120a	1		1			
	10001693	Pseudomonas syringae pv. tagetis str. ICMP 6370	1		1			
	29442	Pseudomonas tolaasii		1		1		
	11604	Puumala virus	32	19	32	19		
	10000485	Puumala virus (STRAIN HALLNAS B1) Vranica/Hallnas	4		4			
	10001238	Puumala virus (strain Umea/hu)	1		1			
	10000483	Puumala virus CG18-20	4		4			
	11605	Puumala virus Hallnas B1		1		1		
	10000484	Puumala virus Kazan	25	7	25	7		
	39002	Puumala virus sotkamo/v-2969/81	196		196			
	272844	Pyrococcus abyssi GE5		1		1		
	3513	Quercus alba		5		5		
	10000507	Rabbit hemorrhagic disease virus Olot/89	1		1			
	32606	Rabbitpox virus		2		2		
	11292	Rabies virus	11	14	11	14		
	11293	Rabies virus AVO1		3		3		
	10000467	Rabies virus CVS	14		14			
	11294	Rabies virus CVS-11	2		2			
	11295	Rabies virus ERA	5	27	6	27	1	
	10000470	Rabies virus Flury LEP		1		1		
	11296	Rabies virus HEP-FLURY	7	1	7	1		
	11298	Rabies virus Nishigahara RCEH	1		1			
	37132	Rabies virus Ontario fox	3		3			
	10000471	Rabies virus RC-HL	4		4			
	103929	Rabies virus strain Pasteur vaccin	2	1	2	1		
	3726	Raphanus sativus	1		1			
	10114	Rattus	11		11			
	10116	Rattus norvegicus	209	465	210	470	1	5
	10001133	Rattus norvegicus DA		3		3		
	10000662	Rattus norvegicus Lewis		1		1		
	10001412	Rattus norvegicus Wistar-Furth		11		11		

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	378809	Ravn virus - Ravn, Kenya, 1987		32		32		
	48483	Reclinomonas americana		1		1		
	1646	Renibacterium salmoninarum	12		12			
	10880	Reoviridae		1		1		
	10891	Reovirus sp.		2		2		
	12814	Respiratory syncytial virus	3	13	3	13		
	186539	Reston ebolavirus		6	1	6	1	
	129003	Reston ebolavirus - Reston	2	27	2	27		
	386032	Reston ebolavirus - Reston (1989)		1		1		
X	10001999	Reticuloendotheliosis virus strain HLJ07I			1		1	
	103930	Rhesus cytomegalovirus strain 68-1		5		5		
	10969	Rhesus rotavirus	8	1	8	1		
	34631	Rhipicephalus appendiculatus	1		1			
	60189	Rhipicephalus decoloratus	5		5			
	34632	Rhipicephalus sanguineus	1		1			
	1063	Rhodobacter sphaeroides		1		1		
	272943	Rhodobacter sphaeroides 2.4.1		1		1		
	43767	Rhodococcus equi	18		18	1		1
	1833	Rhodococcus erythropolis		1		1		
	1828	Rhodococcus fascians		1		1		
	1830	Rhodococcus ruber		1		1		
	316056	Rhodopseudomonas palustris BisB18		1		1		
X	4012	Rhus				1		1
	3988	Ricinus communis	32	4	34	4	2	
	35788	Rickettsia africae		1		1		
	293614	Rickettsia akari str. Hartford		1		1		
	787	Rickettsia australis		1		1		
	391896	Rickettsia bellii OSU 85-389		3		3		
	336407	Rickettsia bellii RML369-C		7		7		
	788	Rickettsia canadensis		1		1		
	781	Rickettsia conorii		13		13		
	272944	Rickettsia conorii str. Malish 7		5		5		
	42862	Rickettsia felis		1		1		
	315456	Rickettsia felis URRWXCal2		6		6		
	35791	Rickettsia massiliae		1		1		
	416276	Rickettsia massiliae MTU5		1		1		
	782	Rickettsia prowazekii		21		21		
	272947	Rickettsia prowazekii str. Madrid E		5		5		
	783	Rickettsia rickettsii		1		1		
	452659	Rickettsia rickettsii str. Iowa		1		1		
	392021	Rickettsia rickettsii str. 'Sheila Smith'		1		1		
	35793	Rickettsia sibirica		4		4		
	272951	Rickettsia sibirica 246		15		15		
	785	Rickettsia typhi		3		3		
	257363	Rickettsia typhi str. Wilmington		5		5		
	11588	Rift Valley fever virus	5	2	5	27		25
	11589	Rift valley fever virus (STRAIN ZH-548 M12)		2		2		
	10000482	Rift Valley fever virus ZH501	2		2			
	11241	Rinderpest virus	2	3	2	3		
	11243	Rinderpest virus (strain L)	6		6			
	36409	Rinderpest virus (strain RBOK)	33	5	33	5		
	10000465	Rinderpest virus LATC	2		2			

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	46920	Rio Mamore virus	1	1	1	1		
	37207	Rio Segundo virus	1		1			
	313596	Robiginitalea biformata HTCC2501		1		1		
	314262	Roseobacter sp. MED193		1		1		
	11029	Ross River virus		1		1		
	11032	Ross river virus (STRAIN T48)	3		3			
	10930	Rotavirus A bovine/B223/G10	2		2			
	72132	Rotavirus G1	1	1	1	1		
	73036	Rotavirus G3		1		1		
	10001216	Rotavirus G3 strain RV-3	1		1			
	11886	Rous sarcoma virus	4	4	4	4		
	11041	Rubella virus	77	96	79	96	2	
	11043	Rubella virus strain M33	3	11	3	11		
	11045	Rubella virus strain Therien	20	35	20	35		
	11044	Rubella virus vaccine strain RA27/3	2	6	2	6		
	159479	Saaremaa virus		9		9		
	45709	Sabia virus		874		879		5
	64284	Saboya virus		1		1		
	4932	Saccharomyces cerevisiae	26	10	26	10		
	545124	Saccharomyces cerevisiae AWRI1631		2		2		
	285006	Saccharomyces cerevisiae RM11-1a		3		3		
X	559292	Saccharomyces cerevisiae S288c			1		1	
	9491	Saguinus imperator	1		1			
	9488	Saguinus mystax	1		1			
	9521	Saimiri sciureus	1		1			
	10381	Saimiriine herpesvirus 2		3		3		
	8030	Salmo salar	30		30			
	590	Salmonella	3		3			
	28901	Salmonella enterica		52		52		
	59203	Salmonella enterica subsp. arizonae		1		1		
	41514	Salmonella enterica subsp. arizonae serovar 62:z4,z23:-		4		4		
	119912	Salmonella enterica subsp. enterica serovar Choleraesuis		2		2		
	321314	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67		5		5		
	98360	Salmonella enterica subsp. enterica serovar Dublin		2		2		
	149539	Salmonella enterica subsp. enterica serovar Enteritidis		2		2		
	10001492	Salmonella enterica subsp. enterica serovar Enteritidis SH1262	3		3			
	29477	Salmonella enterica subsp. enterica serovar Essen	1		1			
	10001569	Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 11	1		1			
	10001570	Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 77	1		1			
	286783	Salmonella enterica subsp. enterica serovar Indiana		1		1		
	10000554	Salmonella enterica subsp. enterica serovar Minnesota R595	2		2			
	596	Salmonella enterica subsp. enterica serovar Muenchen	1		1			
	423368	Salmonella enterica subsp. enterica serovar Newport str. SL254		1		1		
	54388	Salmonella enterica subsp. enterica serovar Paratyphi A		1		1		
	554290	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601		2		2		
	295319	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150		3		3		
	10001709	Salmonella enterica subsp. enterica serovar Paratyphi B strain SPB7		8		8		
	605	Salmonella enterica subsp. enterica serovar Pullorum		1		1		

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	439847	Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29		1		1		
	90370	Salmonella enterica subsp. enterica serovar Typhi	13	111	13	111		
	497977	Salmonella enterica subsp. enterica serovar Typhi str. 404ty		1		1		
	220341	Salmonella enterica subsp. enterica serovar Typhi str. CT18		6		6		
	209261	Salmonella enterica subsp. enterica serovar Typhi str. Ty2		1		5		4
	90371	Salmonella enterica subsp. enterica serovar Typhimurium	15	66	15	69		3
	85569	Salmonella enterica subsp. enterica serovar Typhimurium str. DT104	1		1			
	99287	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2		34		34		
	48409	Salmonella enterica subsp. enterica serovar Virchow		1		1		
	59205	Salmonella enterica subsp. houtenae		1		1		
	59202	Salmonella enterica subsp. salamae		1		1		
	10001511	Salmonella 'group A'	2		2			
	10001722	Salmonella 'group D'	3		3			
	599	Salmonella sp.	1		1			
	72590	Salmonella sp. 'group B'	6		6			
	10001526	Salmonella thompson C1 strain IS40	1		1			
	10000739	Salmonella typhi 620Ty	1		1			
	10000740	Salmonella typhi Ty21a		6		6		
	10000738	Salmonella typhimurium PL5 (O9,12)	1		1			
	10000742	Salmonella typhimurium SH 4809	4		4			
	10000743	Salmonella typhimurium SL3261		4		4		
	151250	Salsola kali		22		22		
	358400	Sangassou virus		6		6		
	234603	Sapovirus Mc114		1		1		
	11607	Sapporo rat virus	1	4	1	4		
	82659	Sapporo virus-Manchester		1		1		
	7386	Sarcophaga peregrina		1		1		
	227859	SARS coronavirus	155	241	155	484		243
	228407	SARS coronavirus BJ01	66	28	66	28		
	229992	SARS coronavirus Frankfurt 1	6	26	6	26		
	627442	SARS coronavirus P2	1		1			
	284672	SARS coronavirus TJF		14		14		
	227984	SARS coronavirus Tor2	171	1965	171	1965		
	228330	SARS coronavirus Urbani	22	52	22	52		
	6181	Schistosoma	3		3			
	6184	Schistosoma bovis	2		2			
	6182	Schistosoma japonicum	43	20	43	20		
	6183	Schistosoma mansoni	74	44	74	44		
	10000385	Schistosoma mansoni Puerto Rico	18	7	18	7		
	5334	Schizophyllum commune		1		1		
X	1133363	Schmallenberg virus			1		1	
X	85552	Scylla paramamosain			3		3	
	4550	Secale cereale	51		51			
	58866	Secale strictum		1		1		
	11033	Semliki forest virus	36	5	36	5		
X	136966	SEN virus				7		7
	11191	Sendai virus	1	9	60	9	59	
	11194	Sendai virus (strain Enders)	7	11	7	11		
	11195	Sendai virus (strain Fushimi)		1		1		
	11196	Sendai virus (strain Harris)	2		2			
	302272	Sendai virus (strain Ohita)	1		1			

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	11198	Sendai virus (Z)		1		1		
	11608	Seoul virus		2		2		
	12557	Seoul virus 80-39		1		1		
	11610	Seoul virus SR11	1		1			
	44026	Sepik virus		1		1		
	615	Serratia marcescens	1	3	1	3		
	399741	Serratia proteamaculans 568		1		1		
	4182	Sesamum indicum	11		11			
	325240	Shewanella baltica OS155		2		2		
	319224	Shewanella putrefaciens CN-32		1		1		
	351745	Shewanella sp. W3-18-1		1		1		
	621	Shigella boydii		2		2		
	344609	Shigella boydii CDC 3083-94		17		17		
	300268	Shigella boydii Sb227		4		4		
	622	Shigella dysenteriae	5	2	5	2		
	358708	Shigella dysenteriae 1012		1		1		
	300267	Shigella dysenteriae Sd197		4		4		
	10000748	Shigella dysenteriae serotype 1	3		3			
	10000749	Shigella dysenteriae serotype 1 114Sd	1		1			
	623	Shigella flexneri	76	10	76	10		
	591020	Shigella flexneri 2002017		1		1		
	42897	Shigella flexneri 2a	31		31			
	198215	Shigella flexneri 2a str. 2457T		2		2		
	198214	Shigella flexneri 2a str. 301		3		3		
	10000750	Shigella flexneri 2b	1		1			
	424717	Shigella flexneri 3a	2		4		2	
	373384	Shigella flexneri 5 str. 8401		21		21		
	424718	Shigella flexneri 5a	2		2			
	10000752	Shigella flexneri 5b	1		1			
	10000754	Shigella flexneri X	1		1			
	424720	Shigella flexneri Y	8		8			
	624	Shigella sonnei		1		1		
	300269	Shigella sonnei Ss046		9		9		
	92652	Shrimp white spot syndrome virus	3		3			
	11723	Simian immunodeficiency virus		154		155		1
	11711	Simian immunodeficiency virus - mac		1		1		
	10000501	Simian immunodeficiency virus - mac - mac 239		279		279		
	10000502	Simian immunodeficiency virus - mac - mac 32H		7		7		
	10000503	Simian immunodeficiency virus - mac - mac BK28		3		3		
	10000504	Simian immunodeficiency virus - mac - mac F965		1		1		
	11735	Simian immunodeficiency virus - mac K6W		72		72		
	31682	Simian immunodeficiency virus - mac1A11		8		8		
	224206	Simian immunodeficiency virus - mon		1		1		
	10000506	Simian immunodeficiency virus - sm - sm PT573		1		1		
	31683	Simian immunodeficiency virus - stm		3		3		
	11737	Simian immunodeficiency virus (F236/SMH4 ISOLATE) (SOOTY MANGABEY)		7		7		
	11736	Simian immunodeficiency virus (K78 ISOLATE)		13		13		
	11733	Simian immunodeficiency virus (MM142-83 ISOLATE)		50		50		
	11734	Simian immunodeficiency virus (MM251 ISOLATE)		1		1		
	160753	Simian immunodeficiency virus 17E-Fr		2		2		
	11942	Simian retrovirus 1	1		1			

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	444186	Simian rotavirus A strain TUCH		5		5		
	10923	Simian rotavirus A/SA11	8	5	8	5		
	37137	Simian rotavirus A/SA11-both	20	2	20	2		
	10633	Simian virus 40	14	42	14	42		
	10001763	Simian virus 40 strain 776		1		1		
	31608	Simian virus 5 (isolate canine/CPI+)	1		1			
	57667	Simian-Human immunodeficiency virus		1		1		
	37705	Sin Nombre virus	1	29	1	29		
	10000544	Sin Nombre virus NM H10	4		4			
	3728	Sinapis alba	2		2			
	11034	Sindbis virus	9		9			
	366394	Sinorhizobium medicae WSM419		1		1		
	382	Sinorhizobium meliloti		1		1		
	266834	Sinorhizobium meliloti 1021		2		2		
	254355	Small ruminant lentivirus	1		1			
	10001307	Small ruminant lentivirus strain It-561	1		1			
	10001308	Small ruminant lentivirus strain It-Pi1	1		1			
	11780	Snyder-Theilen feline sarcoma virus	1		1			
	28375	Soil-borne wheat mosaic virus	1		1			
	4081	Solanum lycopersicum	3		3			
	11307	Sonchus yellow net virus		1		1		
	286542	Soochong virus-2		1		1		
	11984	Southampton virus	1		1			
	58024	Spermatophyta	3		3			
	13687	Sphingomonas		1	1	2	1	1
	185949	Sphingomonas aurantiaca		1		1		
	2133	Spiroplasma citri		1		1		
	7108	Spodoptera frugiperda		3		3		
	240426	Squirrelpox virus		1		1		
	11080	St. Louis encephalitis virus	9	1	9	1		
	11081	St. Louis encephalitis virus (strain MS1-7)	7		7			
	74722	Stachybotrys chartarum	11		11			
	1279	Staphylococcus	1		1			
	1280	Staphylococcus aureus	84	35	86	35	2	
	553583	Staphylococcus aureus A9635	1		1			
	10001662	Staphylococcus aureus Cowan 1	2		2			
	93062	Staphylococcus aureus subsp. aureus COL	17	1	17	1		
	548470	Staphylococcus aureus subsp. aureus MN8	11		11			
	282458	Staphylococcus aureus subsp. aureus MRSA252	40		40			
	158879	Staphylococcus aureus subsp. aureus N315		4		4		
	93061	Staphylococcus aureus subsp. aureus NCTC 8325	4	1	4	1		
	10001974	Staphylococcus epidermidis JCM 2414	1		1			
	1301	Streptococcus	2		2			
	1311	Streptococcus agalactiae	5		5			
	342613	Streptococcus agalactiae 18RS21	2		2			
	208435	Streptococcus agalactiae 2603V/R	1	2	1	2		
X	342614	Streptococcus agalactiae 515			1		1	
	342617	Streptococcus agalactiae CJB111	2		2			
	342615	Streptococcus agalactiae H36B	1		1			
	211110	Streptococcus agalactiae NEM316		1		1		
	355315	Streptococcus agalactiae serogroup Ia	1		1			
	216495	Streptococcus agalactiae serogroup III	12		12			

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	10001900	Streptococcus agalactiae serogroup III M781	1	1	1	1		
	216466	Streptococcus agalactiae serogroup V	1		1			
	10001663	Streptococcus anginosus K214-2K	4		4			
	1317	Streptococcus downei	2	1	2	1		
	119602	Streptococcus dysgalactiae subsp. equisimilis	21		21			
	10001676	Streptococcus dysgalactiae subsp. equisimilis ATCC 12388	2		2			
	10001641	Streptococcus dysgalactiae subsp. equisimilis D181	1		1			
	1336	Streptococcus equi	22	14	22	14		
	1309	Streptococcus mutans	141	89	141	89		
	10000974	Streptococcus mutans GS-5		14		14		
	10000773	Streptococcus mutans MT 8148	40	12	40	12		
	857099	Streptococcus mutans OMZ175	2	1	2	1		
	1303	Streptococcus oralis	12		12			
	1313	Streptococcus pneumoniae	20	6	21	8	1	2
	216600	Streptococcus pneumoniae 23F	5		5			
	10001644	Streptococcus pneumoniae CCUG 1378	1		1			
	10001645	Streptococcus pneumoniae CSR-SCS-2	1		1			
	373153	Streptococcus pneumoniae D39		52		52		
	171101	Streptococcus pneumoniae R6		5		5		
	170187	Streptococcus pneumoniae TIGR4		2		2		
	10001651	Streptococcus pneumoniae type 14	17		17			
	10001731	Streptococcus pneumoniae type 2	1		1			
	10001638	Streptococcus pneumoniae type 27	2		2			
	10001792	Streptococcus pneumoniae type 3	1		1			
	10001646	Streptococcus pneumoniae type 37	2		2			
	10001686	Streptococcus pneumoniae type 6A	2		2			
	10001687	Streptococcus pneumoniae type 6B	5		5			
	10001730	Streptococcus pneumoniae type 6C	1		1			
	1314	Streptococcus pyogenes	122	115	124	115	2	
	10000775	Streptococcus pyogenes 156	1		1			
	10000776	Streptococcus pyogenes 88/25	1		1			
	10000777	Streptococcus pyogenes 88/30	1		1			
	10000778	Streptococcus pyogenes 88/544	1		1			
	10000779	Streptococcus pyogenes 90/85	1		1			
	10000781	Streptococcus pyogenes BSA10	3		3			
	160490	Streptococcus pyogenes M1 GAS	13	1	13	2		1
	286636	Streptococcus pyogenes MGAS10394		1		1		
	10000782	Streptococcus pyogenes NS1	1		1			
	10000783	Streptococcus pyogenes NS14	1		1			
	10000784	Streptococcus pyogenes NS27	1		1			
	10000785	Streptococcus pyogenes NS5	1		1			
	10000786	Streptococcus pyogenes serotype M11	2		2			
	342023	Streptococcus pyogenes serotype M12	3	1	3	1		
	10000780	Streptococcus pyogenes serotype M12 A374	1		1			
	10000787	Streptococcus pyogenes serotype M13	1		1			
	301451	Streptococcus pyogenes serotype M18	1		1			
	404330	Streptococcus pyogenes serotype M2	2		2			
	10000788	Streptococcus pyogenes serotype M22	1		1			
	10000789	Streptococcus pyogenes serotype M24	6	2	6	2		
	301448	Streptococcus pyogenes serotype M3	1		1			
	10000542	Streptococcus pyogenes serotype M3 D58	4		4			
	10000790	Streptococcus pyogenes serotype M30	1		1			

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	404331	Streptococcus pyogenes serotype M4	2		2			
	10000791	Streptococcus pyogenes serotype M41	1		1			
	301452	Streptococcus pyogenes serotype M49	1		1			
	301449	Streptococcus pyogenes serotype M5	56	57	56	57		
	10000792	Streptococcus pyogenes serotype M52	1		1			
	10000793	Streptococcus pyogenes serotype M54	1		1			
	10000794	Streptococcus pyogenes serotype M55	1		1			
	10000795	Streptococcus pyogenes serotype M57	1		1			
	301450	Streptococcus pyogenes serotype M6	9	7	9	7		
	10000824	Streptococcus pyogenes serotype M6 strain D471	4		4			
	10000796	Streptococcus pyogenes serotype M60	1		1			
	10000797	Streptococcus pyogenes serotype M75	1		1			
	10000798	Streptococcus pyogenes serotype M8	1		1			
	410069	Streptococcus pyogenes serotype M80	1		1			
	160491	Streptococcus pyogenes str. Manfredo	3	35	3	35		
	10001975	Streptococcus salivarius JCM 5707	1		1			
	1305	Streptococcus sanguinis		1		1		
	10001439	Streptococcus sanguinis strain BD113-20		6		6		
	1310	Streptococcus sobrinus	1		1			
	246202	Streptococcus sobrinus 6715	4	4	4	4		
	1324	Streptococcus sp. G148	14	5	14	5		
	36470	Streptococcus sp. 'group A'	12		12			
	1319	Streptococcus sp. 'group B'	1		1			
	1307	Streptococcus suis	1		1			
	1349	Streptococcus uberis	8		8			
	1902	Streptomyces coelicolor		2		2		
	100226	Streptomyces coelicolor A3(2)		1		1		
	1946	Streptomyces kasugaensis		1		1		
	1916	Streptomyces lividans	7		8		1	
	80859	Streptomyces ribosidificus		1		1		
	465541	Streptomyces sp. Mg1		1		1		
	35297	Striped Jack nervous necrosis virus	1		1			
	8801	Struthio camelus	2		2			
	7726	Styela plicata	6		6			
	186540	Sudan ebolavirus	2	262	2	279		17
	128948	Sudan ebolavirus - Boniface (1976)	1	1	2	1	1	
	128949	Sudan ebolavirus - Maleo (1979)		30		30		
	386033	Sudan ebolavirus - Uganda (2000)	1	6	1	6		
	10345	Suid herpesvirus 1	2	2	2	2		
	10349	Suid herpesvirus 1 (strain NIA-3)	4		4			
	33703	Suid herpesvirus 1 strain Kaplan	4		4			
	9823	Sus scrofa	104	43	104	44		1
	9825	Sus scrofa domesticus		4		4		
	10000187	Sus scrofa Landrace X Large White	1		1			
	10001097	Sus scrofa Yorkshire	1		1			
	12075	Swine vesicular disease virus	1		1			
	12076	Swine vesicular disease virus (STRAIN H/3 '76)	5		5			
	12077	Swine vesicular disease virus (STRAIN UKG/27/72)	3		3			
	10000809	Swine vesicular disease virus ITL/1/66	1		1			
	10000842	Swine vesicular disease virus NET/1/92	1		1			
	10001002	Swine vesicular disease virus SPA/1/93	16		16			
	10276	Swinepox virus		1		1		

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	32049	Synechococcus sp. PCC 7002		1		1		
	1148	Synechocystis sp. PCC 6803		2		2		
	11631	Tacaribe virus		106		106		
	31616	Tacaribe virus strain V7		1		1		
	6207	Taenia crassiceps	11	1	11	1		
	10000802	Taenia crassiceps Strain ORF	3	3	3	3		
	6203	Taenia ovis	8		8			
	6206	Taenia saginata	6		6			
	6204	Taenia solium	18	4	19	4	1	
	59729	Taeniopygia guttata		1		1		
	186541	Tai Forest ebolavirus		1		1		
	128999	Tai Forest virus - Cote d'Ivoire, Cote d'Ivoire, 1994		3	1	3	1	
	127999	Tanacetum parthenium		1		1		
	425088	Tanganya virus		1		1		
	630277	Tarsius lariang		1		1		
	28871	Taterapox virus		4		4		
	10001712	Taylorella asinigenitalis ATCC 700933	1		1			
	743973	Taylorella equigenitalis ATCC 35865	1		1			
	99883	Tetraodon nigroviridis		1		1		
	398812	TGEV virulent Purdue	4		4			
	5874	Theileria annulata	1		1			
	353154	Theileria annulata strain Ankara		4		4		
	5875	Theileria parva	28	17	28	17		
	10001243	Theileria parva strain Marikebuni		1		1		
	333668	Theileria parva strain Muguga	14	16	14	16		
	10000848	Theileria sergenti Type B1		1		1		
	10000849	Theileria sergenti Type B2		2		2		
	10000850	Theileria sergenti Type C		5		5		
	10000851	Theileria sergenti Type I		1		1		
	12124	Theiler's encephalomyelitis virus		18		18		
	12125	Theiler's encephalomyelitis virus (STRAIN BEAN 8386)	16	52	16	52		
	12126	Theiler's encephalomyelitis virus (STRAIN DA)	3	2	3	2		
	10000855	Theiler's murine encephalomyelitis virus (strain BeAn 8386) (variant M2)		1		1		
	204711	Theilovirus		10		10		
	360549	Themiste hennahi	1		1			
	10479	Thermoproteus tenax virus 1	1		1			
	271	Thermus aquaticus	1		1			
	274	Thermus thermophilus	1	1	1	1		
	13286	Theromyzon tessulatum	1		1			
	4601	Thinopyrum bessarabicum		1		1		
X	83810	Thosea asigna virus				1		1
	11084	Tick-borne encephalitis virus	14	2	14	2		
	11087	Tick-borne encephalitis virus (STRAIN SOFJIN)	6		6			
	10000449	Tick-borne encephalitis virus (WESTERN SUBTYPE) - Neudoerfl	10		10			
	6887	Tityus serrulatus	92		92			
	223337	Tobacco leaf curl Zimbabwe virus		1		1		
	12242	Tobacco mosaic virus	36	13	36	13		
	10001210	Tobacco mosaic virus (strain Ni568)	1		1			
	10001209	Tobacco mosaic virus (strain PM5)	1		1			
	12243	Tobacco mosaic virus (vulgare)	1		1			
	12246	Tobacco mosaic virus strain Dahlemense	2		2			

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	12146	Tomato bushy stunt virus (STRAIN BS-3)	3		3			
	83192	Topografov virus	1		1			
	7787	Torpedo californica	148	75	148	75		
	7788	Torpedo marmorata	3	3	3	3		
X	687385	Torque teno canis virus				1		1
X	687383	Torque teno douroucouli virus				5		5
X	687384	Torque teno felis virus				1		1
X	687369	Torque teno mini virus 1				1		1
X	687371	Torque teno mini virus 3				2		2
X	687375	Torque teno mini virus 7				2		2
X	687376	Torque teno mini virus 8				2		2
X	687386	Torque teno sus virus 1a			10	1	10	1
X	1218488	Torque teno sus virus k2			11		11	
X	687382	Torque teno tamarin virus				2		2
	68887	Torque teno virus	5		5	93		93
X	687340	Torque teno virus 1				3		3
X	687350	Torque teno virus 11				1		1
X	687351	Torque teno virus 12				1		1
X	687353	Torque teno virus 14				5		5
X	687354	Torque teno virus 15				3		3
X	687355	Torque teno virus 16				4		4
X	687341	Torque teno virus 2				4		4
X	687359	Torque teno virus 20				2		2
X	687360	Torque teno virus 21				2		2
X	687362	Torque teno virus 23				2		2
X	687363	Torque teno virus 24				3		3
X	687365	Torque teno virus 26				5		5
X	687367	Torque teno virus 28				3		3
X	687368	Torque teno virus 29				4		4
X	687342	Torque teno virus 3				4		4
X	687346	Torque teno virus 7				3		3
X	687347	Torque teno virus 8				6		6
X	486281	Torque teno virus Chimpanzee/Japan/Pt-TTV6/2000				6		6
X	486278	Torque teno virus Human/China/CT23F/2001				5		5
X	486279	Torque teno virus Human/China/CT39F/2001				2		2
X	486276	Torque teno virus Human/Germany/KAV/2001				2		2
X	487067	Torque teno virus Human/Ghana/GH1/1996				3		3
X	486277	Torque teno virus Human/Japan/SANBAN/1999				5		5
X	486275	Torque teno virus Human/Japan/TRM1/1999				3		3
X	486282	Torque teno virus Japanese macaque/Japan/Mf-TTV9/2000				3		3
X	486280	Torque teno virus VT416				3		3
	6265	Toxocara canis	3		3			
	5811	Toxoplasma gondii	52	60	62	60	10	
	10000353	Toxoplasma gondii 76K	5	5	5	5		
	10000354	Toxoplasma gondii BK	1	1	1	1		
X	10002052	Toxoplasma gondii Gansu Jingtai			16		16	
	507601	Toxoplasma gondii GT1		1		1		
	508771	Toxoplasma gondii ME49	21	7	21	7		
	10000355	Toxoplasma gondii Prugniaud		1		1		
	383379	Toxoplasma gondii RH	24	19	24	19		
X	1209525	Toxoplasma gondii type I				1		1
X	1209523	Toxoplasma gondii type II				1		1

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	432359	Toxoplasma gondii VEG	14		14			
	11149	Transmissible gastroenteritis virus	11		11			
	10001154	Transmissible gastroenteritis virus MAD88	8	1	8	1		
	158	Treponema denticola		1		1		
	160	Treponema pallidum	6	2	6	2		
	10001021	Treponema pallidum subsp. pallidum (strain Chicago)	19		19			
	243276	Treponema pallidum subsp. pallidum str. Nichols	277	9	277	9		
	6334	Trichinella spiralis	7	2	7	2		
	203124	Trichodesmium erythraeum IMS101		2		2		
	5722	Trichomonas vaginalis	2		2			
	81847	Trichophyton quinckeanum	1		1			
	5551	Trichophyton rubrum	2	27	2	27		
	3677	Trichosanthes kirilowii	1		1			
	5554	Trichosporon cutaneum	1		1			
	9337	Trichosurus vulpecula	45		45			
	4565	Triticum aestivum	519	307	577	309	58	2
	4567	Triticum durum		1		1		
	4568	Triticum monococcum		1		1		
	279889	Triticum spelta var. arduini		3		3		
	5691	Trypanosoma brucei	12	6	13	6	1	
	5702	Trypanosoma brucei brucei	5		5			
	31285	Trypanosoma brucei gambiense	2		2			
	31286	Trypanosoma brucei rhodesiense		9		9		
	5693	Trypanosoma cruzi	129	410	129	410		
	10000347	Trypanosoma cruzi Dm28c	2		2			
	10000348	Trypanosoma cruzi G	1		1			
	353153	Trypanosoma cruzi strain CL Brener	2		2			
	10000351	Trypanosoma cruzi Y	1		1			
X	93678	TTV-like mini virus				1		1
X	167758	TTV-like virus DXL1				10		10
	37133	Tula virus	1	9	1	9		
	37347	Tupaia belangeri		1		1		
	63673	Turbo cornutus	2		2			
	11152	Turkey coronavirus	1		1			
	32644	unidentified		1		1		
	11309	unidentified influenza virus		1		1		
	237631	Ustilago maydis 521		1		1		
	10245	Vaccinia virus	1	439	2	452	1	13
	10001973	Vaccinia virus Acambis 2000	1		1			
	332193	Vaccinia Virus Acambis 3000 MVA		2		20		18
	126794	Vaccinia virus Ankara		22		22		
	10001027	Vaccinia virus Connaught	1		1			
	10249	Vaccinia virus Copenhagen	31	549	31	792		243
	502057	Vaccinia virus GLV-1h68		2		2		
	10251	Vaccinia virus IHD-J	1		1			
	10248	Vaccinia virus LC16M8		4		4		
	31531	Vaccinia virus L-IPV		8		8		
	10000388	Vaccinia virus NYCBH - Dryvax		29		29		
	10253	Vaccinia virus Tian Tan		15		15		
	696871	Vaccinia virus Western Reserve		4		4		
	10254	Vaccinia virus WR	26	5527	26	6302		775
	10247	Vaccinia virus WR 65-16		4		4		

NEW 2013	ORGAN-ISM ID	SPECIES/STRAIN	B-12	T-12	B-13	T-13	Δ B	Δ T
	12870	Variola major virus		16		16		
	10000390	Variola major virus India-1967		1		1		
	53258	Variola minor virus		93		93		
	10255	Variola virus		228		228		
	587200	Variola virus human/India/Ind3/1967		1		1		
	11036	Venezuelan equine encephalitis virus		1	2	1	2	
	36382	Venezuelan equine encephalitis virus (strain 3880)		1		1		
	11037	Venezuelan equine encephalitis virus (strain TC-83)	22		22			
	11038	Venezuelan equine encephalitis virus (strain Trinidad donkey)	15		15			
	7742	Vertebrata	4		4			
	11277	Vesicular stomatitis Indiana virus	6	7	6	7		
	11278	Vesicular stomatitis Indiana virus strain Glasgow		1		1		
	11279	Vesicular stomatitis Indiana virus strain Mudd-Summers	1		1			
	11285	Vesicular stomatitis Indiana virus strain San Juan		1		1		
	11280	Vesicular stomatitis New Jersey virus		1		1		
	11276	Vesicular stomatitis virus		8		8		
	7444	Vespa basalis	1		1			
	7453	Vespula maculifrons	1		1			
	7454	Vespula vulgaris	2	95	2	95		
	314288	Vibrio alginolyticus 12G01		3		3		
	55601	Vibrio anguillarum	1		1			
	666	Vibrio cholerae	38	90	38	90		
	412966	Vibrio cholerae 1587		1		1		
	412614	Vibrio cholerae 2740-80		28		28		
	44104	Vibrio cholerae 569B	37		37			
	404974	Vibrio cholerae AM-19226		1		1		
	417400	Vibrio cholerae B33		1		1		
	412967	Vibrio cholerae MAK 757		5		5		
	345072	Vibrio cholerae MO10		1		1		
	417399	Vibrio cholerae NCTC 8457		1		1		
	127906	Vibrio cholerae O1	9		9			
	686	Vibrio cholerae O1 biovar El Tor	3	1	3	1		
	243277	Vibrio cholerae O1 biovar El Tor str. N16961	1	2	1	2		
	10000567	Vibrio cholerae O1 serotype Inaba	1		1			
	10000568	Vibrio cholerae O1 serotype Ogawa	5		5			
	345073	Vibrio cholerae O395		4		4		
	345074	Vibrio cholerae RC385		1		1		
	345075	Vibrio cholerae V51		1		1		
	345076	Vibrio cholerae V52		31		31		
	670	Vibrio parahaemolyticus		57		57		
	563773	Vibrio parahaemolyticus AN-5034		3		3		
	419109	Vibrio parahaemolyticus AQ3810		32		32		
	627611	Vibrio parahaemolyticus K5030		12		12		
	223926	Vibrio parahaemolyticus RIMD 2210633	2	16	2	16		
	70203	Vibrio phage fs1		1		1		
	150340	Vibrio sp. Ex25		9		9		
	314291	Vibrio splendidus 12B01		2		2		
	575788	Vibrio splendidus LGP32		1		1		
	672	Vibrio vulnificus	1	66	1	66		
	216895	Vibrio vulnificus CMCP6		50		50		
	196600	Vibrio vulnificus YJ016		56		56		
	8704	Vipera ammodytes	1		1			

NEW 2013	ORGANISM ID	SPECIES/STRAIN	B-12	T-12	B-13	T-13	Δ B	Δ T
	194601	Vipera aspis aspis	3		3			
	11288	Viral hemorrhagic septicemia virus 07-71	12	1	12	1		
	3972	Viscum album	17		17			
	11743	Visna lentivirus (strain 1514 / clone LV1-1KS1)	4		4			
	11742	Visna lentivirus (strain 1514)	1		1			
	11741	Visna/maedi virus	5	7	5	7		
	12750	Visna/maedi virus EV1	1		1			
	36374	Visna/maedi virus EV1 KV1772	2		2			
	29760	Vitis vinifera	1		1			
	74537	Vladivostok virus	1		1			
	9627	Vulpes vulpes	1		1			
	148360	Watermelon mosaic virus 2 (isolate USA)	2		2			
	43141	Watermelon silver mottle virus	3		3			
	11082	West Nile virus	31	398	48	415	17	17
	10000447	West Nile virus 3000.0259	2		2			
	10000971	West Nile virus NY-99	14	21	14	21		
	449278	West Nile virus SPU116/89		1		1		
	10001047	West Nile virus strain 2741	32		32			
	307044	West Nile virus strain 385-99	22	12	22	12		
	10001879	West Nile virus strain 68856	2		2			
	10001649	West Nile virus strain 956	1		1			
	406269	West Nile virus strain PTRoxo		12		12		
	11039	Western equine encephalitis virus		1		1		
	46919	Whitewater Arroyo virus		344		349		5
	10001617	Whitewater Arroyo virus strain AV9310135		1		1		
	163164	Wolbachia endosymbiont of Drosophila melanogaster		1		1		
	35269	Woodchuck hepatitis virus	4	2	4	6		4
	10430	Woodchuck hepatitis virus 1	3		3			
	341946	Woodchuck hepatitis virus 2	4		4			
	10433	Woodchuck hepatitis virus 8		34		34		
	6293	Wuchereria bancrofti	12	7	12	7		
	280	Xanthobacter autotrophicus		1		1		
	78245	Xanthobacter autotrophicus Py2		1		1		
	8364	Xenopus (Silurana) tropicalis		2		2		
	8355	Xenopus laevis		2		2		
	132475	Yaba-like disease virus		3		3		
	11089	Yellow fever virus		280		373		93
	11090	Yellow fever virus 17D		220		299		79
	617102	Yellow fever virus 17D/Tiantan	4	2	4	5		3
	31641	Yellow fever virus 1899/81		21		21		
	407141	Yellow fever virus isolate Ethiopia/Couma/1961		2		2		
	407134	Yellow fever virus strain Ghana/Asibi/1927		5		5		
	349968	Yersinia bercovieri ATCC 43970		5		5		
	630	Yersinia enterocolitica	6	26	6	26		
	34054	Yersinia enterocolitica (type O:8)		1		1		
	393305	Yersinia enterocolitica subsp. enterocolitica 8081		16		16		
	349966	Yersinia frederiksenii ATCC 33641		1		1		
	28152	Yersinia kristensenii		1		1		
	349967	Yersinia mollaretii ATCC 43969		3		3		
	632	Yersinia pestis	15	140	21	145	6	5
	10000757	Yersinia pestis 195/P	5		5			
	349746	Yersinia pestis Angola		3		3		

NEW 2013	ORGAN-ISM ID	SPECIES/STRAIN	B-12	T-12	B-13	T-13	Δ B	Δ T
	360102	Yersinia pestis Antiqua		34		34		
	412420	Yersinia pestis CA88-4125		21		21		
	214092	Yersinia pestis CO92	4	19	4	19		
	375450	Yersinia pestis FV-1		2		2		
	10000756	Yersinia pestis KIM 5	21		21			
	187410	Yersinia pestis KIM10+		10		10		
	377628	Yersinia pestis Nepal516		110		110		
	386656	Yersinia pestis Pestoides F		1		1		
	633	Yersinia pseudotuberculosis		1		1		
	349747	Yersinia pseudotuberculosis IP 31758		7		7		
	10001895	Yersinia pseudotuberculosis str. 32777		1		1		
	10001504	Yokenella regensburgei PCM 2476	1		1			
	10001505	Yokenella regensburgei PCM 2477	1		1			
	186538	Zaire ebolavirus	5	812	5	833		21
	129000	Zaire ebolavirus - Eckron (Zaire, 1976)		12		12		
	128947	Zaire ebolavirus - Gabon (1994-1997)		18		18		
	128951	Zaire ebolavirus - Zaire (1995)		1		1		
	4577	Zea mays	2	1	3	1	1	
	34245	Zinnia violacea		1		1		
	157914	Ziziphus mauritiana	4		4			

2 Website Features

There were two releases of the IEDB external website during 2013. IEDB 2.11 was released in August and IEDB 2.12 was released in December. In addition, there were two minor releases of the Analysis Resource to fix bugs (Release 2.9.1 and 2.9.2), and two major releases – Release 2.10 in September and Release 2.11 in December. Release 2.10 saw the addition of a new MHC class I immunogenicity tool and a new MHC class I peptide processing prediction tool (MHC-NP). A new version of DiscoTope for predicting discontinuous B cell epitopes was also added. Release 2.11 included Paratome, a new tool to predict the antigen binding regions of antibodies. The features introduced since the last Annual Compendium include:

Main IEDB website:

- Redesigned organism finder and integrated into simple and advanced searches.
- Updated multi-select boxes on Advanced Search screens to be more user-friendly.
- Combined MHC Binding with MHC Ligand Elution data throughout site.
- Added new “alpha” query interface to homepage searches which provides improved filtering capabilities and immediate tabular search results.

Analysis Resource website:

- New tools added:
    - Class I Immunogenicity tool has been added that predicts the immunogenicity of class I peptide-MHC complexes based upon amino acid properties
    - MHC-NP is a new tool to predict class I MHC peptide processing and binding based upon MHC elution data. It was the winner of the 2012 MLI competition and we developed by Sébastien Giguère Alexandre Drouin, Alexandre Lacoste, Mario Marchand, Jacques Corbeil and François Laviolette
    - Version 2.0 of Discotope is now available, in addition to version 1.1
    - Paratome, developed by the lab of Yanay Ofran, can be used to predict the antigen binding regions (ABRs) of antibodies and accepts either a sequence or PDB structure as input.
- MHC I/II binding & processing (web)
    - Form validation updated to identify peptides that are too short for which to make predictions, while making predictions for those that are long enough
    - Prediction limits changed to allow the input box to contain up to 10,000 characters
- Population Coverage Tool - Backend database has been updated to include all high-resolution populations from the Allele Frequency Net database, thanks to data generously provided by Derek Middleton
- Website linkouts updated to point to new tools versions
- New 'Datasets' tab details references and dataset related to benchmarking the predictive tools
- Backend iedb_analysis database updated automatically on a weekly basis to remain in sync with the main website

The IEDB website functionality can be divided into five categories– Browse, Advanced Search, Tools, Support, and More IEDB, 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.

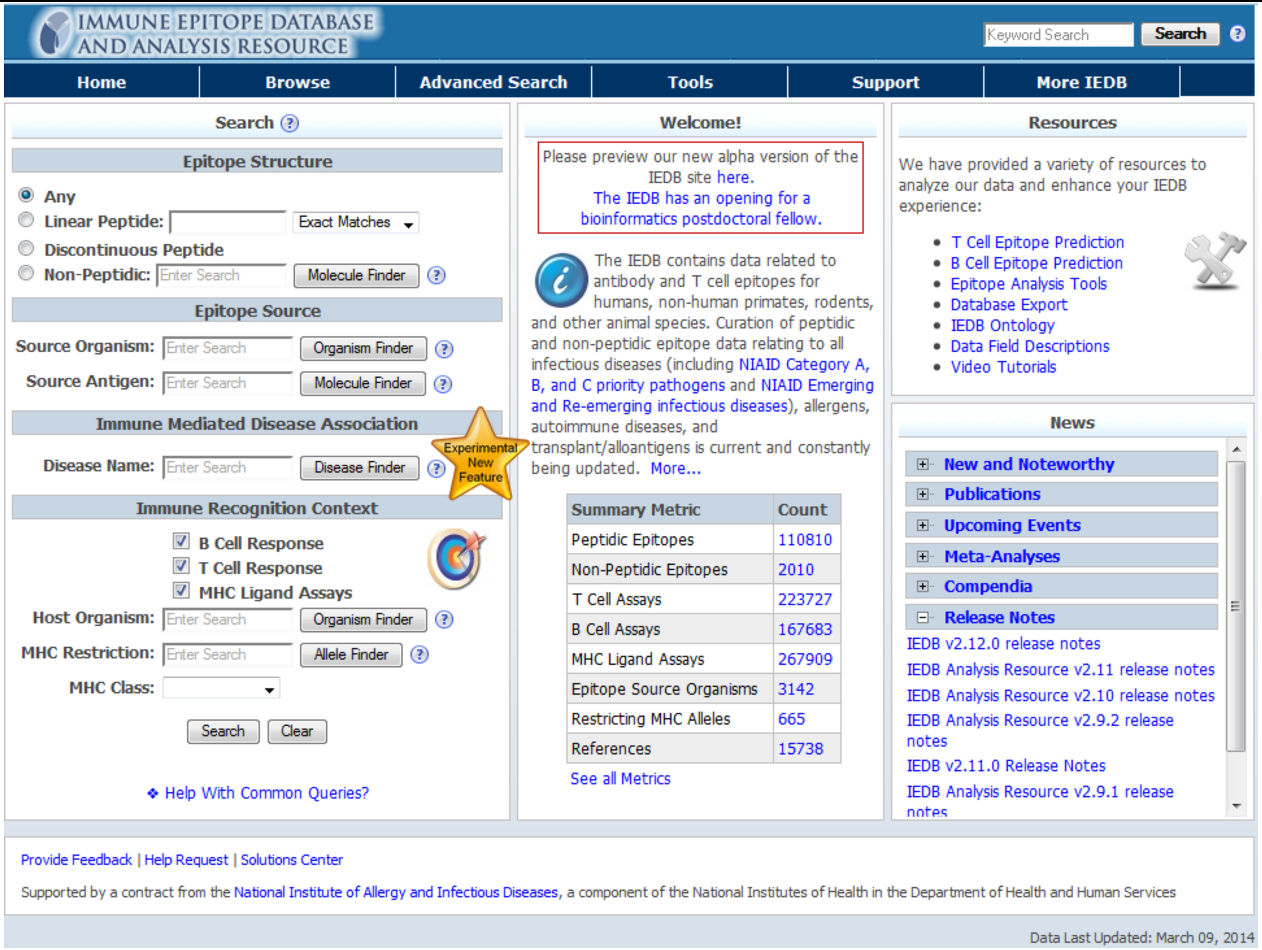
The reader will find it helpful to keep in mind how data are stored in the IEDB. Each item contained in the IEDB consists of a reference (article or submission) containing information about one or more epitopes and associated binding or response information. The same epitope can exist in multiple references.

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 a basic search capability, introductory information, Summary Metrics of the data, available Resources, and project-related News. 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.

Summary Metrics are displayed in the center column of the screen. 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. One change implemented in 2013 was the combining of MHC binding assays and MHC ligand elution assays into one category named MHC ligand assays. Clicking on the "See all Metrics" brings up a Summary Metrics page that shows the positive, negative, and total (all) count for epitopes and assays, and the counts for epitope source organism, host organism, restricting MHC allele, and references. Further detail is revealed when the user clicks on the counts.

The rightmost column has links to a variety of resources, including epitope prediction and analysis tools, database export, the IEDB ontology, and documentation describing data fields. These resources can also be accessed via the pull-down menus on the page. The News panel shows six categories – New and Noteworthy, Publications, Upcoming Events, Meta-analyses, Compendia, and Release Notes. The



Please preview our new alpha version of the IEDB site here.
The IEDB has an opening for a bioinformatics postdoctoral fellow.

The IEDB contains data related to antibody and T cell epitopes for humans, non-human primates, rodents, and other animal species. Curation of peptidic and non-peptidic epitope data relating to all infectious diseases (including NIAID Category A, B, and C priority pathogens and NIAID Emerging and Re-emerging infectious diseases), allergens, autoimmune diseases, and transplant/alloantigens is current and constantly being updated. More...

Summary Metric	Count
Peptidic Epitopes	110810
Non-Peptidic Epitopes	2010
T Cell Assays	223727
B Cell Assays	167683
MHC Ligand Assays	267909
Epitope Source Organisms	3142
Restricting MHC Alleles	665
References	15738

See all Metrics

We have provided a variety of resources to analyze our data and enhance your IEDB experience:

- T Cell Epitope Prediction
- B Cell Epitope Prediction
- Epitope Analysis Tools
- Database Export
- IEDB Ontology
- Data Field Descriptions
- Video Tutorials

⊞ New and Noteworthy
⊞ Publications
⊞ Upcoming Events
⊞ Meta-Analyses
⊞ Compendia
⊟ Release Notes
IEDB v2.12.0 release notes
IEDB Analysis Resource v2.11 release notes
IEDB Analysis Resource v2.10 release notes
IEDB Analysis Resource v2.9.2 release notes
IEDB v2.11.0 Release Notes
IEDB Analysis Resource v2.9.1 release notes

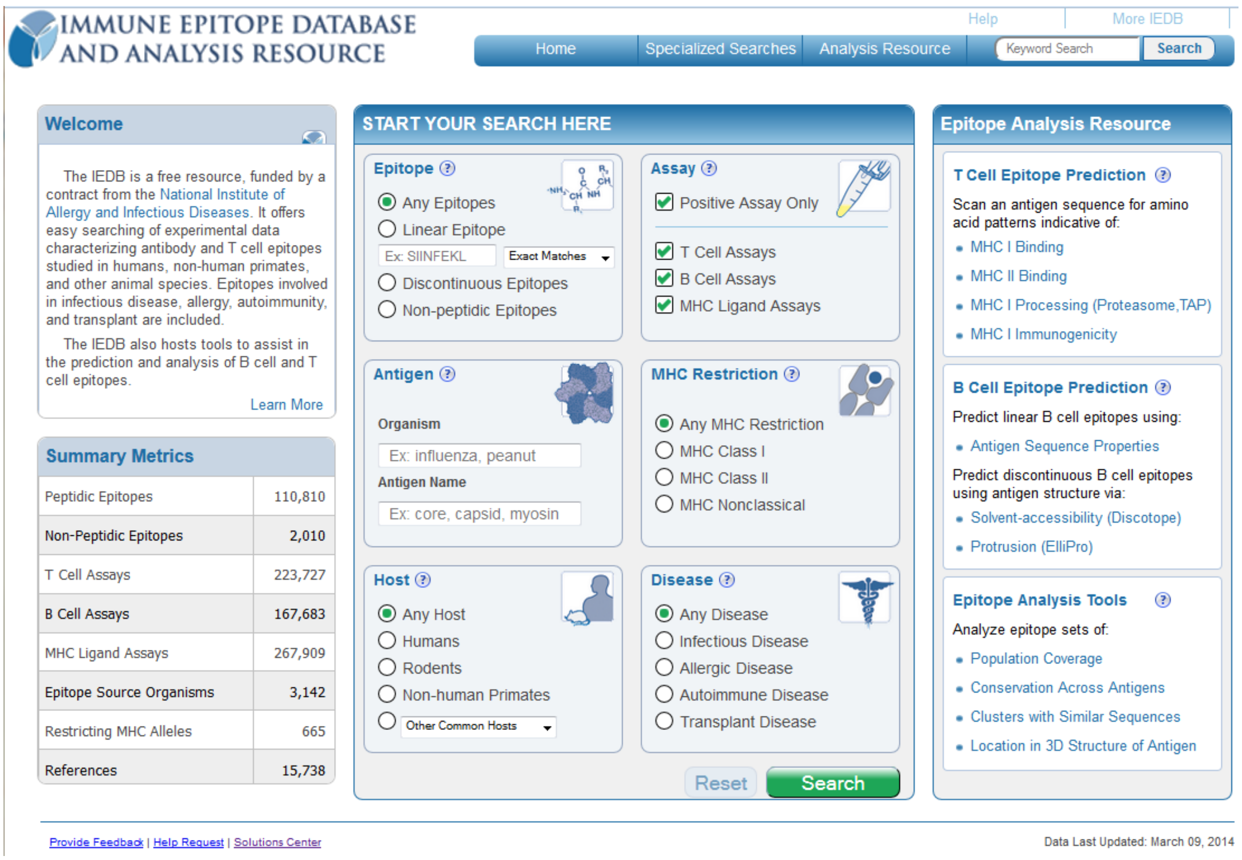
Provide Feedback | Help Request | Solutions Center

Supported by a contract from the National Institute of Allergy and Infectious Diseases, a component of the National Institutes of Health in the Department of Health and Human Services

Figure 2.1 IEDB 2.12 Home page

Newsletter category that existed previously was replaced with a New and Noteworthy category. Each category can be expanded to show its linkable content, as shown in the figure for Release Notes. The date of the latest data update is listed in the lower righthand corner of the home page.

Announcements can also be found in the red-outlined box at the top of the center section. Figure 2.1 contains a link to the IEDB 3.0 alpha website in the red box. The alpha site was deployed in December 2013 and will become the new production website for the IEDB later in 2014. Because it is still under development, it will not be described in this Compendium. The redesigned website incorporates many of the suggestions received from users over the past several years and includes improvements recommended by usability engineers. The overall goal of the redesign effort is to make the IEDB website more intuitive and easier to use. The home page of the redesigned IEDB website is shown in Figure 2.2



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	110,810
Non-Peptidic Epitopes	2,010
T Cell Assays	223,727
B Cell Assays	167,683
MHC Ligand Assays	267,909
Epitope Source Organisms	3,142
Restricting MHC Alleles	665
References	15,738

START YOUR SEARCH HERE

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

Assay
- ☑ Positive Assay Only
- ☑ T Cell Assays
- ☑ B Cell Assays
- ☑ MHC Ligand Assays

Antigen

Organism: Ex: influenza, peanut

Antigen Name: Ex: core, capsid, myosin

MHC Restriction
- ● Any MHC Restriction
- ○ MHC Class I
- ○ MHC Class II
- ○ MHC Nonclassical

Host
- ● Any Host
- ○ Humans
- ○ Rodents
- ○ Non-human Primates
- ○ Other Common Hosts

Disease
- ● Any Disease
- ○ Infectious Disease
- ○ Allergic Disease
- ○ Autoimmune Disease
- ○ Transplant Disease

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:
- Solvent-accessibility (Discotope)
- Protrusion (ElliPro)

Epitope Analysis Tools

Analyze epitope sets of:
- Population Coverage
- Conservation Across Antigens
- Clusters with Similar Sequences
- Location in 3D Structure of Antigen

Data Last Updated: March 09, 2014

Figure 2.2 Home page of the redesigned IEDB website (alpha release)

2.2 Browse

The IEDB allows users to browse for records in three different ways – by MHC allele, by source organism, and by 3D structure.

Browse By MHC Allele ?

- bonobo (Pan paniscus) (1 structure(s)*)
- cattle (Bos taurus) (551 structure(s)*)
- chicken (Gallus gallus) (127 structure(s)*)
- chimpanzee (Pan troglodytes) (777 structure(s)*)
- cotton-top tamarin (Saguinus oedipus) (2 structure(s)*)
- dog (Canis lupus familiaris) (30 structure(s)*)
- gorilla (Gorilla gorilla) (15 structure(s)*)
- horse (Equus caballus) (93 structure(s)*)
- human (Homo sapiens) (72874 structure(s)*)
- mouse (Mus musculus) (21173 structure(s)*)
- organism (all species) (12966 structure(s)*)
- pig (Sus scrofa) (69 structure(s)*)
- rat (Rattus norvegicus) (384 structure(s)*)
- rhesus macaque (Macaca mulatta) (4912 structure(s)*)
  - Class I (4805 structure(s)*)
    - Mamu-A*01 (2166 structure(s)*)
    - Mamu-A*02 (608 structure(s)*)
    - Mamu-A*08 (1 structure(s)*)
    - Mamu-A*11 (926 structure(s)*)
    - Mamu-B*01 (643 structure(s)*)
    - Mamu-B*03 (32 structure(s)*)
    - Mamu-B*04 (9 structure(s)*)
    - Mamu-B*08 (10 structure(s)*)
    - Mamu-B*17 (1373 structure(s)*)
  - Class II (108 structure(s)*)
- sheep (Ovis aries) (8 structure(s)*)

* Indicates the number of distinct molecular structures tested in the context of the selected group of MHC molecules.

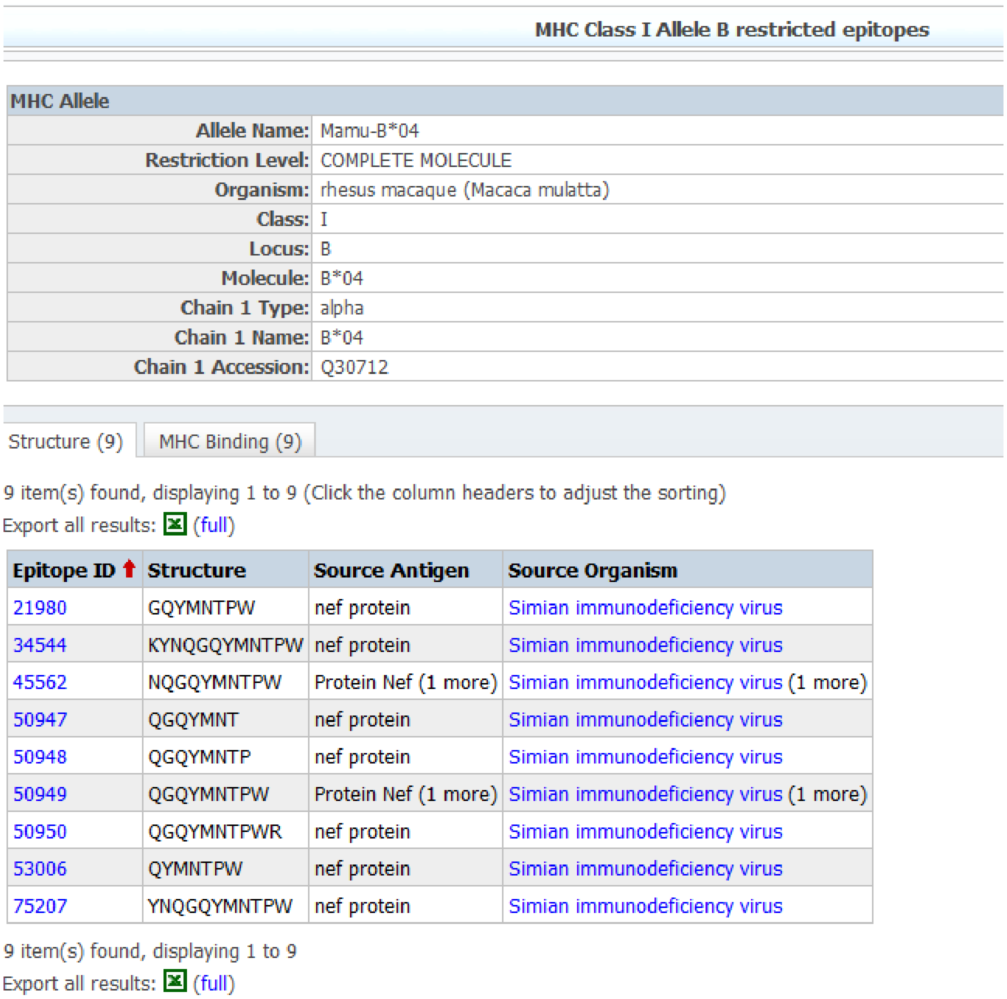
Figure 2.3 Browse by MHC Allele interface

2.2.1 Browse Records by MHC Allele

All users can find records associated with a specific MHC allele by browsing records by allele. To browse records by allele, the user selects *Browse by MHC Allele* under the *Browse* heading on the main menu. The interface for the Browse by MHC Allele is a tree structure that makes it easy for users to find and investigate information on specific MHC alleles. As Figure 2.3 shows, the tree structure expands (and collapses) so users can drill down on species, MHC type, and allele to find the number of distinct molecular structures tested in the context of the selected group of MHC molecules. This number serves as a link that will display the records associated with the selected allele. As an example, clicking on Mamu-B*04 leads to the MHC Class I Allele B restricted epitopes page for that allele (Figure 2.4). A help link, shown as a “?” to the right of the page title directs the user to information in the IEDB Solutions Center.

2.2.2 Browse Records by Source Organism

Users can find records associated with a specific epitope source species by browsing records by source organism. To do this, the user accesses the *Browse by Source Organism* page via the Browse pull-down menu. The interface for the Browse by Source Organism is a tree structure that expands (and collapses) so users can drill down on species as Figure 2.5 shows. Each entry in the tree indicates the number of distinct molecular structures tested from the selected group of source organisms. This number serves as a link that will display the records associated with the selected source organism. The user can also search for names. For example, a search for "human", as shown in Figure 2.6, generates a table of responses for the term and corresponding synonyms. If the user clicks on [Details], Source Organism Information is displayed. The page for the first result, Homo sapiens, is displayed in Figure 2.7, and includes the NCBI taxonomy identifier numbers and information on epitope structure, relevant literature and submission references, source antigens, and assays. If the user clicks on [Highlight] the tree expands and highlights the location. In the case of "Homo sapiens", the tree expands to over 20 levels. Clicking on the number structures displays the same Homo Sapiens Epitope information as seen in Figure 2.7.



MHC Class I Allele B restricted epitopes

MHC Allele

Allele Name:	Mamu-B*04
Restriction Level:	COMPLETE MOLECULE
Organism:	rhesus macaque (Macaca mulatta)
Class:	I
Locus:	B
Molecule:	B*04
Chain 1 Type:	alpha
Chain 1 Name:	B*04
Chain 1 Accession:	Q30712

9 item(s) found, displaying 1 to 9 (Click the column headers to adjust the sorting)

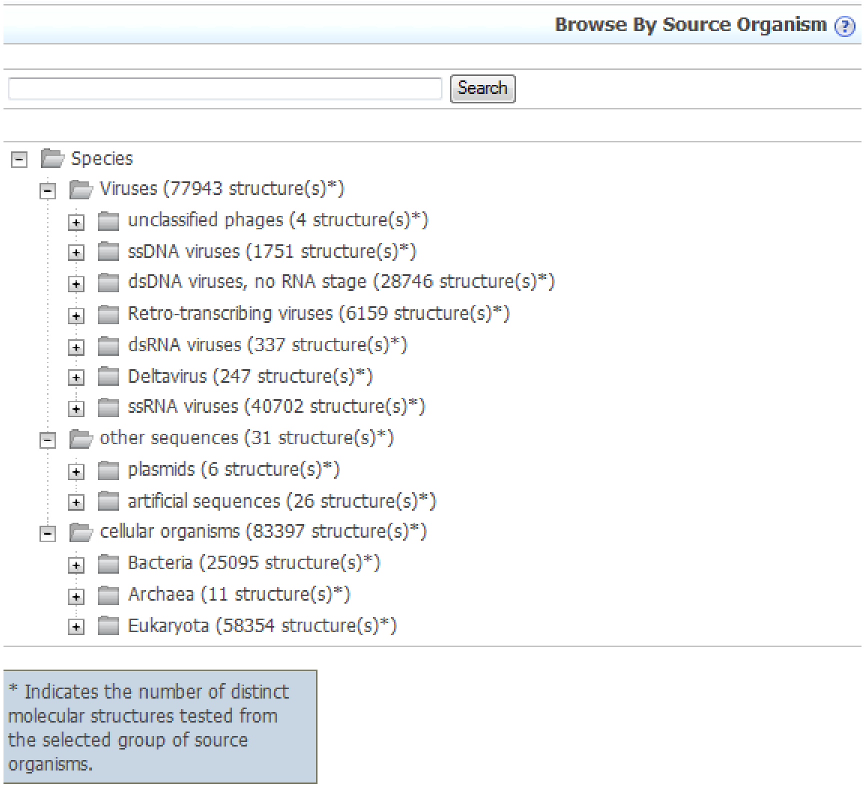
Export all results: (full)

Epitope ID	Structure	Source Antigen	Source Organism
21980	GQYMNTPW	nef protein	Simian immunodeficiency virus
34544	KYNQGQYMNTPW	nef protein	Simian immunodeficiency virus
45562	NQGQYMNTPW	Protein Nef (1 more)	Simian immunodeficiency virus (1 more)
50947	QGQYMNT	nef protein	Simian immunodeficiency virus
50948	QGQYMNTP	nef protein	Simian immunodeficiency virus
50949	QGQYMNTPW	Protein Nef (1 more)	Simian immunodeficiency virus (1 more)
50950	QGQYMNTPWR	nef protein	Simian immunodeficiency virus
53006	QYMNTPW	nef protein	Simian immunodeficiency virus
75207	YNQGQYMNTPW	nef protein	Simian immunodeficiency virus

9 item(s) found, displaying 1 to 9

Export all results: (full)

Figure 2.4 Peptide structures associated with MHC Class I Mamu-B*04 allele



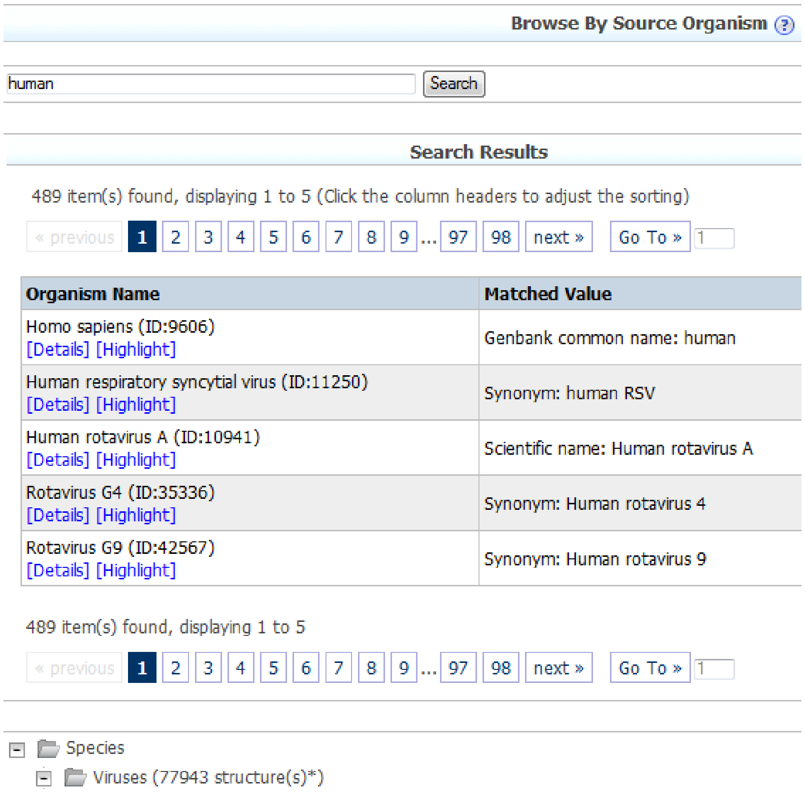
Browse By Source Organism

Search

- Species
  - Viruses (77943 structure(s)*)
    - unclassified phages (4 structure(s)*)
    - ssDNA viruses (1751 structure(s)*)
    - dsDNA viruses, no RNA stage (28746 structure(s)*)
    - Retro-transcribing viruses (6159 structure(s)*)
    - dsRNA viruses (337 structure(s)*)
    - Deltavirus (247 structure(s)*)
    - ssRNA viruses (40702 structure(s)*)
  - other sequences (31 structure(s)*)
    - plasmids (6 structure(s)*)
    - artificial sequences (26 structure(s)*)
  - cellular organisms (83397 structure(s)*)
    - Bacteria (25095 structure(s)*)
    - Archaea (11 structure(s)*)
    - Eukaryota (58354 structure(s)*)

* Indicates the number of distinct molecular structures tested from the selected group of source organisms.

Figure 2.5 Browse by Source Organism interface



Browse By Source Organism

human Search

Search Results

489 item(s) found, displaying 1 to 5 (Click the column headers to adjust the sorting)

« previous 1 2 3 4 5 6 7 8 9 ... 97 98 next » Go To » 1

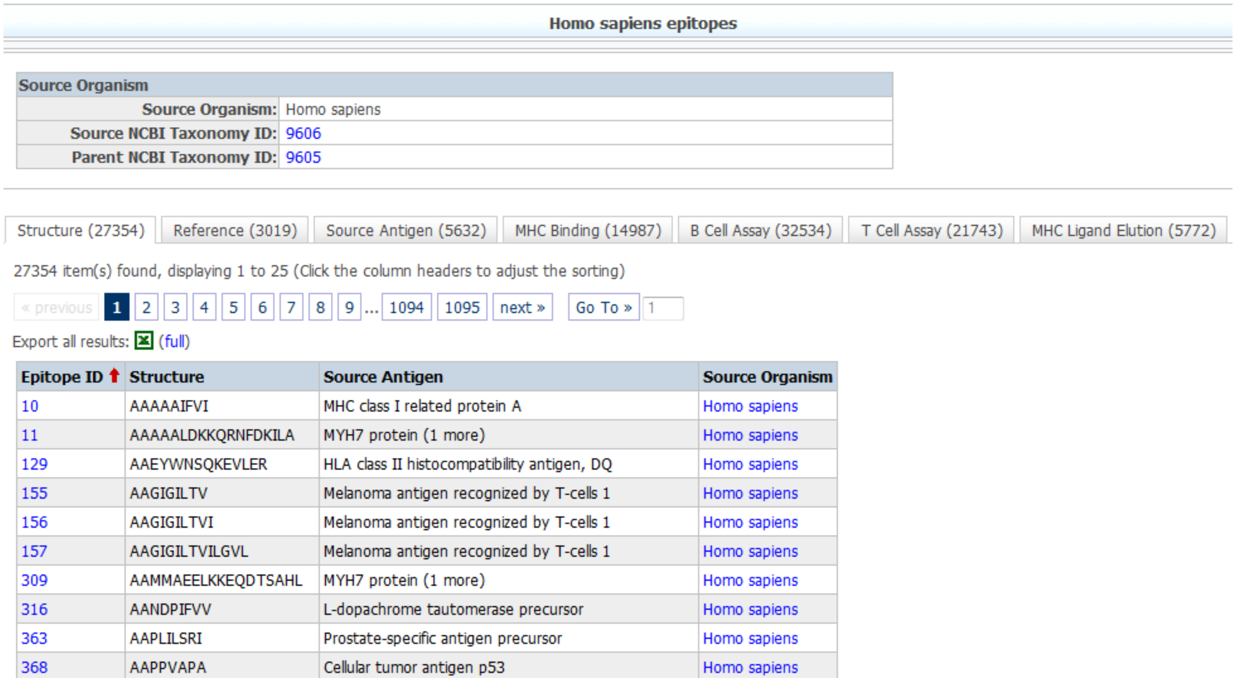
Organism Name	Matched Value
Homo sapiens (ID:9606) [Details] [Highlight]	Genbank common name: human
Human respiratory syncytial virus (ID:11250) [Details] [Highlight]	Synonym: human RSV
Human rotavirus A (ID:10941) [Details] [Highlight]	Scientific name: Human rotavirus A
Rotavirus G4 (ID:35336) [Details] [Highlight]	Synonym: Human rotavirus 4
Rotavirus G9 (ID:42567) [Details] [Highlight]	Synonym: Human rotavirus 9

489 item(s) found, displaying 1 to 5

« previous 1 2 3 4 5 6 7 8 9 ... 97 98 next » Go To » 1

- Species
  - Viruses (77943 structure(s)*)

Figure 2.6 Using the search feature on the Browse by Source Organism page



Homo sapiens epitopes

Source Organism	
Source Organism:	Homo sapiens
Source NCBI Taxonomy ID:	9606
Parent NCBI Taxonomy ID:	9605

27354 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

Epitope ID	Structure	Source Antigen	Source Organism
10	AAAAAIFVI	MHC class I related protein A	Homo sapiens
11	AAAAALDKKQRNFDKILA	MYH7 protein (1 more)	Homo sapiens
129	AAEYWNSQKEVLER	HLA class II histocompatibility antigen, DQ	Homo sapiens
155	AAGIGILTV	Melanoma antigen recognized by T-cells 1	Homo sapiens
156	AAGIGILTVI	Melanoma antigen recognized by T-cells 1	Homo sapiens
157	AAGIGILTVILGVL	Melanoma antigen recognized by T-cells 1	Homo sapiens
309	AAMMAEELKKEQDTSAHL	MYH7 protein (1 more)	Homo sapiens
316	AANDPIFVV	L-dopachrome tautomerase precursor	Homo sapiens
363	AAPLILSRI	Prostate-specific antigen precursor	Homo sapiens
368	AAPPVAPA	Cellular tumor antigen p53	Homo sapiens

Figure 2.7 Source Organism information (epitopes) for Home sapiens

2.2.3 Browse by 3D Structure

All users can find records associated with a curated 3D structure by using *Browse by 3D Structure* found under the *Browse* heading on the main menu. The interface for the Browse by 3D Structure is a tree structure that makes it easy for users to find and investigate information on B cell, T cell, and MHC binding structures. As seen in Figure 2.8, the tree structure expands (and collapses) so users can drill down on species, MHC type, and/or allele to find the number of records in the IEDB for their structure of interest. This entry serves as a link that will display the records associated with the selected structure.

Browse By 3D Structure

The B Cell, T Cell, and MHC Binding trees below are organized by the organism that is the source of the antibody, T Cell, and MHC molecule, respectively.

- B Cell (589 structure(s)*)
  - Camelus dromedarius (20 structure(s)*)
  - Cricetulus migratorius (3 structure(s)*)
  - Ginglymostoma cirratum (1 structure(s)*)
  - Homo sapiens (139 structure(s)*)
  - Lama glama (12 structure(s)*)
  - Mus musculus (407 structure(s)*)
  - Orectolobus maculatus (2 structure(s)*)
  - Oryctolagus cuniculus (1 structure(s)*)
  - Pan troglodytes (1 structure(s)*)
  - Rattus norvegicus (4 structure(s)*)
  - Rattus rattus (1 structure(s)*)
  - Vicugna pacos (2 structure(s)*)
- T Cell (56 structure(s)*)
  - Homo sapiens (31 structure(s)*)
    - Class I (20 structure(s)*)
    - Class II (8 structure(s)*)
      - DQ (2 structure(s)*)
        - HLA-DQ1 (1 structure(s)*)
        - HLA-DQA1*03:01/DQB1*03:02 (1 structure(s)*)
      - DR (7 structure(s)*)
    - Non Classical (3 structure(s)*)
  - Mus musculus (26 structure(s)*)
- MHC Binding (308 structure(s)*)
  - Bos taurus (4 structure(s)*)
  - Gallus gallus (9 structure(s)*)
  - Homo sapiens (181 structure(s)*)
  - Mus musculus (113 structure(s)*)
  - Rattus norvegicus (3 structure(s)*)
  - Sus scrofa (2 structure(s)*)

* Indicates the number of distinct molecular structures.

Figure 2.8 Browse by 3D Structure interface

2.3 Query

In addition to the Browse functions, there are several other ways users can find information in the IEDB. A keyword search is available on the menu bar on each page. 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 will be referred to as Advanced Searches in this document. 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 2.3.4. These methods are elaborated in the subsections below.

2.3.1 Perform a Keyword Search

The keyword search allows users to locate records in the database using a keyword, identifier, or sequence. Wild card characters '*' and '?' can be used in the search field. The '*' character will match zero or more characters and the '?' character will match exactly one character. Additionally, the operators 'AND', 'OR', and 'NOT' can be utilized. A logical ‘OR’ is the default option. These three logical operators can be upper or lowercase. The keyword search is case insensitive, so "ABC" is the same as "abc". Parentheses can be used to refine searches. For example, “(dengue AND malaria) NOT nucleo*” is a legal search.

To perform a search, users enter criteria such as a keyword, identifier, or sequence into the text box in the upper right corner of each page next to the “Search” button (Figure 2.1). They then click the Search button and view the Search Result Summary, which is described in Section 2.3.4.

In addition to using the search function from the menu bar, users can submit searches via a properly constructed URL. The example below will perform a search using the URL for records that contain 'dengue'. This would return the equivalent of typing 'dengue' in the search option on the menu bar and clicking the Search button.

http://www.iedb.org/counts_keyword.php?keyword_search_query_term=dengue

2.3.2 Perform a Home Page Search

The search feature available on the left-hand portion of the home page (Figure 2.9) is designed to simplify the search process for many commonly asked queries by immunologists. It allows greater control in the search than available in the keyword search and is less involved than the Advanced queries. The user specifies the epitope structure with radio button selections for *Any*, *Linear Peptide*, *Discontinuous Peptide*, and *Non-Peptidic*. The user can prescribe a linear peptide sequence and the type of search to be performed on it. When specifying a linear sequence, a window appears in which the user must enter the sequence and press "Apply". 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 user can specify a non-peptidic structure with the Molecule Finder.

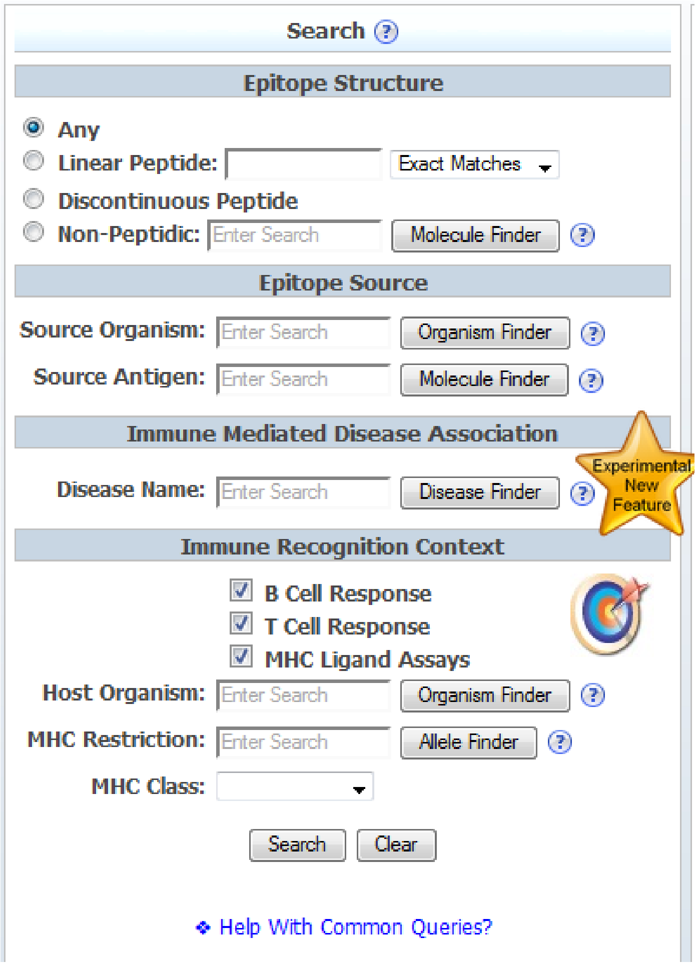
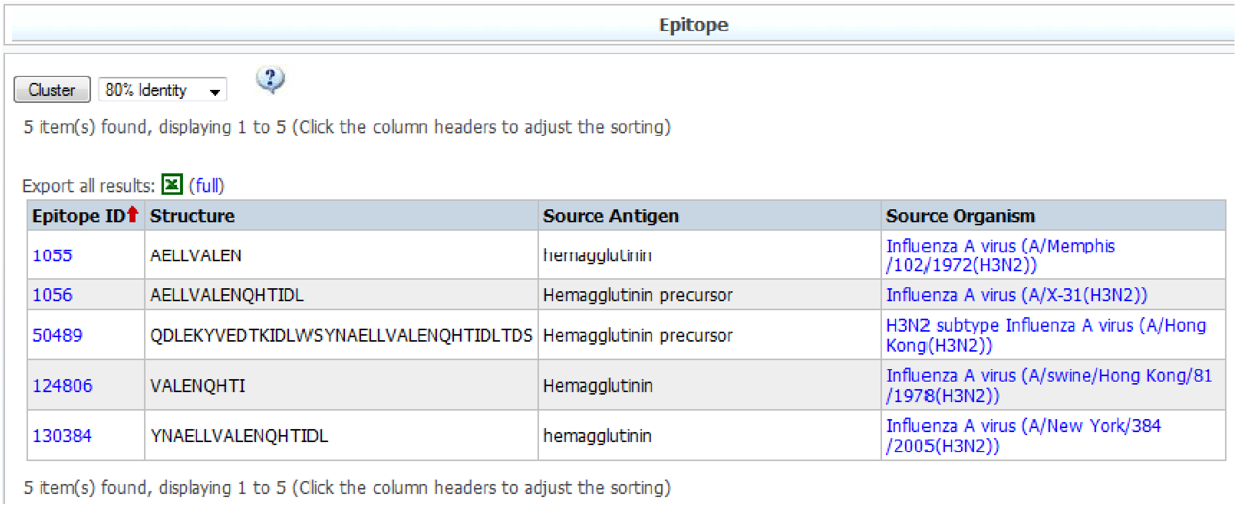


Figure 2.9 Home page Simple Search

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 2.10, 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.



5 item(s) found, displaying 1 to 5 (Click the column headers to adjust the sorting)

Export all results: (full)

Epitope ID	Structure	Source Antigen	Source Organism
1055	AELLVALEN	hemagglutinin	Influenza A virus (A/Memphis /102/1972(H3N2))
1056	AELLVALENQHTIDL	Hemagglutinin precursor	Influenza A virus (A/X-31(H3N2))
50489	QDLEKYVEDTKIDLWSYNAELLVALENQHTIDLTDS	Hemagglutinin precursor	H3N2 subtype Influenza A virus (A/Hong Kong(H3N2))
124806	VALENQHTI	Hemagglutinin	Influenza A virus (A/swine/Hong Kong/81 /1978(H3N2))
130384	YNAELLVALENQHTIDL	hemagglutinin	Influenza A virus (A/New York/384 /2005(H3N2))

5 item(s) found, displaying 1 to 5 (Click the column headers to adjust the sorting)

Figure 2.10 Query results for a substring search performed on the input sequence AELLVALENQHTIDL

An autocomplete feature is available for the Molecule, Organism, Disease, and Allele Finders. For example, as one types “hem” in the Source Antigen field in the Epitope Source section, several choices start to appear in a list below the text field, including “hemolysin”, “hemK protein”, and “hemagglutinin”. 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 Host 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. The autocomplete applies wherever the input field has “Enter Search” in grey. 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 2.3.5.5) and molecule finder (Section 2.3.5.4), 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 2.3.5.1). 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 selecting the Search button and query results can be viewed on the Search Result Summary page, which is described in Section 2.3.4.

The Immune Mediated Disease Association search is an experimental feature on the IEDB home page search and in the Advanced Search pages. It is available on the home page search interface between the *Epitope Source* and the *Immune Recognition Context* field partitions. The Disease Finder in described in in Section 2.3.5.3.

Finally, a link to “Help with Common Queries” is located at the bottom of the Search panel. This links to a series of 16 questions that have been useful in preparing the epitope meta-analyses conducted and published by LIAI. More information about the Common Queries is available in Section 2.5.6.

2.3.3 Advanced query

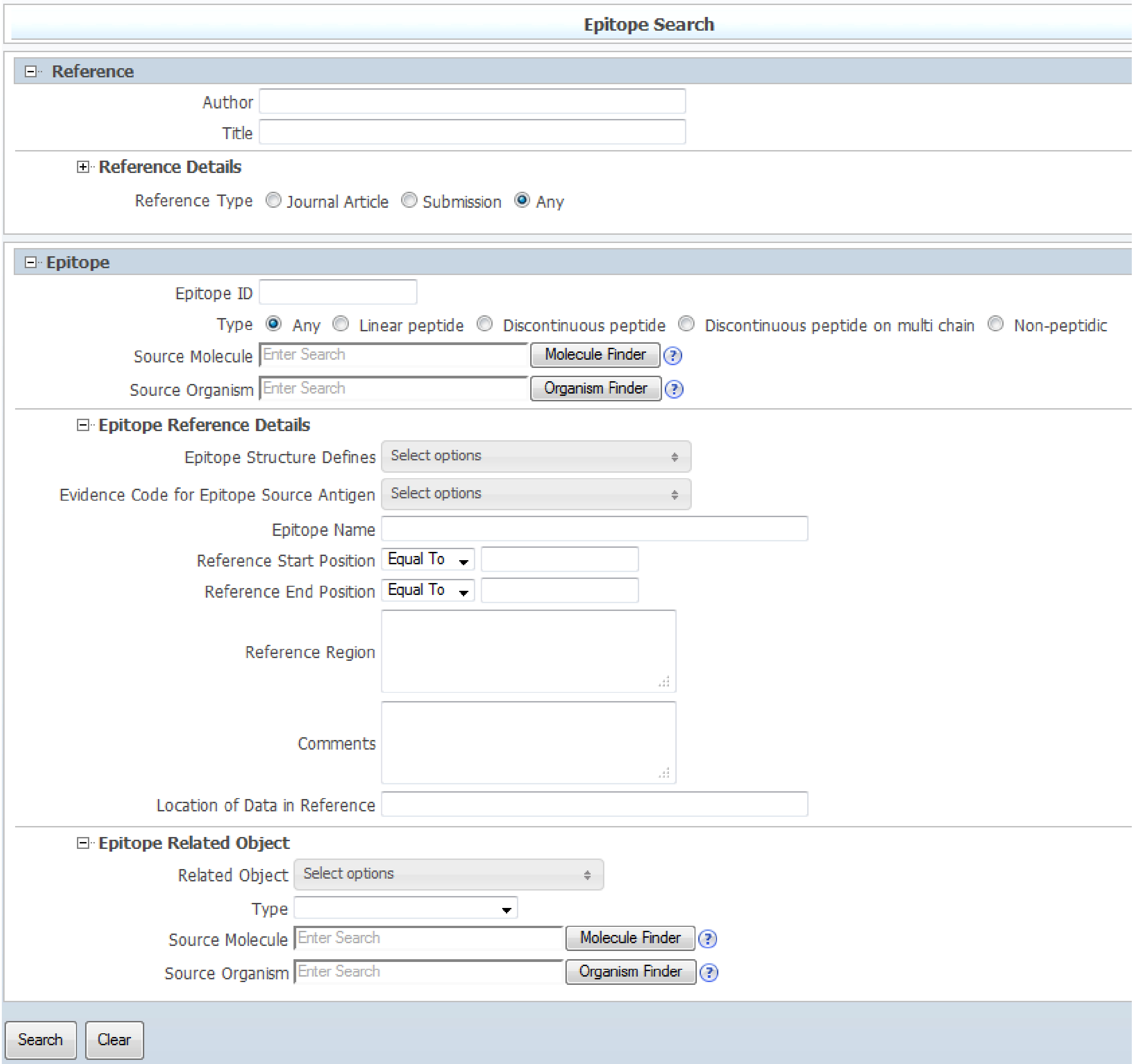
The Advanced queries are based on a standard Query by Example (QBE) approach, which is a method of forming queries where a user can enter conditions for each data field they want included in the query.

The Advanced queries allow users to define example criteria for each field in the system. As there are over 300 fields, the Advanced queries are both powerful and comprehensive.

The fully expanded input screen for the Epitope Search is shown in Figure 2.11. 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. Users can also 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. 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 “Enter Search”. The “?” are links to help pages in the IEDB Solutions Center. Finders are described in further detail in Section 2.3.5.2.

In 2013, the drop-down menus for many fields were replaced with a more convenient and intuitive multiselect menu. Figure 2.12 illustrates the functionality of this feature. This type of multiselect menu can be found throughout the Advanced Search pages. Figure 2.11 shows the fields when “Any” is selected. The fields for the other epitope type selections are shown in Figure 2.13, Figure 2.14, Figure 2.15, and Figure 2.16.



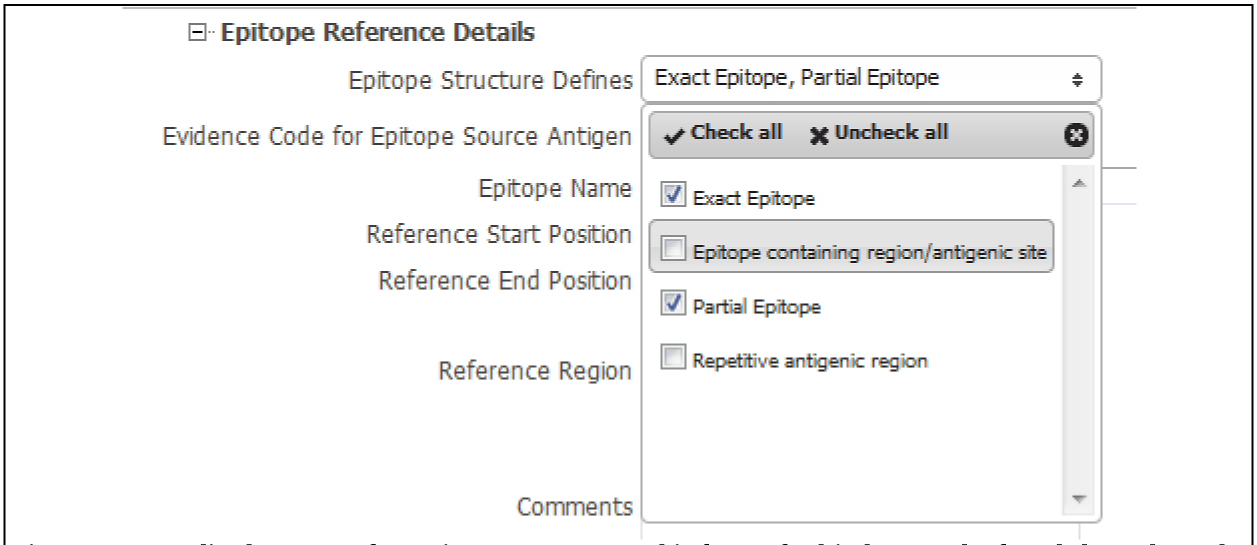
Reference Type ○ Journal Article ○ Submission ● Any

Type ● Any ○ Linear peptide ○ Discontinuous peptide ○ Discontinuous peptide on multi chain ○ Non-peptidic

Reference Start Position: Equal To

Reference End Position: Equal To

Figure 2.11 Epitope Search input screen. Epitope Type is defined as Any



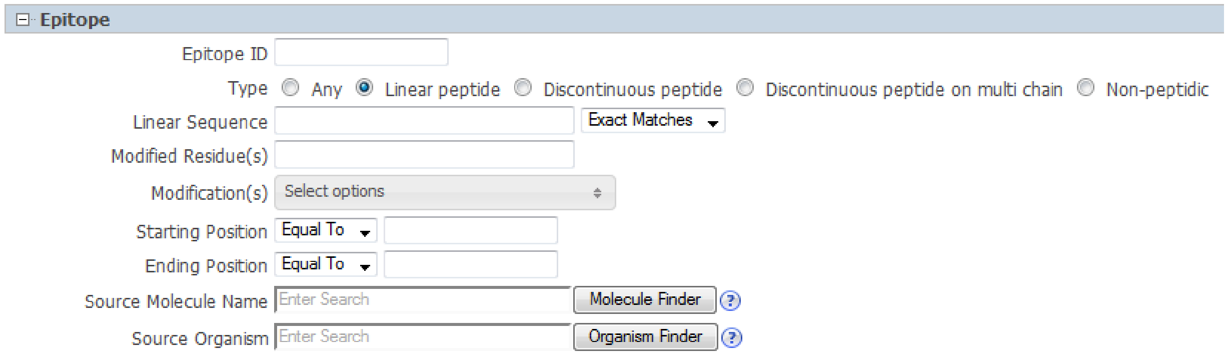
Epitope Reference Details

Epitope Structure Defines: Exact Epitope, Partial Epitope

✓ Check all ✖ Uncheck all

☑ Exact Epitope
☐ Epitope containing region/antigenic site
☑ Partial Epitope
☐ Repetitive antigenic region

Figure 2.12 Mulitselect menu for Epitope Structure. This form of mltiselect can be found throughout the Advanced Search pages



Epitope

Epitope ID:

Type: ○ Any ● Linear peptide ○ Discontinuous peptide ○ Discontinuous peptide on multi chain ○ Non-peptidic

Linear Sequence: Exact Matches

Modified Residue(s):

Modification(s): Select options

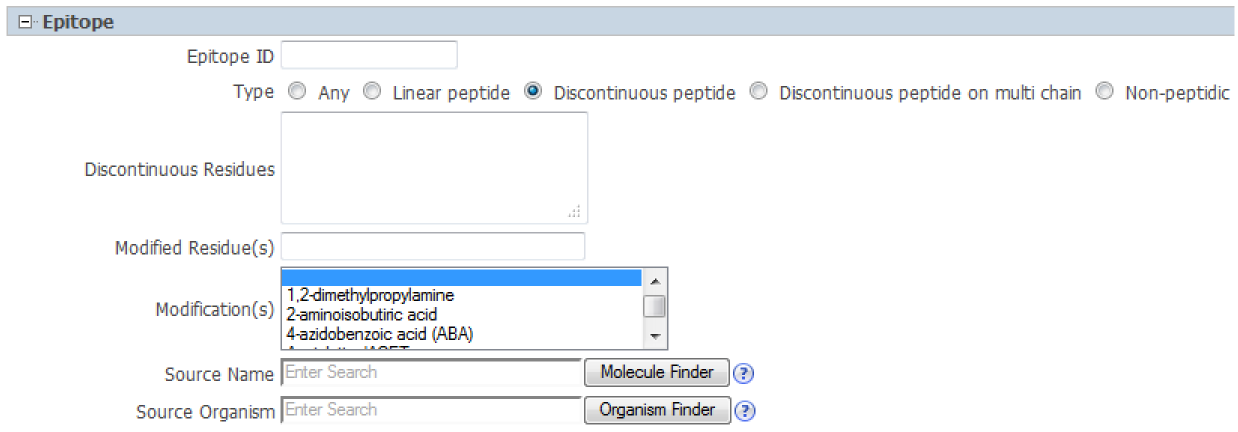
Starting Position: Equal To

Ending Position: Equal To

Source Molecule Name: Enter Search

Source Organism: Enter Search

Figure 2.13 Epitope query fields in the Advanced Search for Linear peptide epitopes



Epitope

Epitope ID:

Type: ○ Any ○ Linear peptide ● Discontinuous peptide ○ Discontinuous peptide on multi chain ○ Non-peptidic

Discontinuous Residues:

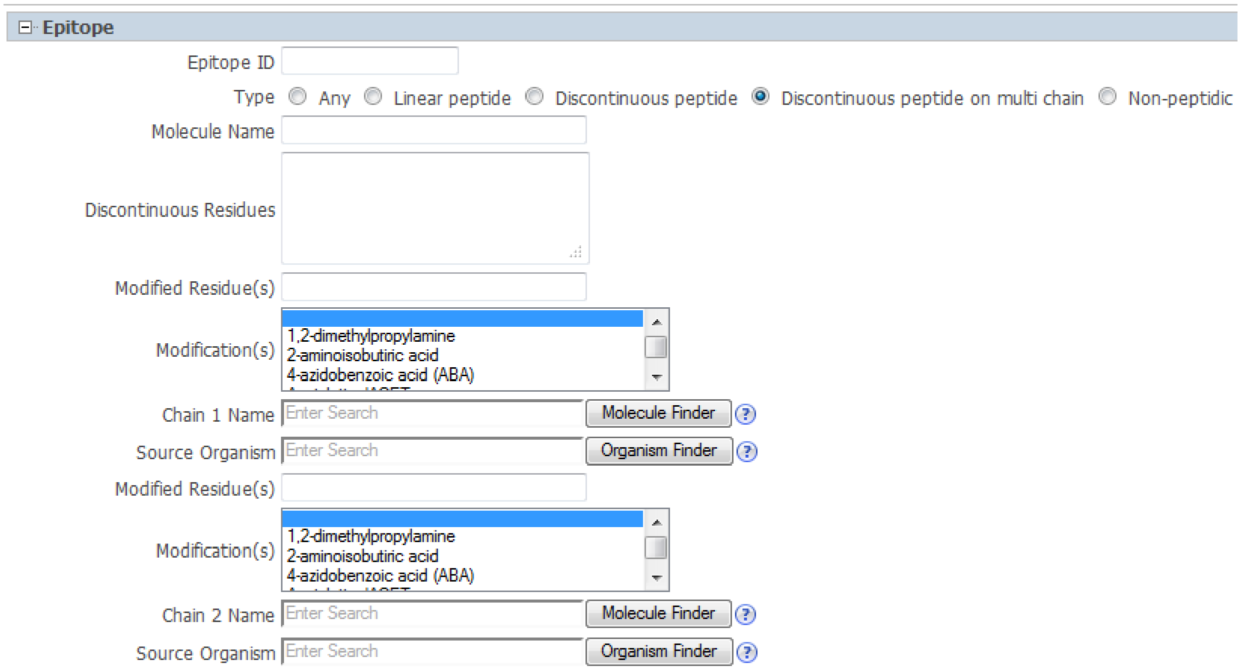
Modified Residue(s):

Modification(s):
1,2-dimethylpropylamine
2-aminoisobutiric acid
4-azidobenzoic acid (ABA)

Source Name: Enter Search

Source Organism: Enter Search

Figure 2.14 Epitope query fields in the Advanced Search for Discontinuous peptide epitopes



⊟ Epitope

Epitope ID

Type ○ Any ○ Linear peptide ○ Discontinuous peptide ● Discontinuous peptide on multi chain ○ Non-peptidic

Molecule Name

Discontinuous Residues

Modified Residue(s)

Modification(s)
1,2-dimethylpropylamine
2-aminoisobutiric acid
4-azidobenzoic acid (ABA)

Chain 1 Name: Enter Search [Molecule Finder] ?

Source Organism: Enter Search [Organism Finder] ?

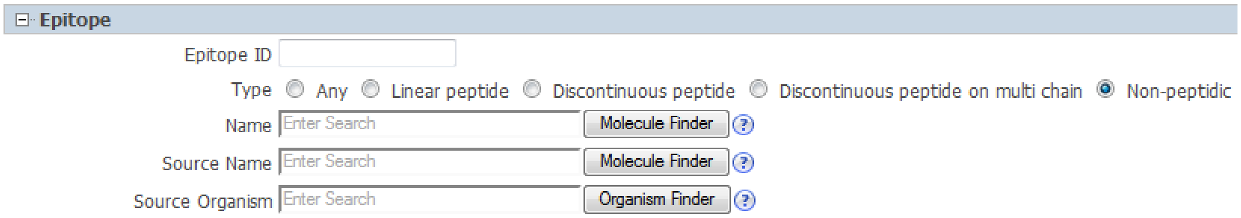
Modified Residue(s)

Modification(s)
1,2-dimethylpropylamine
2-aminoisobutiric acid
4-azidobenzoic acid (ABA)

Chain 2 Name: Enter Search [Molecule Finder] ?

Source Organism: Enter Search [Organism Finder] ?

Figure 2.15 Epitope query fields in the Advanced Search for Discontinuous peptide on multi-chain epitopes



⊟ Epitope

Epitope ID

Type ○ Any ○ Linear peptide ○ Discontinuous peptide ○ Discontinuous peptide on multi chain ● Non-peptidic

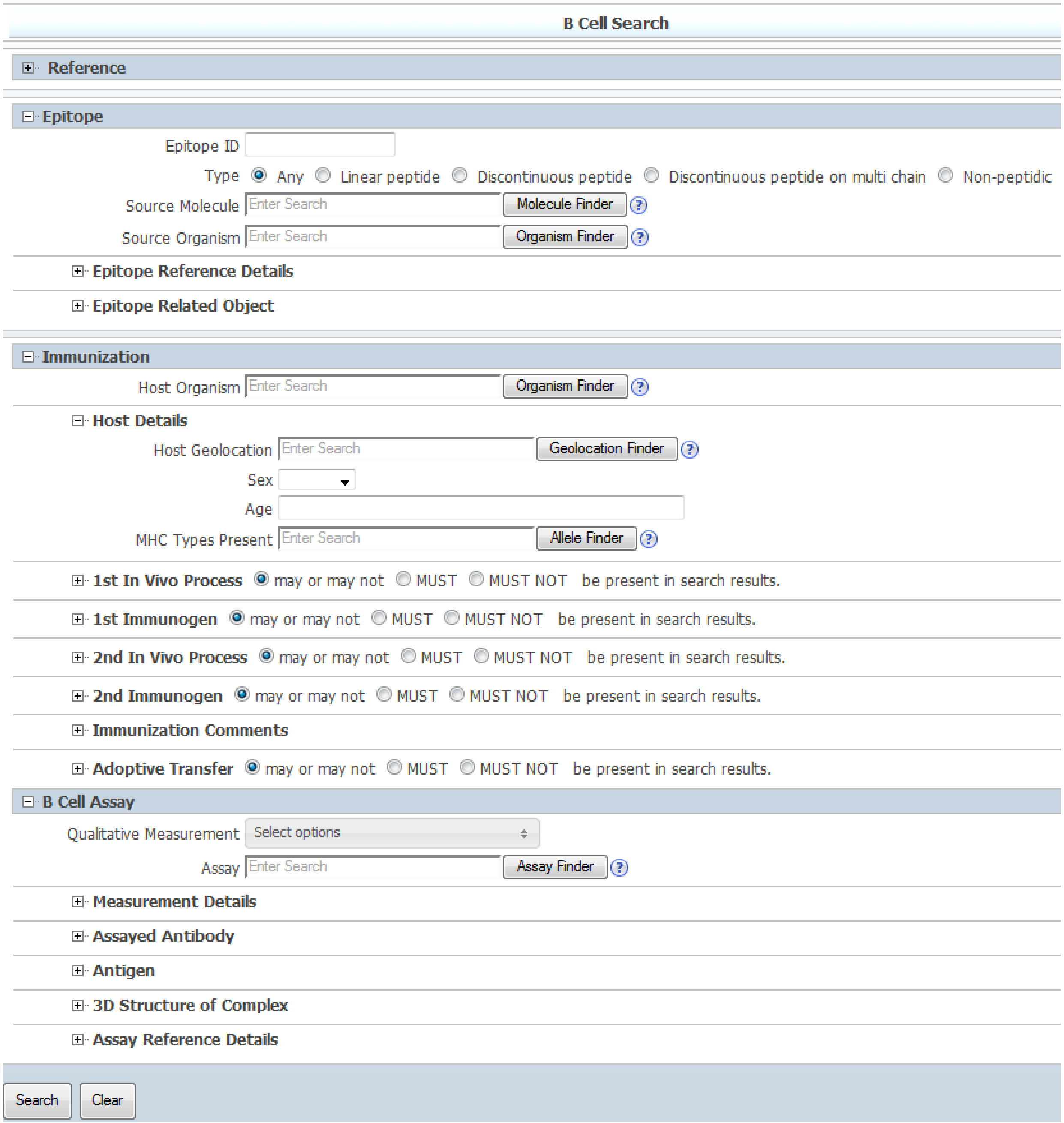
Name: Enter Search [Molecule Finder] ?

Source Name: Enter Search [Molecule Finder] ?

Source Organism: Enter Search [Organism Finder] ?

Figure 2.16 Epitope query fields in the Advanced Search for Non-peptidic epitopes

There are four other Advanced queries that can be used to select search criteria for references, epitopes, and assays. These are B Cell Search, T Cell Search, MHC Ligand Search, and Identifier Search. As an example, the B Cell Search input screen is shown in Figure 2.17. As is the case for all three assay search input screens, the Reference and Epitope criteria fields are listed first, followed by the fields specific for each assay type.



B Cell Search

⊞ Reference

⊟ Epitope

Epitope ID

Type ● Any ○ Linear peptide ○ Discontinuous peptide ○ Discontinuous peptide on multi chain ○ Non-peptidic

Source Molecule Enter Search | Molecule Finder | ?

Source Organism Enter Search | Organism Finder | ?

⊞ Epitope Reference Details

⊞ Epitope Related Object

⊟ Immunization

Host Organism Enter Search | Organism Finder | ?

⊟ Host Details

Host Geolocation Enter Search | Geolocation Finder | ?

Sex

Age

MHC Types Present Enter Search | Allele Finder | ?

⊞ 1st In Vivo Process ● may or may not ○ MUST ○ MUST NOT be present in search results.

⊞ 1st Immunogen ● may or may not ○ MUST ○ MUST NOT be present in search results.

⊞ 2nd In Vivo Process ● may or may not ○ MUST ○ MUST NOT be present in search results.

⊞ 2nd Immunogen ● may or may not ○ MUST ○ MUST NOT be present in search results.

⊞ Immunization Comments

⊞ Adoptive Transfer ● may or may not ○ MUST ○ MUST NOT be present in search results.

⊟ B Cell Assay

Qualitative Measurement Select options

Assay Enter Search | Assay Finder | ?

⊞ Measurement Details

⊞ Assayed Antibody

⊞ Antigen

⊞ 3D Structure of Complex

⊞ Assay Reference Details

Figure 2.17 B Cell Search input screen

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. Figure 2.17 shows the Geolocation Finder under the Host Details subsection under Immunization section and another example of the multiselect menu under the B Cell Assay section for specifying Qualitative Measurement. Both can also be found in the T Cell Search and MHC Ligand Search. A description of the Geolocation Finder can be found in Section 2.3.5.6.

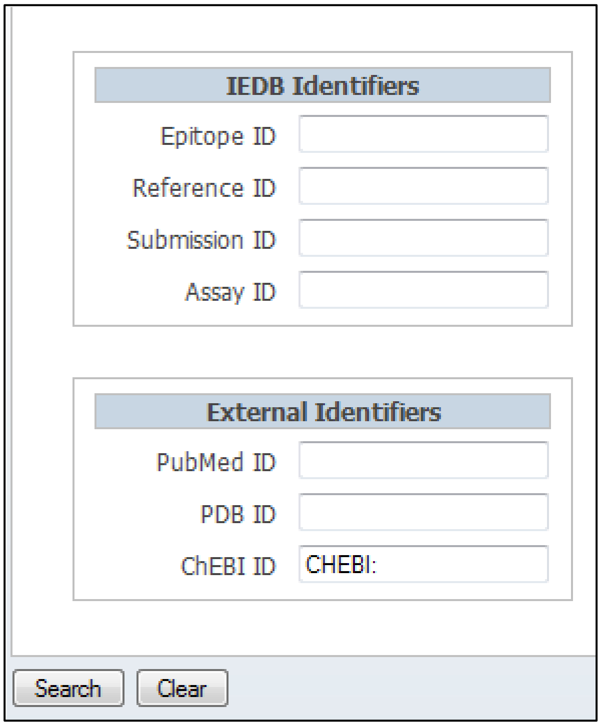


Figure 2.18 Identifier Search input screen

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.

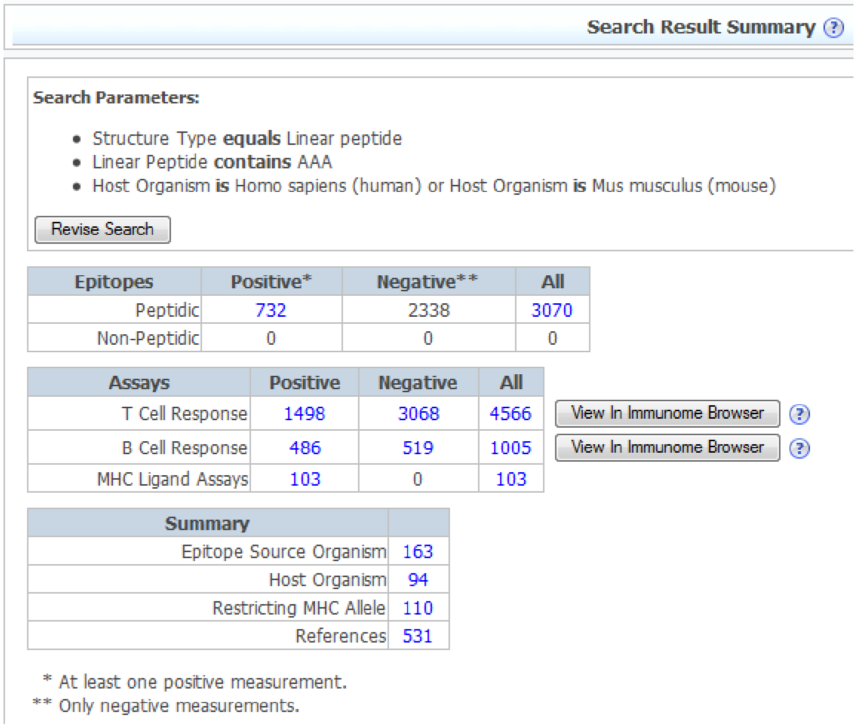
The Identifier Search input screen is shown in Figure 2.18. If users know the epitope, reference, submission, or assay identifier they are seeking, they can enter that information into one of the four IEDB Identifiers fields. Users can also look for information based on the PubMed ID of a reference or the PDB ID of a structure by using the External Identifiers fields.

2.3.4 Search Results Summary

The Search Results Summary page displays the results of all the different queries. An example is displayed in Figure 2.19, which was generated with the Home page Simple Search for the linear sequence substring "AAA" for human and mouse host organisms. The Search Results Summary allows the user to quickly assess the results of their search and drill down the level of detail that is of interest. Search Parameters are displayed on the Search Result Summary page, along with the ability to revise the search criteria. Clicking on the “Revise Search” button will take the user back to the original search form, either the home page for the Simple Search or to the appropriate Advanced Search form.

The number of peptidic and non-peptidic epitopes are displayed in the topmost table on the Result Summary. Because the IEDB captures both positive and negative assay responses, some “epitopes” lack a positive binding value and therefore are not actually epitopes; the number of these molecular structures is indicated in the Negative column of the table. The user can click on the number in the Positive and All columns to view all the results for that category, as seen in Figure 2.19 for the positive peptidic epitopes. The columns displayed include the number of corresponding epitope, source antigen, and source species.

Figure 2.19 also shows the Immunome Browser, which is described in detail in Section 2.3.4.4. The Immunome Browser visualizes large sets of epitope data by aligning epitope sequences with reference proteomes to ensure consistency. A user can map query results for T Cell and B Cell assays to a set of antigens and determine the position of a given pitope within an antigen.



Search Result Summary

Search Parameters:

- Structure Type **equals** Linear peptide
- Linear Peptide **contains** AAA
- Host Organism **is** Homo sapiens (human) or Host Organism **is** Mus musculus (mouse)

Epitopes	Positive*	Negative**	All
Peptidic	732	2338	3070
Non-Peptidic	0	0	0

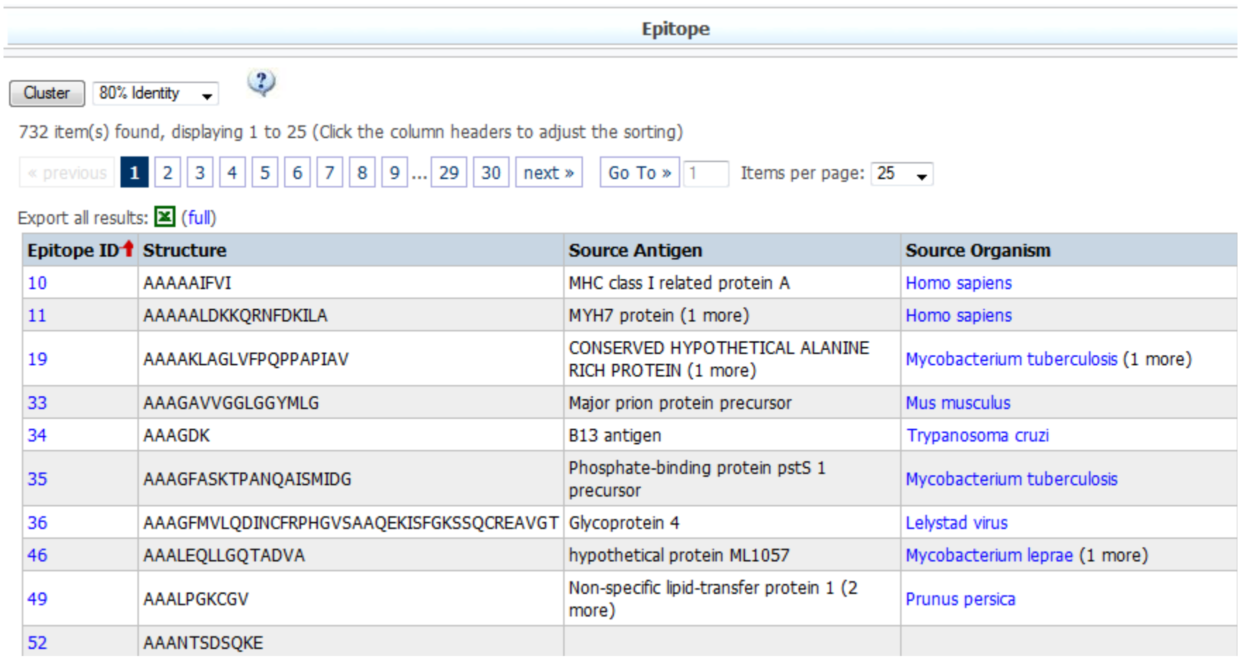
Assays	Positive	Negative	All
T Cell Response	1498	3068	4566
B Cell Response	486	519	1005
MHC Ligand Assays	103	0	103

Summary	
Epitope Source Organism	163
Host Organism	94
Restricting MHC Allele	110
References	531

* At least one positive measurement.
** Only negative measurements.

Figure 2.19 Sample of Search Result Summary

As Figure 2.20 and subsequent figures show, comma separated values (CSV) file exports are available on-demand from all list pages and list tabs throughout the site, except for the patent list, which is only provided in PDF format. The CSV file exports are generated in two formats, a compact format that only contains the data presented in the list the user is viewing, and a full record format that contains all of the data associated with the records in the list the user is viewing. On some results pages, only the full format is available. The CSV format can be easily manipulated using a spreadsheet program, such as Microsoft Excel, or edited with a word processing program, such as Microsoft Word or Notepad.



Epitope

732 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

Export all results: (full)

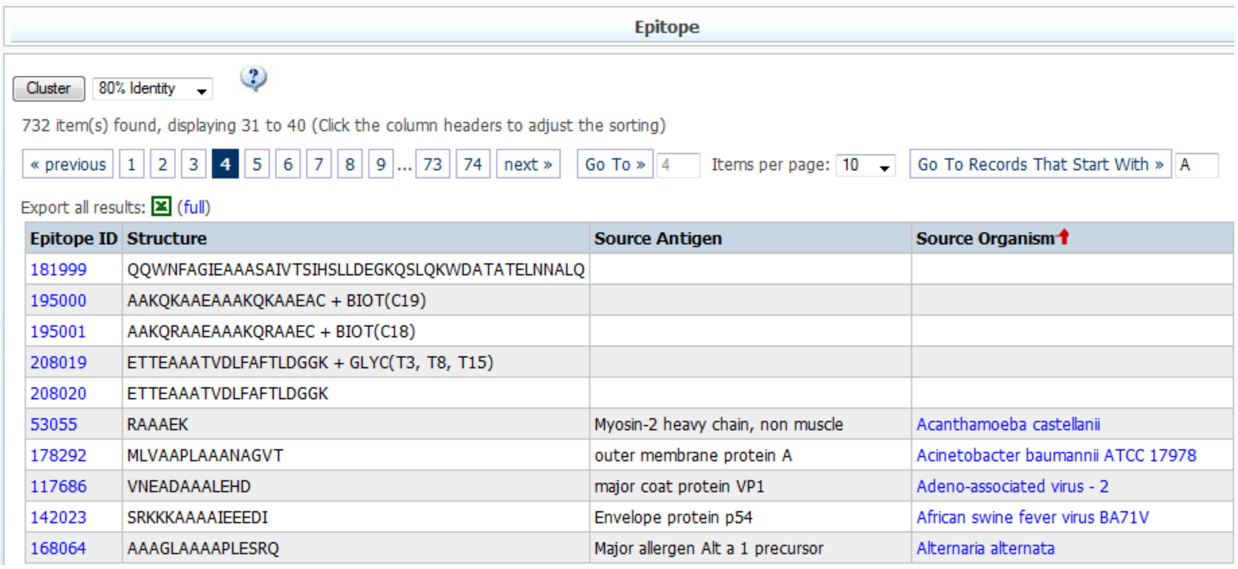
Epitope ID	Structure	Source Antigen	Source Organism
10	AAAAAIFVI	MHC class I related protein A	Homo sapiens
11	AAAAALDKKQRNFDKILA	MYH7 protein (1 more)	Homo sapiens
19	AAAAKLAGLVFPQPPAPIAV	CONSERVED HYPOTHETICAL ALANINE RICH PROTEIN (1 more)	Mycobacterium tuberculosis (1 more)
33	AAAGAVVGGLGGYMLG	Major prion protein precursor	Mus musculus
34	AAAGDK	B13 antigen	Trypanosoma cruzi
35	AAAGFASKTPANQAISMIDG	Phosphate-binding protein pstS 1 precursor	Mycobacterium tuberculosis
36	AAAGFMVLQDINCFRPHGVSAAQEKISFGKSSQCREAVGT	Glycoprotein 4	Lelystad virus
46	AAALEQLLGQTADVA	hypothetical protein ML1057	Mycobacterium leprae (1 more)
49	AAALPGKCGV	Non-specific lipid-transfer protein 1 (2 more)	Prunus persica
52	AAANTSDSQKE		

Figure 2.20 Screen generated by drilling down on the positive epitope hyperlink in the Search Result Summary

The user can cluster query results by the sequence identity of the epitope structure. Clustering has been implemented to simplify query results, especially since the amount of data returned in many queries has grown as the amount of data in the IEDB has grown. As an example, if the user would query for all Vaccinia virus epitopes they would get a list of over 10,000 records. If they then hit the 'Cluster' button, the epitopes would be grouped according to their sequence identity and the user would end up with a 'cleaned up' view of the results.

An algorithm for grouping the sequences has been developed and tested with several IEDB data sets. It groups related sequences based on sequence identity and allows the user to specify the sequence identity threshold from 70%-100%. As an example, at 85% identity, 7,512 Vaccinia virus epitopes form 2,528 clusters. This drastically reduces the number of results displayed to the user and should result in more efficient navigation. In terms of sorting the clusters of epitopes so that the most relevant ones are displayed first, bioinformaticians at LIAI have developed a metric called the 'evidence score'. This metric takes into account the number of references, number of positive assays, and total number of assays for each epitope. It is used initially to seed the clusters and is summed over all of the epitopes in the cluster to get the 'cluster score' (CScore). Clusters are then sorted by the CScore in a descending order by default.

Figure 2.20 shows the initial results page without any clustering. The user can select from four levels of sequence identity for the clustering, 70, 80, 90, or 100%, with 80% being the default (see Figure). Users can sort on each column in the table. If the column is alphanumeric in nature, and not strictly numeric as is the case for Epitope ID, a field labeled "Go To Records That Start With" appears to the right of field that specifies the number of items per page. The user can input a single character and the display will jump to the first occurrence of that character starting a string in that column. An example of the results sorted by Source Organism and starting with the letter "A" is shown in Figure 2.21.



732 item(s) found, displaying 31 to 40 (Click the column headers to adjust the sorting)

Epitope ID	Structure	Source Antigen	Source Organism
181999	QQWNFAGIEAAASAIVTSIHSLLDEGKQSLQKWDATATELNNALQ		
195000	AAKQKAAEAAAKQKAAEAC + BIOT(C19)		
195001	AAKQRAAEAAAKQRAAEC + BIOT(C18)		
208019	ETTEAAATVDLFAFTLDGGK + GLYC(T3, T8, T15)		
208020	ETTEAAATVDLFAFTLDGGK		
53055	RAAAEK	Myosin-2 heavy chain, non muscle	Acanthamoeba castellanii
178292	MLVAAPLAAANAGVT	outer membrane protein A	Acinetobacter baumannii ATCC 17978
117686	VNEADAAALEHD	major coat protein VP1	Adeno-associated virus - 2
142023	SRKKKAAAAIEEEDI	Envelope protein p54	African swine fever virus BA71V
168064	AAAGLAAAAPLESRQ	Major allergen Alt a 1 precursor	Alternaria alternata

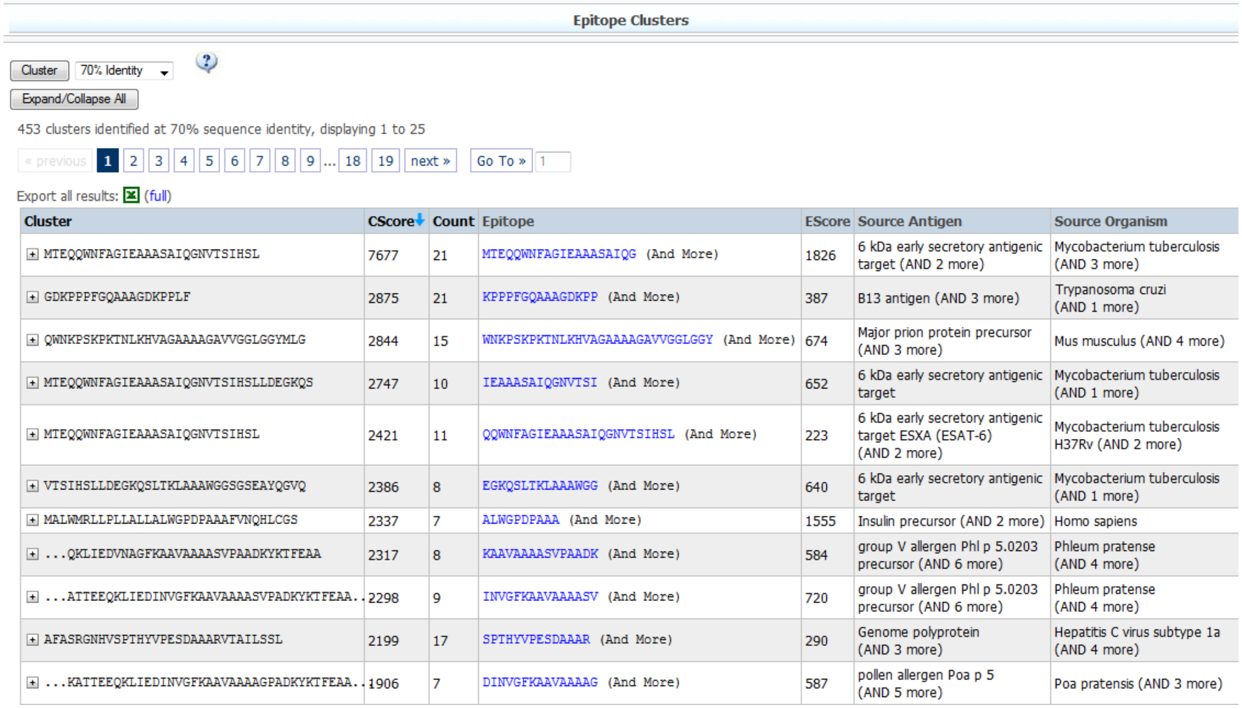
Figure 2.21 Epitope results sorted by Source Organism, showing the first record starting with an "A" as specified in the "Go To Records That Start With" field in the upper right.

Clustering is initiated when the user clicks the *Cluster* button. Figure 2.22 shows clustering by 70% sequence identity. A description of the epitope clustering algorithm and additional screen shots of the clustered results can be found in the IEDB Solutions Center under the *Tutorials and Reference Materials* folder (http://iedb.zendesk.com/entries/306422-iedb-epitope-clustering-help). Help can also be reached by clicking on the '?' icon to the right of the *% Identify* button.

The second table in Figure 2.19 summarizes the positive and negative assay responses for the four general assay types. The user can drill down on any of these values to see the corresponding epitopes. The detail page for the positive T Cell Responses of this search is displayed in Figure 2.23.

The third table lists the number of epitope source organisms, host organisms, restricting MHC alleles, and references resulting from the input search criteria. As before, the user can drill down on the values in the table to find more detail related to each category, as seen in Figure 2.24, Figure 2.25, Figure 2.26, and Figure 2.27.

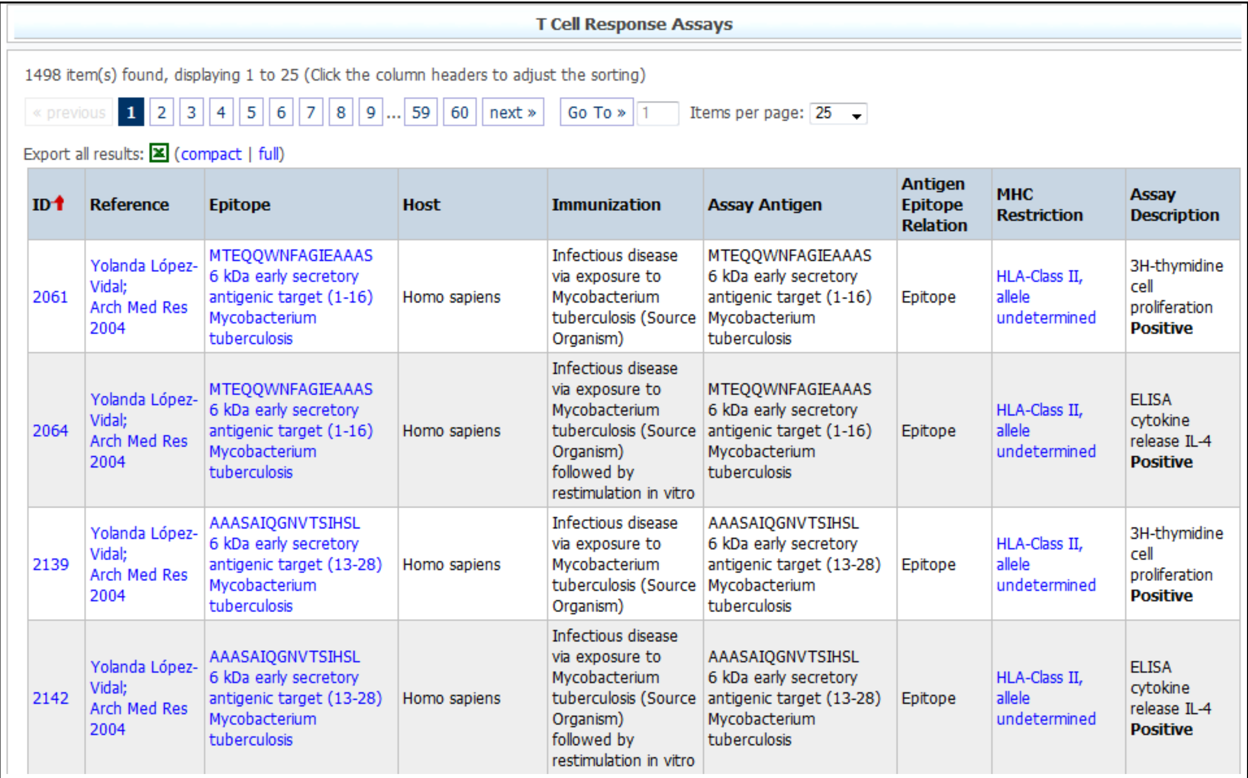
Users can specify the number of items on a result page from a pull-down list of four values – 10, 25, 50, and 100. On other result pages, users can also jump to pages that feature results starting with a specified character, as seen in Figure 2.24, Figure 2.25, and Figure 2.26. Users can select columns by which to sort by clicking on the column headers. Clicking again will reverse the sort order.



453 clusters identified at 70% sequence identity, displaying 1 to 25

Cluster	CScore	Count	Epitope	EScore	Source Antigen	Source Organism
⊞ MTEQQWNFAGIEAAASAIQGNVTSIHSL	7677	21	MTEQQWNFAGIEAAASAIQG (And More)	1826	6 kDa early secretory antigenic target (AND 2 more)	Mycobacterium tuberculosis (AND 3 more)
⊞ GDKPPPFGQAAAGDKPPLF	2875	21	KPPPFGQAAAGDKPP (And More)	387	B13 antigen (AND 3 more)	Trypanosoma cruzi (AND 1 more)
⊞ QWNKPSKPKTNLKHVAGAAAAGAVVGGLGGYMLG	2844	15	WNKPSKPKTNLKHVAGAAAAGAVVGGLGGY (And More)	674	Major prion protein precursor (AND 3 more)	Mus musculus (AND 4 more)
⊞ MTEQQWNFAGIEAAASAIQGNVTSIHSLLDEGKQS	2747	10	IEAAASAIQGNVTSI (And More)	652	6 kDa early secretory antigenic target	Mycobacterium tuberculosis (AND 1 more)
⊞ MTEQQWNFAGIEAAASAIQGNVTSIHSL	2421	11	QQWNFAGIEAAASAIQGNVTSIHSL (And More)	223	6 kDa early secretory antigenic target ESXA (ESAT-6) (AND 2 more)	Mycobacterium tuberculosis H37Rv (AND 2 more)
⊞ VTSIHSLLDEGKQSLTKLAAAWGGSGSEAYQGVQ	2386	8	EGKQSLTKLAAAWGG (And More)	640	6 kDa early secretory antigenic target	Mycobacterium tuberculosis (AND 1 more)
⊞ MALWMRLLPLLALLALWGPDPAAAFVNQHLCGS	2337	7	ALWGPDPAAA (And More)	1555	Insulin precursor (AND 2 more)	Homo sapiens
⊞ ...QKLIEDVNAGFKAAVAAAASVPAADKYKTFEAA	2317	8	KAAVAAAASVPAADK (And More)	584	group V allergen Phl p 5.0203 precursor (AND 6 more)	Phleum pratense (AND 4 more)
⊞ ...ATTEEQKLIEDINVGFKAAVAAAASVPADKYKTFEAA..	2298	9	INVGFKAAVAAAASV (And More)	720	group V allergen Phl p 5.0203 precursor (AND 6 more)	Phleum pratense (AND 4 more)
⊞ AFASRGNHVSPTHYVPESDAAARVTAILSSL	2199	17	SPTHYVPESDAAAR (And More)	290	Genome polyprotein (AND 3 more)	Hepatitis C virus subtype 1a (AND 4 more)
⊞ ...KATTEEQKLIEDINVGFKAAVAAAAGPADKYKTFEAA..	1906	7	DINVGFKAAVAAAAG (And More)	587	pollen allergen Poa p 5 (AND 5 more)	Poa pratensis (AND 3 more)

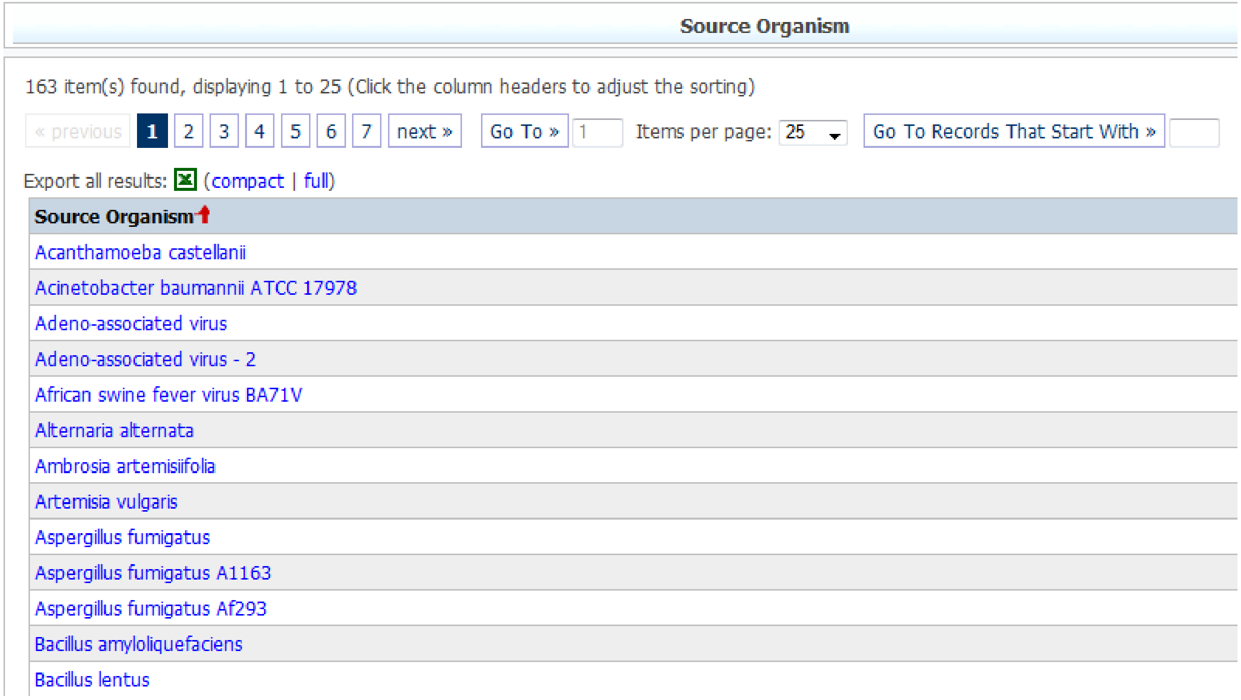
Figure 2.22 Query results for clustering at 70% sequence identity



1498 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

ID	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	MHC Restriction	Assay Description
2061	Yolanda López-Vidal; Arch Med Res 2004	MTEQQWNFAGIEAAAS 6 kDa early secretory antigenic target (1-16) Mycobacterium tuberculosis	Homo sapiens	Infectious disease via exposure to Mycobacterium tuberculosis (Source Organism)	MTEQQWNFAGIEAAAS 6 kDa early secretory antigenic target (1-16) Mycobacterium tuberculosis	Epitope	HLA-Class II, allele undetermined	3H-thymidine cell proliferation **Positive**
2064	Yolanda López-Vidal; Arch Med Res 2004	MTEQQWNFAGIEAAAS 6 kDa early secretory antigenic target (1-16) Mycobacterium tuberculosis	Homo sapiens	Infectious disease via exposure to Mycobacterium tuberculosis (Source Organism) followed by restimulation in vitro	MTEQQWNFAGIEAAAS 6 kDa early secretory antigenic target (1-16) Mycobacterium tuberculosis	Epitope	HLA-Class II, allele undetermined	ELISA cytokine release IL-4 **Positive**
2139	Yolanda López-Vidal; Arch Med Res 2004	AAASAIQGNVTSIHSL 6 kDa early secretory antigenic target (13-28) Mycobacterium tuberculosis	Homo sapiens	Infectious disease via exposure to Mycobacterium tuberculosis (Source Organism)	AAASAIQGNVTSIHSL 6 kDa early secretory antigenic target (13-28) Mycobacterium tuberculosis	Epitope	HLA-Class II, allele undetermined	3H-thymidine cell proliferation **Positive**
2142	Yolanda López-Vidal; Arch Med Res 2004	AAASAIQGNVTSIHSL 6 kDa early secretory antigenic target (13-28) Mycobacterium tuberculosis	Homo sapiens	Infectious disease via exposure to Mycobacterium tuberculosis (Source Organism) followed by restimulation in vitro	AAASAIQGNVTSIHSL 6 kDa early secretory antigenic target (13-28) Mycobacterium tuberculosis	Epitope	HLA-Class II, allele undetermined	ELISA cytokine release IL-4 **Positive**

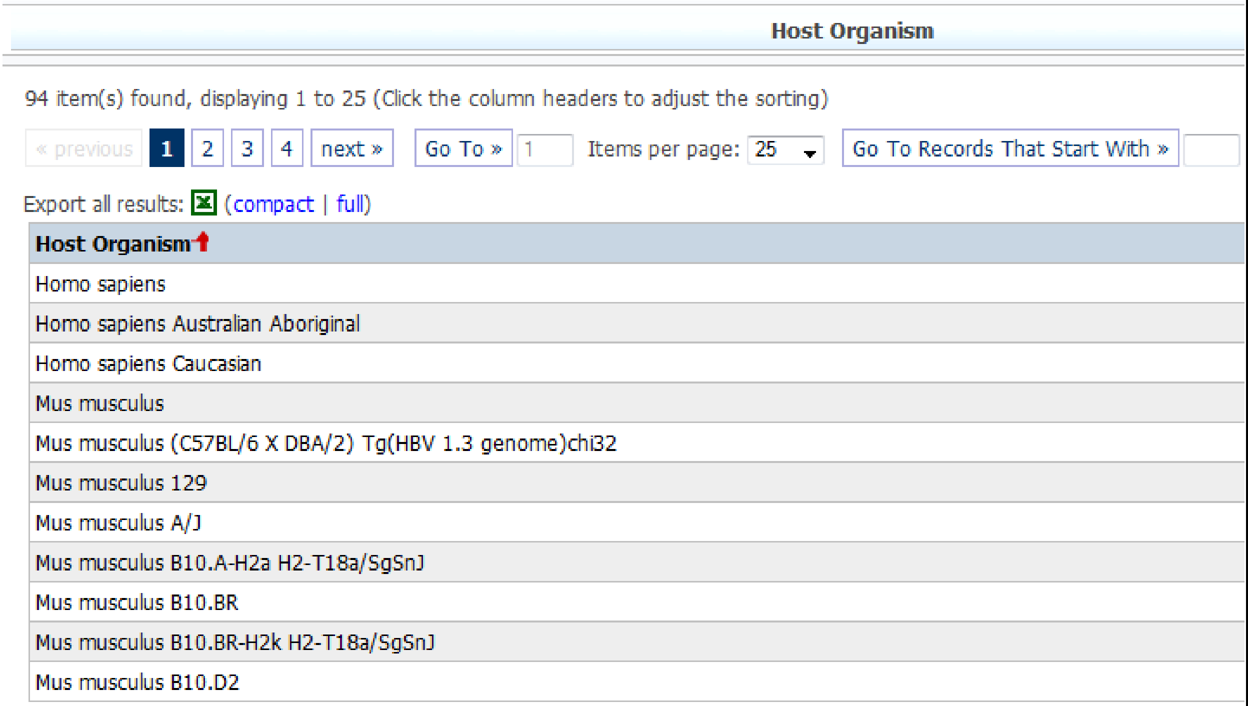
Figure 2.23 Screen generated by drilling down on the positive T cell assay hyperlink in the Search Result Summary



163 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

Source Organism
Acanthamoeba castellanii
Acinetobacter baumannii ATCC 17978
Adeno-associated virus
Adeno-associated virus - 2
African swine fever virus BA71V
Alternaria alternata
Ambrosia artemisiifolia
Artemisia vulgaris
Aspergillus fumigatus
Aspergillus fumigatus A1163
Aspergillus fumigatus Af293
Bacillus amyloliquefaciens
Bacillus lentus

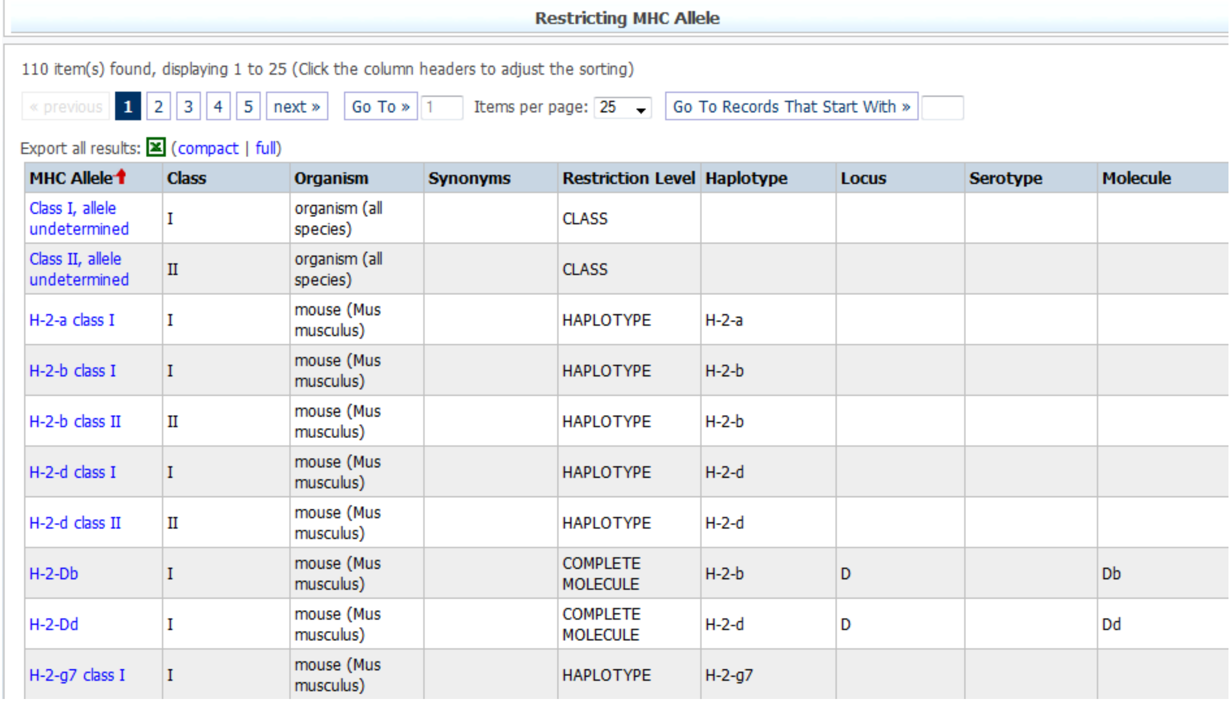
Figure 2.24 Screen generated by drilling down on the Epitope Source Organism link in the Search Result Summary



94 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

Host Organism
Homo sapiens
Homo sapiens Australian Aboriginal
Homo sapiens Caucasian
Mus musculus
Mus musculus (C57BL/6 X DBA/2) Tg(HBV 1.3 genome)chi32
Mus musculus 129
Mus musculus A/J
Mus musculus B10.A-H2a H2-T18a/SgSnJ
Mus musculus B10.BR
Mus musculus B10.BR-H2k H2-T18a/SgSnJ
Mus musculus B10.D2

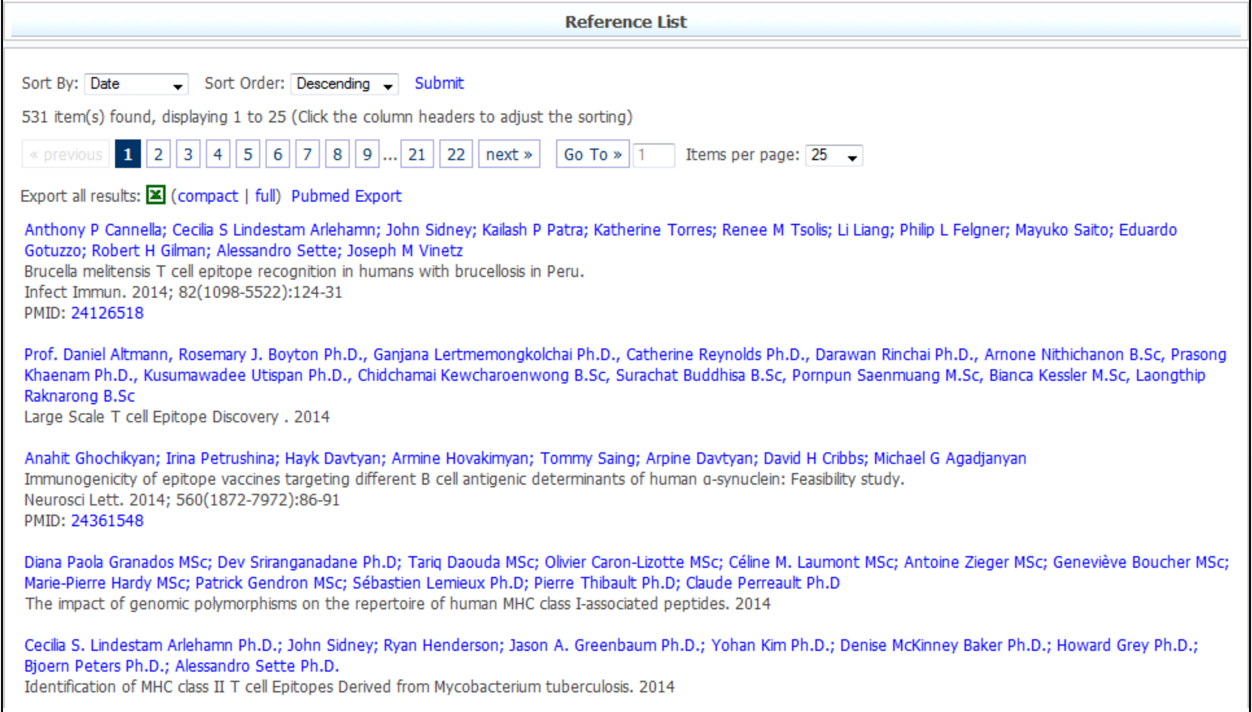
Figure 2.25 Screen generated by drilling down on the Host Organism link in the Search Result Summary



110 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

MHC Allele	Class	Organism	Synonyms	Restriction Level	Haplotype	Locus	Serotype	Molecule
Class I, allele undetermined	I	organism (all species)		CLASS				
Class II, allele undetermined	II	organism (all species)		CLASS				
H-2-a class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-a			
H-2-b class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-b			
H-2-b class II	II	mouse (Mus musculus)		HAPLOTYPE	H-2-b			
H-2-d class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-d			
H-2-d class II	II	mouse (Mus musculus)		HAPLOTYPE	H-2-d			
H-2-Db	I	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-b	D		Db
H-2-Dd	I	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-d	D		Dd
H-2-g7 class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-g7			

Figure 2.26 Screen generated by drilling down on the Restricting MHC Allele link in the Search Result Summary



Reference List

Sort By: Date Sort Order: Descending Submit

531 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

« previous 1 2 3 4 5 6 7 8 9 ... 21 22 next » Go To » 1 Items per page: 25

Export all results: (compact | full) Pubmed Export

Anthony P Cannella; Cecilia S Lindestam Arlehamn; John Sidney; Kailash P Patra; Katherine Torres; Renee M Tsolis; Li Liang; Philip L Felgner; Mayuko Saito; Eduardo Gotuzzo; Robert H Gilman; Alessandro Sette; Joseph M Vinetz
Brucella melitensis T cell epitope recognition in humans with brucellosis in Peru.
Infect Immun. 2014; 82(1098-5522):124-31
PMID: 24126518

Prof. Daniel Altmann, Rosemary J. Boyton Ph.D., Ganjana Lertmemongkolchai Ph.D., Catherine Reynolds Ph.D., Darawan Rinchai Ph.D., Arnone Nithichanon B.Sc, Prasong Khaenam Ph.D., Kusumawadee Utispan Ph.D., Chidchamai Kewcharoenwong B.Sc, Surachat Buddhisa B.Sc, Pornpun Saenmuang M.Sc, Bianca Kessler M.Sc, Laongthip Raknarong B.Sc
Large Scale T cell Epitope Discovery . 2014

Anahit Ghochikyan; Irina Petrushina; Hayk Davtyan; Armine Hovakimyan; Tommy Saing; Arpine Davtyan; David H Cribbs; Michael G Agadjanyan
Immunogenicity of epitope vaccines targeting different B cell antigenic determinants of human α-synuclein: Feasibility study.
Neurosci Lett. 2014; 560(1872-7972):86-91
PMID: 24361548

Diana Paola Granados MSc; Dev Sriranganadane Ph.D; Tariq Daouda MSc; Olivier Caron-Lizotte MSc; Céline M. Laumont MSc; Antoine Zieger MSc; Geneviève Boucher MSc; Marie-Pierre Hardy MSc; Patrick Gendron MSc; Sébastien Lemieux Ph.D; Pierre Thibault Ph.D; Claude Perreault Ph.D
The impact of genomic polymorphisms on the repertoire of human MHC class I-associated peptides. 2014

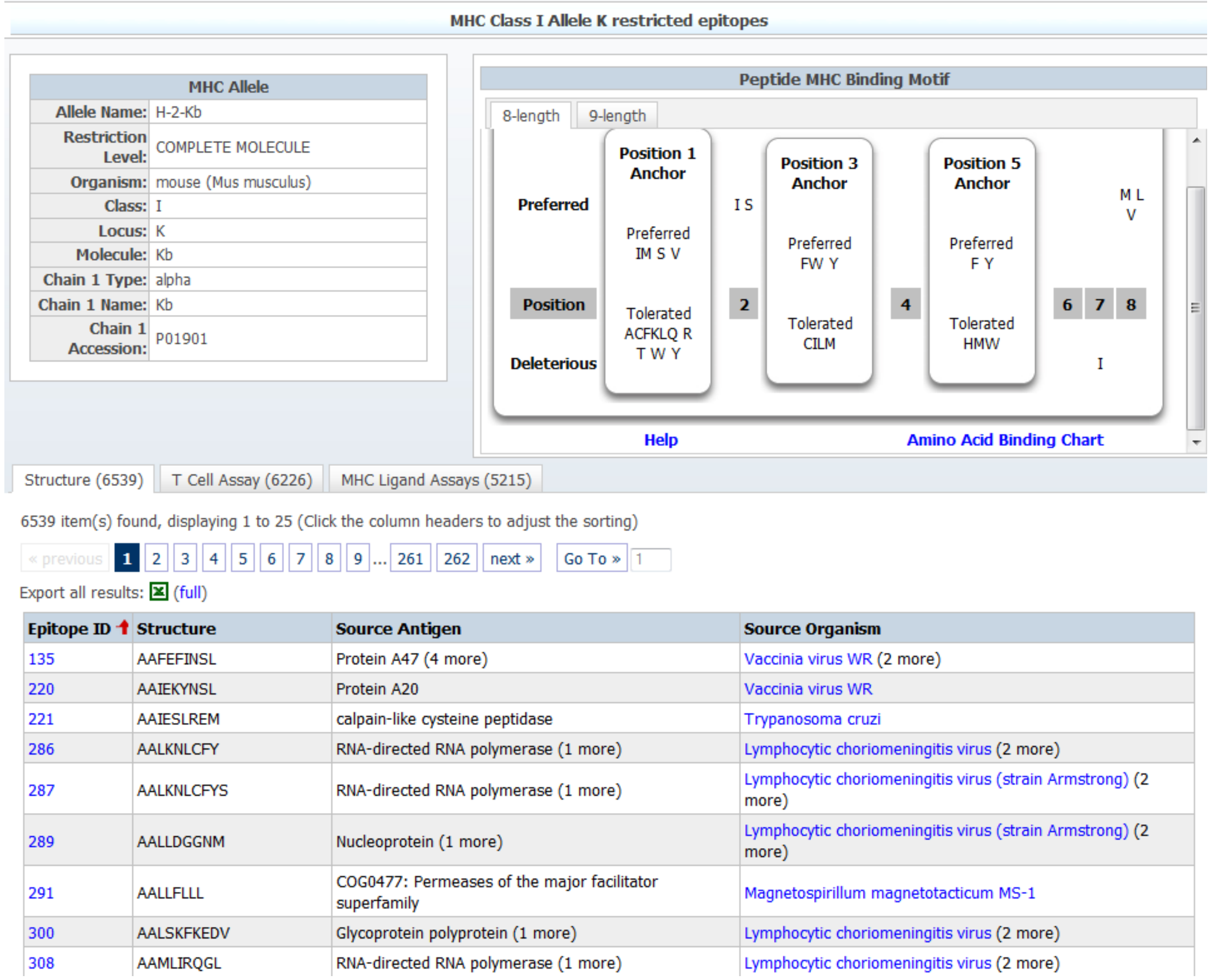
Cecilia S. Lindestam Arlehamn Ph.D.; John Sidney; Ryan Henderson; Jason A. Greenbaum Ph.D.; Yohan Kim Ph.D.; Denise McKinney Baker Ph.D.; Howard Grey Ph.D.; Bjoern Peters Ph.D.; Alessandro Sette Ph.D.
Identification of MHC class II T cell Epitopes Derived from Mycobacterium tuberculosis. 2014

Figure 2.27 Screen generated by drilling down on the reference hyperlink in the Search Result Summary

When users click on the number of references on the Search Results Summary screen, the system will display the Reference List, as seen in Figure 2.27. This list will display all the references that matched the user's search criteria. Enough information is listed to identify each reference uniquely, including authors, article title, year, PubMed ID, and journal name. To view all the information related to a given reference, click the highlighted author line. The list can be sorted by date, author, PubMed ID, and title in ascending or descending order. Clicking on the PubMed identifier will open the PubMed citation in a new window. Users can also retrieve the PubMed records for all the references by clicking on “PubMed Export” adjacent to the Compact and Full export options at the top and bottom of the page.

2.3.4.1 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 Information page. This page can be reached from the Restricting MHC Allele page shown in Figure 2.26. Clicking on H-2-Kb in the left MHC Allele column in the 22nd row, the user is brought to its MHC Allele Information page (Figure 2.28). 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 Class I Allele K restricted epitopes

MHC Allele	
Allele Name:	H-2-Kb
Restriction Level:	COMPLETE MOLECULE
Organism:	mouse (Mus musculus)
Class:	I
Locus:	K
Molecule:	Kb
Chain 1 Type:	alpha
Chain 1 Name:	Kb
Chain 1 Accession:	P01901

Peptide MHC Binding Motif

8-length | 9-length

Position	Position 1 Anchor	2	Position 3 Anchor	4	Position 5 Anchor	6	7	8
Preferred	Preferred IM S V	I S	Preferred FW Y		Preferred F Y			M L V
	Tolerated ACFKLQ R T W Y		Tolerated CILM		Tolerated HMW			
Deleterious							I	

6539 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

Epitope ID	Structure	Source Antigen	Source Organism
135	AAFEFINSL	Protein A47 (4 more)	Vaccinia virus WR (2 more)
220	AAIEKYNSL	Protein A20	Vaccinia virus WR
221	AAIESLREM	calpain-like cysteine peptidase	Trypanosoma cruzi
286	AALKNLCFY	RNA-directed RNA polymerase (1 more)	Lymphocytic choriomeningitis virus (2 more)
287	AALKNLCFYS	RNA-directed RNA polymerase (1 more)	Lymphocytic choriomeningitis virus (strain Armstrong) (2 more)
289	AALLDGGNM	Nucleoprotein (1 more)	Lymphocytic choriomeningitis virus (strain Armstrong) (2 more)
291	AALLFLLL	COG0477: Permeases of the major facilitator superfamily	Magnetospirillum magnetotacticum MS-1
300	AALSKFKEDV	Glycoprotein polyprotein (1 more)	Lymphocytic choriomeningitis virus (2 more)
308	AAMLIRQGL	RNA-directed RNA polymerase (1 more)	Lymphocytic choriomeningitis virus (2 more)

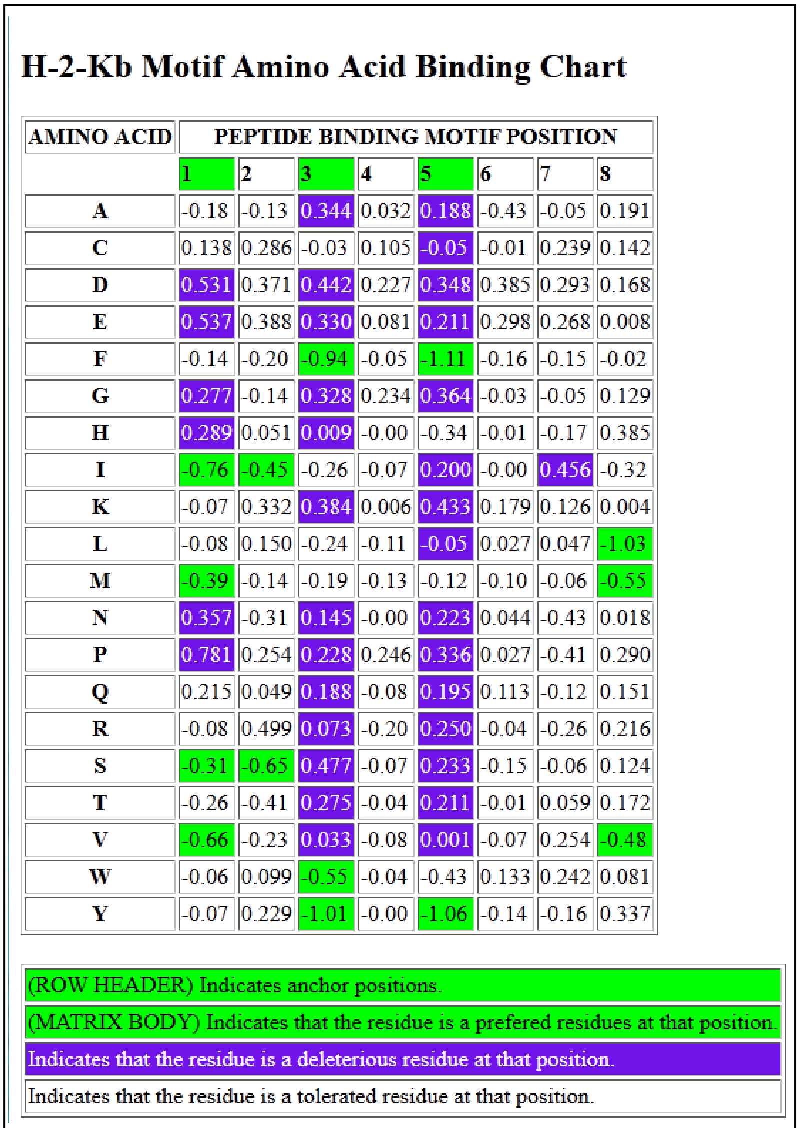
Figure 2.28 Sample MHC Allele Information page with Peptide MHC Binding Motif diagram for H-2-Kb. Note the link to the corresponding Amino Acid Binding Chart on the bottom right of the diagram

The Peptide MHC Binding Motif diagram summarizes the results of the amino acid binding for each position, which is shown in Figure 2.29. 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 2.4.1.1. 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



H-2-Kb Motif Amino Acid Binding Chart

AMINO ACID	PEPTIDE BINDING MOTIF POSITION							
	1	2	3	4	5	6	7	8
A	-0.18	-0.13	0.344	0.032	0.188	-0.43	-0.05	0.191
C	0.138	0.286	-0.03	0.105	-0.05	-0.01	0.239	0.142
D	0.531	0.371	0.442	0.227	0.348	0.385	0.293	0.168
E	0.537	0.388	0.330	0.081	0.211	0.298	0.268	0.008
F	-0.14	-0.20	-0.94	-0.05	-1.11	-0.16	-0.15	-0.02
G	0.277	-0.14	0.328	0.234	0.364	-0.03	-0.05	0.129
H	0.289	0.051	0.009	-0.00	-0.34	-0.01	-0.17	0.385
I	-0.76	-0.45	-0.26	-0.07	0.200	-0.00	0.456	-0.32
K	-0.07	0.332	0.384	0.006	0.433	0.179	0.126	0.004
L	-0.08	0.150	-0.24	-0.11	-0.05	0.027	0.047	-1.03
M	-0.39	-0.14	-0.19	-0.13	-0.12	-0.10	-0.06	-0.55
N	0.357	-0.31	0.145	-0.00	0.223	0.044	-0.43	0.018
P	0.781	0.254	0.228	0.246	0.336	0.027	-0.41	0.290
Q	0.215	0.049	0.188	-0.08	0.195	0.113	-0.12	0.151
R	-0.08	0.499	0.073	-0.20	0.250	-0.04	-0.26	0.216
S	-0.31	-0.65	0.477	-0.07	0.233	-0.15	-0.06	0.124
T	-0.26	-0.41	0.275	-0.04	0.211	-0.01	0.059	0.172
V	-0.66	-0.23	0.033	-0.08	0.001	-0.07	0.254	-0.48
W	-0.06	0.099	-0.55	-0.04	-0.43	0.133	0.242	0.081
Y	-0.07	0.229	-1.01	-0.00	-1.06	-0.14	-0.16	0.337

(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.

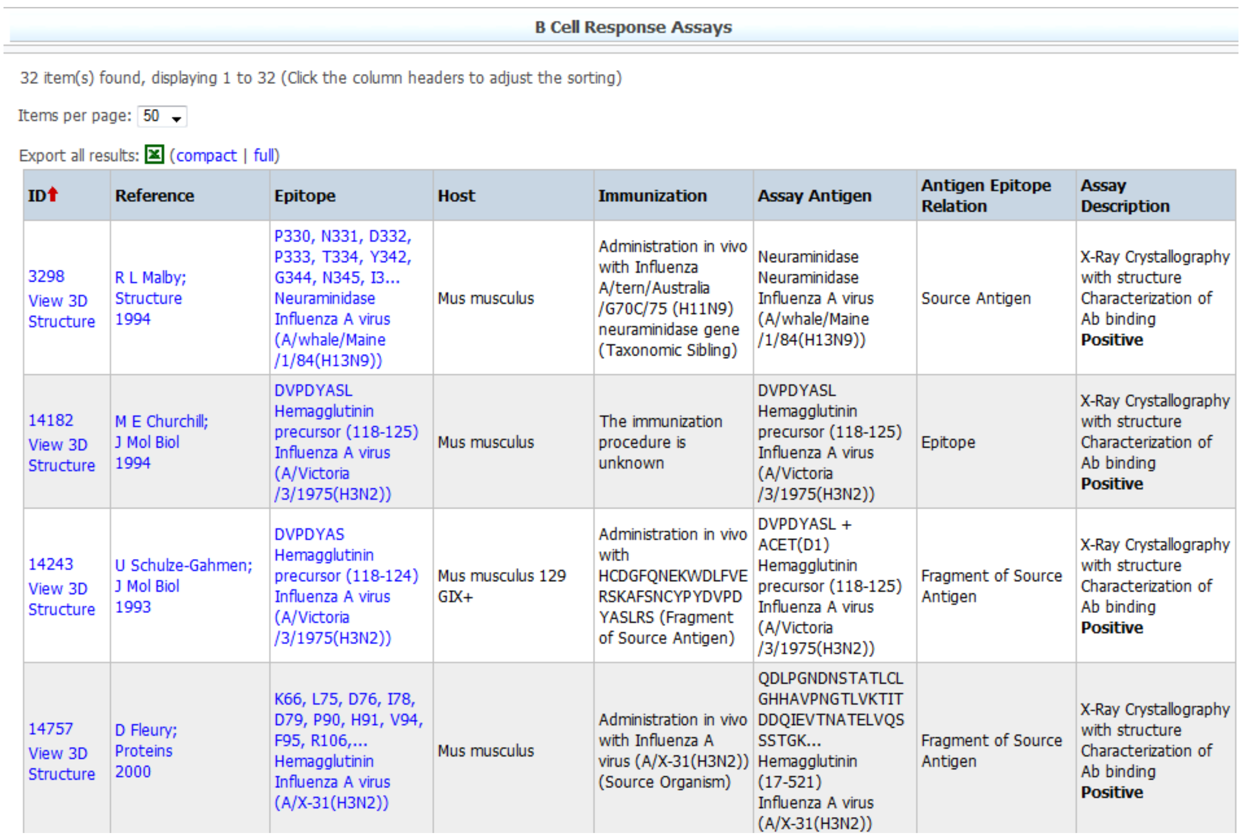
Figure 2.29 Amino acid binding matrix for MHC allele H-2-Db

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

2.3.4.2 Accessing the EpitopeViewer

The EpitopeViewer is an application for three dimensional viewing of receptor-antigen interactions that can be accessed from the Assay List screens. The EpitopeViewer can be used with all assays that have receptor-antigen interaction data available. It is not available for epitopes and assays, and when it is available, a link is provided in the leftmost ID column, as illustrated by the “View 3D Structure” in Figure 2.30. The 32 B cell response assays shown are a result of using the B Cell Search for Epitope Source Organism = Influenza A and Assay Type = X-Ray Crystallography.



B Cell Response Assays

32 item(s) found, displaying 1 to 32 (Click the column headers to adjust the sorting)

Items per page: 50

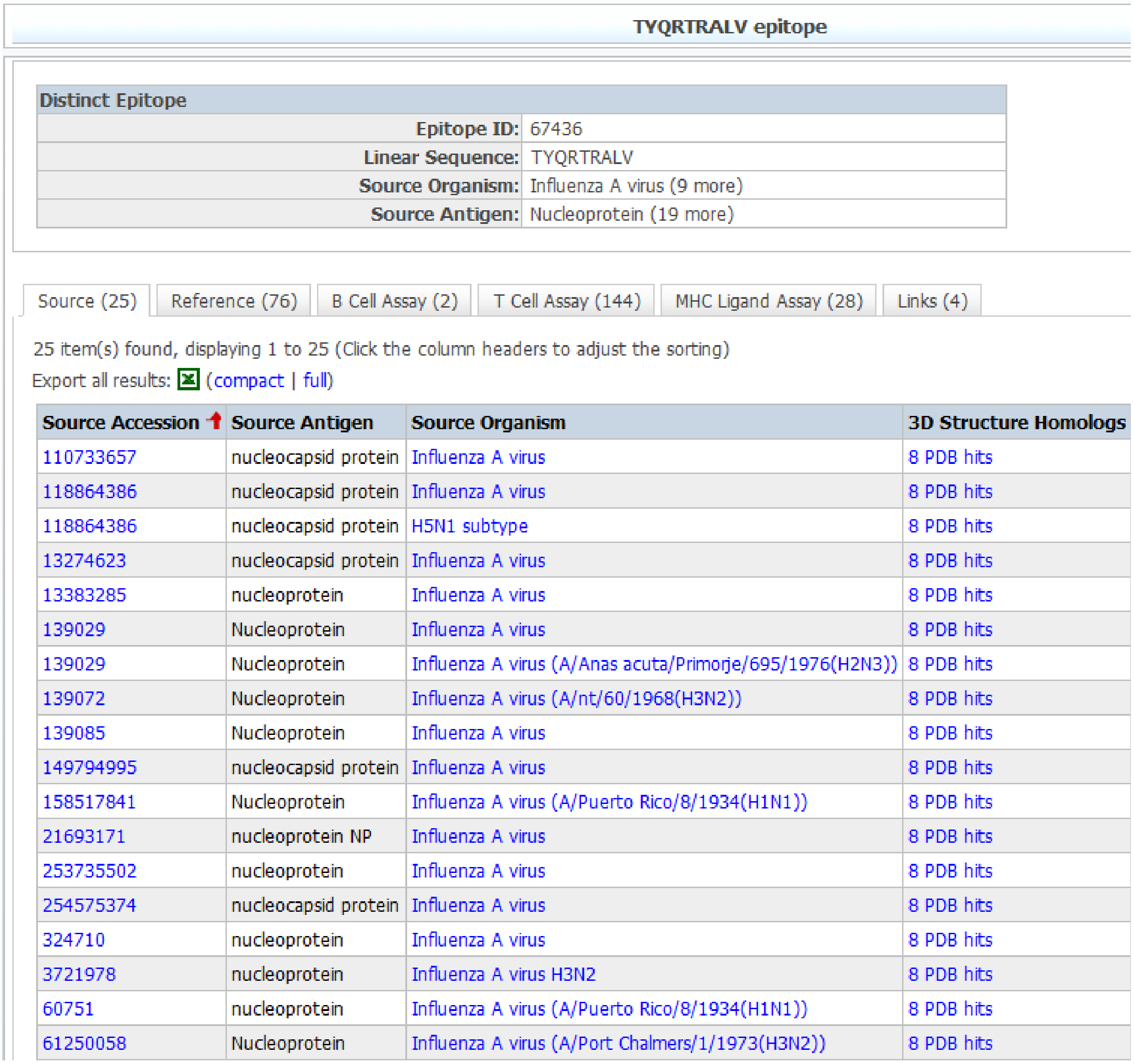
Export all results: (compact | full)

ID	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	Assay Description
3298 View 3D Structure	R L Malby; Structure 1994	P330, N331, D332, P333, T334, Y342, G344, N345, I3... Neuraminidase Influenza A virus (A/whale/Maine /1/84(H13N9))	Mus musculus	Administration in vivo with Influenza A/tern/Australia /G70C/75 (H11N9) neuraminidase gene (Taxonomic Sibling)	Neuraminidase Neuraminidase Influenza A virus (A/whale/Maine /1/84(H13N9))	Source Antigen	X-Ray Crystallography with structure Characterization of Ab binding **Positive**
14182 View 3D Structure	M E Churchill; J Mol Biol 1994	DVPDYASL Hemagglutinin precursor (118-125) Influenza A virus (A/Victoria /3/1975(H3N2))	Mus musculus	The immunization procedure is unknown	DVPDYASL Hemagglutinin precursor (118-125) Influenza A virus (A/Victoria /3/1975(H3N2))	Epitope	X-Ray Crystallography with structure Characterization of Ab binding **Positive**
14243 View 3D Structure	U Schulze-Gahmen; J Mol Biol 1993	DVPDYAS Hemagglutinin precursor (118-124) Influenza A virus (A/Victoria /3/1975(H3N2))	Mus musculus 129 GIX+	Administration in vivo with HCDGFQNEKWDLFVE RSKAFSNCYPYDVPD YASLRS (Fragment of Source Antigen)	DVPDYASL + ACET(D1) Hemagglutinin precursor (118-125) Influenza A virus (A/Victoria /3/1975(H3N2))	Fragment of Source Antigen	X-Ray Crystallography with structure Characterization of Ab binding **Positive**
14757 View 3D Structure	D Fleury; Proteins 2000	K66, L75, D76, I78, D79, P90, H91, V94, F95, R106,... Hemagglutinin Influenza A virus (A/X-31(H3N2))	Mus musculus	Administration in vivo with Influenza A virus (A/X-31(H3N2)) (Source Organism)	QDLPGNDNSTATLCL GHHAVPNGTLVKTIT DDQIEVTNATELVQS SSTGK... Hemagglutinin (17-521) Influenza A virus (A/X-31(H3N2))	Fragment of Source Antigen	X-Ray Crystallography with structure Characterization of Ab binding **Positive**

Figure 2.30 B Cell Response screen with Epitope Viewer links in the leftmost column

2.3.4.3 Result Tabs

As users drill down on hyperlinks to further explore the results of a query, they will find the information organized by tabs. As seen in Figure 2.31 for Epitope ID 67436, there are 25 source organisms listed from 76 references. There is also assay information for MHC binding, B cells, T cells, and MHC ligand assays. The Links tab (Figure 2.32) contains links to relevant tools in the Analysis Resource. Links can also appear to the Bioinformatics Resource Centers (BRC). In the example shown, there is a link to the Influenza Research Database (IRD).



TYQRTRALV epitope

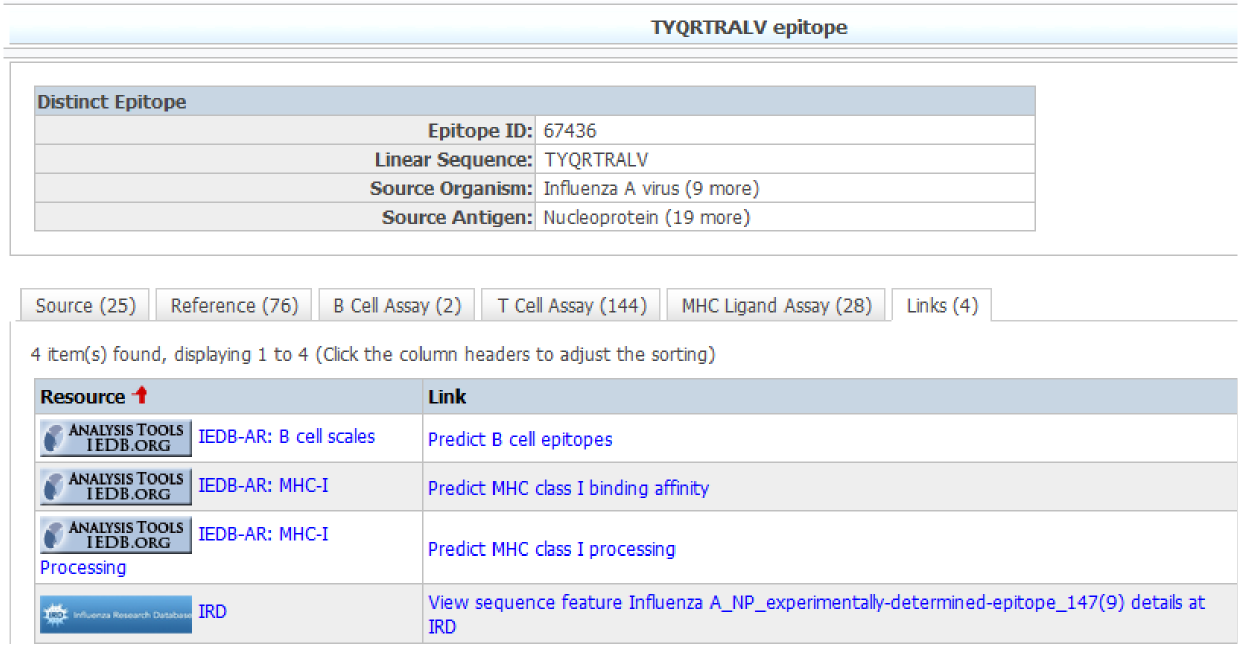
Distinct Epitope	
Epitope ID:	67436
Linear Sequence:	TYQRTRALV
Source Organism:	Influenza A virus (9 more)
Source Antigen:	Nucleoprotein (19 more)

25 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

Export all results: (compact | full)

Source Accession	Source Antigen	Source Organism	3D Structure Homologs
110733657	nucleocapsid protein	Influenza A virus	8 PDB hits
118864386	nucleocapsid protein	Influenza A virus	8 PDB hits
118864386	nucleocapsid protein	H5N1 subtype	8 PDB hits
13274623	nucleocapsid protein	Influenza A virus	8 PDB hits
13383285	nucleoprotein	Influenza A virus	8 PDB hits
139029	Nucleoprotein	Influenza A virus	8 PDB hits
139029	Nucleoprotein	Influenza A virus (A/Anas acuta/Primorje/695/1976(H2N3))	8 PDB hits
139072	Nucleoprotein	Influenza A virus (A/nt/60/1968(H3N2))	8 PDB hits
139085	Nucleoprotein	Influenza A virus	8 PDB hits
149794995	nucleocapsid protein	Influenza A virus	8 PDB hits
158517841	Nucleoprotein	Influenza A virus (A/Puerto Rico/8/1934(H1N1))	8 PDB hits
21693171	nucleoprotein NP	Influenza A virus	8 PDB hits
253735502	nucleoprotein	Influenza A virus	8 PDB hits
254575374	nucleocapsid protein	Influenza A virus	8 PDB hits
324710	nucleoprotein	Influenza A virus	8 PDB hits
3721978	nucleoprotein	Influenza A virus H3N2	8 PDB hits
60751	nucleoprotein	Influenza A virus (A/Puerto Rico/8/1934(H1N1))	8 PDB hits
61250058	Nucleoprotein	Influenza A virus (A/Port Chalmers/1/1973(H3N2))	8 PDB hits

Figure 2.31 Many results pages have information organized into tabs



TYQRTRALV epitope

Distinct Epitope	
Epitope ID:	67436
Linear Sequence:	TYQRTRALV
Source Organism:	Influenza A virus (9 more)
Source Antigen:	Nucleoprotein (19 more)

4 item(s) found, displaying 1 to 4 (Click the column headers to adjust the sorting)

Resource	Link
IEDB-AR: B cell scales	Predict B cell epitopes
IEDB-AR: MHC-I	Predict MHC class I binding affinity
IEDB-AR: MHC-I Processing	Predict MHC class I processing
IRD	View sequence feature Influenza A_NP_experimentally-determined-epitope_147(9) details at IRD

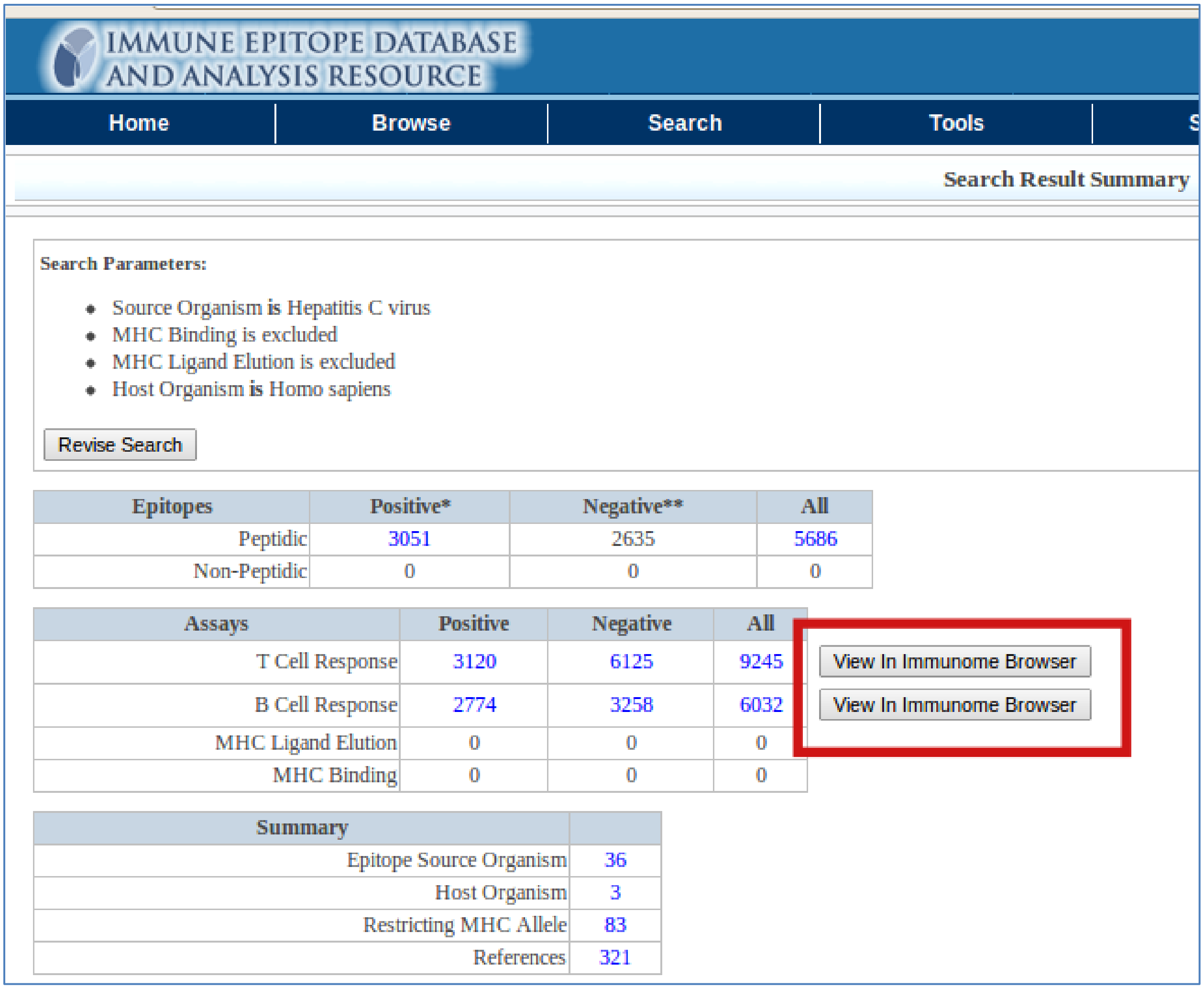
Figure 2.32 The Links tab contains links to relevant tools in the Analysis Resource and links to relevant data from the Bioinformatics Resource Centers. For this case, there is a link to the Influenza Research Database

2.3.4.4 Immunome Browser

The Immunome Browser is a feature integrated into the IEDB to more efficiently display large sets of immune epitope data. The Immunome Browser 'maps' query results from the IEDB onto a reference proteome. A reference proteome is used because the positions of epitopes and names of antigens reported by different investigators are inconsistent due to many versions of protein sequences and differences between strains. 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. Currently, only linear peptide epitopes with T cell or B cell responses are supported for viewing using the Immunome Browser.

Getting Started

To start using the Immunome Browser, just make a query as before and look for the new '**View In Immunome Browser**' buttons, as shown below (Figure 2.33). Clicking on these buttons passes your query results to the Immunome Browser.



Search Result Summary

Search Parameters:

- Source Organism is Hepatitis C virus
- MHC Binding is excluded
- MHC Ligand Elution is excluded
- Host Organism is Homo sapiens

Epitopes	Positive*	Negative**	All
Peptidic	3051	2635	5686
Non-Peptidic	0	0	0

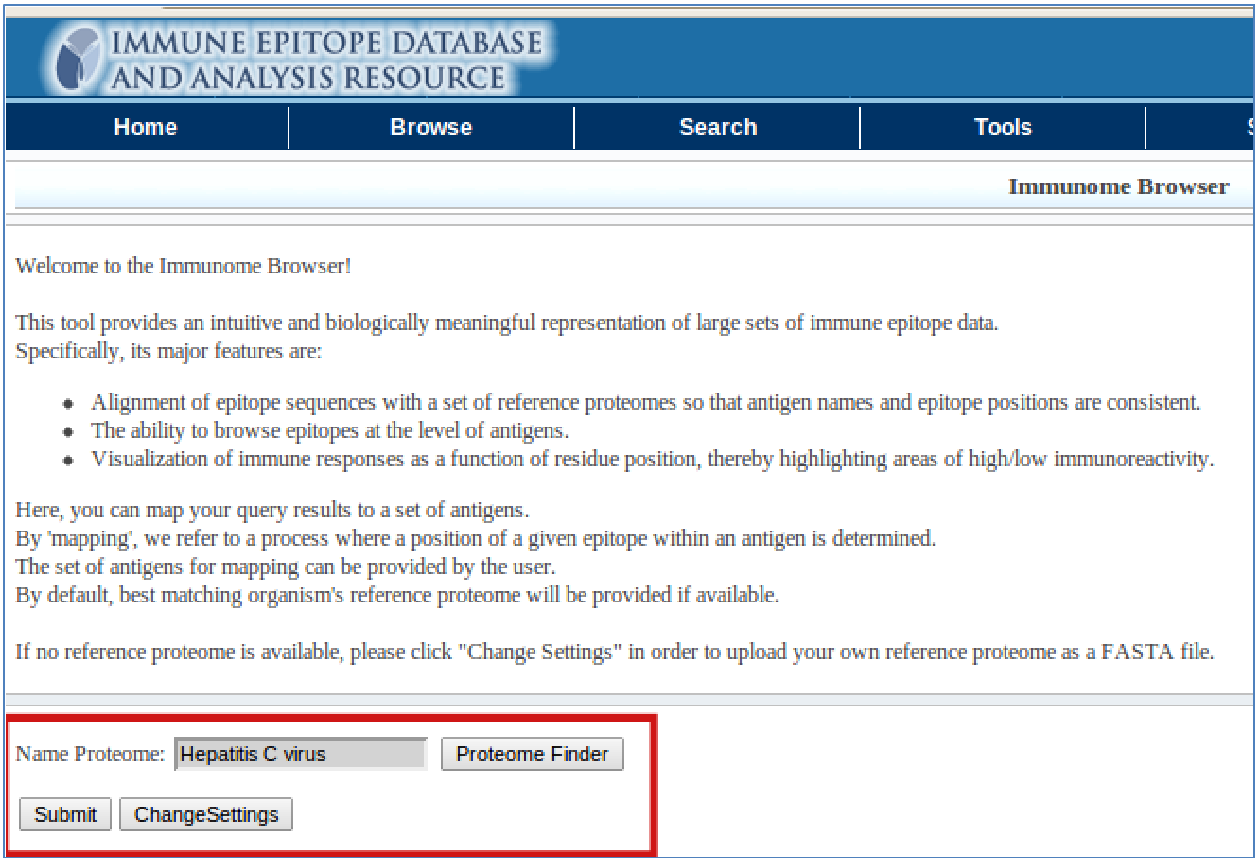
Assays	Positive	Negative	All
T Cell Response	3120	6125	9245
B Cell Response	2774	3258	6032
MHC Ligand Elution	0	0	0
MHC Binding	0	0	0

Summary	
Epitope Source Organism	36
Host Organism	3
Restricting MHC Allele	83
References	321

Figure 2.33 Search result summary page returned by the IEDB website

Defining Peptide:Antigen Mapping Parameters

Once in the Immunome Browser, the default parameters are set and the best matching reference proteome is displayed (Figure 2.34).



Welcome to the Immunome Browser!

This tool provides an intuitive and biologically meaningful representation of large sets of immune epitope data.
Specifically, its major features are:

- Alignment of epitope sequences with a set of reference proteomes so that antigen names and epitope positions are consistent.
- The ability to browse epitopes at the level of antigens.
- Visualization of immune responses as a function of residue position, thereby highlighting areas of high/low immunoreactivity.

Here, you can map your query results to a set of antigens.
By 'mapping', we refer to a process where a position of a given epitope within an antigen is determined.
The set of antigens for mapping can be provided by the user.
By default, best matching organism's reference proteome will be provided if available.

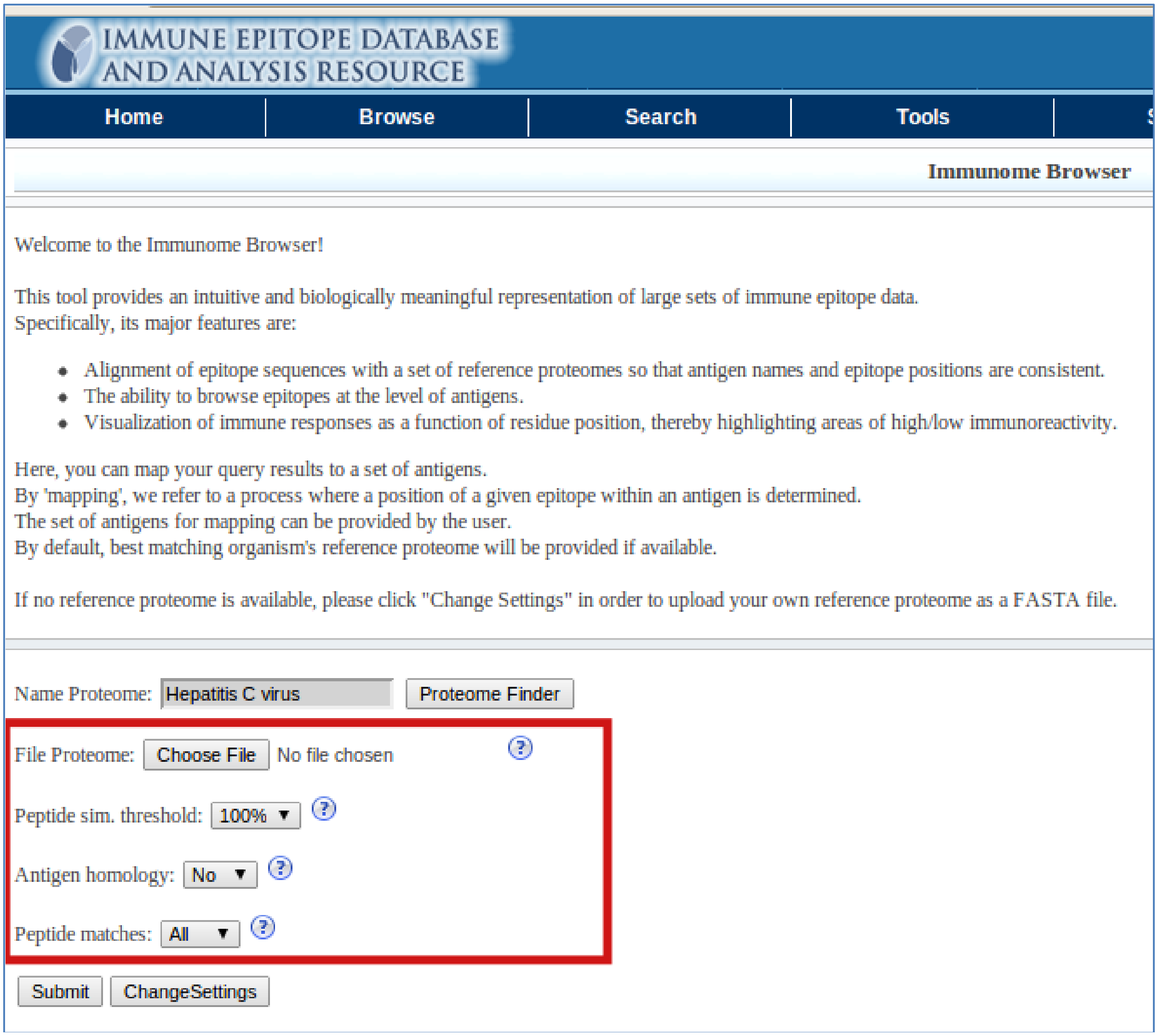
If no reference proteome is available, please click "Change Settings" in order to upload your own reference proteome as a FASTA file.

Name Proteome: Hepatitis C virus

Figure 2.34 Default parameter setting for mapping query results to a selected reference proteome

To override a default proteome or change other default mapping parameters, click '**Change Settings**' to reveal additional fields.

After clicking **Change Settings**, all parameters are shown in Figure 2.35:



Welcome to the Immunome Browser!

This tool provides an intuitive and biologically meaningful representation of large sets of immune epitope data.
Specifically, its major features are:

- Alignment of epitope sequences with a set of reference proteomes so that antigen names and epitope positions are consistent.
- The ability to browse epitopes at the level of antigens.
- Visualization of immune responses as a function of residue position, thereby highlighting areas of high/low immunoreactivity.

Here, you can map your query results to a set of antigens.
By 'mapping', we refer to a process where a position of a given epitope within an antigen is determined.
The set of antigens for mapping can be provided by the user.
By default, best matching organism's reference proteome will be provided if available.

If no reference proteome is available, please click "Change Settings" in order to upload your own reference proteome as a FASTA file.

Name Proteome: Hepatitis C virus

File Proteome: No file chosen

Peptide sim. threshold: 100%

Antigen homology: No

Peptide matches: All

Figure 2.35 Parameters needed to map query results onto the reference proteome

Use each of the fields to adjust mapping settings as follows:

Name Proteome
This name refers to the best matching reference proteome for the query entered by the user. In the case where no match is found, the user must provide a set of antigens against which to map peptides. To provide the proteome or override a default proteome, use the '**File Proteome**' field.

File Proteome
This button allows the user to submit a set of protein sequences, overriding the selected reference proteome. Use '**Choose File**' to provide your own antigen sequences in a FASTA format.

Peptide Similarity Threshold
This allows the user to change the similarity threshold between the epitope sequences and the protein they are being mapped to. A lower threshold may be desirable for proteins that display high sequence variability such as HCV.The sequence alignment step uses the USEARCH [http://www.drive5.com/usearch/] algorithm, to achieve fast sequence searches. Specifically, the

command 'usearch search_local' is used. In our experience, usearch is faster than BLAST. Furthermore, USEARCH is a heuristic algorithm (BLAST is also heuristic). Hence, for low similarity thresholds, some valid epitopes may be missed.

Antigen Homology

This field allows the user to place the additional constraint that the proteins to which the epitopes are mapped must be homologous to the source protein of the epitopes, as described in the manuscript the epitope was described in.

Peptide Matches

Using this field the user decides between two different types of mappings; either ‘All’, where all possible epitope:protein matches are presented, or ‘Best’ where only the best matches are presented. In the case of 'Best' matches, ties are kept if multiple best matches are available.

Once all parameters are set as desired, click the ‘**Submit**’ button. This will initiate mapping of the query results to the chosen reference proteome.

Navigating the Mapping Results

After clicking the ‘**Submit**’ button, results of mapping the query results to the reference proteome are displayed in Figure 2.36. Shown at the top is a navigation panel to display different types of mapping results. For example, by default, all proteins in the reference proteome are listed. If the user wants to see only those proteins with epitopes mapped, then ‘ORFs containing epitopes’ should be chosen.

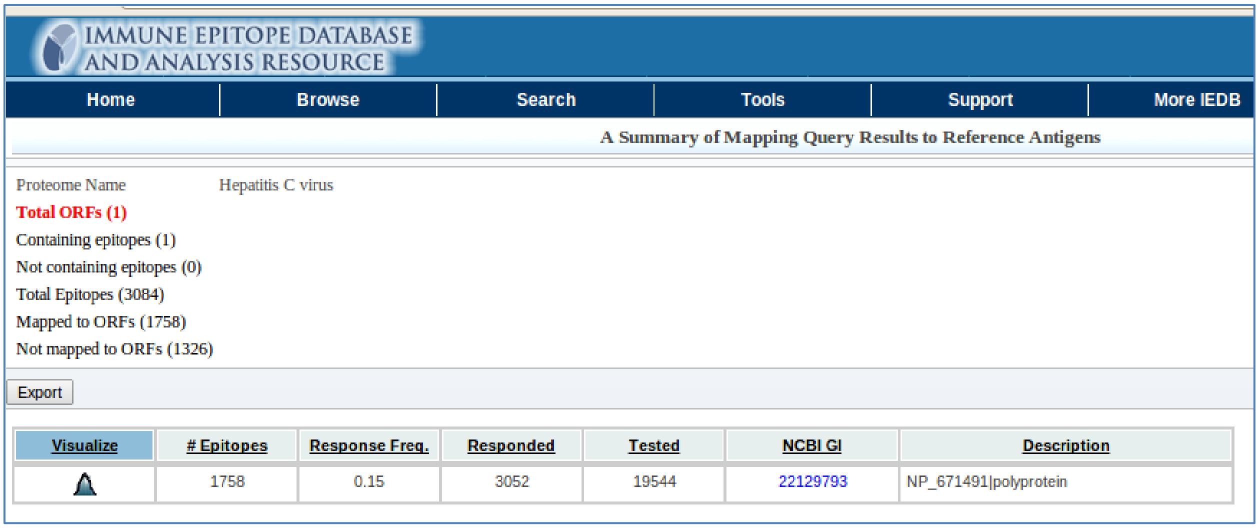
In the bottom panel, either a list of proteins or epitopes is shown based on the selection made in the navigation panel shown above. Of special note, in the case of ‘ORFs containing epitopes’, by clicking icons in column ‘Visualize’, one can visualize profiles of epitope prominence scores for corresponding antigens.

Visualizing a Profile of Epitope Prominence Scores for Each Antigen

After clicking any one of the icons in column ‘Visualize’ from the page showing mapping results, a screen such as Figure 2.37 is shown. The top panel provides a visualization of where on the antigen epitopes are mapped. The x-axis shows residue positions and the y-axis shows epitope prominence scores. The bottom panel lists epitopes mapped to the antigen, their mapped positions and their epitope prominence scores (e.g. Response Freq. Score).

Different types of ‘epitope prominence scores’ are possible. By default, response frequency scores are chosen, which correlate with how often subjects responded to a given epitope. In addition, a score based on the number of assays is also provided. As the name indicates, for each epitope, the number of assays associated with it is collected and plotted. Thus, an epitope with a higher ‘num assay’ score would mean that it has been studied more often. Additional details of the different epitope prominence scores are provided in the section that follows.

To illustrate the usefulness of epitope prominence scores, a region in the HCV polyprotein containing the immunodominant epitope (NS3, 1248-1261) [4] is shown in Figure 2.38. In the figure, a peak in the region (1248-1261), which contains the immunodominant epitope indicating relatively high response frequency scores, is visible. In Figure 2.39, a list of peptides mapped to the region and sorted based on positions of their first residue is shown. Epitopes responsible for the peak visualized can be found based on response frequency scores listed in the last column.



A Summary of Mapping Query Results to Reference Antigens

Proteome Name Hepatitis C virus

Total ORFs (1)

Containing epitopes (1)

Not containing epitopes (0)

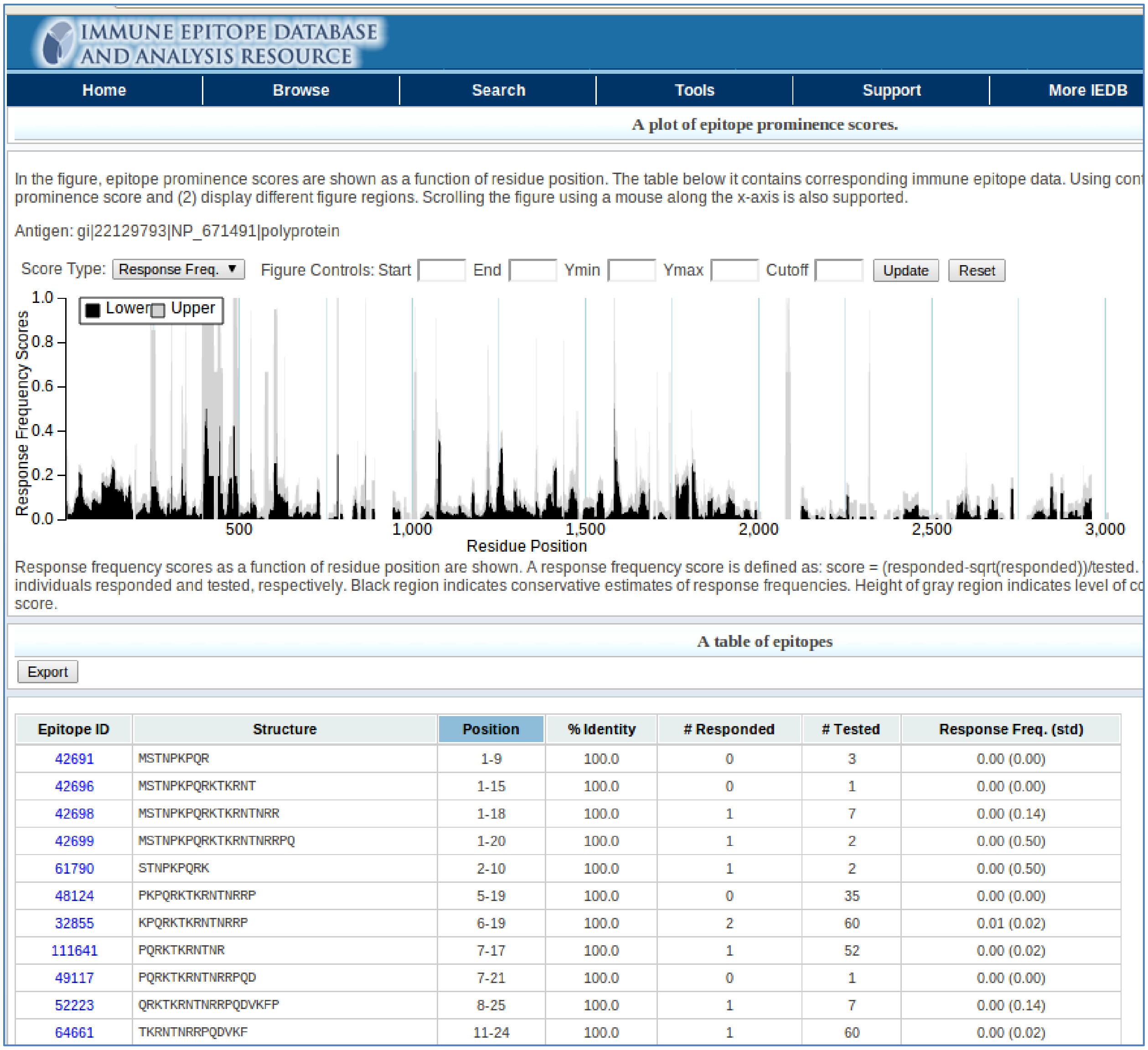
Total Epitopes (3084)

Mapped to ORFs (1758)

Not mapped to ORFs (1326)

Visualize	# Epitopes	Response Freq.	Responded	Tested	NCBI GI	Description
▲	1758	0.15	3052	19544	22129793	NP_671491|polyprotein

Figure 2.36 Mapping results



A plot of epitope prominence scores.

In the figure, epitope prominence scores are shown as a function of residue position. The table below it contains corresponding immune epitope data. Using cont prominence score and (2) display different figure regions. Scrolling the figure using a mouse along the x-axis is also supported.

Antigen: gi|22129793|NP_671491|polyprotein

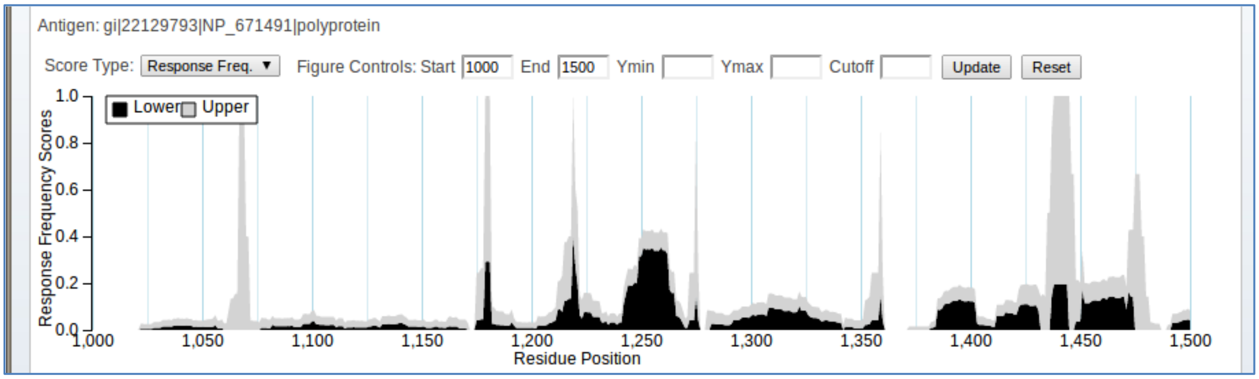
Score Type: Response Freq. ▼ Figure Controls: Start End Ymin Ymax Cutoff

Response frequency scores as a function of residue position are shown. A response frequency score is defined as: score = (responded-sqrt(responded))/tested. individuals responded and tested, respectively. Black region indicates conservative estimates of response frequencies. Height of gray region indicates level of co score.

A table of epitopes

Epitope ID	Structure	Position	% Identity	# Responded	# Tested	Response Freq. (std)
42691	MSTNPKPQR	1-9	100.0	0	3	0.00 (0.00)
42696	MSTNPKPQRKTKRNT	1-15	100.0	0	1	0.00 (0.00)
42698	MSTNPKPQRKTKRNTNRR	1-18	100.0	1	7	0.00 (0.14)
42699	MSTNPKPQRKTKRNTNRRPQ	1-20	100.0	1	2	0.00 (0.50)
61790	STNPKPQRK	2-10	100.0	1	2	0.00 (0.50)
48124	PKPQRKTKRNTNRRP	5-19	100.0	0	35	0.00 (0.00)
32855	KPQRKTKRNTNRRP	6-19	100.0	2	60	0.01 (0.02)
111641	PQRKTKRNTNR	7-17	100.0	1	52	0.00 (0.02)
49117	PQRKTKRNTNRRPQD	7-21	100.0	0	1	0.00 (0.00)
52223	QRKTKRNTNRRPQDVKFP	8-25	100.0	1	7	0.00 (0.14)
64661	TKRNTNRRPQDVKF	11-24	100.0	1	60	0.00 (0.02)

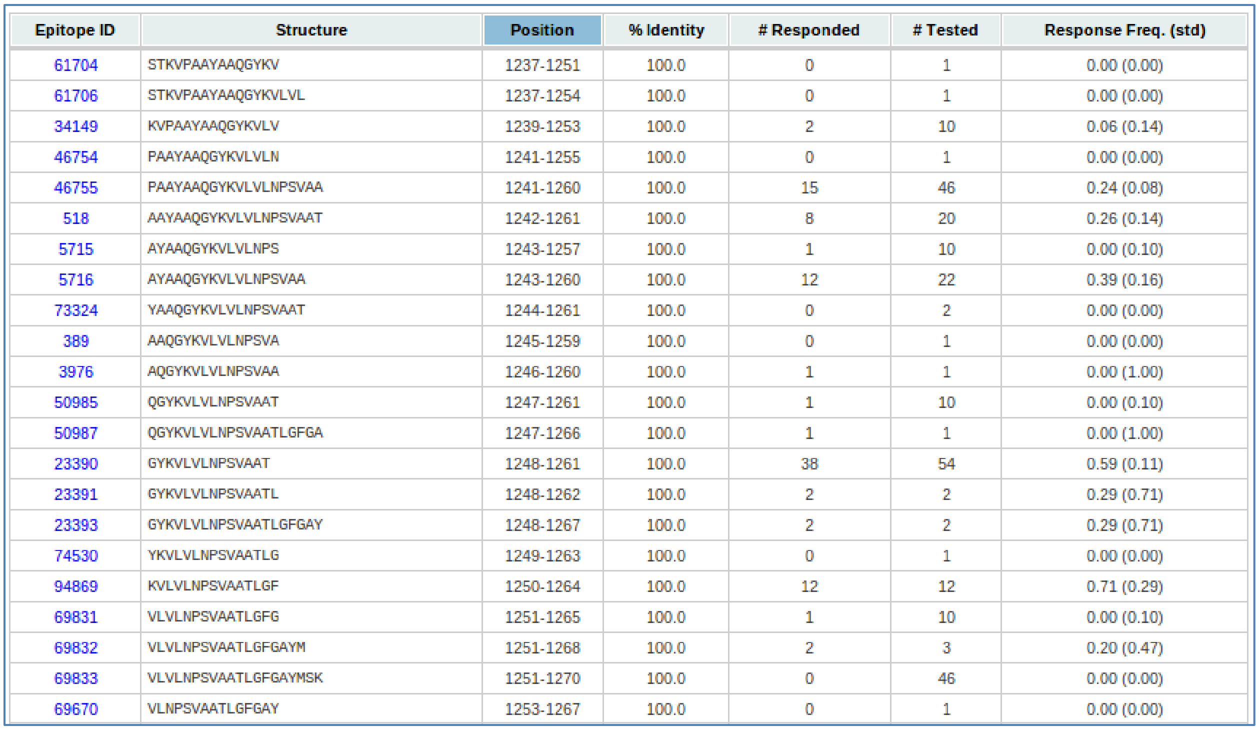
Figure 2.37 Visualization of mapped query results to an HCV polyprotein



Antigen: gi|22129793|NP_671491|polyprotein

Score Type: Response Freq. ▼ Figure Controls: Start 1000 End 1500 Ymin Ymax Cutoff

Figure 2.38 A zoom-in of a region of the HCV polyprotein containing the immunodominant epitope at positions 1248-1261 in the NS3 protein



Epitope ID	Structure	Position	% Identity	# Responded	# Tested	Response Freq. (std)
61704	STKVPAAYAAQGYKV	1237-1251	100.0	0	1	0.00 (0.00)
61706	STKVPAAYAAQGYKVLVL	1237-1254	100.0	0	1	0.00 (0.00)
34149	KVPAAYAAQGYKVLV	1239-1253	100.0	2	10	0.06 (0.14)
46754	PAAYAAQGYKVLVLN	1241-1255	100.0	0	1	0.00 (0.00)
46755	PAAYAAQGYKVLVLNPSVAA	1241-1260	100.0	15	46	0.24 (0.08)
518	AAYAAQGYKVLVLNPSVAAT	1242-1261	100.0	8	20	0.26 (0.14)
5715	AYAAQGYKVLVLNPS	1243-1257	100.0	1	10	0.00 (0.10)
5716	AYAAQGYKVLVLNPSVAA	1243-1260	100.0	12	22	0.39 (0.16)
73324	YAAQGYKVLVLNPSVAAT	1244-1261	100.0	0	2	0.00 (0.00)
389	AAQGYKVLVLNPSVA	1245-1259	100.0	0	1	0.00 (0.00)
3976	AQGYKVLVLNPSVAA	1246-1260	100.0	1	1	0.00 (1.00)
50985	QGYKVLVLNPSVAAT	1247-1261	100.0	1	10	0.00 (0.10)
50987	QGYKVLVLNPSVAATLGFGA	1247-1266	100.0	1	1	0.00 (1.00)
23390	GYKVLVLNPSVAAT	1248-1261	100.0	38	54	0.59 (0.11)
23391	GYKVLVLNPSVAATL	1248-1262	100.0	2	2	0.29 (0.71)
23393	GYKVLVLNPSVAATLGFGAY	1248-1267	100.0	2	2	0.29 (0.71)
74530	YKVLVLNPSVAATLG	1249-1263	100.0	0	1	0.00 (0.00)
94869	KVLVLNPSVAATLGF	1250-1264	100.0	12	12	0.71 (0.29)
69831	VLVLNPSVAATLGFG	1251-1265	100.0	1	10	0.00 (0.10)
69832	VLVLNPSVAATLGFGAYM	1251-1268	100.0	2	3	0.20 (0.47)
69833	VLVLNPSVAATLGFGAYMSK	1251-1270	100.0	0	46	0.00 (0.00)
69670	VLNPSVAATLGFGAY	1253-1267	100.0	0	1	0.00 (0.00)

Figure 2.39 A screen shot of the table of peptides for the region containing the immunodominant epitope at positions 1248-1261 of the NS3 protein

Different Types of Epitope Prominence Scores

As mentioned earlier, two different types of epitope prominence scores have been implemented, reflecting different ways an epitope's importance can be measured. Details of their calculations are provided below.

Response Frequency Scores

For a given peptide, its response frequency score is defined as: (responded – sqrt(responded))/subjects. The variables 'responded' and 'subjects' refer to the number of subjects that gave positive immune response and the total number of subjects, respectively. The term 'sqrt(responded)' is used to take into account statistical uncertainty associated with low counts. For example, response frequencies of 10/10 and 100/100 have the same ratios, however the latter has greater significance. Response frequency scores (RFScores) take this into account, and thus the ratios have RFScores of 0.68 and 0.9, respectively.

Number of Assays

For a given peptide, num_assay scores is a count of its assay records. Thus those peptides that are studied more often will get higher num_assay scores. In addition, scores can be broken down into those assay records with positive or negative results.

2.3.5 Finders Overview

Several finders (Allele, Assay, Disease, Molecule, Geolocation, and Organism) are available to help facilitate selections and control vocabulary usage (improves result outputs). 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 except the keyword query. Multiple selections can be made when utilizing finders during a query.

2.3.5.1 Allele Finder

The MHC Allele Finder facilitates the selection of one or more MHC alleles. Initially the Allele Finder lists all alleles ordered by allele name. The Allele Finder allows the user to find alleles by organism, class {I, II, non-classical}, and allele in the Find box (Figure 2.40). 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 any alleles that contain the value in the name field and match the class selected.

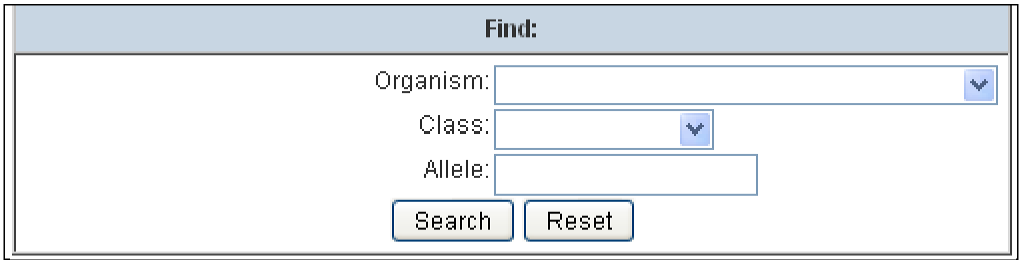
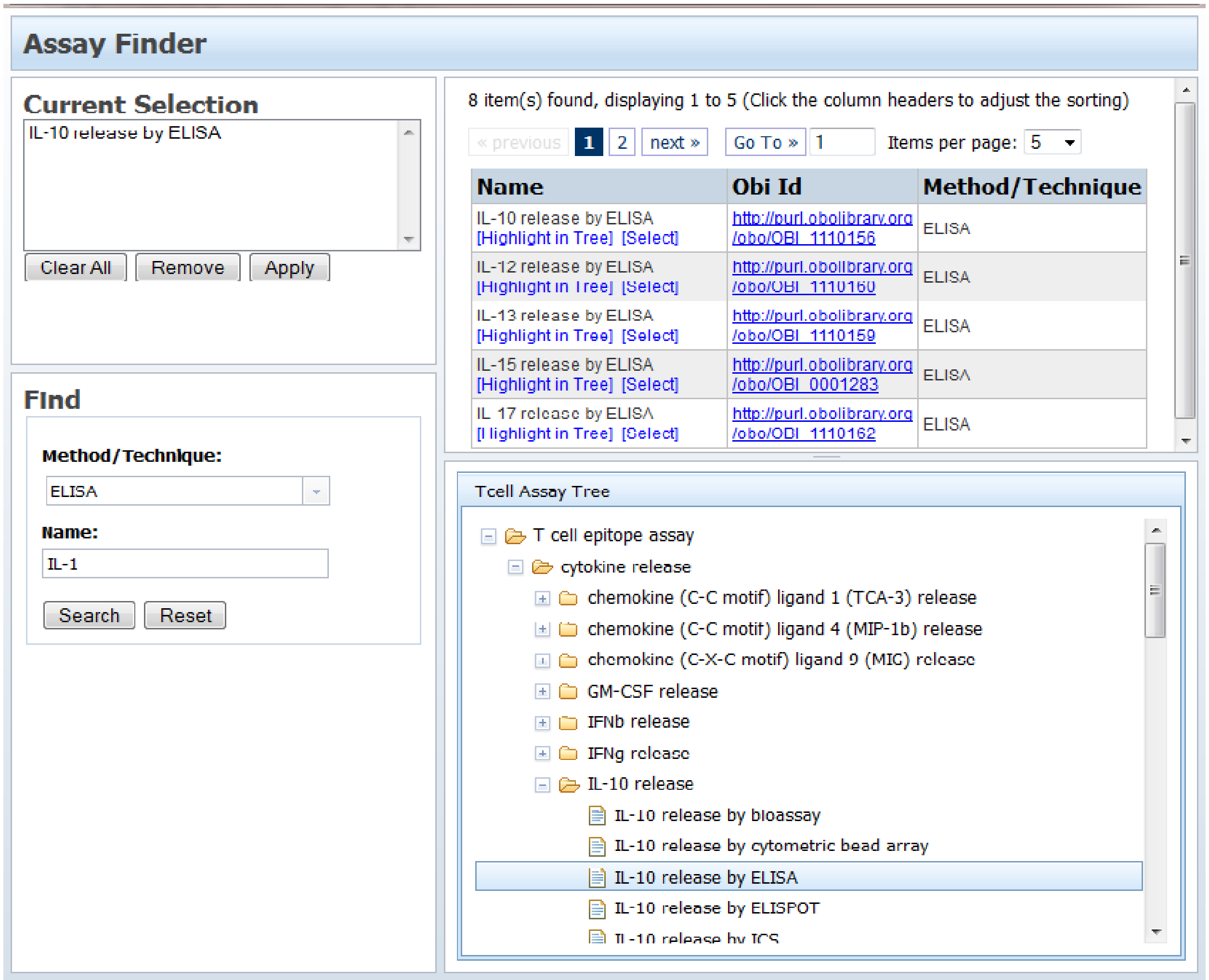


Figure 2.40 Find form on the Allele Finder

2.3.5.2 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. There are three versions of the Assay Finder, each specifically designed for B cell, T cell, and MHC ligand assays. All three organize and display assays in a tree structure, as seen in Figure 2.41 for the T Cell assays.



IL-10 release by ELISA

Method/Technique: ELISA

Name: IL-1

8 item(s) found, displaying 1 to 5 (Click the column headers to adjust the sorting)

Go To » 1 Items per page: 5

Name	Obi Id	Method/Technique
IL-10 release by ELISA [Highlight in Tree] [Select]	http://purl.obolibrary.org/obo/OBI_1110156	ELISA
IL-12 release by ELISA [Highlight in Tree] [Select]	http://purl.obolibrary.org/obo/OBI_1110160	ELISA
IL-13 release by ELISA [Highlight in Tree] [Select]	http://purl.obolibrary.org/obo/OBI_1110159	ELISA
IL-15 release by ELISA [Highlight in Tree] [Select]	http://purl.obolibrary.org/obo/OBI_0001283	ELISA
IL-17 release by ELISA [Highlight in Tree] [Select]	http://purl.obolibrary.org/obo/OBI_1110162	ELISA

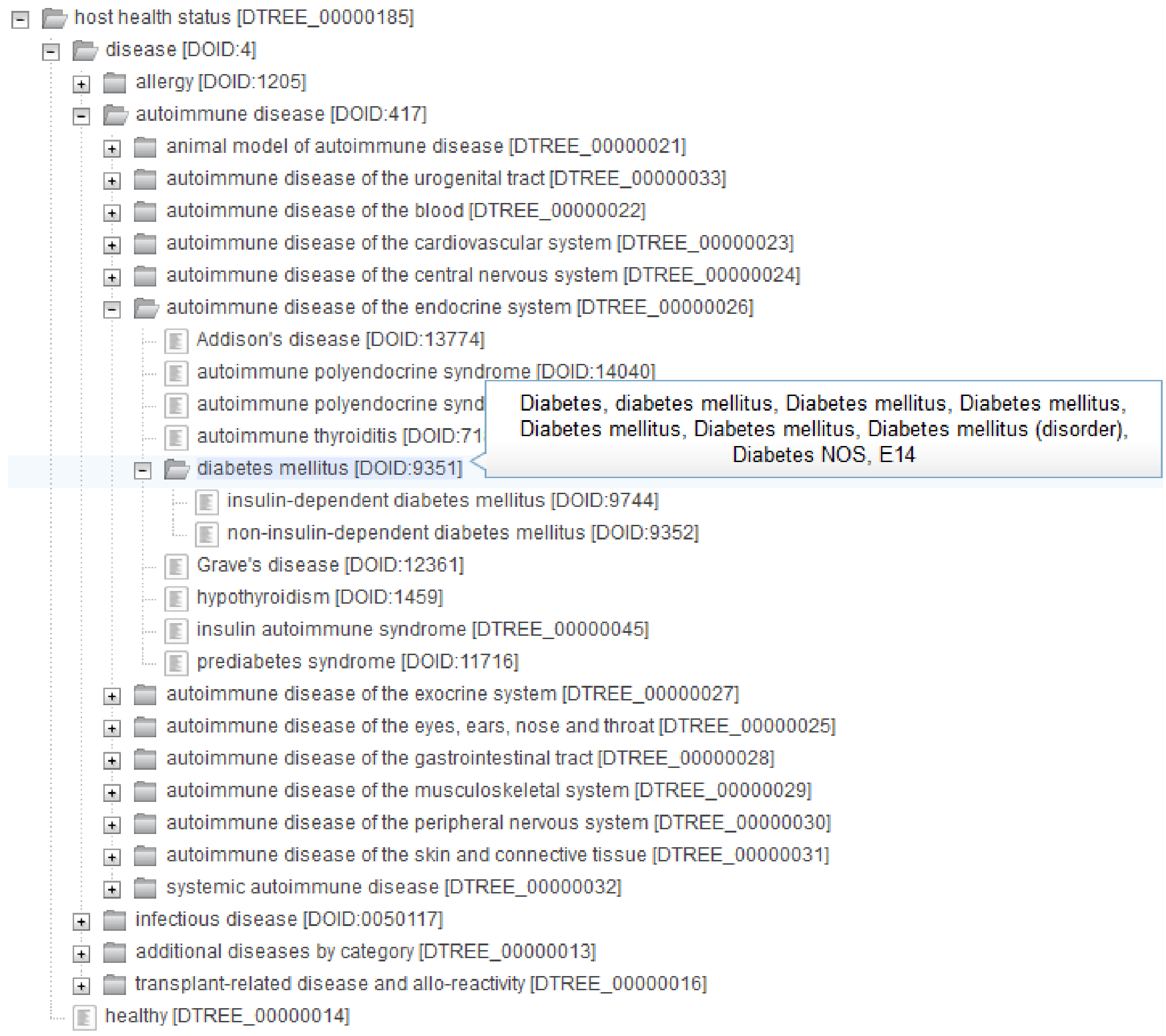
- ⊟ T cell epitope assay
  - ⊟ cytokine release
    - ⊞ chemokine (C-C motif) ligand 1 (TCA-3) release
    - ⊞ chemokine (C-C motif) ligand 4 (MIP-1b) release
    - ⊞ chemokine (C-X-C motif) ligand 9 (MIG) release
    - ⊞ GM-CSF release
    - ⊞ IFNb release
    - ⊞ IFNg release
    - ⊟ IL-10 release
      - IL-10 release by bioassay
      - IL-10 release by cytometric bead array
      - IL-10 release by ELISA
      - IL-10 release by ELISPOT
      - IL-10 release by ICS

Figure 2.41 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.

2.3.5.3 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 (including ICD10 codes) 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. When initially introduced, the Disease Finder was functional for only Allergy and Autoimmunity. In 2013 its functionality was expanded to include the other three categories. Additional refinements, especially in the categorization of allergic diseases, will be made in 2014. Infectious disease searches are also well accommodated by the Source Organism Finder.

Figure 2.42 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. A mouse-over balloon provides additional information on each node of the tree, as shown in the figure.



- host health status [DTREE_00000185]
  - disease [DOID:4]
    - allergy [DOID:1205]
    - autoimmune disease [DOID:417]
      - animal model of autoimmune disease [DTREE_00000021]
      - autoimmune disease of the urogenital tract [DTREE_00000033]
      - autoimmune disease of the blood [DTREE_00000022]
      - autoimmune disease of the cardiovascular system [DTREE_00000023]
      - autoimmune disease of the central nervous system [DTREE_00000024]
      - autoimmune disease of the endocrine system [DTREE_00000026]
        - Addison's disease [DOID:13774]
        - autoimmune polyendocrine syndrome [DOID:14040]
        - autoimmune polyendocrine synd
        - autoimmune thyroiditis [DOID:71
        - diabetes mellitus [DOID:9351]
          - insulin-dependent diabetes mellitus [DOID:9744]
          - non-insulin-dependent diabetes mellitus [DOID:9352]
        - Grave's disease [DOID:12361]
        - hypothyroidism [DOID:1459]
        - insulin autoimmune syndrome [DTREE_00000045]
        - prediabetes syndrome [DOID:11716]
      - autoimmune disease of the exocrine system [DTREE_00000027]
      - autoimmune disease of the eyes, ears, nose and throat [DTREE_00000025]
      - autoimmune disease of the gastrointestinal tract [DTREE_00000028]
      - autoimmune disease of the musculoskeletal system [DTREE_00000029]
      - autoimmune disease of the peripheral nervous system [DTREE_00000030]
      - autoimmune disease of the skin and connective tissue [DTREE_00000031]
      - systemic autoimmune disease [DTREE_00000032]
    - infectious disease [DOID:0050117]
    - additional diseases by category [DTREE_00000013]
    - transplant-related disease and allo-reactivity [DTREE_00000016]
  - healthy [DTREE_00000014]

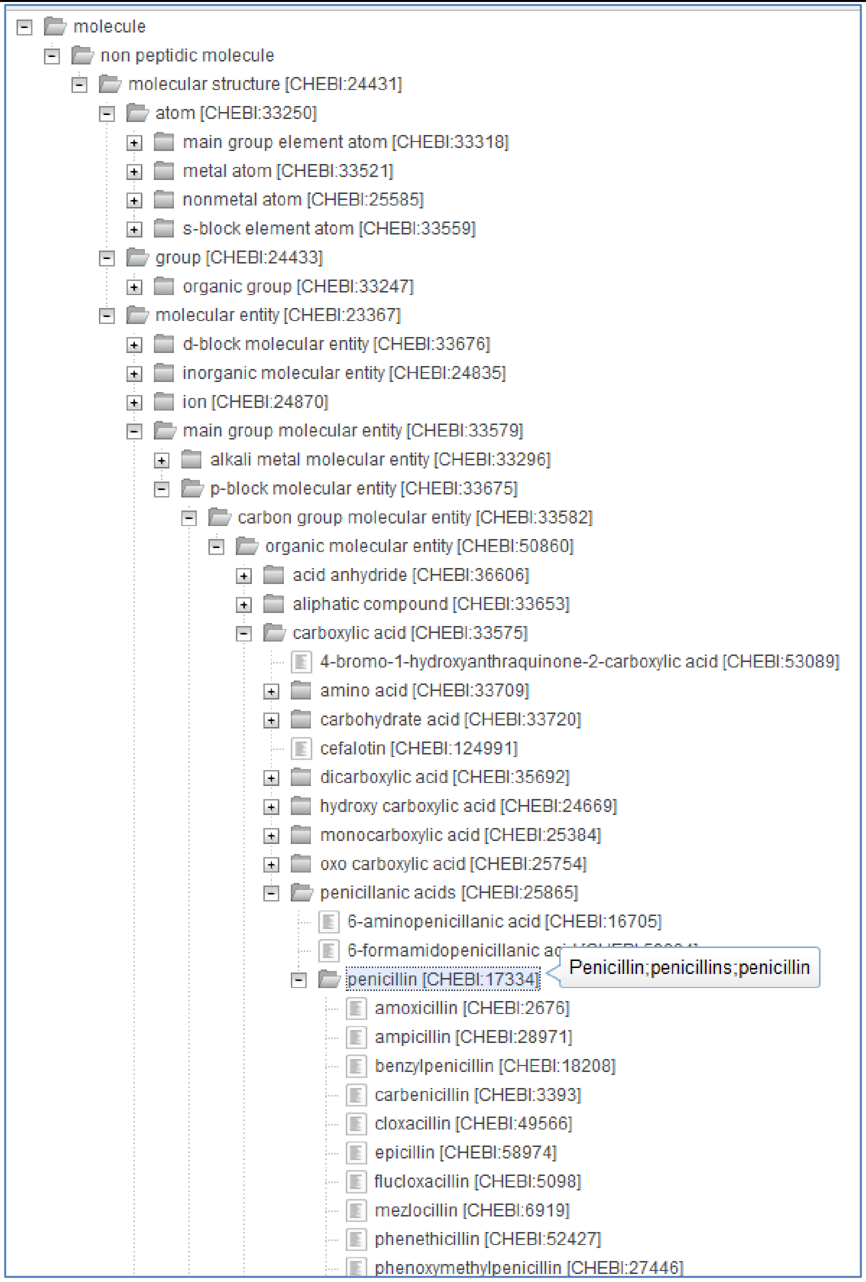
Diabetes, diabetes mellitus, Diabetes mellitus, Diabetes mellitus, Diabetes mellitus, Diabetes mellitus, Diabetes mellitus (disorder), Diabetes NOS, E14

Figure 2.42 The disease finder can be found within the Immune Mediated Disease Association section of the Home Page search and within the In Vivo Process section of the relevant Advanced Searches. In the example shown, diabetes is highlighted. A balloon also indicates its synonyms.

2.3.5.4 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 and another that includes peptidic and non-peptidic branches. Both versions can be found in the Home Page Search (Section 2.3.2) and on the Advanced Search pages. The non-peptidic version is used when the epitope type is specified as non-peptidic. The more general version is used to specify the epitope source molecule. Records in the Source Finder come from GenPept, ChEBI, and UniProt databases. When not available in these sources, the IEDB creates an internal IEDB source identifier.

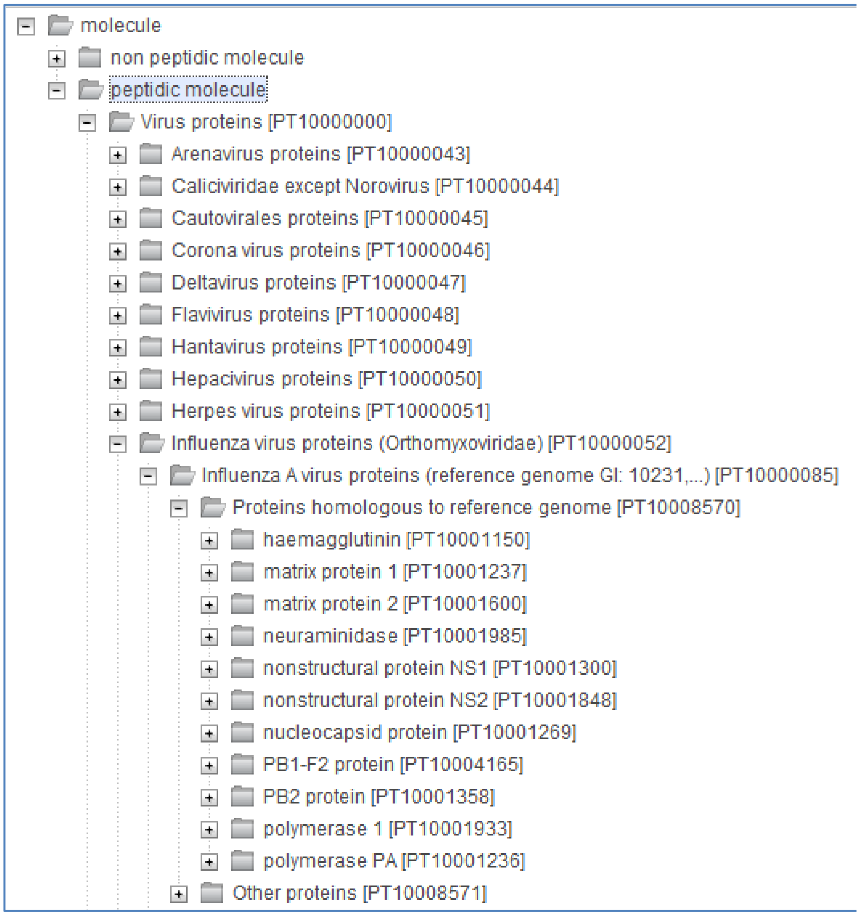
The Molecule Finder for specifying the source molecule is designed to include two parallel trees, one for non-peptidics and the other for protein molecules. The former contains the structures curated by the Chemical Entities of Biological Interest (ChEBI) database. An example is shown in Figure 2.43.



- molecule
  - non peptidic molecule
    - molecular structure [CHEBI:24431]
      - atom [CHEBI:33250]
        - main group element atom [CHEBI:33318]
        - metal atom [CHEBI:33521]
        - nonmetal atom [CHEBI:25585]
        - s-block element atom [CHEBI:33559]
      - group [CHEBI:24433]
        - organic group [CHEBI:33247]
      - molecular entity [CHEBI:23367]
        - d-block molecular entity [CHEBI:33676]
        - inorganic molecular entity [CHEBI:24835]
        - ion [CHEBI:24870]
        - main group molecular entity [CHEBI:33579]
          - alkali metal molecular entity [CHEBI:33296]
          - p-block molecular entity [CHEBI:33675]
            - carbon group molecular entity [CHEBI:33582]
              - organic molecular entity [CHEBI:50860]
                - acid anhydride [CHEBI:36606]
                - aliphatic compound [CHEBI:33653]
                - carboxylic acid [CHEBI:33575]
                  - 4-bromo-1-hydroxyanthraquinone-2-carboxylic acid [CHEBI:53089]
                  - amino acid [CHEBI:33709]
                  - carbohydrate acid [CHEBI:33720]
                  - cefalotin [CHEBI:124991]
                  - dicarboxylic acid [CHEBI:35692]
                  - hydroxy carboxylic acid [CHEBI:24669]
                  - monocarboxylic acid [CHEBI:25384]
                  - oxo carboxylic acid [CHEBI:25754]
                  - penicillanic acids [CHEBI:25865]
                    - 6-aminopenicillanic acid [CHEBI:16705]
                    - 6-formamidopenicillanic ac
                    - penicillin [CHEBI:17334]
                      - amoxicillin [CHEBI:2676]
                      - ampicillin [CHEBI:28971]
                      - benzylpenicillin [CHEBI:18208]
                      - carbenicillin [CHEBI:3393]
                      - cloxacillin [CHEBI:49566]
                      - epicillin [CHEBI:58974]
                      - flucloxacillin [CHEBI:5098]
                      - mezlocillin [CHEBI:6919]
                      - phenethicillin [CHEBI:52427]
                      - phenoxymethylpenicillin [CHEBI:27446]

Figure 2.43 Example of the non-peptidic branch of the Molecule Finder tree showing the branches before and after penicillin. Notice the pop-up balloon adding information for each entry

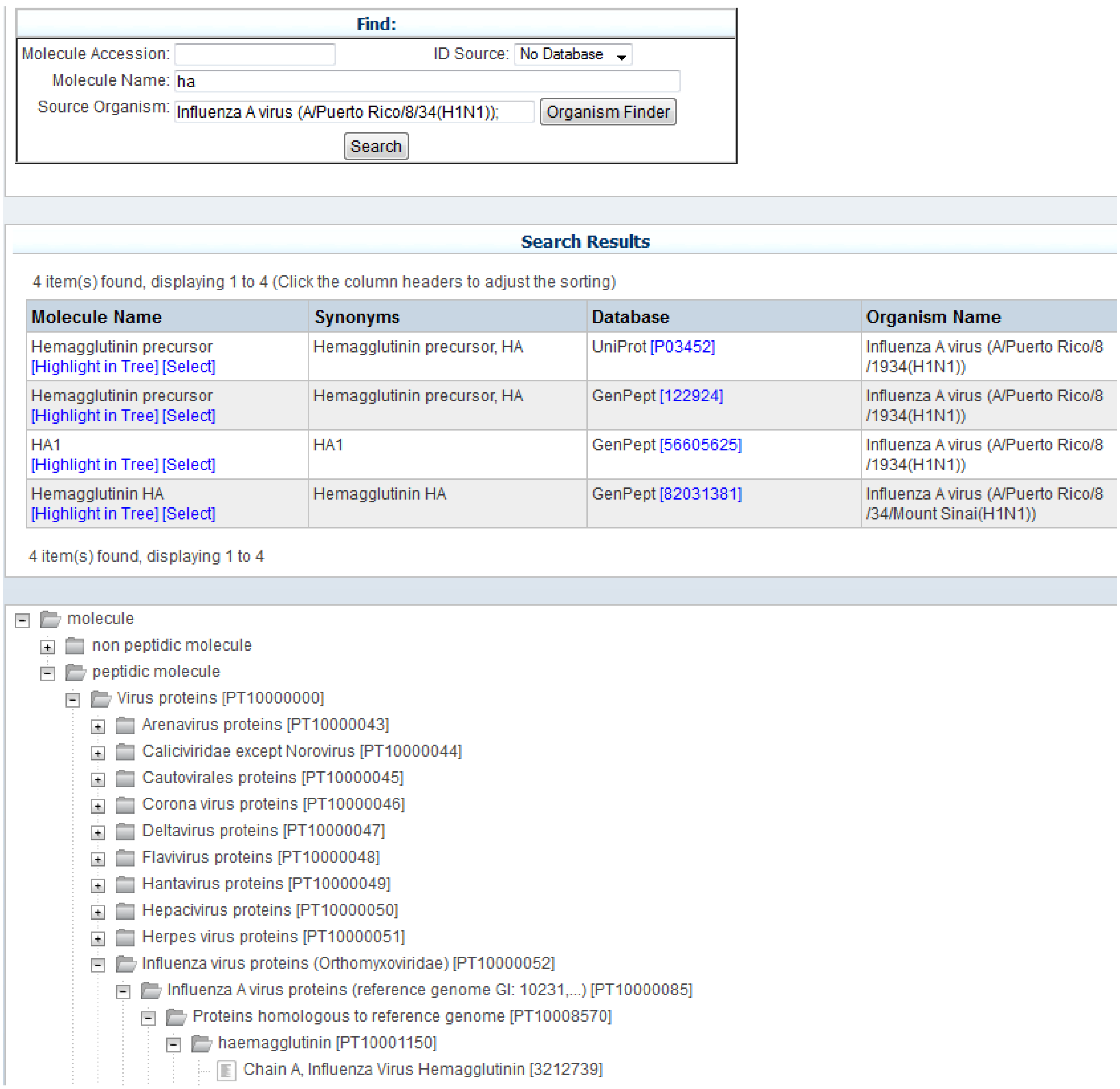
The development team determined that the most logical way to group the proteins was by organism. In order to accomplish this, the NCBI species was determined for each of the proteins in the database. For viruses and bacteria, this involved traversing the NCBI taxonomy from the sub-species (strain) level up to the species level. For each species, a set of reference proteins was selected from the NCBI protein database based upon the availability of a complete genome for the species. All proteins for each species were BLASTed against the reference protein set to determine their homologs. These data were used to build the protein tree in a way that mirrors a pruned version of the NCBI taxonomy. The result is a coherent tree that is divided along major taxonomic categories and is quickly traversed with proteins grouped logically below each species. The user can perform a free text search to see where a protein is placed in the tree. It is possible, for example, to select all Influenza A haemagglutinin (HA) proteins by selecting one node of the tree rather than individually clicking on the 100+ different HA proteins in the database. This can be seen in Figure 2.44.



- molecule
  - non peptidic molecule
  - peptidic molecule
    - Virus proteins [PT10000000]
      - Arenavirus proteins [PT10000043]
      - Caliciviridae except Norovirus [PT10000044]
      - Cautovirales proteins [PT10000045]
      - Corona virus proteins [PT10000046]
      - Deltavirus proteins [PT10000047]
      - Flavivirus proteins [PT10000048]
      - Hantavirus proteins [PT10000049]
      - Hepacivirus proteins [PT10000050]
      - Herpes virus proteins [PT10000051]
      - Influenza virus proteins (Orthomyxoviridae) [PT10000052]
        - Influenza A virus proteins (reference genome GI: 10231,...) [PT10000085]
          - Proteins homologous to reference genome [PT10008570]
            - haemagglutinin [PT10001150]
            - matrix protein 1 [PT10001237]
            - matrix protein 2 [PT10001600]
            - neuraminidase [PT10001985]
            - nonstructural protein NS1 [PT10001300]
            - nonstructural protein NS2 [PT10001848]
            - nucleocapsid protein [PT10001269]
            - PB1-F2 protein [PT10004165]
            - PB2 protein [PT10001358]
            - polymerase 1 [PT10001933]
            - polymerase PA [PT10001236]
          - Other proteins [PT10008571]

Figure 2.44 Example of the protein tree as found in the Source Antigen Molecule Finder on the IEDB home page

The search interface at the top of the Molecule Finder is shown in Figure 2.45. It has a comprehensive and flexible search form, and includes the Organism Finder. Users can highlight results in the molecule tree or select specific molecules directly by clicking on the corresponding “Select” link. User can also specify the molecule database. Figure 2.45 shows the results for searching for ha (Hemagglutinin) in a strain for Influenza A virus.



Molecule Accession:
ID Source: No Database
Molecule Name: ha
Source Organism: Influenza A virus (A/Puerto Rico/8/34(H1N1));

4 item(s) found, displaying 1 to 4 (Click the column headers to adjust the sorting)

Molecule Name	Synonyms	Database	Organism Name
Hemagglutinin precursor [Highlight in Tree] [Select]	Hemagglutinin precursor, HA	UniProt [P03452]	Influenza A virus (A/Puerto Rico/8 /1934(H1N1))
Hemagglutinin precursor [Highlight in Tree] [Select]	Hemagglutinin precursor, HA	GenPept [122924]	Influenza A virus (A/Puerto Rico/8 /1934(H1N1))
HA1 [Highlight in Tree] [Select]	HA1	GenPept [56605625]	Influenza A virus (A/Puerto Rico/8 /1934(H1N1))
Hemagglutinin HA [Highlight in Tree] [Select]	Hemagglutinin HA	GenPept [82031381]	Influenza A virus (A/Puerto Rico/8 /34/Mount Sinai(H1N1))

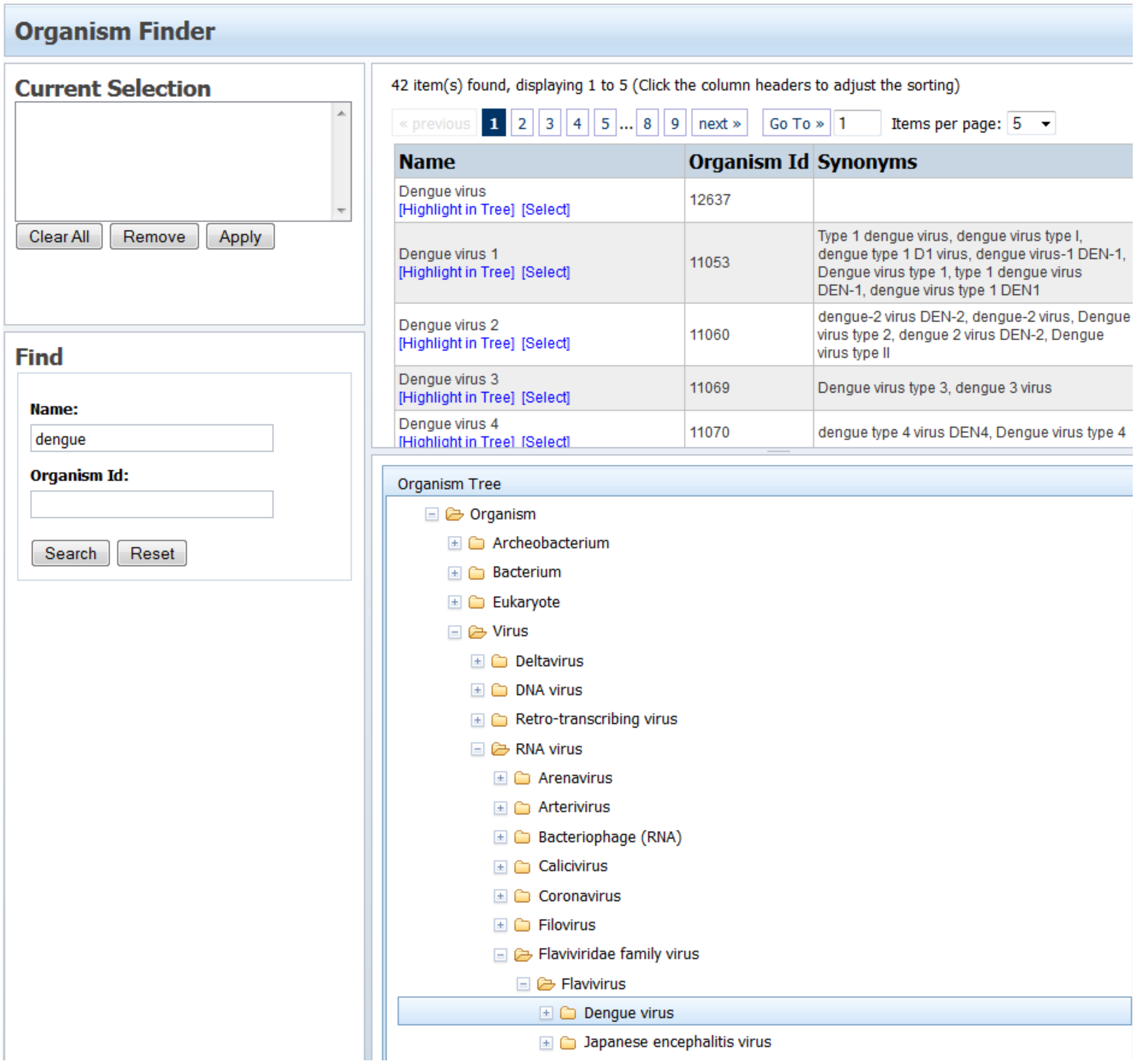
4 item(s) found, displaying 1 to 4

- molecule
  - non peptidic molecule
  - peptidic molecule
    - Virus proteins [PT10000000]
      - Arenavirus proteins [PT10000043]
      - Caliciviridae except Norovirus [PT10000044]
      - Cautovirales proteins [PT10000045]
      - Corona virus proteins [PT10000046]
      - Deltavirus proteins [PT10000047]
      - Flavivirus proteins [PT10000048]
      - Hantavirus proteins [PT10000049]
      - Hepacivirus proteins [PT10000050]
      - Herpes virus proteins [PT10000051]
      - Influenza virus proteins (Orthomyxoviridae) [PT10000052]
        - Influenza A virus proteins (reference genome GI: 10231,...) [PT10000085]
          - Proteins homologous to reference genome [PT10008570]
            - haemagglutinin [PT10001150]
              - Chain A, Influenza Virus Hemagglutinin [3212739]

Figure 2.45 Results for searching for ha (Hemagglutinin) molecules for a strain of Influenza A virus

2.3.5.5 Organism Finder

The organism finder was redesigned in 2013. The 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 Find box. In the example shown in Figure 2.46, a search for "dengue" is performed, which results in 42 items being found. The user can select one or more of the items. The user can also choose to highlight the item in the tree, as shown in the figure. To see the synonyms for a selection, users can place their computer mouse over the scientific name. When the Organism Finder is adjacent to a Host Organism field, only the source organisms for which data exists in the IEDB are displayed in the tree structure.



Name: dengue

Organism Id:

42 item(s) found, displaying 1 to 5 (Click the column headers to adjust the sorting)

Go To » 1 Items per page: 5

Name	Organism Id	Synonyms
Dengue virus [Highlight in Tree] [Select]	12637	
Dengue virus 1 [Highlight in Tree] [Select]	11053	Type 1 dengue virus, dengue virus type I, dengue type 1 D1 virus, dengue virus-1 DEN-1, Dengue virus type 1, type 1 dengue virus DEN-1, dengue virus type 1 DEN1
Dengue virus 2 [Highlight in Tree] [Select]	11060	dengue-2 virus DEN-2, dengue-2 virus, Dengue virus type 2, dengue 2 virus DEN-2, Dengue virus type II
Dengue virus 3 [Highlight in Tree] [Select]	11069	Dengue virus type 3, dengue 3 virus
Dengue virus 4 [Highlight in Tree] [Select]	11070	dengue type 4 virus DEN4, Dengue virus type 4

- Organism
  - Archeobacterium
  - Bacterium
  - Eukaryote
  - Virus
    - Deltavirus
    - DNA virus
    - Retro-transcribing virus
    - RNA virus
      - Arenavirus
      - Arterivirus
      - Bacteriophage (RNA)
      - Calicivirus
      - Coronavirus
      - Filovirus
      - Flaviviridae family virus
        - Flavivirus
          - Dengue virus
          - Japanese encephalitis virus

Figure 2.46 Organism Finder showing a search for dengue with dengue highlighted in the tree

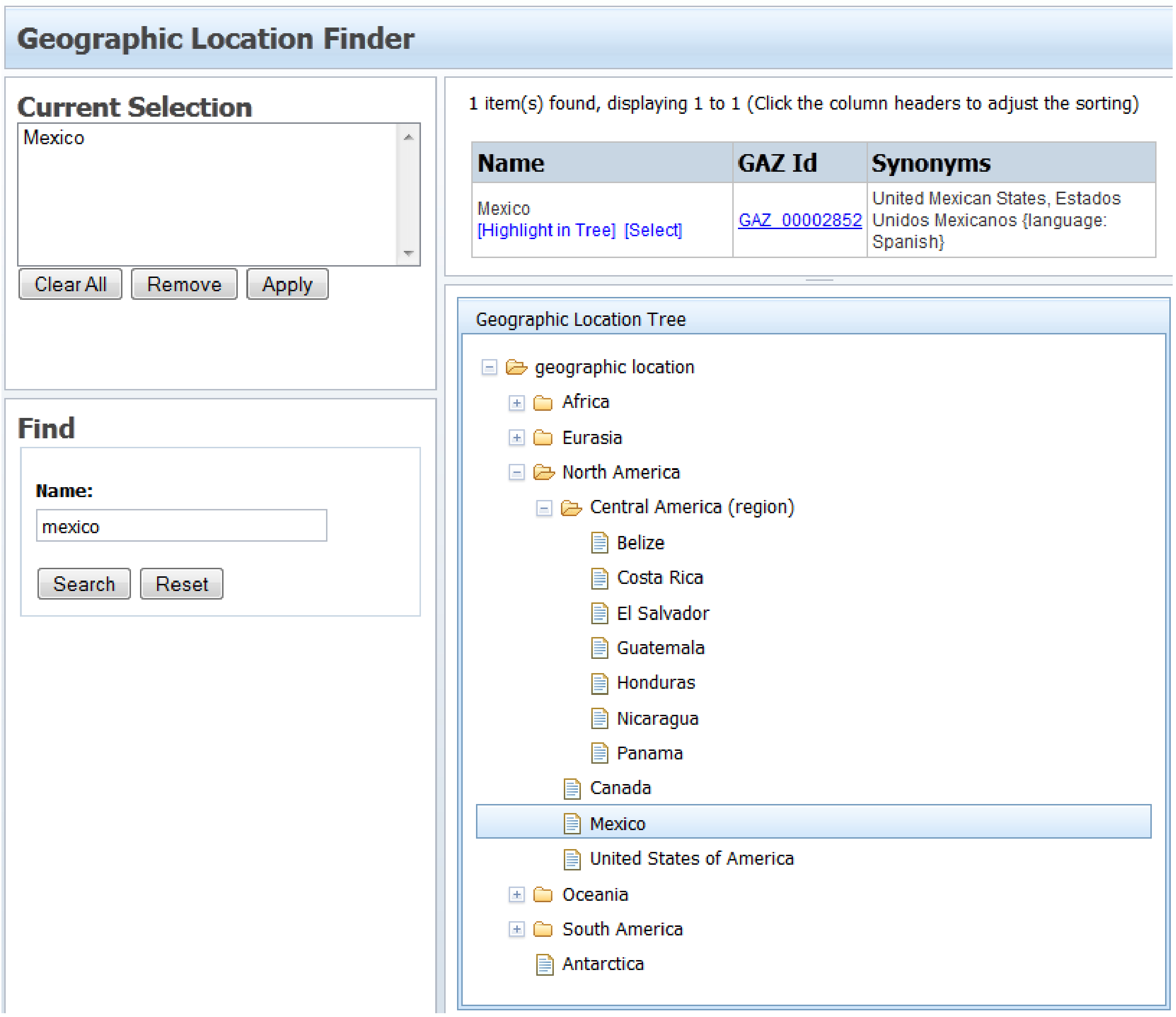
2.3.5.6 Geolocation Finder

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 advanced 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 "Find" feature and type free text to search the tree. The Find feature accepts synonyms as search criteria. Its use is shown in Figure 2.47 for 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: Mexico

Name: mexico

1 item(s) found, displaying 1 to 1 (Click the column headers to adjust the sorting)

Name	GAZ Id	Synonyms
Mexico [Highlight in Tree] [Select]	GAZ_00002852	United Mexican States, Estados Unidos Mexicanos {language: Spanish}

Figure 2.47 Geolocation finder. This example shows the tree structure by continent, region, and country. A search was made for Mexico within the tree using the Find 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.

2.4 Tools

The Tools pull-down menu accesses the IEDB Analysis Resource and has three items – T Cell Epitope Prediction, B Cell Epitope Prediction, and Analysis Tools. 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.

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
- B-cell epitope prediction

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

2.4.1 T Cell Epitope Prediction

2.4.1.1 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 seven 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, and NetMHCpan. 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, and a consensus method derived from the ARB, SMM_align, Sturniolo methods, and NetMHCIIpan. 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 2.4.4.

2.4.1.1.1 Peptide Binding to MHC Class I Molecules

Users can select from seven different methods for predicting class I epitopes – ANN, SMM, SMMPMBEC, Comblib_Sidney2008, Consensus, NetMHCpan, 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. The training data in this case are peptide sequences with quantitative affinities for a specific MHC molecule.

Many different implementations of artificial neural networks exist. The one utilized here is described for HLA-A2 binding predictions by Nielsen et al. (Protein Science, 2003) and has been applied to a number of different alleles (http://www.cbs.dtu.dk/services/NetMHC/).

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 predicts binding of peptides to a MHC class I molecule using artificial neural networks (ANN). It predicts binding for over 1,650 alleles, including HLA-A, B, C, E, G; non-human primates; mouse; pig; and user-supplied MHC sequence. Predictions can be made for peptide sequences of 8 to 11 residues in length. The method has been trained on over 110,000 peptide/MHC interactions.

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.

2.4.1.1.2 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 paper specifically describing the class II tool will be published in 2010.

Consensus
The consensus method was developed by the IEDB team by exploiting features of the other three aforementioned methods. The method was updated with the introduction of NN-align, so the revised Consesnus 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).

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 describe the method in detail (PMID: 19765293).

NetMHCIIpan
NetMHCIIpan predicts binding of peptides for over 500 HLA-DR alleles using artificial neural networks. A paper describing the method was published by Nielsen et al. in Immunome Research, November 2010.

The datasets used in assessing the performance of the ARB, SMM-align, and Sturniolo methods and in developing the Consensus method, as described in Wang et al., can be found at http://mhcbindingpredictions.immuneepitope.org/MHCII/. The three datasets can be used for developing algorithms that predict peptides binding to MHC class II molecules and/or activating CD4+ T cells. The first is a comprehensive dataset consisting of more than 10,000 previously unpublished MHC-peptide binding affinities for 16 alleles (peptide_affinity_dataset.zip). The second dataset is a text file of 29 peptide/MHC crystal structures found in the PDB that can be used for binding core predictions (non_redundant_pdb_core_pep_allele.txt). The third dataset contains 664 peptide sequences experimentally tested for CD4+ T-cell responses (LCMV_T_cell_activation.txt).

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.

2.4.1.2 T Cell Epitopes – MHC I Processing Prediction

2.4.1.2.1 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, ARB, SMMPMBEC, Comblib, NetMHCpan, and IEDB Recommended, which are described in Section 0.

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.

2.4.1.2.2 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).

2.4.1.2.3 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.

2.4.1.3 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)

2.4.2 B Cell Epitope Prediction

2.4.2.1 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. It is described in Larsen et al. (Immunome Research, 2006).

2.4.2.2 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).

2.4.2.3 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).

2.4.2.4 Paratome – Prediction of antigen binding regions

Paratome is an automated tool for the identification of Antigen Binding Regions (ABRs) in antibodies. It accepts as an input the amino acid sequences or 3D structures (in PDB format) of antibodies. It is constructed by structurally aligning a non-redundant set of all known Antibody-Antigen complexes in the PDB, from which structural consensus elements that are commonly involved in antigen binding across antibodies are identified. The list of all train and test sets ABRs and Ab-Ag contacts which were used to construct Paratome can be found at http://ofranservices.biu.ac.il/site/services/paratome/index.html. The method is described in Kunik et al. (Nucleic Acids Res, 2012

2.4.3 Epitope Analysis Tools

2.4.3.1 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 database (http://www.allelefrequencies.net/). At present, Allele Frequency database provides allele frequencies for 115 countries and 21 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).

2.4.3.2 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).

2.4.3.3 Epitope Cluster Analysis

This tool 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.

2.4.3.4 Homology Mapping Tool and EpitopeViewer

This Homology Mapping Tool maps linear epitopes to 3D structures of proteins (Beaver, et al., Immunome Res 2007). This is done by comparing the epitope source protein sequence with that of proteins with known 3D structures in the PDB. The tool generates an alignment between the query sequence of the epitope source sequence and a homologous sequence from the PDB, and visualizes the result in an EpitopeViewer. For input, the tool uses the SwissProt ID of the antigen protein, the epitope sequence, and the position of the epitope in the antigen sequence as curated within the IEDB or input by the user. The tool applies the NCBI BLAST algorithm for performing sequence homology search, and provides options for the sophisticated user to choose cutoff values on parameters used in the search programs (such as e-value and penalty on gap initiation and gap extension). The tool output page displays the alignment between the query sequence of the antigen containing the epitope and the sequence from the PDB representing significant hits (matches). The region within the epitope is highlighted in the alignment, and the sequence identity for the epitope and homologous region is provided. The EpitopeViewer application for visualization of homologous epitope/antigen and its further structural analysis is launched from the output page.

Functionality was added to the homology mapping tool in 2010 to allow users to input their own conformational epitopes and map them to protein structures. This feature was documented on the "Example 5" tab of the homology mapping web page. The "Help" tab was also updated.

The convenient and easy to use EpitopeViewer, a Java application running JOGL, has been developed for three-dimensional visualization of immune epitopes and analyses of their interactions with antigen-specific receptors of the immune system (antibodies, T cell receptors, MHC molecules) for structures available in the Protein Data Bank (PDB). The EpitopeViewer is based on the Molecular Biology Toolkit (MBT; http://mbt.sdsc.edu/) developed at the San Diego Supercomputer Center (SDSC). It uses data both from the PDB and the IEDB, and visualizes one epitope at a time from a particular PDB structure (Beaver, et al., Immunome Res 2007).

The EpitopeViewer provides the following functionality:

- Link to the PDB web-page displaying a particular structure.
- Visualization of the 3D structure of epitope/antigen in complex with immune receptor(s) as curated within the IEDB and available in the PDB.
- Visualization of the 3D structure of epitope and antigen mapped to a PDB structure using the Homology Mapping tool.

- Visualization of sequences of epitope/antigen and immune receptor(s).
- 3D-visualization of intermolecular (epitope-paratope, epitope-antibody CDR, epitope-MHC, pMHC-TCR, pMHC-TCR CDR), inter-atom and inter-residue interactions curated within the IEDB and/or calculated on the fly from the PDB file with essential details (contact type, atoms, distance) provided;
- 2D-plot of inter-residue interactions between epitope and immune receptor.
- Generation of publication-quality pictures of structures, sequences, and plots of contacting residues.

2.4.4 Benchmark references and data sets

A new “Datasets” tab was added to the Analysis Resource in 2013. The associated page 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:

- 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

2.4.5 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 for T cell epitopes. 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 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 users that would like to run the analysis resource locally, a virtual machine image file is available upon request. All tools are included except MHC-NP and Paratome, which were not developed by the IEDB team. The image is kept in sync with the current version of the IEDB Analysis Resource and is updated on a six month cycle. This is also freely available for non-profit/academic users through an open-source license. Commercial licenses are also available. Requests for either license can be sent to license@iedb.org or via the IEDB help desk.

2.5 Support Overview

The Support 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.

2.5.1 Solutions Center

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 and subsequently track a help request via the Solutions Center, users must follow a simple registration procedure in order to provide an email address, name, and password. The Solutions Center can also be accessed by a link at the bottom of each web page.

2.5.2 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.

2.5.3 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 "SUBMIT A 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. Requests that are specific to analytical tools or the method used to curate data are answered initially to inform the requestor that their question/comment is being forwarded to team specialists, and an approximate date of full response is provided. Based on the complexity of the request or if that request prompts the team to make changes to the system or curate additional data/source organisms, requests are resolved immediately in some cases, while others are resolved in future IEDB system builds, or later curation.

2.5.4 Data Field Descriptions

The Data Field Descriptions item in the Support pull-down menu gives the user access to the Curation Manual. 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.

2.5.5 Video Tutorials

There is a link to the IEDB video tutorials in the Solutions Center. The tutorial on Using the Organism Finder had become obsolete so the link was removed. Many of the other tutorials from previous years have become partially out-of-date, but given the ongoing website redesign effort, it was decided not to expend the effort to revise them. Eight new Analysis Resource videos, however, were produced in 2013. Presentations from the 2013 IEDB User Workshop were recorded and made available as video tutorials. They cover the use of the T cell and B cell epitope prediction tools and the analysis tools. The eighteen tutorials are listed in Table 2.1

Category	Topic
Overview of the IEDB	Introduction to the IEDB site and Search Options
	Simple Search Overview
Searching the IEDB	Simple Search: Finding Epitopes from a Protein
	Peptide/Protein Homology Search
	Linear Sequence Queries
	Advanced Search Overview
	Advanced B cell search: Example of finding antibody cross-reaction
	How do I generate a list of all proteins from which epitopes have been identified for an organism of interest?
	Using the Disease Finder
Understanding Query Results	Results: Epitope Listing, Details of Individual Entries and Using the Export Function
2013 User Workshop Analysis Resource Webinars	Overview of the epitope prediction and analysis tools available, presented by Dr. Bjoern Peters (22 minutes)
	MHC class I binding prediction tools, presented by Dr. Yohan Kim (35 minutes)
	MHC class II binding prediction tools and API, presented by Dr. Sinu Paul (49 minutes)
	MHC class I processing and immunogenicity tools, presented by Dr. Bjoern Peters (23 minutes)
	Analysis Tools (population coverage, epitope conservancy analysis, epitope cluster analysis), presented by Dr. Bjoern Peters (8 minutes)
	B cell epitope prediction tools, presented by Dr. Julia Ponomarenko (56 minutes)
	Homology mapping tools, presented by Dr. Julia Ponomarenko (9 minutes)
	EpitopeViewer, presented by Dr. Julia Ponomarenko (8 minutes)

Table 2.1 Available IEDB video tutorials

2.5.6 Help with Common Queries

A series of 16 queries has been designed to parallel the IEDB meta-analysis efforts. A link to this information can be found at the bottom of the Home Page Search. Meta-analyses are performed at intervals to query the database for all data relating to subjects of interest (e.g. Influenza, Malaria, Tuberculosis). The queries represent a simplified version of such analysis. Two examples from the series are “How do I generate a list of all the different species and strains reported for an organism of interest?” and “How do I search for human data and specify geographic region?” The user can click on the button (+) next to each query for step-by-step instructions on how to find the answer. Data generated through use of the tutorial can be downloaded for further analysis using Excel. When available, the option to download data appears in the upper left-hand side of the page (Excel icon). Tools for performing specific analyses are also available through the Analysis Resource on the IEDB website.

2.6 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.

2.6.1 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.

2.6.2 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: www.iedb.org

2. The journal reference for the IEDB was updated after the release of IEDB 2.0. The IEDB should be cited as:

   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. 2010 Jan; 38(Database issue):D854-62. Epub 2009 Nov 11.

2.6.3 Database Export

The contents of the Immune Epitope Database are exported weekly to files in XML format. The database export page (Figure 2.47) 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.

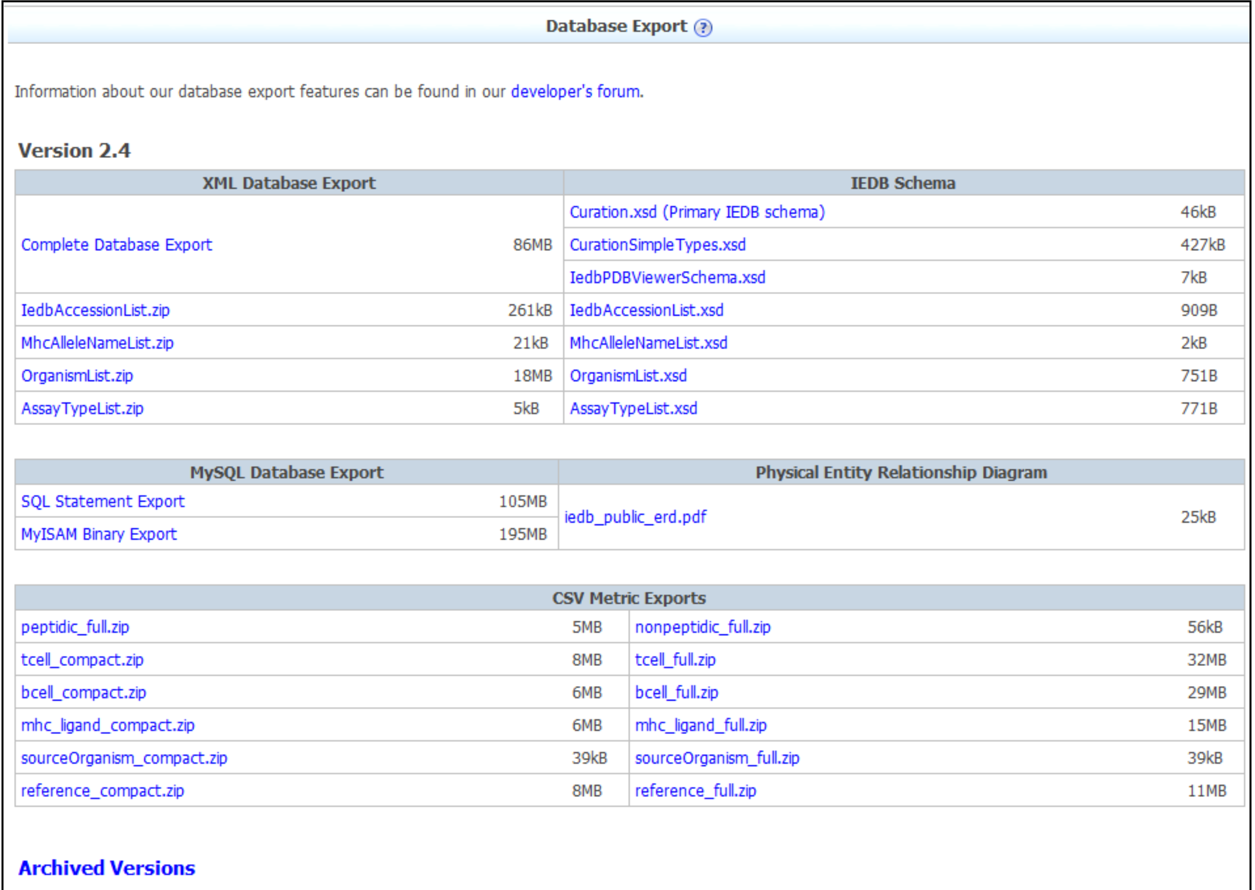
The database export page also provides the relevant XML Schema Definition (XSD) files for each of the XML files provided. The XSD file(s) for a particular XML file will be located in the second column of the export table. In the case of the complete database export, multiple schemas are provided, with 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 MySQL v5.5 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 compress file that contains an XML for each reference. The corresponding XSD files are also available for download.

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, except for the patent list, which is only provided in PDF format. The CSV file exports are available in two formats, a compact format that only contains the data presented in the list the user is viewing, and a full record format that contains all of the data associated with the records in the list the user is viewing.

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. For example, reference_compact.zip and reference_full.zip contain the list of all references (literature and submissions) in the database. The compact version contains reference ID, reference type, PubMed ID, Author(s), Title, Abstract, Journal, and Year. The full version contains the same information plus author affiliations, Journal volume, Article pages, MeSH terms, and all other reference related information captured in the database. Files are available for all peptidic epitopes, non-peptidic epitopes, T cell assays, B cell assays, MHC ligand assays, and source organisms.



Database Export

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

Version 2.4

XML Database Export		IEDB Schema	
Complete Database Export	86MB	Curation.xsd (Primary IEDB schema)	46kB
		CurationSimpleTypes.xsd	427kB
		IedbPDBViewerSchema.xsd	7kB
IedbAccessionList.zip	261kB	IedbAccessionList.xsd	909B
MhcAlleleNameList.zip	21kB	MhcAlleleNameList.xsd	2kB
OrganismList.zip	18MB	OrganismList.xsd	751B
AssayTypeList.zip	5kB	AssayTypeList.xsd	771B

MySQL Database Export		Physical Entity Relationship Diagram	
SQL Statement Export	105MB	iedb_public_erd.pdf	25kB
MyISAM Binary Export	195MB		

CSV Metric Exports			
peptidic_full.zip	5MB	nonpeptidic_full.zip	56kB
tcell_compact.zip	8MB	tcell_full.zip	32MB
bcell_compact.zip	6MB	bcell_full.zip	29MB
mhc_ligand_compact.zip	6MB	mhc_ligand_full.zip	15MB
sourceOrganism_compact.zip	39kB	sourceOrganism_full.zip	39kB
reference_compact.zip	8MB	reference_full.zip	11MB

Archived Versions

Figure 2.48 IEDB Database Export web page

2.6.4 Documents

A variety of IEDB reference materials is available for download by all users. The Documents page lists the files available for download by category. The files available for download include an Introduction to IEDB and Analysis Resource, a System Architecture and Database Design Specification, IEDB Annual Workshop Executive Summaries, and the Annual Compendia. Additional reference materials will be added for download over time. Users can also find much of this material and more in the folders at http://help.iedb.org.

2.6.5 IEDB Ontology

Selecting IEDB Ontology from the pull-down menu 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.

2.6.6 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 Links under the Resources heading on the main menu. 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

2.6.7 Patent List

As part of the IEDB curation effort, the Derwent World Patent Index has been searched for potentially relevant patent items. These are presented in a table on the Patent List web page that lists the publication number, patent title, inventors, assignee name, patent abstract, date filed, and date published. The enhanced abstracts of all of the 774 listed patent items have been reviewed, but the actual patents have not been read or curated. This information is presented for those users who wish to explore these patent items further.

The list mostly includes patents related to Category A-C priority pathogens, emerging and re-emerging infectious diseases, Malaria, Hepatitis B, Clostridium tetani, Leishmania, and Candida albicans, as well as other diseases. Users can search the table by using the "find" feature of their browser. The list contains patents through the year 2006 and can be viewed in a web browser or downloaded as a pdf file. It is not updated.

2.6.8 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.

2.6.9 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.

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 seven 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 2013, ten articles were published, 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 68 scientific articles about the IEDB in the last nine years.

3.1.1 2013

1. 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.
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3.2 Publications Citing the IEDB in 2013

In years past, the analysis of publications citing the IEDB was conducted by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the IEDB papers. In 2013, this resulted in finding 378 references that cited at least one of the 68 papers written by the IEDB team over the past ten years. This represents an increase of 55 citations over 2012. The list excludes self-citations by the 68 IEDB papers.

The papers have been categorized by the type of IEDB paper they cited – General IEDB (G), Analysis Resource (AR), Curation (C), 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 (2009) 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 “Analysis Resource” as a category and not having “General” have been listed in the “Analysis Resource” list below. A similar hierarchy has been applied for the Curation papers. That means all papers listed under “Meta-analysis” below only belong to that category.

When not adhering to this hierarchy, 444 references cited at least one of the 68 papers written by the IEDB team in the past ten years. The “General” category IEDB papers were cited 147 times in 2013. The Analysis Resource papers received 225 citations. The Curation category papers received 4. The meta-analysis papers received 68. There may be an overap in citations among these categories.

Adhering to the hierarchy, 378 references cited at least one of the 68 papers written by the IEDB team in the past ten years. The “General” category IEDB papers were cited 147 times in 2013. The Analysis Resource papers received 172 citations. The Curation category papers received 4. The meta-analysis papers received 55.

After observing that many papers were making use of the IEDB but not citing any of its papers in their reference section, the team developed an automated full-text search of papers in Google Scholar looking for the strings “IEDB” or “Immune Epitope Database”. References found in this manner that were not included in the original 378 were processed to find their corresponding PubMed ID. The papers in this list were then manually inspected to find citations to the IEDB and to categorize them. Most of these papers cited the IEDB URL and mentioned the IEDB in the paper’s text. At the end of the process, 55 additional references were found, 18 in the General category, 36 in the Analysis Resource category, and 1 in the Curation category. These papers are indicated in the lists below with an astericks “*”.

Accounting for these additional papers, the adjusted hierarchical counts are 433 total citations for 2013. The “General” category IEDB papers received 165 citations, the Analysis Resource papers received 208, the Curation category papers received 5, and the meta-analysis papers received 55.

3.2.1 General IEDB

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3.2.2 Analysis Resource

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