

Contract No. HHSN272201200010C

Immune Epitope Database and Analysis Program

2015 Annual IEDB Compendium

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

858-752-6923
858-752-6987 (fax)
wfleri@lji.org

6 May 2016

This page intentionally left blank

Table of Contents

Table of Contents.....	i
Table of Figures.....	iii
Introduction.....	1
1 Antibody and T Cell Epitopes.....	2
2 Website Features.....	68
2.1 Home Page.....	68
2.2 Query.....	69
2.2.1 Perform a Home Page Search.....	69
2.2.2 Specialized Searches.....	71
2.2.3 Search Results Page.....	78
2.2.3.1 Peptide MHC Binding Motif Displays.....	85
2.2.3.2 Immunome Browser.....	87
2.2.4 Finders Overview.....	90
2.2.4.1 Allele Finder.....	90
2.2.4.2 Assay Finder.....	91
2.2.4.3 Disease Finder.....	92
2.2.4.4 Molecule Finder.....	93
2.2.4.5 Organism Finder.....	96
2.2.4.6 Geolocation Finder.....	97
2.3 Tools.....	98
2.3.1 T Cell Epitope Prediction.....	99
2.3.1.1 T Cell Epitopes - MHC binding prediction.....	99
2.3.1.1.1 Peptide Binding to MHC Class I Molecules.....	99
2.3.1.1.2 Peptide Binding to MHC Class II Molecules.....	101
2.3.1.2 T Cell Epitopes – MHC I Processing Prediction.....	103
2.3.1.2.1 Proteasomal cleavage/TAP transport/MHC class I combined predictor ..	103
2.3.1.2.2 Neural network based prediction of proteasomal cleavage sites (NetChop) and T cell epitopes (NetCTL/NetCTLpan).....	103
2.3.1.2.3 MHC-NP – Prediction of peptides naturally processed by the MHC.....	104
2.3.1.3 T cell class I pMHC immunogenicity predictor.....	104
2.3.2 B Cell Epitope Prediction.....	104
2.3.2.1 Prediction of linear epitopes from protein sequence.....	104
2.3.2.2 DiscoTope - Prediction of epitopes from protein structure.....	104
2.3.2.3 ElliPro - Epitope prediction based upon structural protrusion.....	105
2.3.2.4 Prediction of ImmunoGlobulin Structure (PIGS).....	105
2.3.2.5 Methods for modeling and docking of antibody and protein 3D structures...	105
2.3.3 Epitope Analysis Tools.....	105
2.3.3.1 Population coverage.....	105
2.3.3.2 Epitope conservancy.....	106
2.3.3.3 Epitope Cluster Analysis.....	107
2.3.3.4 Homology Mapping Tool and EpitopeViewer.....	107
2.3.3.5 Computational Methods for Mapping Mimotopes to Protein Antigens.....	107
2.3.4 IEDB Analysis Resource Labs.....	108
2.3.5 Benchmark references and data sets.....	109
2.3.6 Other Ways to Access Tools.....	110
2.4 Help Overview.....	110
2.4.1 Support.....	110

2.4.2	Help Request	111
2.4.3	Provide Feedback	111
2.4.4	Video Tutorials	111
2.5	More IEDB	112
2.5.1	Database Export	113
2.5.2	Meta-Analyses	114
2.5.3	Citing the IEDB	114
2.5.4	Release Notes	115
2.5.5	Links to External Sources	115
2.6	Learn More	115
2.6.1	Support	116
2.6.2	About the Data	117
2.6.3	About Us	117
3	Scientific Publications	119
3.1	Publications of the IEDB team by Year	119
3.1.1	2015	119
3.1.2	2014	120
3.1.3	2013	120
3.1.4	2012	121
3.1.5	2011	122
3.1.6	2010	122
3.1.7	2009	123
3.1.8	2008	123
3.1.9	2007	124
3.1.10	2006	125
3.1.11	2005	125
3.1.12	2004	126
3.2	Publications Citing the IEDB in 2014	126
3.2.1	General IEDB	126
3.2.2	Analysis Resource	138
3.2.3	Curation	158
3.2.4	Epitope Meta-Analyses	159
4	References	163

Table of Figures

Figure 2.1 IEDB 3.3 Home page	69
Figure 2.2 Home page Simple Search	70
Figure 2.3 Query results for a substring search performed on the input sequence AELLVALENQHTIDL	71
Figure 2.4 Epitope Detail Search input screen	73
Figure 2.5 Epitope panel on the Specialized Search page expanded to show input fields.....	74
Figure 2.6 Epitope query fields in the Advanced Search for Linear peptide epitopes	75
Figure 2.7 Epitope query fields in the Advanced Search for Discontinuous peptide epitopes ...	75
Figure 2.8 Epitope query fields in the Advanced Search for Discontinuous peptide on multi- chain epitopes.....	76
Figure 2.9 Epitope query fields in the Advanced Search for Non-peptidic epitopes	76
Figure 2.10 MHC Assay Detailed Search web page.....	77
Figure 2.11 Identifier Search input screen.....	78
Figure 2.12 The Epitope tab of the search results page	79
Figure 2.13 An example of the epitope detail page	79
Figure 2.14 The Antigens tab of the search results page	80
Figure 2.15 The Results filtered by the Nucleoprotein of the Influenza A virus. This was achieved by clicking on the filter icon in the antigen column. The content of the other tabs contain data specific to this antigen.....	81
Figure 2.16 The Assays tab of the search results page. The page contains three additional tabs for T Cell, B Cell, and MHC Ligand Assays	82
Figure 2.17 The top three sections of a sample T cell assay detail page.....	83
Figure 2.18 The References tab of the search results page	84
Figure 2.19 An example of the Reference detail page.....	85
Figure 2.20 Sample MHC Allele Details page with Peptide MHC Binding Motif diagram for HLA- A*02:01. Note the link to the corresponding Amino Acid Binding Chart on the bottom left of the diagram.....	86
Figure 2.21 Amino acid binding matrix for MHC allele HLA-A*02:01	87
Figure 2.22 The Immunome Browser is accessed by clicking on the icon shown on the Antigen tab on the results page of a query	88
Figure 2.23 Immunome Browser graphical output displaying assay results mapped onto a reference proteome by residue position	89
Figure 2.24 Immunome Browser tabular output.....	89
Figure 2.25 Allele Finder. Alleles are displayed in a tree structure and users can search by allele name, source organism, and MHC class (I, II, or non-classical).....	91
Figure 2.26 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	92
Figure 2.27 The disease finder is particularly helpful in specifying epitopes related to autoimmune diseases. In the example shown, diabetes is highlighted and selected.	93
Figure 2.28 The non-peptidic version of the Molecule Finder. This finder is accessed in the Epitope filter on the search results page.	94
Figure 2.29 An example of the protein branch of the Molecule Finder.....	95
Figure 2.30 Organism Finder showing a search for dengue with dengue highlighted in the tree	97
Figure 2.31 Geolocation finder. This example shows the tree structure by continent, and country. A search was made for Mexico within the tree using the Search By box on the left, which produced one result. This was then highlighted in the tree, as shown. Clicking on “Mexico” in the tree populated the Current Selection field in the upper left corner of the finder. 98	

Figure 2.32 IEDB Database Export web page.....114
Figure 2.33 The Learn More page, accessed from the Welcome message in the upper left
corner of the IEDB home page.....116

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 eleventh 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 2016. The second section describes the features of the IEDB 3.3 website and the Analysis Resource 2.14. The third section lists the scientific publications in 2015 for which the IEDB played a contributory role.

Since the publication of last year's 2014 Annual Compendium, the quantity of data available in the IEDB has increased significantly with the addition of 622 fully curated references and 15 data submissions. 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 2015, 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 2014 and 2015. Of the 3313 species/strains listed, 150 were added in 2015. 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 2015" indicates with an "X" if epitopes for the species/strain was added to the IEDB in 2015. 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-14", "T-14", "B-15", and "T-15" indicate the cumulative number of distinct B cell and T cell epitopes in the database at the end of 2014 and 2015, respectively. The two rightmost columns display the differences in the B and T cell epitope counts from 2014 to 2015. The changes in B and T cell epitope counts are shown in red. In 2015, the number of B cell epitopes increased by 3,963 from 34,098 to 38,061, and the number of T cell epitopes increased by 46,579 from 91,570 to 138,149.

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

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	3816	Abrus precatorius	1		1			
	5755	Acanthamoeba castellanii	14	3	14	3		
	57068	Acanthisitta chloris		1		1		
	4026	Acer pseudoplatanus	1		1			
	104102	Acetobacter tropicalis		1		1		
	2147	Acholeplasma	1		1			
	264635	Acholeplasma granularum	1		1			
	2148	Acholeplasma laidlawii		2		2		
X	1003200	Achromobacter insuavis AXX-A			1		1	
X	72556	Achromobacter piechaudii			1		1	
	349163	Acidiphilium cryptum JF-5		1		1		
X	920	Acidithiobacillus ferrooxidans				1		1
X	1214225	Acidocella sp. MX-AZ02			1		1	
	351607	Acidothermus cellulolyticus 11B		2		2		
	470	Acinetobacter baumannii		1		1		
	400667	Acinetobacter baumannii ATCC 17978	10	13	10	13		
	509173	Acinetobacter baumannii AYE		1		1		
	471	Acinetobacter calcoaceticus		1		1		
	29430	Acinetobacter haemolyticus	1		1			
	10001530	Acinetobacter haemolyticus strain 57	1		1			
	10001531	Acinetobacter haemolyticus strain 61	1		1			
	40214	Acinetobacter johnsonii		1		1		
	10001503	Acinetobacter lwoffii F78	1		1			
	62977	Acinetobacter sp. ADP1		2		2		
	7902	Acipenser gueldenstaedtii	1		1			
	715	Actinobacillus pleuropneumoniae		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		
X	85106	Adeno-associated virus - 1				11		11
	10804	Adeno-associated virus - 2	42	67	42	81		14
	82300	Adeno-associated virus - 5	9		9			
	202812	Adeno-associated virus - 7		2		2		
	202813	Adeno-associated virus - 8	17	7	17	14		7
	235455	Adeno-associated virus 9	9		9			
	7160	Aedes albopictus	7		7			
	4494	Aegilops markgrafii		1		1		
	4487	Aegilops searsii	1		1			
	37682	Aegilops tauschii		1		1		
	6100	Aequorea victoria	3	4	3	5		1
	105751	Aeromonas bestiarum		1		1		
X	644	Aeromonas hydrophila			4	1	4	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	4		4
	10497	African swine fever virus	1		1			
	10498	African swine fever virus BA71V	46		46			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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	1	1	
	11966	Aids-associated retrovirus		2		2		
	10000828	Ajellomyces dermatitidis ATCC 60636		2		2		
	65690	AK7 murine leukemia virus		1		1		
	11791	AKR (endogenous) murine leukemia virus		12		12		
	11790	AKT8 murine leukemia virus	1		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			
	1263035	Alistipes finegoldii CAG:68		1		1		
	172148	Alkhumra hemorrhagic fever virus		4		4		
	3517	Alnus glutinosa		17		17		
	9502	Alouatta caraya	1		1			
	333754	Alphapapillomavirus 10	4		4			
	333766	Alphapapillomavirus 13		1		1		
	337043	Alphapapillomavirus 4		1		1		
	337042	Alphapapillomavirus 7	9		9			
	5599	Alternaria alternata	5	36	5	36		
X	28108	Alteromonas macleodii				1		1
	314275	Alteromonas mediterranea		1		1		
	261202	Alto Paraguay hantavirus		3		3		
	45218	Amapari mammarenavirus		3		3		
	1338344	Ambigolimax valentianus	1		1			
	4212	Ambrosia artemisiifolia	4	32	4	130		98
	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	63		64		1	
X	97477	Anaerobaculum mobile				1		1
	4615	Ananas comosus	3		3			
	769	Anaplasma centrale		1		2		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		
	948	Anaplasma phagocytophilum	29		29			
	212042	Anaplasma phagocytophilum str. HZ	21		21			
	10001573	Anatid herpesvirus 1 Clone-03	1		1			
X	53326	Ancylostoma ceylanicum				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	24		24			
	6860	Androctonus mauritanicus mauritanicus	1		1			
	334426	Angiostrongylus costaricensis	1	1	1	1		
	59799	Angomonas deanei		2		2		
	6269	Anisakis simplex	20		38	28	18	28

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	155017	Anogeissus	1		1			
	7165	Anopheles gambiae	8	2	8	2		
	180454	Anopheles gambiae str. PEST	1	2	6	2	5	
	33934	Anoxybacillus flavithermus		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		
	63363	Aquifex aeolicus	2		2			
	224324	Aquifex aeolicus VF5	1	4	1	4		
	3702	Arabidopsis thaliana	2	10	2	10		
	201444	Aracatuba virus		5		5		
	3818	Arachis hypogaea	386	157	411	157	25	
	308159	Araucaria virus		6		6		
	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	69		1
	29320	Arthrobacter nicotinovorans	1		1			
	290399	Arthrobacter sp. FB24		2		2		
	6253	Ascaris suum	1	1	1	1		
	746128	Aspergillus fumigatus	126	86	126	86		
	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		15		11
	11861	Avian erythroblastosis virus	1		1			
	172851	Avian hepatitis E virus	17		20		3	
	11127	Avian infectious bronchitis virus (strain M41)	4	3	4	3		
	231428	Avian infectious bronchitis virus (strain Vic S)	11	8	11	8		
X	363020	Avian leukosis virus HPRS103			1		1	
	10001967	Avian leukosis virus isolate CAUHM01	1		1			
	10001965	Avian leukosis virus strain NX0101	1		1			
	38171	Avian reovirus strain S1133	5		5			
	195700	Avian rotavirus PO-13	6		6			
	354	Azotobacter vinelandii		2		2		
	322710	Azotobacter vinelandii DJ		2		2		
	5866	Babesia bigemina		3		3		
	5865	Babesia bovis	3	8	3	8		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	10001459	Babesia bovis Argentina R1A	4		4			
	10000382	Babesia bovis Mexico	1	4	1	4		
	10000383	Babesia bovis Mexico Mo7	1	33	1	33		
	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	3	18	3		
	1392	Bacillus anthracis	399	203	399	203		
	486619	Bacillus anthracis str. A0193		3		3		
	592021	Bacillus anthracis str. A0248		1		1		
	486623	Bacillus anthracis str. A0389		5		5		
	486621	Bacillus anthracis str. A0442		1		1		
	486620	Bacillus anthracis str. A0465		5		5		
	486624	Bacillus anthracis str. A0488		91		91		
	191218	Bacillus anthracis str. A2012		29		29		
	198094	Bacillus anthracis str. Ames		2		2		
	261594	Bacillus anthracis str. 'Ames Ancestor'		1		1		
	568206	Bacillus anthracis str. CDC 684		3		3		
	260799	Bacillus anthracis str. Sterne	5	4	5	4		
	10000291	Bacillus anthracis str. Sterne 34F2	1		1			
	405536	Bacillus anthracis str. Tsiankovskii-I		1		1		
	212045	Bacillus anthracis str. Western North America USA6153		1		1		
	1396	Bacillus cereus	1	5	1	5		
	572264	Bacillus cereus 03BB102		2		2		
	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		
	526974	Bacillus cereus BDRD-ST24		1		1		
	347495	Bacillus cereus F837/76		1		1		
	269801	Bacillus cereus G9241		41		41		
	405531	Bacillus cereus G9842		3		3		
	451708	Bacillus cereus H3081.97		12		12		
	451707	Bacillus cereus NVH0597-99		7		7		
	405917	Bacillus cereus W		1		1		
	66692	Bacillus clausii KSM-K16		1		1		
	441769	Bacillus coahuilensis m4-4		1		1		
	315749	Bacillus cytotoxicus NVH 391-98		3		3		
	1467	Bacillus lentus		1		1		
	1402	Bacillus licheniformis		10		10		
	1404	Bacillus megaterium		1		1		
	1408	Bacillus pumilus		1		1		
	313627	Bacillus sp. NRRL B-14911		2		2		
	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	1	6	1	1	
	527019	Bacillus thuringiensis IBL 200		1		1		
	339854	Bacillus thuringiensis serovar israelensis ATCC 35646		7		7		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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 tochiensis BGSC 4Y1		1		1		
	412694	Bacillus thuringiensis str. Al Hakam		8		8		
	315730	Bacillus weihenstephanensis KBAB4		5		5		
	2	Bacteria	11		45		34	
	483215	Bacteroides finegoldii DSM 17565		1		1		
	817	Bacteroides fragilis		1		2		1
	329854	Bacteroides intestinalis		1		1		
X	667015	Bacteroides salanitronis DSM 18170				1		1
	12040	Barley yellow dwarf virus-PAV	1		1			
	360095	Bartonella bacilliformis KC583		1		1		
	283166	Bartonella henselae str. Houston-1		1		1		
	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			
X	1022	Beggiatoa alba			1		1	
	3645	Bertholletia excelsa	7	24	7	24		
	161934	Beta vulgaris	5		5			
X	1263720	Betacoronavirus England 1			4		4	
	3505	Betula pendula	75	357	75	357		
	1681	Bifidobacterium bifidum		1		1		
	1685	Bifidobacterium breve		1		1		
	205913	Bifidobacterium longum DJO10A		2		2		
	10629	BK polyomavirus		52	1	52	1	
	10001761	BK polyomavirus strain Dunlop		1		1		
	65743	Blackcurrant reversion virus	2		2			
	1146883	Blastococcus saxosidens DD2		1		1		
X	5039	Blastomyces dermatitidis				1		1
X	447095	Blastomyces dermatitidis ATCC 26199				1		1
	6973	Blattella germanica	22	56	22	56		
	40697	Blomia tropicalis	19		19			
	40051	Bluetongue virus	9		9			
	10904	Bluetongue virus (serotype 1 / isolate Australia)	7		7			
	10900	Bluetongue virus (serotype 10 / American isolate)	3		3			
	33717	Bluetongue virus (serotype 13 / isolate USA)	2		2			
	33718	Bluetongue virus (serotype 17 / isolate USA)	4		4			
	35327	Bluetongue virus 1	4		4			
	10906	Bluetongue virus 10	3		3			
	35329	Bluetongue virus 11	6		6			
X	94966	Bluetongue virus 12			15		15	
	35330	Bluetongue virus 13	1		1			
X	35331	Bluetongue virus 15			7		7	
	45029	Bluetongue virus 16	3		3			
	10002028	Bluetongue virus 16 Beatrice Hill/1987	2		2			
	10002006	Bluetongue virus 16 BN96/16	2		2			
	10002027	Bluetongue virus 16 Kumamoto/1985	2		2			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	10903	Bluetongue virus 17	4		4			
	94967	Bluetongue virus 4	7		7			
	197780	Bluetongue virus 8	2	21	2	21		
	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	250	95	336	218	86	123
	10002069	Bordetella pertussis 509		7		7		
	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			
	390236	Borrelia afzelii PKo	2		2			
	498740	Borrelia burgdorferi 64b		2		2		
	224326	Borrelia burgdorferi B31	103	10	103	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			
	10000530	Borrelia garinii IP90	3		3			
	29518	Borrelia afzelii	2	1	2	1		
	139	Borrelia burgdorferi	57	40	58	40	1	
	29519	Borrelia garinii	5	29	5	29		
	9913	Bos taurus	1216	494	1221	517	5	23
	8722	Bothrops asper	1		1			
	8726	Bothrops jararacussu	13		13			
	11128	Bovine coronavirus	7		7			
	10002018	Bovine coronavirus Kakegawa	1		1			
	233262	Bovine enteric coronavirus (strain 98TXSF-110-ENT)		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	5	40	1	
	10000404	Bovine herpesvirus 1 Lam	1		1			
	263683	Bovine herpesvirus 5 strain TX89	2		2			
	79889	Bovine herpesvirus type 1.1	1		2		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	33	29	33	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	3	1	3	
	11246	Bovine respiratory syncytial virus	3	2	3	2		
	31611	Bovine respiratory syncytial virus (strain 391-2)	3		3			
	11249	Bovine respiratory syncytial virus (strain RB94)	4		4			
	82823	Bovine respiratory syncytial virus strain Ielystad	1		1			
	82824	Bovine respiratory syncytial virus strain snook	1	75	1	75		
	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		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	11099	Bovine viral diarrhoea virus 1	1	11	1	12		1
	11100	Bovine viral diarrhoea virus 1-NADL	4	3	4	3		
	54315	Bovine viral diarrhoea virus 2	1		1			
	82470	Bovine viral diarrhoea virus strain Oregon C24V	5	3	5	3		
	158474	Bovine viral diarrhoea virus strain Trangie Y546	1		1			
	221918	Bovine viral diarrhoea virus VEDEVAC	6		6			
X	15368	Brachypodium distachyon			1		1	
	288000	Bradyrhizobium sp. BTAi1		1		1		
	3707	Brassica juncea	9		9			
X	234	Brucella				28		28
	235	Brucella abortus	4	29	6	36	2	7
	359391	Brucella abortus 2308		31		31		
	262698	Brucella abortus bv. 1 str. 9-941		1		1		
	520450	Brucella abortus bv. 2 str. 86/8/59		1		1		
	575591	Brucella abortus NCTC 8038		1		1		
	430066	Brucella abortus S19		15		15		
	641140	Brucella abortus str. 2308 A		1		1		
	10001424	Brucella abortus W99	1		1			
	483179	Brucella canis ATCC 23365		9		9		
	29459	Brucella melitensis	6	93	15	93	9	
	224914	Brucella melitensis bv. 1 str. 16M	6	16	6	16		
	520464	Brucella melitensis bv. 1 str. Rev.1	1		1			
	703352	Brucella melitensis M5-90		26		26		
	236	Brucella ovis		1		1		
	10001886	Brucella ovis 020	2		2			
	10001888	Brucella ovis 63/290	1		1			
	444178	Brucella ovis ATCC 25840		10		10		
	10001887	Brucella ovis Reo 198	1		1			
	29461	Brucella suis		7	1	7	1	
	204722	Brucella suis 1330	1	29	1	29		
	470137	Brucella suis ATCC 23445	1	6	1	6		
	6279	Brugia malayi	3	5	3	5		
	6280	Brugia pahangi	1		1			
	89462	Bubalus bubalis	7	1	7	1		
	32605	Buffalopox virus		1		1		
	565995	Bundibugyo virus	1		1			
X	8613	Bungarus fasciatus			1		1	
	8616	Bungarus multicinctus	17	3	17	3		
	32008	Burkholderia	1		1			
	339670	Burkholderia ambifaria AMMD		4		4		
	331271	Burkholderia cenocepacia AU 1054		8		8		
	331272	Burkholderia cenocepacia HI2424		1		1		
	350702	Burkholderia cenocepacia PC184		1		1		
	292	Burkholderia cepacia	3	1	3	1		
	386056	Burkholderia ferrariae		1		1		
	134537	Burkholderia fungorum	1		1			
	482957	Burkholderia lata		2		2		
	13373	Burkholderia mallei		45		45		
	243160	Burkholderia mallei ATCC 23344		40		40		
	334802	Burkholderia mallei FMH		1		1		
	320390	Burkholderia mallei GB8 horse 4		1		1		
	334803	Burkholderia mallei JHU		2		2		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	412022	Burkholderia mallei NCTC 10229		10		10		
	320388	Burkholderia mallei SAVP1		31		31		
	28450	Burkholderia pseudomallei	5	2	12	6	7	4
	357348	Burkholderia pseudomallei 1106a		2		2		
	441160	Burkholderia pseudomallei 14		1		1		
	320372	Burkholderia pseudomallei 1710b		4		4		
	425067	Burkholderia pseudomallei 305		3		3		
	360118	Burkholderia pseudomallei 406e		2		2		
	320373	Burkholderia pseudomallei 668		12		12		
	441158	Burkholderia pseudomallei 9		1		1		
	441159	Burkholderia pseudomallei 91		2		2		
	272560	Burkholderia pseudomallei K96243	3	417	3	734		317
	331978	Burkholderia pseudomallei Pasteur 52237		1		1		
	320374	Burkholderia pseudomallei S13		2		2		
	271848	Burkholderia thailandensis E264		2		2		
	269482	Burkholderia vietnamiensis G4		9		9		
	60879	Cabassou virus		1		1		
X	6238	Caenorhabditis briggsae			1		1	
	6239	Caenorhabditis elegans	2	10	2	10		
	351627	Caldicellulosiruptor saccharolyticus DSM 8903		1		1		
	35305	California encephalitis virus		1		1		
	9483	Callithrix jacchus		4		4		
X	9244	Calypte anna				1		1
	28873	Camelpox virus		2		2		
	203172	Camelpox virus CMS		28		28		
	203174	Camelpox virus CP1		1		1		
	203173	Camelpox virus M-96		133		133		
X	195	Campylobacter coli				1		1
	306254	Campylobacter coli RM2228		3		3		
	32019	Campylobacter fetus subsp. fetus	3		3			
	197	Campylobacter jejuni	26	22	26	22		
	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		4		4		
	482628	Campylobacter jejuni subsp. jejuni BH-01-0142		1		1		
	360112	Campylobacter jejuni subsp. jejuni HB93-13		2		2		
	567106	Campylobacter jejuni subsp. jejuni IA3902		1		1		
	192222	Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819	10	23	10	23		
	10002003	Campylobacter jejuni subsp. jejuni serotype HS:15	1		1			
	306263	Campylobacter lari RM2100		1		1		
	28080	Campylobacter upsaliensis	3		3			
	306264	Campylobacter upsaliensis RM3195		1		1		
	44088	Canarypox virus		8		8		
	5476	Candida albicans	101	68	101	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			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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		
	170325	Canid herpesvirus 1		1		1		
	292348	Canine calicivirus (strain 48)	2		2			
	11232	Canine distemper virus	4	8	4	8		
	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	76	6	154		78
	60135	Cano Delgadito virus		1		1		
	521097	Capnocytophaga ochracea DSM 7271		1		1		
	712212	Capnocytophaga sp. oral taxon 326		1		1		
	9925	Capra hircus	11		11			
	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	1	3	1		
	64289	Carey Island virus		2		2		
	32201	Carya illinoensis	19		19			
	10185	Castor fiber		1		1		
	129052	Catelliglobospora koreensis		1		1		
X	304895	Catenulispora acidiphila				1		1
	10141	Cavia porcellus	32	73	32	75		2
	33706	Caviid herpesvirus 2	2	3	2	3		
	6878	Centruroides noxius	8		8			
	260965	Cercopithecine herpesvirus 1 (strain E2490)	18		18			
	10317	Cercopithecine herpesvirus 2		1		1		
	9864	Cervus canadensis nelsoni	4		5		1	
	9860	Cervus elaphus	2		2			
	9721	Cetacea	1		1			
X	38033	Chaetomium globosum			1		1	
X	759272	Chaetomium thermophilum var. thermophilum DSM 1495			1		1	
	13415	Chamaecyparis obtusa	1	68	1	68		
	266779	Chelativorans sp. BNC1		4		4		
	12618	Chicken anemia virus	3		3			
	37124	Chikungunya virus	23	3	41	3	18	
	10001934	Chikungunya virus Singapore/11/2008	3		3			
	10001997	Chikungunya virus strain LR2006_OPY1 IMT/Reunion Island/2006	1		1			
X	371094	Chikungunya virus strain S27-African prototype			24		24	
	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		3		2
	243161	Chlamydia muridarum str. Nigg		28		42		14
	83558	Chlamydia pneumoniae	57	23	57	23		
	83554	Chlamydia psittaci	78	2	78	2		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	331636	Chlamydia psittaci 6BC	1		1			
	813	Chlamydia trachomatis	122	65	128	67	6	2
	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		26		25
	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	12	15	12		
	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			
	337090	Chlorobium chlorochromatii		1		1		
X	340177	Chlorobium chlorochromatii CaD3				1		1
	9534	Chlorocephus aethiops		3		3		
	169173	Choclo virus		3		3		
	7777	Chondrichthyes	1		1			
	544	Citrobacter	1		1			
	546	Citrobacter freundii	1		1			
	12162	Citrus tristeza virus	8		8			
	29918	Cladosporium herbarum		18		18		
	11096	Classical swine fever virus	12	3	13	4	1	1
	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			
X	358812	Classical swine fever virus - C			2		2	
	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			
	68621	Classical swine fever virus strain Riems		5		5		
	36911	Clavispota lusitaniae	1		1			
X	272562	Clostridium acetobutylicum ATCC 824				1		1
	1137848	Clostridium arbusti		1		1		
	1491	Clostridium botulinum	178	76	194	80	16	4
	36826	Clostridium botulinum A	46		46			
	10000293	Clostridium botulinum A 1	1		1			
	10000294	Clostridium botulinum A 2	2		2			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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			
	935198	Clostridium botulinum B str. Eklund 17B (NRP)		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			
	10000307	Clostridium difficile BART'S W1	1		1			
	10001847	Clostridium difficile BI / NAP1/ 027	1		1			
X	10002079	Clostridium difficile VPI 10463			2		2	
	386415	Clostridium novyi NT		2		2		
	29362	Clostridium papyrosolvens	1	1	1	1		
	1502	Clostridium perfringens	10	1	10	1		
	107819	Clostridium perfringens D	1		1			
	195102	Clostridium perfringens str. 13		1		1		
X	29371	Clostridium termitidis			1		1	
	1513	Clostridium tetani	77	244	77	245		1
	212717	Clostridium tetani E88		16		16		
	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		9		10		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		
X	410072	Coprococcus comes			1		1	
	13451	Corylus avellana	27	53	27	53		
	43765	Corynebacterium amycolatum		1		1		
	1717	Corynebacterium diphtheriae	13	52	15	52	2	
	152794	Corynebacterium efficiens		5		5		
	196164	Corynebacterium efficiens YS-314		4		4		
	1718	Corynebacterium glutamicum		26		26		
	196627	Corynebacterium glutamicum ATCC 13032		14		14		
	306537	Corynebacterium jeikeium K411		1		1		
	12264	Cowpea mosaic virus		1		1		
	10243	Cowpox virus		25		25		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	265872	Cowpox virus (Brighton Red)		1		1		
	10000571	Cowpox virus (Brighton Red) White-pock		1		1		
	777	Coxiella burnetii	2	198	2	198		
	434923	Coxiella burnetii CbuG_Q212		1		1		
	434924	Coxiella burnetii CbuK_Q154		1		1		
	434922	Coxiella burnetii Dugway 5J108-111		8		8		
	360116	Coxiella burnetii 'MSU Goat Q177'		8		8		
	360117	Coxiella burnetii Q321		14		14		
	360115	Coxiella burnetii RSA 331		9		9		
	227377	Coxiella burnetii RSA 493		14		14		
	12066	Coxsackievirus	1		1			
	31704	Coxsackievirus A16	2		2			
	42782	Coxsackievirus A20	1		1			
	12067	Coxsackievirus A9	30		30			
	12071	Coxsackievirus B1	12		12			
	82639	Coxsackievirus B2	2		2			
	12072	Coxsackievirus B3	7	15	7	15		
	103903	Coxsackievirus B3 (strain Nancy)	13	30	13	30		
	12073	Coxsackievirus B4	17	50	17	50		
	103905	Coxsackievirus B4 (strain E2)	7	41	7	41		
	103906	Coxsackievirus B4 (strain JVB / Benschoten / New York/51)		76		76		
	10029	Cricetulus griseus	1		1			
	11593	Crimean-Congo hemorrhagic fever virus	14	1	20	1	6	
	368445	Crocodilepox virus		2		2		
	8732	Crotalus durissus terrificus	4		4			
	5207	Cryptococcus neoformans	2	1	2	2		1
	178876	Cryptococcus neoformans var. grubii	1		1			
	283643	Cryptococcus neoformans var. neoformans B-3501A	1	3	1	3		
	10001132	Cryptococcus neoformans var. neoformans Serotype A	1		1			
	10001120	Cryptococcus neoformans var. neoformans Serotype D	1		1			
	3369	Cryptomeria japonica	44	182	44	182		
	237895	Cryptosporidium hominis		3		3		
	5807	Cryptosporidium parvum	3	30	3	30		
	353152	Cryptosporidium parvum Iowa II		84		84		
	220837	Cryptosporidium sp. MNJ-1		1		1		
	7515	Ctenocephalides felis		2		2		
	12305	Cucumber mosaic virus	1		1			
	117125	Cucumber mosaic virus (strain Pepo)	1		1			
	3656	Cucumis melo	13		13			
	208899	Cupixi mammarenavirus		1		1		
	13469	Cupressus sempervirens		8		8		
	266264	Cupriavidus metallidurans CH34		3		3		
	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		12		12		
	7955	Danio rerio	1	3	1	3		
	4039	Daucus carota		1		1		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	305674	Deerpox virus W-848-83		2		2		
	243164	Dehalococcoides mccartyi 195		1		1		
X	68909	Deinococcus geothermalis			1		1	
	337052	Deltapapillomavirus 4	8		8			
	12637	Dengue virus	22	424	22	429		5
	11053	Dengue virus 1	21	109	21	203		94
	408685	Dengue virus 1 Brazil/97-11/1997		1058		1058		
	10001582	Dengue virus 1 Mochizuki	4		4			
	11059	Dengue virus 1 Nauru/West Pac/1974	4	50	4	50		
	10001945	Dengue virus 1 PVP159	2		2			
	33741	Dengue virus 1 Singapore/S275/1990		242		242		
	11057	Dengue virus 1 Thailand/AHF 82-80/1980		1		1		
	11060	Dengue virus 2	104	191	120	325	16	134
	31635	Dengue virus 2 16681-PDK53	4	31	4	31		
	10002010	Dengue virus 2 D2/SG/05K4155DK1/2005		49		49		
	11064	Dengue virus 2 Jamaica/1409/1983	263	1254	264	1254	1	
	11062	Dengue virus 2 Malaysia M2	1		1			
	10001583	Dengue virus 2 New Guinea C	1	4	1	4		
	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	32	21	32	21		
	10001768	Dengue virus 2 S-16803	10		10			
X	10001636	Dengue virus 2 S221				42		42
	10001705	Dengue virus 2 strain 43	1		1			
	31634	Dengue virus 2 Thailand/16681/84	30	62	32	62	2	
	11065	Dengue virus 2 Thailand/NGS-C/1944	17	37	17	37		
	11067	Dengue virus 2 Tonga/EKB194/1974		3		3		
	11069	Dengue virus 3	39	248	41	295	2	47
	408690	Dengue virus 3 China/80-2/1980		84		84		
	408691	Dengue virus 3 Martinique/1243/1999		889		889		
	408870	Dengue virus 3 Philippines/H87/1956	8	13	8	13		
	408693	Dengue virus 3 Singapore/8120/1995		69		69		
	408692	Dengue virus 3 Sri Lanka/1266/2000		66		66		
	10001619	Dengue virus 3 strain 16652	16		16			
	10001944	Dengue virus 3 Thailand/PaH881/1988	1		2		1	
	11070	Dengue virus 4	32	88	45	146	13	58
X	10002112	Dengue virus 4 1036			1		1	
	10001943	Dengue virus 4 Burma/63632/1976	1		3		2	
	408871	Dengue virus 4 Dominica/814669/1981	1	256	1	256		
X	10002148	Dengue virus 4 Mexico/BC287/1997			1		1	
	408686	Dengue virus 4 Philippines/H241/1956	4	947	4	947		
	408687	Dengue virus 4 Singapore/8976/1995		5		5		
	408688	Dengue virus 4 Thailand/0348/1991		15		15		
	408689	Dengue virus 4 Thailand/0476/1997		2		2		
X	10002111	Dengue virus 4 TVP-376			1		1	
	10000965	Dengue virus type 1 FGA/89	2		4		2	
	10000440	Dengue virus type 1 Hawaii	19	10	29	22	10	12
	10000961	Dengue virus type 1 strain 16007	15		15			
	10000442	Dengue virus type 3 CH53489		7		7		
	6954	Dermatophagoides farinae	16	77	16	82		5
	6956	Dermatophagoides pteronyssinus	74	226	76	226	2	
	439235	Desulfatibacillum alkenivorans AK-01		1		1		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	272564	Desulfitobacterium hafniense DCB-2		3		3		
X	60893	Desulfobacca acetoxidans				1		1
	1286635	Desulfotignum phosphitoxidans DSM 13687		1		1		
	281689	Desulfuromonas acetoxidans DSM 684		1		1		
	11319	Dhuri virus (strain Indian/1313/61)	1		1			
	44689	Dictyostelium discoideum		1		1		
	261658	Dictyostelium fasciculatum		1		1		
	4163	Digitalis	1		1			
	86600	Discosoma sp.		1		1		
	12506	Dobrava-Belgrade virus		25		25		
	7441	Dolichovespula maculata	11	20	11	20		
	292633	Dragon grouper nervous necrosis virus	20		20			
	7227	Drosophila melanogaster	4	15	7	15	3	
X	7234	Drosophila persimilis			1		1	
X	46245	Drosophila pseudoobscura pseudoobscura			1		1	
X	7244	Drosophila virilis				1		1
X	10002132	Duck hepatitis A virus 1 HP-1			1		1	
X	10002151	Duck hepatitis A virus 1 LY0801			1		1	
X	10002152	Duck hepatitis A virus 3 SD1201			1		1	
	12639	Duck hepatitis B virus	262	20	262	20		
	38767	Duvenhage virus		2		2		
X	231455	Dyella japonica			1		1	
	11021	Eastern equine encephalitis virus	42	1	42	1		
	11022	Eastern equine encephalitis virus (STRAIN VA33[TEN BROECK])		1		1		
	10000439	Eastern equine encephalitis virus SV	8		8			
	129000	Ebola virus - Eckron (Zaire, 1976)		12		12		
	128947	Ebola virus - Gabon (1994-1997)		18		18		
	128952	Ebola virus - Mayinga, Zaire, 1976	19	13	27	13	8	
	128951	Ebola virus - Zaire (1995)		1		1		
	205488	Ebola virus sp.		10		10		
	53751	Echinacea purpurea	1		1			
	6210	Echinococcus granulosus	39		39			
	6211	Echinococcus multilocularis	6		6			
	99586	Echis ocellatus	5		5			
	33758	Echovirus		1		1		
	12078	Echovirus E11	1		1			
	12060	Echovirus E9	1		1			
	12643	Ectromelia virus		6		6		
	944	Ehrlichia canis	7	1	7	1		
	269484	Ehrlichia canis str. Jake	16		16			
	945	Ehrlichia chaffeensis	14	1	14	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		
	8005	Electrophorus electricus	3		3			
X	2903	Emiliania huxleyi				1		1
	280463	Emiliania huxleyi CCMP1516		1		1		
	6035	Encephalitozoon cuniculi		5		5		
	284813	Encephalitozoon cuniculi GB-M1		28		28		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	1178016	Encephalitozoon romaleae SJ-2008		1		1		
	12104	Encephalomyocarditis virus		1		1		
	370354	Entamoeba dispar SAW760		20		20		
	5759	Entamoeba histolytica	29	13	29	13		
	294381	Entamoeba histolytica HM-1:IMSS		103		103		
	885311	Entamoeba histolytica KU27		1		1		
	10000352	Entamoeba histolytica YS-27	1		1			
X	550	Enterobacter cloacae					9	9
	12340	Enterobacteria phage 933J	1		1			
	10730	Enterobacteria phage 933W	1		1			
	10863	Enterobacteria phage f1	1	1	1	1		
	10864	Enterobacteria phage fd	7	1	7	1		
	10710	Enterobacteria phage lambda	2	6	2	6		
	10754	Enterobacteria phage P22	5		5			
	10847	Enterobacteria phage phiX174	1		1			
	10658	Enterobacteria phage PRD1	2		2			
	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			
	138948	Enterovirus A	1		1			
	39054	Enterovirus A71	20	1	23	1	3	
	10002056	Enterovirus A71 TW/2086/98	1		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	7		7	218		218
	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	6		6			
	10000405	Equid herpesvirus 4 TH20	2		2			
	82831	Equid herpesvirus type 2 strain 86/87	1		1			
	11047	Equine arteritis virus	2		3		1	
	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	48	45	48	45		
	9798	Equus przewalskii		1		1		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	9538	Erythrocebus patas		1		1		
	562	Escherichia coli	228	141	236	141	8	
	10001633	Escherichia coli 055:B5	3		3			
	358709	Escherichia coli 101-1		5		5		
	10001145	Escherichia coli 1471	2		2			
	10000727	Escherichia coli 180/C3	1		1			
	362663	Escherichia coli 536		66		66		
	344610	Escherichia coli 53638		1		1		
	525281	Escherichia coli 83972		4		4		
	405955	Escherichia coli APEC O1		8		8		
	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		25		25		
	550676	Escherichia coli B185		1		1		
	340184	Escherichia coli B7A		5		5		
	199310	Escherichia coli CFT073	1	2	1	2		
	340186	Escherichia coli E110019		2		2		
	340185	Escherichia coli E22		13		13		
	316401	Escherichia coli ETEC H10407	64	31	64	31		
	340197	Escherichia coli F11		12		12		
	10001528	Escherichia coli F515	1		1			
	10001463	Escherichia coli F576	1		1			
	331112	Escherichia coli HS		14		14		
	585034	Escherichia coli IAI1	3		3			
X	1432555	Escherichia coli ISC7				1		1
	10001502	Escherichia coli J-5	1		1			
	10001753	Escherichia coli K1		1		1		
	83333	Escherichia coli K-12	20	19	20	19		
	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			
	331111	Escherichia coli O139:H28 str. E24377A		36		36		
	83334	Escherichia coli O157:H7		103		103		
	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	32	3	32	1	
	386585	Escherichia coli O157:H7 str. Sakai		17		17		
	10000733	Escherichia coli O5:K4:H4	1		1			
	244320	Escherichia coli O55:H7		1		1		
	217992	Escherichia coli O6		7		7		
	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		3		3		
	511145	Escherichia coli str. K-12 substr. MG1655		31		31		
	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			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	6958	Euroglyphus maynei		10		10		
	1323	Faecalicoccus pleomorphus		1		1		
	3617	Fagopyrum esculentum	40		40			
	62330	Fagopyrum tataricum	5		5			
	6690	Farfantepenaeus aztecus	51	31	51	31		
	46835	Fasciola gigantica	2		2			
	6192	Fasciola hepatica	270	28	270	28		
	11978	Feline calicivirus	4		4			
	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)	15	14	15	14		
	10001624	Feline infectious peritonitis virus (strain KU-2)	22	43	22	43		
	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	40	99	40	99		
	29960	Fenneropenaeus indicus	2		2			
	4606	Festuca arundinacea	1		1			
	1260	Finogoldia magna		1		1		
	156586	Flavobacteria bacterium BBFL7		2		2		
	487797	Flavobacteria bacterium MS024-3C		1		1		
	12110	Foot-and-mouth disease virus	24	5	24	5		
	12111	Foot-and-mouth disease virus - type A		5		5		
	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	9	3	9	3		
	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	2		2			
	12116	Foot-and-mouth disease virus - type C	6	26	6	26		
	12118	Foot-and-mouth disease virus - type O	34	5	35	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	1	21	1		
	12115	Foot-and-mouth disease virus (strain A24 Cruzeiro)	17	10	17	10		
	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			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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)	43	8	43	8		
	10000806	Foot-and-mouth disease virus (strain O1) (O1 Manisa)	5		5			
	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	43	12	43	12		
	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		
	12121	Foot-and-mouth disease virus C1	1	4	1	4		
	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	15	17	15	17		
	31621	Four Corners hantavirus	2	8	2	8		
	10261	Fowlpox virus		7		7		
	10263	Fowlpox virus isolate HP-438/Munich		1		1		
	928301	Fowlpox virus strain NVSL		3		3		
	263	Francisella tularensis	4	13	4	13		
	351581	Francisella tularensis subsp. holarctica FSC200		1		1		
	458234	Francisella tularensis subsp. holarctica FTNF002-00		1		1		
	376619	Francisella tularensis subsp. holarctica LVS	9	291	10	291	1	
	393011	Francisella tularensis subsp. holarctica OSU18		6		6		
	401614	Francisella tularensis subsp. novicida U112		1		1		
	119856	Francisella tularensis subsp. tularensis		5		5		
	430557	Francisella tularensis subsp. tularensis FSC033		27		27		
	393115	Francisella tularensis subsp. tularensis FSC198		85		85		
	177416	Francisella tularensis subsp. tularensis SCHU S4		90		90		
	418136	Francisella tularensis subsp. tularensis WY96-3418		2		2		
	298653	Frankia sp. EAN1pec		2		2		
X	81475	Frateuria aurantia			1		1	
	38873	Fraxinus excelsior		3		3		
	11795	Friend murine leukemia virus	6	52	6	52		
	209882	Fusobacterium nucleatum subsp. vincentii ATCC 49256		2		2		
	8049	Gadus morhua	30		31		1	
	8053	Gadus morhua callarias	10		10			
	7137	Galleria mellonella	1		1			
	395494	Gallionella capsiferriformans ES-2		1		1		
	9031	Gallus gallus	317	220	319	320	2	100
	373098	Gambierdiscus toxicus	6		6			
	566466	gamma proteobacterium NOR5-3		1		1		
	11824	Gardner-Arnstein feline leukemia oncovirus B	13		13			
	54290	GB virus C	16		16			
	471223	Geobacillus sp. WCH70		2		2		
	1422	Geobacillus stearothermophilus	2	1	2	1		
	5741	Giardia intestinalis		10		10		
	598745	Giardia intestinalis ATCC 50581		7		7		
	184922	Giardia lamblia ATCC 50803		249		249		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	658858	Giardia lamblia P15		1		1		
	37546	Glossina morsitans morsitans	2		2			
	3847	Glycine max	143	2	143	2		
	61466	Gnathostoma binucleatum	10		10			
	38251	Goose parvovirus	7		7			
	9593	Gorilla gorilla		2		2		
	9595	Gorilla gorilla gorilla		5		5		
X	940614	Granulicella mallensis				1		1
	55951	Grapevine leafroll-associated virus 3	1		1			
	35288	Grapevine virus A	19		19			
	655863	Grosmania clavigera kw1407		1		1		
	45219	Guanarito mammarenavirus		840		840		
	10001616	Guanarito virus strain INH-95551		1		1		
	114727	H1N1 subtype	12	33	12	43		10
	10000477	H1N1 subtype Influenza A virus (A/Netherlands/306/00 (H1N1))		1		1		
	10001225	H1N1 subtype Influenza A/Oklahoma/7485/01		5		5		
	36420	H1N1 swine influenza virus		12		12		
	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		
	170500	H1N9 subtype	1		1			
	114729	H2N2 subtype		1		1		
	119210	H3N2 subtype	4	21	4	21		
	10001157	H3N2 subtype Influenza A virus (A/Hong Kong(H3N2))		15		15		
	102793	H5N1 subtype	17	31	18	31	1	
	119218	H7N7 subtype		1		1		
	333278	H7N9 subtype		11	1	11	1	
	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		3		2	
	197575	Haemophilus aegyptius	1		1			
	730	Haemophilus ducreyi	3	1	3	2		1
	233412	Haemophilus ducreyi 35000HP	1		1			
	727	Haemophilus influenzae	24	65	30	66	6	1
	374927	Haemophilus influenzae 22.1-21		3		3		
	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			
	374933	Haemophilus influenzae PittII		3		3		
	262727	Haemophilus influenzae R2846		6		6		
	262728	Haemophilus influenzae R2866		2		2		
	375432	Haemophilus influenzae R3021		3		3		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	71421	Haemophilus influenzae Rd KW20		3		3		
	1000860	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			
	1000861	Haemophilus influenzae Variant d1	18		18			
	738	Haemophilus parasuis	1		1			
	205914	Haemophilus somnus 129PT		2		2		
	228400	Haemophilus somnus 2336	1		1			
	6454	Haliotis rufescens	1		1			
	62319	Halococcus saccharolyticus		1		1		
	10626	Hamster polyomavirus	11		11			
	11599	Hantaan virus	2	51	2	51		
	11602	Hantaan virus 76-118	13	35	13	53		18
	370830	Hantaan virus Q32		4		4		
	470918	Hantaanvirus CGHu1		1		1		
	458678	Hantaanvirus CGRn93P8		2		2		
	11598	Hantavirus		15		15		
	74942	Hantavirus CRF355		1		1		
	308061	Hantavirus HPR/02-73		1		1		
	42358	Hantavirus Monongahela-3		5		5		
	279233	Hantavirus Z37		2		2		
	13557	Hapalemur griseus		1		1		
	489455	HBV genotype A	1		1			
	489460	HBV genotype B	1		1			
	489466	HBV genotype C	4		4			
	489483	HBV genotype D	1	3	1	3		
	4232	Helianthus annuus	18		18			
	32025	Helicobacter hepaticus		1		1		
	235279	Helicobacter hepaticus ATCC 51449	2		2			
	210	Helicobacter pylori	42	11	43	15	1	4
	85962	Helicobacter pylori 26695	13	11	13	11		
	10001667	Helicobacter pylori 487	1		1			
	10001794	Helicobacter pylori B128 Gerbil-adapted variant 7.13	1		1			
	563041	Helicobacter pylori G27	2		2			
X	992121	Helicobacter pylori Hp M5			1		1	
	10000718	Helicobacter pylori J223	2		2			
	85963	Helicobacter pylori J99		53		53		
	637383	Helicobacter pylori NCTC 11639		2		2		
	570508	Helicobacter pylori P12		2		2		
X	1337393	Helicobacter pylori PZ5056			1		1	
X	1352357	Helicobacter pylori SouthAfrica50			1		1	
	102617	Helicobacter pylori SS1	3	3	3	3		
	10000720	Helicobacter pylori UA948	2		2			
	10000721	Helicobacter pylori UA955	1		1			
	148363	Helicoverpa armigera nucleopolyhedrovirus G4	2		2			
	6339	Heligmosomoides polygyrus	3		3			
	6536	Helix pomatia	1		1			
	63330	Hendra virus	7		7			
	10407	Hepatitis B virus	260	620	261	637	1	17

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	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		
	482134	Hepatitis B virus adw/Japan/Nishioka/1983		1		1		
	10415	Hepatitis B virus adw/Okinawa/PODW282		4		4		
	45410	Hepatitis B virus adw4/Brazil/isolate w4b		6		6		
	10411	Hepatitis B virus alpha1		16		16		
	489469	Hepatitis B virus ayw/China/Tibet127/2002	1		1			
	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			
X	10000435	Hepatitis B virus genotype D				6		6
	10414	Hepatitis B virus LSH/chimpanzee		2		2		
	10001156	Hepatitis B virus subtype AD	3	2	3	2		
	106820	Hepatitis B virus subtype adr	23	25	23	25		
	106821	Hepatitis B virus subtype adw	17	59	17	59		
	10408	Hepatitis B virus subtype adw2	77	60	77	60		
	10419	Hepatitis B virus subtype adyw	2	35	2	35		
	10000436	Hepatitis B virus subtype AY	7		7			
	10000437	Hepatitis B virus subtype AYR		1		1		
	10418	Hepatitis B virus subtype ayw	57	166	57	166		
	11103	Hepatitis C virus	654	1010	665	1051	11	41
	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	65		22
	333284	Hepatitis C virus (isolate Con1)	4	3	4	3		
	356419	Hepatitis C virus (isolate EUH1480)		4		4		
	329389	Hepatitis C virus (isolate Glasgow)	3	1	3	1		
	11108	Hepatitis C virus (isolate H)	130	80	134	80	4	
	63746	Hepatitis C virus (isolate H77)	94	207	102	207	8	
	356410	Hepatitis C virus (isolate HC-G9)	2	1	2	1		
	356416	Hepatitis C virus (isolate HCV-K3a/650)		14		14		
	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	14	3	14		
	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	102	2	134		32
	40271	Hepatitis C virus genotype 2	41	6	41	6		
	356114	Hepatitis C virus genotype 3	121	13	121	17		4
	33745	Hepatitis C virus genotype 4		2		2		
	33746	Hepatitis C virus genotype 5		2		2		
	42182	Hepatitis C virus genotype 6		7		7		
	11110	Hepatitis C virus HCT18	1		1			
	31644	Hepatitis C virus HCV-KF	1	1	1	1		
	421877	Hepatitis C virus isolate HC-J1	3	26	3	26		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
X	420174	Hepatitis C virus isolate HC-J4				127		127
	11113	Hepatitis C virus isolate HC-J6	8	2	8	2		
	11115	Hepatitis C virus isolate HC-J8	2	1	2	1		
	356411	Hepatitis C virus JFH-1	6	1	7	1	1	
	31646	Hepatitis C virus subtype 1a	194	369	200	391	6	22
	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	539	234	604	243	65	9
	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	4	103	4	2	
	356426	Hepatitis C virus subtype 3a	8	77	8	77		
	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	56	7	8	
	10000523	Hepatitis delta virus TW2667		5		5		
	12461	Hepatitis E virus	134	27	148	27	14	
	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		
	185579	Hepatitis E virus type 1	1		3		2	
X	185580	Hepatitis E virus type 4			1		1	
	39113	Hepatitis GB virus B		4		4		
	12092	Hepatovirus A	23	22	23	22		
	28300	Heron hepatitis B virus		1		1		
	10299	Herpes simplex virus (type 1 / strain 17)	44	40	44	40		
	10301	Herpes simplex virus (type 1 / strain Angelotti)		1		1		
	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		1		1		
	49011	Hesperocyparis arizonica	2	6	2	6		
	93621	Heteropneustes fossilis		1		1		
	3981	Hevea brasiliensis	170	43	170	43		
	471721	HIV-1 CRF01_AE	1		1			
	388799	HIV-1 group O	1		1			
	505184	HIV-1 M:A	6	1	6	1		
	505185	HIV-1 M:B	3	1	4	1	1	
	11685	HIV-1 M:B_ARV2/SF2	1	43	1	43		
	11706	HIV-1 M:B_HXB2R	11	12	13	12	2	
	11696	HIV-1 M:B_MN	9	21	9	21		
	505186	HIV-1 M:C	6		8		2	
	327105	HIV-1 O_ANT70	1		1			
	11583	HoJo virus		1		1		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	29679	Holcus lanatus	14	2	14	2		
	9606	Homo sapiens	6407	20148	6840	60937	433	40789
X	63221	Homo sapiens neanderthalensis				1		1
	4513	Hordeum vulgare		2		23		21
X	77009	Hordeum vulgare subsp. spontaneum				1		1
X	112509	Hordeum vulgare subsp. vulgare				12		12
	397342	Horsepox virus		6		6		
	10533	Human adenovirus 1		1		1		
	10541	Human adenovirus 11		12		12		
X	343463	Human adenovirus 11a			1		1	
	343462	Human adenovirus 11p	7		7			
	28282	Human adenovirus 12	10	2	10	2		
X	10521	Human adenovirus 14			1		1	
	28276	Human adenovirus 15	1		1			
	10515	Human adenovirus 2	28	6	28	8		2
	10529	Human adenovirus 31		1		1		
	28284	Human adenovirus 40	2	1	2	1		
	46941	Human adenovirus 46	1		1			
	28285	Human adenovirus 5	25	175	25	177		2
	10519	Human adenovirus 7	4		4			
	10001392	Human adenovirus B strain Harbin04B	5		5			
	45659	Human adenovirus B3	29	1	29	1		
X	714978	Human adenovirus B55			4		4	
	46921	Human adenovirus D13	1		1			
	31545	Human adenovirus D8	1	1	1	1		
X	1235996	Human betacoronavirus 2c EMC/2012			7		7	
	689403	Human bocavirus 1	8		8			
	573977	Human bocavirus 2	4		4			
	638313	Human bocavirus 3	6		6			
	158465	Human calicivirus Hu/NLV/GII/MD145-12/1987/US	1		1			
	11137	Human coronavirus 229E		2		2		
	31631	Human coronavirus OC43		1		1		
	10002015	Human coxsackievirus A16 shzh05-1	92		92			
	10001213	Human coxsackievirus B3 (strain RK)	1		1			
	11827	Human endogenous retrovirus	1	1	1	1		
	64382	Human Endogenous Retrovirus IDDMK1,2-22	3		3			
	45617	Human endogenous retrovirus K	14		14			
	69153	Human enterovirus 71 (strain BR CR)	1		1			
	10001902	Human enterovirus 71 NUH0083/SIN/08	4		4			
	10000548	Human enterovirus 71 Subgenogroup C2	19		19			
	10000549	Human enterovirus 71 Subgenogroup C4	3		3			
	208726	Human hepatitis A virus	4		4			
	12098	Human hepatitis A virus Hu/Australia/HM175/1976	86	83	86	83		
	10298	Human herpesvirus 1	150	142	150	144		2
	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	102	205	102	205		
	10312	Human herpesvirus 2 strain 186	1	1	1	1		
	10313	Human herpesvirus 2 strain 333	2	5	2	5		
	10315	Human herpesvirus 2 strain HG52		31		31		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	10335	Human herpesvirus 3	9	90	9	117		27
	10000406	Human herpesvirus 3 H-551	26	15	26	15		
	10338	Human herpesvirus 3 strain Dumas		28		29		1
X	341980	Human herpesvirus 3 strain Oka vaccine			3		3	
	10376	Human herpesvirus 4	132	527	138	536	6	9
	10377	Human herpesvirus 4 (strain B95-8)	107	310	107	353		43
	31525	Human herpesvirus 4 (strain CAO)		1		1		
	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	13	4	13		
	12509	Human herpesvirus 4 type 2	2	9	2	10		1
	10000427	Human herpesvirus 4 type A		5		5		
	10359	Human herpesvirus 5	84	501	88	519	4	18
	10360	Human herpesvirus 5 strain AD169	33	395	228	395	195	
	295027	Human herpesvirus 5 strain Merlin		2	1	3	1	1
X	311339	Human herpesvirus 5 strain Toledo			9		9	
	10363	Human herpesvirus 5 strain Towne	5	26	5	26		
X	10000408	Human herpesvirus 5 TB40				1		1
	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	2	7	2	7		
	32604	Human herpesvirus 6B	2	26	2	42		16
	10000535	Human herpesvirus 6B HST	1		1			
	10372	Human herpesvirus 7	2	3	2	4		1
	57278	Human herpesvirus 7 strain JI		1		1		
	37296	Human herpesvirus 8	26	482	26	482		
	11676	Human immunodeficiency virus 1	106	393	132	416	26	23
	10000500	Human immunodeficiency virus 1 IIIB	1	2	1	2		
	11709	Human immunodeficiency virus 2	1	6	1	7		1
	11682	Human immunodeficiency virus type 1 (BH5 ISOLATE)		1		1		
	11686	Human immunodeficiency virus type 1 (BRU ISOLATE)	1	4	1	4		
	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)	10	21	15	21	5	
	11694	Human immunodeficiency virus type 1 (JH3 ISOLATE)		3		3		
	11688	Human immunodeficiency virus type 1 (JRCSF ISOLATE)	2	35	3	35	1	
	11697	Human immunodeficiency virus type 1 (MAL ISOLATE)		8		8		
	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)	15		15			
	31678	Human immunodeficiency virus type 1 (WMJ1 isolate)		15		15		
	11705	Human immunodeficiency virus type 1 (WMJ2 ISOLATE)		1		1		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	11683	Human immunodeficiency virus type 1 (Z2/CDC-Z34 ISOLATE)		1		1		
	11678	Human immunodeficiency virus type 1 BH10	2	22	2	22		
	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)		6		6		
	73484	Human immunodeficiency virus type 2 (isolate KR)		2		2		
	11718	Human immunodeficiency virus type 2 (ISOLATE SBLISY)		2		2		
	129875	Human mastadenovirus A		1		1		
X	108098	Human mastadenovirus B			1		1	
	129951	Human mastadenovirus C	1	3	1	3		
	130309	Human mastadenovirus F	1		1			
	162145	Human metapneumovirus	8	121	8	121		
	10566	Human papillomavirus	1		1	1		1
	10580	Human papillomavirus type 11	9	40	9	40		
	10573	Human papillomavirus type 13	1	1	1	1		
	333760	Human papillomavirus type 16	329	400	330	413	1	13
	333761	Human papillomavirus type 18	24	83	25	83	1	
	10583	Human papillomavirus type 1a	8	14	8	14		
	333751	Human papillomavirus type 2		7		7		
	333762	Human papillomavirus type 26		1		1		
	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	9	7	9	7		
	333763	Human papillomavirus type 32	1	1	1	1		
	10586	Human papillomavirus type 33	5	9	5	9		
	10587	Human papillomavirus type 35		1	1	1	1	
	10588	Human papillomavirus type 39		1	1	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	1	5	1	
	333923	Human papillomavirus type 5	1		1			
	10595	Human papillomavirus type 51	1	1	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	3	32	4	32	1	
	37115	Human papillomavirus type 59		1	1	1	1	
	31552	Human papillomavirus type 6	12	4	12	4		
	45240	Human papillomavirus type 68		1		1		
	37121	Human papillomavirus type 69		1		1		
	10600	Human papillomavirus type 6b	11	25	11	25		
	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			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	12063	Human parechovirus 1	6		7		1	
	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	49	31	49	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	27	197	27	199		2
	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	124	16	124	16		
	10001456	Human respiratory syncytial virus A strain RGH	1		1			
	11259	Human respiratory syncytial virus A2	57	127	60	127	3	
	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	84	13	84		
	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 lymphotropic virus type 1 (Caribbean isolate)		5		5		
	10001004	Human T-cell lymphotropic virus type 1 (Caribbean isolate) (Strain HS35)	1		1			
	11928	Human T-cell lymphotropic virus type 1 (isolate MT-2)	1		1			
	11926	Human T-cell lymphotropic virus type 1 (strain ATK)	30	118	30	118		
	39015	Human T-cell lymphotropic virus type 1 (african isolate)		2		2		
	11908	Human T-lymphotropic virus 1	234	280	234	280		
	11909	Human T-lymphotropic virus 2	63	2	63	2		
	9580	Hylobates lar		1		1		
	11120	Infectious bronchitis virus	7	1	7	1		
	10000825	Infectious bronchitis virus Avian strain D207	11		11			
	10001431	Infectious bronchitis virus CK/CH/LDL/97I	1		1			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	633557	Infectious bronchitis virus CK/CH/LHLJ/04V	1		1			
	10995	Infectious bursal disease virus	10		12		2	
	10997	Infectious bursal disease virus 002-73/AUS	1		1			
	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	65	485	68	494	3	9
	229051	Influenza A virus (A/81/HO)		6		6		
X	425551	Influenza A virus (A/AA/Huston/1945(H1N1))			1		1	
	387139	Influenza A virus (A/Aichi/2/1968(H3N2))	11	10	11	10		
	203129	Influenza A virus (A/Aichi/2/1994(H3N2))		1		1		
	1391655	Influenza A virus (A/Aichi/2-1/1968(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))	3		3			
X	1481964	Influenza A virus (A/Anhui/1-DEWH730/2013(H7N9))			1	26	1	26
X	1663996	Influenza A virus (A/Anhui/1-YK_RG01/2013(H7N9))			1		1	
	370811	Influenza A virus (A/Anhui/2/2005(H5N1))	1		1			
X	1413188	Influenza A virus (A/Anhui/PA-1/2013(H7N9))			1	3	1	3
	464314	Influenza A virus (A/Anhui/T2/2006(H5N1))	1		1			
	384498	Influenza A virus (A/Ann Arbor/6/1960(H2N2))	1	181	1	182		1
	947939	Influenza A virus (A/aquatic bird/Korea/w44/2005(H7N3))		1		1		
	62446	Influenza A virus (A/Argentina/3779/94(H3N2))		1		1		
	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))	1	5	1	5		
	223931	Influenza A virus (A/Bangkok/10/1983(H1N1))		1		1		
	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))		2		2		
	476294	Influenza A virus (A/Brisbane/10/2007(H3N2))	5		5			
	504904	Influenza A virus (A/Brisbane/59/2007(H1N1))	24	12	26	12	2	
	385587	Influenza A virus (A/budgerigar/Hokkaido/1/1977(H4N6))		4		4		
	641501	Influenza A virus (A/California/04/2009(H1N1))	61	95	62	95	1	
	535852	Influenza A virus (A/California/06/2008(H1N1))		1		1		
	641809	Influenza A virus (A/California/07/2009(H1N1))	7	317	15	317	8	
	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			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	205946	Influenza A virus (A/Chicken/Beijing/1/95(H9N2))		1		1		
	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))		6		6		
	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		
	352348	Influenza A virus (A/chicken/Hong Kong/17/1977(H6N1))		1		1		
X	100835	Influenza A virus (A/Chicken/Hong Kong/258/97 (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		
X	1342397	Influenza A virus (A/chicken/Hong Kong/TP38/2003(H9N2))				3		3
	292039	Influenza A virus (A/chicken/HongKong/SF1/03(H9N2))	1		1			
	292045	Influenza A virus (A/chicken/HongKong/YU427/03(H9N2))	1		1			
	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			
	1403514	Influenza A virus (A/chicken/Jiangsu/x1/2004(H9N2))	7		7			
	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		
	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		5		4	
	996581	Influenza A virus (A/chicken/Shanghai/Q0808-1/2008(H9N2))		1		1		
	404408	Influenza A virus (A/chicken/Shanxi/2/2006(H5N1))	1		1			
	371214	Influenza A virus (A/chicken/Taiwan/O329/01(H6N1))	5		5			
	449656	Influenza A virus (A/chicken/Taiwan/2838V/00(H6N1))	14		15		1	
X	1082519	Influenza A virus (A/chicken/Taixing/10/2010(H9N2))			2		2	
	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		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	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		
X	284190	Influenza A virus (A/Ck/Viet Nam/36/2004(H5N1))			1		1	
	284195	Influenza A virus (A/Ck/YN/115/2004(H5N1))		1		1		
	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			
	1727172	Influenza A virus (A/duck/Bavaria/1/1977(H1N1))		2		2		
	387203	Influenza A virus (A/duck/Bavaria/2/1977(H1N1))		1		1		
	658578	Influenza A virus (A/duck/Beijing/MG0617/2005(H9N2))		1		1		
	383550	Influenza A virus (A/duck/England/1/1956(H11N6))		2		2		
	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))		2		2		
	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		
	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		
	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		
X	510222	Influenza A virus (A/duck/Vietnam/NCVD-9/2007(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	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		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	137578	Influenza A virus (A/England/939/69 x A/PR/8/34)		2		2		
	680689	Influenza A virus (A/England/AV877/1996(H7N7))		1		1		
X	680785	Influenza A virus (A/environment/Hong Kong/156/1997(H5N1))			1		1	
	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			
X	159471	Influenza A virus (A/eq/Sussex/89/(H3N8))			4		4	
	387213	Influenza A virus (A/equine/Alaska/1/1991(H3N8))		1		1		
	475493	Influenza A virus (A/equine/California/8560/2002(H3N8))		2		2		
X	1122279	Influenza A virus (A/equine/Guangxi/3/2011(H9N2))				1		1
	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/Massachusetts/213/2003(H3N8))		1		1		
	387223	Influenza A virus (A/equine/Miami/1963(H3N8))	5		5			
X	475478	Influenza A virus (A/equine/New Market/1/1979(H3N8))			1		1	
	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))		47		47		
	260806	Influenza A virus (A/FPV/Dutch/1927(H7N7))	1		1			
	107558	Influenza A virus (A/France/75/97(H3N2))		1		1		
	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))	1	6	1	6		
	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))		14		14		
	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))		3		3		
	645724	Influenza A virus (A/Hong Kong/01/2009(H1N1))	3		3			
	506350	Influenza A virus (A/Hong Kong/1/1968(H3N2))	8	2	9	2	1	
	130760	Influenza A virus (A/Hong Kong/1073/99(H9N2))	1	25	1	25		
	680690	Influenza A virus (A/Hong Kong/1074/1999(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		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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		
X	715494	Influenza A virus (A/Hong Kong/33982/2009(H9N2))				3		3
	155218	Influenza A virus (A/Hong Kong/482/97(H5N1))	7	1	7	1		
	88104	Influenza A virus (A/Hong Kong/483/1997(H5N1))	3	10	3	10		
	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		
	153969	Influenza A virus (A/Hong Kong/497/97(H3N2))		1		1		
	155225	Influenza A virus (A/Hong Kong/507/97(H5N1))		5		5		
	155226	Influenza A virus (A/Hong Kong/514/97(H5N1))		1		1		
	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))		2		2		
	697610	Influenza A virus (A/India/GWMH05/2009(H1N1))		1		1		
	1081253	Influenza A virus (A/Indiana/08/2011(H3N2))		6		6		
	400788	Influenza A virus (A/Indonesia/5/2005(H5N1))	1	2	1	3		1
	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		4		2	
	400830	Influenza A virus (A/Indonesia/CDC699/2006(H5N1))	2		2			
	472511	Influenza A virus (A/Indonesia/TLL007/2006(H5N1))	1		1			
	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))	4	29	4	29		
	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		
	644289	Influenza A virus (A/Korea/01/2009(H1N1))	3		3			
	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))		5		5		
	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))		7		7		
	383577	Influenza A virus (A/Memphis/1/1990(H3N2))		1		1		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	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		
	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			
	383578	Influenza A virus (A/Memphis/4/1980(H3N2))		1		1		
	383571	Influenza A virus (A/Memphis/6/1986(H3N2))	4		4			
	761251	Influenza A virus (A/Mexico City/WR1704T/2009(H1N1))		1		1		
	887118	Influenza A virus (A/Mexico/UASLP-012/2008(H3N2))		1		1		
	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		
	224819	Influenza A virus (A/Nagasaki/76/98(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		
	251297	Influenza A virus (A/Netherlands/127/03(H7N7))		1		1		
	936115	Influenza A virus (A/Netherlands/18/1994(H3N2))		1		1		
	680693	Influenza A virus (A/Netherlands/219/2003(H7N7))	1		1			
	132884	Influenza A virus (A/Netherlands/458/98 (H3N2))		1		1		
	643212	Influenza A virus (A/Netherlands/602/2009(H1N1))		14		14		
	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	227	5	227	2	
	311695	Influenza A virus (A/New York/124/2001(H3N2))		1		1		
	311775	Influenza A virus (A/New York/205/2001(H1N1))		12		12		
	335358	Influenza A virus (A/New York/232/2004(H3N2))		110		110		
	327205	Influenza A virus (A/New York/348/2003(H1N1))		141		146		5
	335333	Influenza A virus (A/New York/384/2005(H3N2))		62		62		
	335337	Influenza A virus (A/New York/388/2005(H3N2))		14		14		
	342508	Influenza A virus (A/New York/444/2001(H1N1))		24		24		
	342546	Influenza A virus (A/New York/490/2003(H1N2))		1		1		
	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))		3		3		
	384505	Influenza A virus (A/nt/60/1968(H3N2))		68		68		
	155917	Influenza A virus (A/NWS/33HA-A/tern/Australia/G70C/75NA(H1N9))	1		1			
	62503	Influenza A virus (A/Ohio/3/95(H3N2))		1		1		
	1163697	Influenza A virus (A/Oklahoma/309/2006(H3N2))	4	3	4	3		
	223935	Influenza A virus (A/Okuda/1957(H2N2))	1	9	1	9		
	754366	Influenza A virus (A/Ontario/309862/2009(H1N1))	1		1			
	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))		4		4		
	137886	Influenza A virus (A/parakeet/Narita/92A/98(H9N2))		2		2		
	11448	Influenza A virus (A/parrot/Ulster/73(H7N1))		1		1		
	654811	Influenza A virus (A/Perth/16/2009(H3N2))	1		1			
	382825	Influenza A virus (A/Philippines/2/1982(H3N2))		1	1	1	1	
	385624	Influenza A virus (A/Port Chalmers/1/1973(H3N2))	7	1	7	1		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B 14	T 14	B 15	T 15	D B	D T
	385600	Influenza A virus (A/Puerto Rico/8/1934(Cambridge))(H1N1))	1		1			
	211044	Influenza A virus (A/Puerto Rico/8/1934(H1N1))	29	424	30	451	1	27
	183764	Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))	7	98	7	99		1
	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			
	682728	Influenza A virus (A/Quebec/144147/2009(H1N1))	10		10			
	411167	Influenza A virus (A/Queensland/11/2001(H3N2))		1		1		
	647923	Influenza A virus (A/reassortant/NYMC X-179A(California/07/2009 x NYMC X-157)(H1N1))	7		7			
	286239	Influenza A virus (A/red knot/Delaware/2561/1987(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		
	715091	Influenza A virus (A/Roma/ISS1941/2009(H1N1))		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		
	1144025	Influenza A virus (A/Shandong/9/1993(H3N2))	13		13			
	62512	Influenza A virus (A/Shangdong/5/94(H3N2))		1		1		
X	1332244	Influenza A virus (A/Shanghai/02/2013(H7N9))			1		1	
	383568	Influenza A virus (A/Shanghai/11/1987(H3N2))		1		1		
	1093545	Influenza A virus (A/shorebird/Delaware Bay/277/2000(H9N7))		1		1		
	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))		5		5		
	382781	Influenza A virus (A/Singapore/1/1957(H2N2))	1	31	1	31		
	1331560	Influenza A virus (A/Singapore/H2011.447/2011(H3N2))	1		1			
	742305	Influenza A virus (A/slaty-backed gull/Japan/6KS0185/2006(H4N8))		1		1		
	464623	Influenza A virus (A/Solomon Islands/3/2006(H1N1))	2		6		4	
	59375	Influenza A virus (A/South Carolina/1/1918(H1N1))	8	1	8	1		
	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		
X	614035	Influenza A virus (A/swine/Belgium/1/1998(H1N1))			1		1	
	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		
	168278	Influenza A virus (A/swine/Finistere/127/99(H3N2))		4		4		
	1068705	Influenza A virus (A/swine/Guangdong/221/2009(H1N1))		1		1		
	522740	Influenza A virus (A/swine/Hannover/1/1981(H1N1))		12		12		
	915014	Influenza A virus (A/swine/Heilongjiang/44/2009(H1N1))	1		1			
	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		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	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))		12		12		
	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))		15		15		
	1176042	Influenza A virus (A/swine/Italy/1513-1/1998(H1N1))		1		1		
	169166	Influenza A virus (A/swine/Italy/1521/98(H1N2))		4		4		
	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))		4		4		
	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))		2		2		
	986174	Influenza A virus (A/swine/Korea/4382/2009(H1N2))		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		
	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		
	1171336	Influenza A virus (A/swine/Nebraska/A01116984/2011(H3N2))		1		1		
	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		
X	292590	Influenza A virus (A/swine/Ontario/42729A/01(H3N3))			1		1	
	55532	Influenza A virus (A/swine/Quebec/1192/1986(H1))		1		1		
	172149	Influenza A virus (A/swine/Quebec/192/81(H1N1))	1		1			
	83206	Influenza A virus (A/swine/Scotland/410440/94(H1N2))		5		5		
	332747	Influenza A virus (A/swine/Tennessee/25/1977(H1N1))	1		1			
	1470614	Influenza A virus (A/swine/Thailand/CU-S3673N/2012(H3N2))		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		
	380964	Influenza A virus (A/Texas/36/1991(H1N1))		1		1		
X	266827	Influenza A virus (A/Thailand/1(KAN-1)/2004(H5N1))			3		3	
	414044	Influenza A virus (A/Thailand/1(KAN-1A)/2004(H5N1))	1		1			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	411157	Influenza A virus (A/Thailand/271/2005(H1N1))	1		1			
	270945	Influenza A virus (A/Thailand/4(SP-528)/2004(H5N1))		21		21		
	908203	Influenza A virus (A/Thailand/CU-H126/2009(H1N1))		1		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))		5		5		
	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		
	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))		1		1		
	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))		4		4		
	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))		5		5		
	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))	45	8	45	9		1
	284218	Influenza A virus (A/Viet Nam/1203/2004(H5N1))	66	123	69	123	3	
	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))	11	4	12	4	1	
	357210	Influenza A virus (A/Vietnam/CL100/2004(H5N1))	1		1			
	357208	Influenza A virus (A/Vietnam/CL26/2004(H5N1))		78		79		1
	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		
	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))		110		110		
	157642	Influenza A virus (A/Wisconsin/10/1998(H1N1))		1		1		
	380346	Influenza A virus (A/Wisconsin/3523/1988(H1N1))	2		2			
	461772	Influenza A virus (A/Wisconsin/43/2006(H3N2))	1		1			
	380979	Influenza A virus (A/Wisconsin/4754/1994(H1N1))		1		1		
	380978	Influenza A virus (A/Wisconsin/4755/1994(H1N1))		5		5		
	393902	Influenza A virus (A/Wisconsin/67/2005(H3N2))	1	5	1	5		
	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))		8		8		
	432094	Influenza A virus (A/Wyoming/3/2003-X-147(H3N2))		1		1		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	430417	Influenza A virus (A/Wyoming/3e5/2003(H3))	1		1			
	132504	Influenza A virus (A/X-31(H3N2))	77	189	77	189		
	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		
	255682	Influenza A virus (A/Yokohama/47/2002(H1N2))		1		1		
	11408	Influenza A virus (STRAIN A/EQUINE/NEW MARKET/76)		1		1		
	41857	Influenza A virus H3N2	1	47	1	49		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		
	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		
	604436	Influenza B virus (B/Brisbane/60/2008)	2		2			
	107406	Influenza B virus (B/Chiba/447/98)		1		1		
	461739	Influenza B virus (B/Florida/4/2006)	1		1			
	206203	Influenza B virus (B/Hong Kong/330/2001)		23		23		
	427826	Influenza B virus (B/Hong Kong/8/1973)		1		1		
	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			
	518987	Influenza B virus (B/Lee/1940)	5	3	5	3		
	464417	Influenza B virus (B/Malaysia/2506/2004)	1		1			
	289338	Influenza B virus (B/Nanchang/12/98)		1		1		
	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		
	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			
X	224197	Influenza C virus (C/Nara/1/85)				1		1
	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		11			1

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	313589	Janibacter sp. HTCC2649		1		1		
	11072	Japanese encephalitis virus	39	74	40	74	1	
	1000444	Japanese encephalitis virus CH2195LA	1		1			
	1000445	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	6	1	6	1		
	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	35	7	39	6	4
	10001762	JC polyomavirus strain MAD1		1		1		
	16719	Juglans nigra	1		1			
	51240	Juglans regia	34		34	17		17
	11619	Junin mammarenavirus	3	872	3	872		
	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		
	151250	Kali turgidum		22		22		
	122291	Kappapapillomavirus 1	2		2			
	10623	Kappapapillomavirus 2	5	7	5	7		
	156230	Karenia brevis	1		1			
	42894	Khabarovsk virus		1		1		
	10638	Kilham polyomavirus		1		1		
	266940	Kineococcus radiotolerans SRS30216 = ATCC BAA-149		2		2		
	452652	Kitasatospora setae KM-6054		1		1		
	573	Klebsiella pneumoniae	23	8	23	8		
	272620	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	28		28			
	484021	Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044		1		1		
X	749535	Klebsiella sp. MS 92-3				1		1
	28448	Komagataeibacter xylinus		1		1		
X	11092	Kumlinge virus			26		26	
	11077	Kunjin virus	11	1	12	1	1	
	11078	Kunjin virus (STRAIN MRM61C)		4		4		
	11577	La Crosse virus	2	1	2	1		
	11578	La Crosse virus L74		2		2		
	8753	Lachesis muta muta	21		21			
	658655	Lachnospiraceae bacterium 1_4_56FAA		1		1		
	300015	Lactate dehydrogenase elevating virus C	1		1			
	300016	Lactate dehydrogenase elevating virus Plagemann	1		1			
	11048	Lactate dehydrogenase-elevating virus	14		14			
X	1604	Lactobacillus amylovorus				1		1
	219334	Lactobacillus casei subsp. casei ATCC 393	2		2			
X	28038	Lactobacillus curvatus				1		1
	1585	Lactobacillus delbrueckii subsp. bulgaricus	1		1			
	10001913	Lactobacillus johnsonii JCM 1022	3		3			
	557433	Lactobacillus reuteri JCM 1112	3		3			
X	1599	Lactobacillus sakei				1		1
	1358	Lactococcus lactis		5		5		
	100641	Lactococcus lactis phage p2	2		2			
	35345	Lactococcus phage TP901-1	3		3			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	9519	Lagothrix lagotricha	1		1			
	61172	Laguna Negra virus		12		12		
	378830	Lake Victoria marburgvirus - Angola2005	6	18	6	18		
	33728	Lake Victoria marburgvirus - Popp	2	14	2	14		
	35258	Lambdapapillomavirus 2		25		25		
	80365	Laminaria digitata	2		2			
	11085	Langat virus		1		1		
	136371	Lasallia papulosa	1		1			
	11620	Lassa mammarenavirus	13	670	13	670		
	11621	Lassa virus GA391		47		47		
	11622	Lassa virus Josiah		387		387		
	6925	Latrodectus tredecimguttatus		1		1		
	85223	Laurus nobilis		1		1		
X	316068	Leadbetterella byssophila				1		1
	69245	Lechiguanas virus		9		9		
	661367	Legionella longbeachae NSW150		1		1		
	1498499	Legionella norrlandica		1		1		
	446	Legionella pneumophila		1		1		
	272624	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	1		1			
	5658	Leishmania	2		2			
	5667	Leishmania aethiopica	16		16			
	5659	Leishmania amazonensis		15		15		
	5660	Leishmania braziliensis	6		6			
	420245	Leishmania braziliensis MHOM/BR/75/M2904	11		14	8	3	8
	44271	Leishmania chagasi	3		3			
	5661	Leishmania donovani	15	41	15	41		
	99875	Leishmania donovani donovani	1		1			
	10000341	Leishmania donovani donovani 1S2D	1		1			
	5671	Leishmania infantum	96	4	97	4	1	
	435258	Leishmania infantum JPCM5	28	5	28	5		
	10000345	Leishmania infantum LEM 75	14		14			
	5664	Leishmania major	16	124	17	124	1	
	347515	Leishmania major strain Friedlin	29	25	29	38		13
	5665	Leishmania mexicana	2	3	2	3		
	929439	Leishmania mexicana MHOM/GT/2001/U1103		1		1		
	5679	Leishmania panamensis	3	7	3	7		
	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		
	211882	Leptospira interrogans serovar Australis	2		2			
	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		
X	29507	Leptospira kirschneri			1		1	
	10000847	Leptospira sp. Akiyami A AUT10	1		1			
	1245	Leuconostoc mesenteroides	1		1			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	6850	Limulus polyphemus		1		1		
	1641	Listeria grayi		1		1		
	1642	Listeria innocua	2	3	2	3		
	1638	Listeria ivanovii	1	1	1	1		
	1639	Listeria monocytogenes	18	90	19	93	1	3
	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	64	5	64		
	393128	Listeria monocytogenes F6900		1		1		
	393117	Listeria monocytogenes FSL J1-194		2		2		
	393124	Listeria monocytogenes FSL N3-165		2		2		
	393125	Listeria monocytogenes FSL R2-503		1		1		
	393126	Listeria monocytogenes FSL R2-561		1		1		
	552536	Listeria monocytogenes HCC23		2		2		
	401650	Listeria monocytogenes HPB2262		3		3		
	393130	Listeria monocytogenes J0161		6		6		
	267409	Listeria monocytogenes serotype 1/2a str. F6854		3		3		
	568819	Listeria monocytogenes serotype 4b str. CLIP 80459		6		6		
	265669	Listeria monocytogenes serotype 4b str. F2365		6		6		
	267410	Listeria monocytogenes serotype 4b str. H7858		25		25		
	386043	Listeria welshimeri serovar 6b str. SLCC5334		3		3		
	6299	Litomosoides carinii	3		3			
	6689	Litopenaeus vannamei	118		140		22	
	217686	Little cherry virus 1		1		1		
	4522	Lolium perenne	36	121	36	121		
	36386	Louping ill virus (strain 31)	1		1			
	58216	Loxosceles gaucho	1		1			
	58218	Loxosceles intermedia	14		14			
	58217	Loxosceles laeta	2		2			
	11623	Lymphocytic choriomeningitis mammarenavirus	3	644	4	649	1	5
	11624	Lymphocytic choriomeningitis virus (strain Armstrong)		1143		1143		
	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)		61		61		
	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	2	3	2	3		
	9544	Macaca mulatta	2	5	2	5		
	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		24		24		
	11628	Machupo mammarenavirus		800		800		
	10001615	Machupo virus strain Carvalho		1		1		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
X	35725	<i>Macrophomina phaseolina</i>				1		1
	1126212	<i>Macrophomina phaseolina</i> MS6		1		1		
	9322	<i>Macropus</i> sp.	1		1			
	431944	<i>Magnetosporium gryphiswaldense</i> MSR-1		1		1		
	272627	<i>Magnetosporium magnetotacticum</i> MS-1		4		4		
	76777	<i>Malassezia sympodialis</i>	1		1			
	3750	<i>Malus domestica</i>	27	38	27	48		10
	1239567	Mamastrovirus 3	2		2			
	40674	Mammalia	2		2			
	351073	Mammalian orthoreovirus		1		1		
	7130	<i>Manduca sexta</i>		3		3		
	29780	<i>Mangifera indica</i>	1		1			
	45201	<i>Mannheimia haemolytica</i> serotype 1	82		82			
	221988	<i>Mannheimia succiniciproducens</i> MBEL55E		2		2		
	11269	Marburg marburgvirus	1	95	1	95		
	33727	Marburg virus - Musoke, Kenya, 1980	3	84	3	84		
X	1006	<i>Marivirga tractuosa</i>				1		1
	38020	marmosets	3		3			
	11234	Measles virus	63	38	63	39		1
	10000462	Measles virus CAM/RB		1		1		
	262307	Measles virus genotype A	4		4			
	171264	Measles virus genotype D3	1		1			
	11235	Measles virus strain Edmonston	167	210	167	210		
	70146	Measles virus strain Edmonston-B	2	13	2	78		65
	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	<i>Megathura crenulata</i>	1		1			
	9103	<i>Meleagris gallopavo</i>	3		3			
	152219	Menangle virus	2		2			
	12107	Mengo virus	5	13	5	13		
	493803	Merkel cell polyomavirus		2	2	2	2	
	10036	<i>Mesocricetus auratus</i>	55		56		1	
	243232	<i>Methanocaldococcus jannaschii</i> DSM 2661	2	2	3	2	1	
	39152	<i>Methanococcus maripaludis</i>	1		1			
	187420	<i>Methanothermobacter thermautotrophicus</i> str. Delta H		2		2		
	420662	<i>Methylibium petroleiphilum</i> PM1		1		1		
X	1270	<i>Micrococcus luteus</i>			2		2	
	38832	Micromonas		1		1		
	1464048	<i>Micromonospora parva</i>		1		1		
X	313606	<i>Microscilla marina</i> ATCC 23134				1		1
X	54390	<i>Micrurus corallinus</i>			116		116	
X	1335626	Middle East respiratory syndrome coronavirus			4		4	
	10793	Mink enteritis virus strain Abashiri	1		1			
	467144	Modified Vaccinia Ankara virus		21		22		1
	11801	Moloney murine leukemia virus		5		5		
	10244	Monkeypox virus	5	2	5	2		
	13616	<i>Monodelphis domestica</i>	1	4	1	4		
	1000585	Montano virus	3		3			
	264732	<i>Moorella thermoacetica</i> ATCC 39073		1		1		
	300180	Mopeia Lassa virus reassortant 29		4		4		
	11629	Mopeia mammarenavirus		14		14		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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		6		3	
	334203	Mupapillomavirus 1	1	37	1	38		1
	10366	Murid herpesvirus 1	2	49	2	52		3
	10000411	Murid herpesvirus 1 deltaMS94.5		2		2		
	10000412	Murid herpesvirus 1 Isolate G4		1		1		
	10000413	Murid herpesvirus 1 Isolate K6		1		1		
	33708	Murid herpesvirus 4	1	52	1	53		1
	10000536	Murid herpesvirus 4 G2.4		3		3		
	10000537	Murid herpesvirus 4 WUMS		3		19		16
	1440122	Murid herpesvirus 68		2		2		
	10530	Murine adenovirus 1	1	2	1	2		
	69156	Murine cytomegalovirus (strain K181)	2	14	2	14		
	10367	Murine cytomegalovirus (strain Smith)		32		32		
	10001396	Murine cytomegalovirus (strain Smith) MW97.01		5		5		
	35275	Murine endogenous retrovirus		13		13		
	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	16		1
	11786	Murine leukemia virus	1	16	1	23		7
	10001207	Murine leukemia virus LP-BM5		1		1		
	223997	Murine norovirus 1	4		4	1		1
	10002026	Murine norovirus 1 Mu/NoV/GV/MNV1/2002/USA		1		1		
	463722	Murine norovirus GV/CR6/2005/USA		1		1		
	11263	Murine pneumonia virus		14		14		
	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	8	21	8		
	301478	Murray valley encephalitis virus (strain MVE-1-51)	11	14	11	14		
	10090	Mus musculus	596	4159	615	6526	19	2367
	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		11		9
	57486	Mus musculus molossinus		1		1		
X	763552	Mus musculus papillomavirus type 1				1		1
	4641	Musa acuminata	50	1	50	1		
	214697	Musa acuminata AAA Group	1		1			
	37325	Muscovy duck parvovirus	4		4			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	10001918	Muscovy duck reovirus S12	2		2			
	9666	Mustela lutreola	1		1			
	1763	Mycobacterium	3	15	3	15		
	36809	Mycobacterium abscessus		18		19		1
	1198627	Mycobacterium abscessus subsp. bolletii str. GO 06		1		1		
	1764	Mycobacterium avium	6	13	6	13		
	243243	Mycobacterium avium 104		43		43		
	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	101	13	104	13	3	
	262316	Mycobacterium avium subsp. paratuberculosis K-10	3	57	4	58	1	1
	10000328	Mycobacterium avium subsp. paratuberculosis Strain Ben		1		1		
	1765	Mycobacterium bovis	48	130	48	130		
	233413	Mycobacterium bovis AF2122/97		50		50		
	10000322	Mycobacterium bovis AN5	9	28	9	28		
	33892	Mycobacterium bovis BCG	12	146	12	146		
	410289	Mycobacterium bovis BCG str. Pasteur 1173P2	1	229	1	229		
	10000323	Mycobacterium bovis T/91/1378		6		6		
	1774	Mycobacterium chelonae	1		1			
	1041522	Mycobacterium colombiense CECT 3035		20		20		
	1766	Mycobacterium fortuitum		1		1		
	144549	Mycobacterium fortuitum subsp. fortuitum		1		1		
	10000331	Mycobacterium gastri W471	1		1			
X	1804	Mycobacterium gilvum				1		1
	350054	Mycobacterium gilvum PYR-GCK		64		64		
	278137	Mycobacterium gilvum Spyr1		53		53		
	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	409	119	410		1
	272631	Mycobacterium leprae TN		30		30		
X	1781	Mycobacterium marinum				1		1
	216594	Mycobacterium marinum M		29		29		
X	1795	Mycobacterium neoaurum				1		1
	525368	Mycobacterium parascrofulaceum ATCC BAA-614		35		35		
	43304	Mycobacterium peregrinum	2		2			
	1771	Mycobacterium phlei		1		1		
	1783	Mycobacterium scrofulaceum	4		4			
	875328	Mycobacterium sinense		10		10		
	1772	Mycobacterium smegmatis		2		2		
	246196	Mycobacterium smegmatis str. MC2 155		61		61		
	164757	Mycobacterium sp. JLS		77		77		
	189918	Mycobacterium sp. KMS		69		69		
	164756	Mycobacterium sp. MCS		73		73		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	1380386	Mycobacterium sp. URHB0044		1		1		
	1773	Mycobacterium tuberculosis	502	2095	525	2173	23	78
	10000329	Mycobacterium tuberculosis 103	1		1			
	348776	Mycobacterium tuberculosis C		176		176		
	83331	Mycobacterium tuberculosis CDC1551		39		42		3
	336982	Mycobacterium tuberculosis F11		24		24		
	419947	Mycobacterium tuberculosis H37Ra		111		130		19
	83332	Mycobacterium tuberculosis H37Rv	56	843	58	861	2	18
	652616	Mycobacterium tuberculosis str. Erdman = ATCC 35801	15	19	15	19		
	395095	Mycobacterium tuberculosis str. Haarlem		127		127		
	182785	Mycobacterium tuberculosis subsp. tuberculosis		1		1		
	75922	Mycobacterium tusciae		2		2		
	1809	Mycobacterium ulcerans		7		8		1
	362242	Mycobacterium ulcerans Agy99		16		16		
	350058	Mycobacterium vanbaalenii PYR-1		55		55		
	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	1	8	1		
	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			
	57372	Mycoplasma suis	3		3			
	13618	Myrmecia pilosula	2		2			
X	76832	Myroides odoratimimus				1		1
X	83455	Myxococcus stipitatus				1		1
	1278073	Myxococcus stipitatus DSM 14675		1		1		
	246197	Myxococcus xanthus DK 1622		1		1		
	10273	Myxoma virus		4		4		
X	744533	Naegleria gruberi strain NEG-M			1		1	
	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		5		5		
	485	Neisseria gonorrhoeae	24	11	25	11	1	
	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	62	23	83	23	21	
	272831	Neisseria meningitidis FAM18	1		1			
	909420	Neisseria meningitidis H44/76	1		1			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	10001560	Neisseria meningitidis M982B	2		2			
	122586	Neisseria meningitidis MC58	17		17			
	65699	Neisseria meningitidis serogroup A	5		5			
	10001051	Neisseria meningitidis serogroup A Strain 8659	1		1			
	491	Neisseria meningitidis serogroup B	40	1	40	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			
X	10001860	Neisseria meningitidis serogroup X			3		3	
	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		
	44755	New York virus		2		2		
	11176	Newcastle disease virus	14	4	14	5		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			
	4097	Nicotiana tabacum	1		5		4	
	1285600	Nile crocodilepox virus		2		2		
	121791	Nipah virus	5		5			
	314278	Nitrococcus mobilis Nb-231		1		1		
	37329	Nocardia farcinica		1		1		
	37333	Nocardia transvalensis		1		1		
X	280240	Nocardiopsis baichengensis			1		1	
X	239984	Nocardiopsis ganjiahuensis				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 GI.1	1		1			
	122928	Norovirus GI	2		2			
	647514	Norovirus GI.1	1		1			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	647515	Norovirus GI.2	1		1			
	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	2	1	2		
	508775	Norovirus GII.9	1	1	1	1		
	524364	Norovirus Hu/1968/US	1	1	1	1		
	1286616	Norovirus Hu/GII.3/693/425/2008/AU	6		6			
	1182144	Norovirus Hu/GII.4/Minerva/2006/USA	2		2			
	1156983	Norovirus Hu/GII.4/Minerva/CS1258/2006/USA	1		1			
X	1241973	Norovirus Hu/GII.4/Sydney/NSW0514/2012/AU			1		1	
	588533	Norovirus Hu/GII/GZ-1/2008/CHN	1		1			
X	546980	Norovirus Hu/GII-4/Saga1/2006/JP			1		1	
X	489822	Norovirus Hu/Houston/TCH186/2002/US			2		2	
	150080	Norovirus isolates	1		1			
	11983	Norwalk virus	2	1	4	1	2	
	63737	Nostoc punctiforme PCC 73102		2		2		
	8663	Notechis scutatus	2		2			
X	48935	Novosphingobium aromaticivorans				1		1
	8996	Numida meleagris	1		1			
	9978	Ochotona princeps		1		1		
X	9874	Odocoileus virginianus			1		1	
X	1005962	Ogataea parapolyomorpha				1		1
	871575	Ogataea parapolyomorpha DL-1		1		1		
	4146	Olea europaea	70	19	70	19		
	42764	Oliveros mammaronavirus		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		
X	265619	Ornithodoros erraticus			22		22	
X	6938	Ornithodoros moubata			20		20	
	9258	Ornithorhynchus anatinus		1		1		
	9986	Oryctolagus cuniculus	52	9	53	10	1	1
X	4530	Oryza sativa			2		2	
	39947	Oryza sativa Japonica Group	5	1	5	1		
	8090	Oryzias latipes	1	1	1	1		
	34862	Otospermophilus beecheyi		1		1		
	28869	Ovine respiratory syncytial virus	1		1			
	9940	Ovis aries	91	17	91	17		
	8667	Oxyuranus scutellatus scutellatus	4		4			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
X	324057	Paenibacillus sp. JDR-2			1		1	
	9597	Pan paniscus		1		1		
	9598	Pan troglodytes	7	23	7	25		2
	188763	Panine herpesvirus 2		3		3		
	59538	Pantholops hodgsonii		1		1		
	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 mammarenavirus		1		1		
	33127	Parietaria judaica	65	2	65	2		
	13187	Parietaria officinalis	2		2			
	147272	Paspalum notatum		16		16		
	747	Pasteurella multocida		10	1	10	1	
	272843	Pasteurella multocida subsp. multocida str. Pm70		5		5		
	10000759	Pasteurella multocida X-73	2		2			
	554	Pectobacterium carotovorum	2		2			
	1254	Pediococcus acidilactici	1		1			
	338966	Pelobacter propionicus DSM 2379		3		3		
	6687	Penaeus monodon	10	4	10	23		19
	5076	Penicillium chrysogenum	45	19	45	19		
	5077	Penicillium citrinum	13		13			
	1496	Peptoclostridium difficile	53		53			
X	1169127	Peptoclostridium difficile genomovar ribotype_087			1		1	
	69248	Pergamino virus		1		1		
	6978	Periplaneta americana	10	3	13	3	3	
	31276	Perkinsus marinus		1		1		
	31604	Peste-des-petits-ruminants virus	13	1	13	1		
	10001020	Peste-des-petits-ruminants virus (strain Nigeria 75/1)		1		1		
X	10002123	Peste-des-petits-ruminants virus China/Tibet/Geg/07-30			31		31	
X	97097	Phaethon lepturus				1		1
	28479	Phalaris aquatica		12		12		
	3885	Phaseolus vulgaris	5	1	5	1		
	9057	Phasianus colchicus colchicus	1		1			
	15957	Phleum pratense	58	1127	59	1129	1	2
	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		
	121723	Photobacterium sp. SKA34		1		1		
	72539	Physalis mottle virus	2		2			
	9755	Physeter catodon	1	31	1	32		1
	11630	Pichinde mammarenavirus		10		10		
	10001618	Pichinde virus strain Munchique		1		1		
	3318	Pinaceae	2		2			
	3352	Pinus taeda	4		4			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	60876	Pixuna virus		1		1		
	39414	Plantago lanceolata		2		2		
	2439	Plasmid ColB2	1		1			
	2465	Plasmid F	1		1			
	5820	Plasmodium	4	5	4	5		
	5821	Plasmodium berghei	14	49	14	49		
	5823	Plasmodium berghei ANKA	7	11	7	11		
	10000356	Plasmodium berghei NK65	2	2	2	2		
	5824	Plasmodium brasilianum	2		2			
	5825	Plasmodium chabaudi	4	4	4	4		
	10000357	Plasmodium chabaudi adami DS	2	37	2	37		
	31271	Plasmodium chabaudi chabaudi		3		3		
	5827	Plasmodium cynomolgi	2		2			
	5833	Plasmodium falciparum	690	803	730	804	40	1
	10000358	Plasmodium falciparum 366		1		1		
	36329	Plasmodium falciparum 3D7	163	209	168	209	5	
	57266	Plasmodium falciparum 7G8	42	50	42	50		
	10000363	Plasmodium falciparum Brazil-608	1	1	1	1		
	5835	Plasmodium falciparum CAMP/Malaysia	36	2	36	2		
	5836	Plasmodium falciparum CDC/Honduras	18		18			
	5837	Plasmodium falciparum FC27/Papua New Guinea	43	60	47	60	4	
	10000366	Plasmodium falciparum FCB-2	1		1			
	5838	Plasmodium falciparum FCR-3/Gambia	94		94			
	10000369	Plasmodium falciparum FVO		5		5		
	10000371	Plasmodium falciparum Indochina I/CDC	32		32			
	10002007	Plasmodium falciparum isolate UAS22	4		4			
	10002009	Plasmodium falciparum isolate UAS29	2		2			
	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	38		38			
	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	8	7	1	
	5852	Plasmodium knowlesi strain Nuri		3		3		
	5858	Plasmodium malariae	1		1			
	5854	Plasmodium reichenowi		2		2		
	5859	Plasmodium simium	2		2			
	5855	Plasmodium vivax	95	147	98	147	3	
	10000378	Plasmodium vivax NK		2		2		
X	1035514	Plasmodium vivax North Korean			1		1	

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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.	3		3			
	5861	Plasmodium yoelii	17	38	17	38		
	73239	Plasmodium yoelii yoelii	22	31	22	31		
	352914	Plasmodium yoelii yoelii 17XNL	6	3	6	3		
	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		
	703	Plesiomonas shigelloides		2		2		
	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	35	34	35		
	365044	Polaromonas naphthalenivorans CJ2		2		2		
	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		2		2		
	9600	Pongo pygmaeus		2		2		
	46221	Porcine circovirus		49		49		
	10001964	Porcine circovirus 1 strain 1/G	7		7			
	10001881	Porcine circovirus 2 -A	3		3			
	10001239	Porcine circovirus strain ISU31	7		7			
	85709	Porcine circovirus type 2-B	2		2			
	133704	Porcine circovirus-1	5		5			
	85708	Porcine circovirus-2	27		27			
	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			
	10002000	Porcine epidemic diarrhea virus CH/SHH/06	1		1			
	229032	Porcine epidemic diarrhea virus CV777	4		5		1	
	10796	Porcine parvovirus	37		40		3	
	28344	Porcine reproductive and respiratory syndrome virus	80	34	85	34	5	
	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	4	1	4	1		
X	10002089	Porcine reproductive and respiratory syndrome virus SY0608			17		17	
	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			
	10915	Porcine rotavirus (SEROTYPE 5 / STRAIN OSU)	1		1			
	10919	Porcine rotavirus (STRAIN YM)	2	1	2	1		
	101350	Porcine rotavirus strain A253	2		2			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B 14	T 14	B 15	T 15	D B	D T
	10917	Porcine rotavirus strain Gottfried	2		2			
	53179	Porcine rubulavirus	3		3			
	1225860	Porcine torque teno virus 1	2		2			
	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	84	20	87	21	3	1
	10001079	Porphyromonas gingivalis 381	71	55	71	55		
	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			
	12216	Potato virus Y	1		2		1	
X	12219	Potato virus Y strain N			1		1	
	12220	Potato virus Y strain O	6		7		1	
	11083	Powassan virus		3		3		
	28130	Prevotella disiens		1		1		
	93058	Prochlorococcus marinus str. MIT 9202	1		1			
X	1747	Propionibacterium acnes				1		1
	765103	Propionibacterium acnes HL030PA1		1		1		
	1752	Propionibacterium freudenreichii subsp. shermanii		1		1		
	11603	Prospect Hill virus	1	2	1	2		
	290512	Prosthecochloris aestuarii DSM 271		1		1		
	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	21		21			
	36596	Prunus armeniaca	4		4			
	42229	Prunus avium	3	1	3	1		
	3758	Prunus domestica	4		4			
	3755	Prunus dulcis	19		19			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B 14	T 14	B 15	T 15	D B	D T
	3760	Prunus persica	18	51	18	51		
	8671	Pseudechis porphyriacus	3		3			
	342610	Pseudoalteromonas atlantica T6c		1		1		
X	549169	Pseudogulbenkiania ferrooxidans				1		1
	286	Pseudomonas	1		1			
	287	Pseudomonas aeruginosa	76	55	77	122	1	67
	350703	Pseudomonas aeruginosa 2192		2		2		
	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		12		12		
	10000725	Pseudomonas aeruginosa PAK	7	3	7	3		
	10000815	Pseudomonas aeruginosa PAO	2	2	2	2		
	208964	Pseudomonas aeruginosa PAO1	1	5	1	5		
	10001519	Pseudomonas aeruginosa serotype O11	1		1			
	208963	Pseudomonas aeruginosa UCBPP-PA14		23		23		
	237609	Pseudomonas alkylphenolia		1		1		
	129138	Pseudomonas amygdali pv. morsprunorum	2		2			
	384676	Pseudomonas entomophila L48		1		1		
	294	Pseudomonas fluorescens		4		4		
	300	Pseudomonas mendocina		1		1		
	10879	Pseudomonas phage phi6	7		7			
X	122355	Pseudomonas psychrophila			1			1
	303	Pseudomonas putida	1	8	1	8		
	351746	Pseudomonas putida F1		6		6		
	76869	Pseudomonas putida GB-1		1		1		
	319	Pseudomonas savastanoi pv. phaseolicola	1		1			
	264730	Pseudomonas savastanoi pv. phaseolicola 1448A		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			
	10001700	Pseudomonas syringae pv. morsprunorum str. CFBP 1650	1		1			
	10001698	Pseudomonas syringae pv. morsprunorum str. GSPB 883	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		
X	571800	Psychrobacter sp. G			1			1
	11604	Puumala virus	32	20	32	20		
	10000485	Puumala virus (STRAIN HALLNAS B1) Vranica/Hallnas	4		4			
	10001238	Puumala virus (strain Umea/hu)	1		1			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	1337063	Puumala virus bank vole/CG1820/Russia/1984		1		1		
	10000483	Puumala virus CG18-20	4		4			
	11605	Puumala virus Hallnas B1		1		1		
	10000484	Puumala virus Kazan	26	7	26	7		
	39002	Puumala virus sotkamo/v-2969/81	196		196			
	272844	Pyrococcus abyssi GE5		1		1		
	114742	Pythium insidiosum	2		2			
	3513	Quercus alba		5		5		
	10000507	Rabbit hemorrhagic disease virus Olot/89	1		1			
	32606	Rabbitpox virus		2		2		
	11292	Rabies virus	10	14	11	14	1	
	11293	Rabies virus AVO1		3		3		
	10000467	Rabies virus CVS	14		14			
	11294	Rabies virus CVS-11	2		2			
	11295	Rabies virus ERA	6	27	6	27		
	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		
	381666	Ralstonia eutropha H16		1		1		
	3726	Raphanus sativus	1		1			
	10114	Rattus	8		8			
	10116	Rattus norvegicus	226	493	230	577	4	84
	10001133	Rattus norvegicus DA		3		3		
	10000662	Rattus norvegicus Lewis		1		1		
	10001412	Rattus norvegicus Wistar-Furth		11		11		
	10117	Rattus rattus		1		1		
	378809	Ravn virus - Ravn, Kenya, 1987		32	1	32	1	
	48483	Reclinomonas americana		1		1		
	314283	Reinekea blandensis MED297		1		1		
	1646	Renibacterium salmoninarum	12		12			
	10891	Reovirus sp.		2		2		
	12814	Respiratory syncytial virus	3	13	3	13		
	186539	Reston ebolavirus	1	11	1	11		
	129003	Reston ebolavirus - Reston	2	27	2	27		
	386032	Reston ebolavirus - Reston (1989)		4		4		
	11636	Reticuloendotheliosis virus		5		5		
	10001999	Reticuloendotheliosis virus strain HLJ071	1		1			
	103930	Rhesus cytomegalovirus strain 68-1		5		5		
	10969	Rhesus rotavirus	10	1	10	1		
	10002082	Rhesus rotavirus MMU 18006		3		3		
	34631	Rhipicephalus appendiculatus	1		1			
	60189	Rhipicephalus decoloratus	5		5			
	34632	Rhipicephalus sanguineus	1		1			
	384	Rhizobium leguminosarum		1		1		
X	1035271	Rhizobium nepotum				1		1
	1063	Rhodobacter sphaeroides		1		1		
	272943	Rhodobacter sphaeroides 2.4.1		1		1		
	349101	Rhodobacter sphaeroides ATCC 17029		1		1		
	43767	Rhodococcus equi	18	1	18	2		1

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	1833	Rhodococcus erythropolis		1		2		1
	1828	Rhodococcus fascians		1		2		1
	1830	Rhodococcus ruber		1		1		
	1268303	Rhodococcus sp. AW25M09		1	1	1	1	
X	1076	Rhodopseudomonas palustris				2		2
	316056	Rhodopseudomonas palustris BisB18		1		1		
	4012	Rhus		1		1		
	3988	Ricinus communis	44	4	44	4		
	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 URRWXCa2		7		7		
	35791	Rickettsia massiliae		1		1		
	416276	Rickettsia massiliae MTU5		2		2		
	782	Rickettsia prowazekii		21		21		
	272947	Rickettsia prowazekii str. Madrid E		10		10		
	783	Rickettsia rickettsii		1		1		
	452659	Rickettsia rickettsii str. Iowa		1		1		
	392021	Rickettsia rickettsii str. 'Sheila Smith'		3		3		
	35793	Rickettsia sibirica		4		4		
	272951	Rickettsia sibirica 246		27		27		
	785	Rickettsia typhi		3		3		
	257363	Rickettsia typhi str. Wilmington		6		6		
	11588	Rift Valley fever virus	5	27	5	27		
	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			
	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	81	96	81	96		
	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		
	203119	Ruminiclostridium thermocellum ATCC 27405		1		1		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	1265	Ruminococcus flavefaciens		1		1		
X	106	Runella slithyformis				1		1
	761193	Runella slithyformis DSM 19594		1		1		
	159479	Saaremaa virus		21		21		
	45709	Sabia mammarenavirus		879		879		
	64284	Saboya virus		1		1		
	4932	Saccharomyces cerevisiae	27	11	27	11		
	545124	Saccharomyces cerevisiae AWRI1631		2		2		
	643680	Saccharomyces cerevisiae EC1118		1		1		
	285006	Saccharomyces cerevisiae RM11-1a		3		3		
	559292	Saccharomyces cerevisiae S288c	2		6		4	
	1095631	Saccharomyces cerevisiae x Saccharomyces kudriavzevii VIN7		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	31		31			
	590	Salmonella	3	18	3	18		
	28901	Salmonella enterica		53		54		1
	59203	Salmonella enterica subsp. arizonae		1		1		
	41514	Salmonella enterica subsp. arizonae serovar 62:z4,z23:-		4		4		
	440534	Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701		1		1		
	119912	Salmonella enterica subsp. enterica serovar Choleraesuis		3		3		
	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		3		3		
	295319	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150		3		3		
	1016998	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7		7		7		
	10001709	Salmonella enterica subsp. enterica serovar Paratyphi B strain SPB7		8		8		
	605	Salmonella enterica subsp. enterica serovar Pullorum		1		1		
	439847	Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29		1		1		
	439843	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633	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		92		92		
	497976	Salmonella enterica subsp. enterica serovar Typhi str. E00-7866		1		1		
	209261	Salmonella enterica subsp. enterica serovar Typhi str. Ty2		5		5		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B 14	T 14	B 15	T 15	D B	D T
	90371	Salmonella enterica subsp. enterica serovar Typhimurium	15	71	15	75		4
	85569	Salmonella enterica subsp. enterica serovar Typhimurium str. DT104	1		1	1		1
	99287	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2		78		79		1
	216597	Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344		2		2		
	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	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		
	358400	Sangassou virus		6		6		
	9515	Sapajus apella	1		1			
	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	162	496	162	496		
	228407	SARS coronavirus BJ01	64	28	64	28		
	229992	SARS coronavirus Frankfurt 1	5	26	5	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	24	52	24	52		
	6181	Schistosoma	3		3			
	6184	Schistosoma bovis	2		2			
	6182	Schistosoma japonicum	43	31	43	31		
	6183	Schistosoma mansoni	74	44	74	46		2
	10000385	Schistosoma mansoni Puerto Rico	20	7	20	7		
	5334	Schizophyllum commune		1		1		
	1133363	Schmallenberg virus	1		1			
	85552	Scylla paramamosain	3		7		4	
	4550	Secale cereale	51		51	31		31
X	155091	Secale cereale subsp. afghanicum				2		2
X	49318	Secale cereale x Triticum aestivum				1		1
	58866	Secale strictum		1		1		
	88036	Selaginella moellendorffii		1		1		
	11033	Semliki Forest virus	36	5	36	5		
	136966	SEN virus		7		7		
	11191	Sendai virus	63	10	63	10		
	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			
	11198	Sendai virus (Z)		1		1		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D B	D T
	11608	Seoul virus		5		5		
	12557	Seoul virus 80-39		3		3		
	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		20		20		
	300268	Shigella boydii Sb227		5		5		
	622	Shigella dysenteriae	5	2	6	2	1	
	358708	Shigella dysenteriae 1012		1		1		
	300267	Shigella dysenteriae Sd197		5		5		
	10000748	Shigella dysenteriae serotype 1	3		3			
	10000749	Shigella dysenteriae serotype 1 114Sd	1		1			
	623	Shigella flexneri	77	11	77	11		
	591020	Shigella flexneri 2002017		1		1		
	42897	Shigella flexneri 2a	35		35			
	198215	Shigella flexneri 2a str. 2457T		2		2		
	198214	Shigella flexneri 2a str. 301		4		4		
	1288825	Shigella flexneri 2b	1		1			
	10000750	Shigella flexneri 2b	1		1			
	424717	Shigella flexneri 3a	4		4			
	373384	Shigella flexneri 5 str. 8401		23		23		
	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		156		157		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			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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		
X	46771	Simian virus 12			1		1	
	10633	Simian virus 40	14	42	16	42	2	
	10001763	Simian virus 40 strain 776		1		1		
	31608	Simian virus 5 (isolate canine/CPI+)	1		1			
	37705	Sin Nombre virus	1	35	1	35		
	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		3		3		
	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			
X	743722	Sphingobacterium sp. 21			1		1	
	13687	Sphingomonas	1	3	1	4		1
	185949	Sphingomonas aurantiaca		1		1		
	317655	Sphingopyxis alaskensis RB2256		1		1		
	2133	Spiroplasma citri		1		1		
X	108	Spirosoma linguale			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	94	35	104	36	10	1
	553583	Staphylococcus aureus A9635	1		1			
X	10002122	Staphylococcus aureus Becker			2		2	
	10001662	Staphylococcus aureus Cowan 1	2		2			
X	10002121	Staphylococcus aureus Reynolds			2		2	
X	10002129	Staphylococcus aureus RN4850			1		1	
	93062	Staphylococcus aureus subsp. aureus COL	17	1	17	1		
	548470	Staphylococcus aureus subsp. aureus MN8	11		11			
	282458	Staphylococcus aureus subsp. aureus MRSA252	85		86		1	
	158879	Staphylococcus aureus subsp. aureus N315		5		5		
	93061	Staphylococcus aureus subsp. aureus NCTC 8325	5	1	5	1		
X	426430	Staphylococcus aureus subsp. aureus str. Newman			1		1	
	29388	Staphylococcus capitis	1		1			
	525374	Staphylococcus epidermidis BCM-HMP0060		1		1		
	10001974	Staphylococcus epidermidis JCM 2414	1		1			
	1301	Streptococcus	4		5		1	

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	1311	Streptococcus agalactiae	5		5			
	342613	Streptococcus agalactiae 18RS21	2		2			
	208435	Streptococcus agalactiae 2603V/R	1	2	1	2		
	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			
	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		
X	1334	Streptococcus dysgalactiae			3		3	
	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	146	89	146	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	70	8	76	8	6	
	216600	Streptococcus pneumoniae 23F	6		6			
	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		12		12		
	170187	Streptococcus pneumoniae TIGR4		2		2		
	10001651	Streptococcus pneumoniae type 14	18		18			
	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	127	115	127	115		
	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	2	13	2		
	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			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	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			
	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'	13		13			
	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	10		10			
	80859	Streptomyces ribosidificus		1		1		
	465541	Streptomyces sp. Mg1		1		1		
	1463841	Streptomyces sp. NRRL F-2580		1		1		
	35297	Striped Jack nervous necrosis virus	1		1			
	8801	Struthio camelus	2		2			
	7726	Styela plicata	6		6			
	186540	Sudan ebolavirus	2	280	2	280		
	128949	Sudan ebolavirus - Maleo (1979)		30		30		
	386033	Sudan ebolavirus - Uganda (2000)	1	6	1	6		
	128948	Sudan virus - Boniface, Sudan,1976	2	1	2	1		
	10345	Suid herpesvirus 1	2	2	3	2	1	
	10349	Suid herpesvirus 1 (strain NIA-3)	4		4			
	33703	Suid herpesvirus 1 strain Kaplan	4		4			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	387093	Sulfurovum sp. NBC37-1		1		1		
	9823	Sus scrofa	104	49	105	53	1	4
	9825	Sus scrofa domesticus		5		5		
	10000187	Sus scrofa Landrace X Large White	1		1			
	10001097	Sus scrofa Yorkshire	1		1			
X	63421	Swine hepatitis E virus			3		3	
	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		2		2		
	32049	Synechococcus sp. PCC 7002		1		1		
	1148	Synechocystis sp. PCC 6803		2		2		
	11631	Tacaribe mammarenavirus		106		106		
	928313	Tacaribe virus strain Franze-Fernandez		6		6		
	31615	Tacaribe virus strain V5		1		1		
	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	19	4	28	4	9	
	59729	Taeniopygia guttata		1		1		
	186541	Tai Forest ebolavirus		1		1		
	128999	Tai Forest virus - Cote d'Ivoire, Cote d'Ivoire, 1994	1	3	1	3		
	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			
	392734	Terriglobus roseus		1		1		
	99883	Tetraodon nigroviridis		2		2		
	398812	TGEV virulent Purdue	4		4			
	5874	Theileria annulata	1		1			
	353154	Theileria annulata strain Ankara		4		4		
	5872	Theileria equi	8		8			
	5875	Theileria parva	28	17	28	18		1
	10001243	Theileria parva strain Marikebuni		1		1		
	333668	Theileria parva strain Muguga	14	18	14	18		
	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		17		18		1
	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		

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	360549	Themiste hennahi	1		1			
	10479	Thermoproteus tenax virus 1	1		1			
	271	Thermus aquaticus	1		1			
	274	Thermus thermophilus	1	1	1	1		
	300852	Thermus thermophilus HB8		1		1		
	13286	Theromyzon tessulatum	1		1			
	4601	Thinopyrum bessarabicum		1		1		
	222994	Thinopyrum ponticum x Triticum aestivum		7		7		
	83810	Thosea asigna virus		1		1		
	11084	Tick-borne encephalitis virus	14	135	14	136		1
	11087	Tick-borne encephalitis virus (STRAIN SOFJIN)	6		6			
	10000449	Tick-borne encephalitis virus (WESTERN SUBTYPE) - Neudoerfl	10		10			
X	94827	Tinamus guttatus				1		1
	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			
	742503	Tokudaia muenninki		1		1		
	12146	Tomato bushy stunt virus (STRAIN BS-3)	3		3			
	83192	Topografov virus	1		1			
	7787	Torpedo californica	149	75	149	75		
	7788	Torpedo marmorata	3	3	3	3		
	687385	Torque teno canis virus		1		1		
	687383	Torque teno douroucouli virus		5		5		
	687384	Torque teno felis virus		1		1		
	687369	Torque teno mini virus 1		1		1		
	687371	Torque teno mini virus 3		2		2		
	687375	Torque teno mini virus 7		2		2		
	687376	Torque teno mini virus 8		2		2		
	687386	Torque teno sus virus 1a	12	1	12	1		
	1218488	Torque teno sus virus k2	11		11			
	687382	Torque teno tamarin virus		2		2		
	68887	Torque teno virus	5	94	5	94		
	687340	Torque teno virus 1		3		3		
	687350	Torque teno virus 11		1		1		
	687351	Torque teno virus 12		1		1		
	687353	Torque teno virus 14		5		5		
	687354	Torque teno virus 15		3		3		
	687355	Torque teno virus 16		4		4		
	687358	Torque teno virus 19		5		5		
	687341	Torque teno virus 2		4		4		
	687359	Torque teno virus 20		2		2		
	687360	Torque teno virus 21		2		2		
	687362	Torque teno virus 23		2		2		
	687363	Torque teno virus 24		3		3		
	687364	Torque teno virus 25		3		3		
	687365	Torque teno virus 26		5		5		
	687366	Torque teno virus 27		5		5		
	687367	Torque teno virus 28		3		3		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	687368	Torque teno virus 29		4		4		
	687342	Torque teno virus 3		4		4		
	687343	Torque teno virus 4		6		6		
	687345	Torque teno virus 6		2		2		
	687346	Torque teno virus 7		3		3		
	687347	Torque teno virus 8		6		6		
	487067	Torque teno virus Human/Ghana/GH1/1996		3		3		
	486280	Torque teno virus VT416		3		3		
	6265	Toxocara canis	3		3			
	5811	Toxoplasma gondii	62	60	64	74	2	14
	10000353	Toxoplasma gondii 76K	5	5	5	5		
	10000354	Toxoplasma gondii BK	1	1	1	1		
	10002052	Toxoplasma gondii Gansu Jingtai	16		27		11	
	507601	Toxoplasma gondii GT1		1		1		
	508771	Toxoplasma gondii ME49	21	10	21	10		
	10000355	Toxoplasma gondii Prugniaud		1		1		
	383379	Toxoplasma gondii RH	24	20	27	23	3	3
	1209525	Toxoplasma gondii type I		2		2		
	1209523	Toxoplasma gondii type II		2		2		
	398031	Toxoplasma gondii type III		1		1		
	432359	Toxoplasma gondii VEG	14		14			
	11149	Transmissible gastroenteritis virus	11	1	11	1		
	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		
X	754027	Treponema phagedenis F0421				1		1
	6334	Trichinella spiralis	8	2	8	2		
	203124	Trichodesmium erythraeum IMS101		2		2		
	5722	Trichomonas vaginalis	2	1	2	1		
	81847	Trichophyton quinckeanum	1		1			
	5551	Trichophyton rubrum	2	27	2	27		
	3677	Trichosanthes kirilowii	1		1			
	1186058	Trichosporon asahii var. asahii CBS 2479		1		1		
	5554	Trichosporon cutaneum	1		1			
	9337	Trichosurus vulpecula	45		45			
	4565	Triticum aestivum	589	409	633	465	44	56
	488177	Triticum aestivum x Lophopyrum elongatum		1		1		
	4568	Triticum monococcum		1		1		
	279889	Triticum spelta var. arduini		3		3		
	4567	Triticum turgidum subsp. durum		1		1		
	4572	Triticum urartu	1		1	1		1
	5691	Trypanosoma brucei	13	6	13	6		
	5702	Trypanosoma brucei brucei	5		5			
	185431	Trypanosoma brucei brucei TREU927		1		1		
	31285	Trypanosoma brucei gambiense	2		2			
	679716	Trypanosoma brucei gambiense DAL972		1		1		
	31286	Trypanosoma brucei rhodesiense		9		9		
	5693	Trypanosoma cruzi	152	411	159	421	7	10
	10000347	Trypanosoma cruzi Dm28c	2		2			
	10000348	Trypanosoma cruzi G	1		1			

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	353153	Trypanosoma cruzi strain CL Brener	7	1	2053	10	2046	9
	10000351	Trypanosoma cruzi Y	1		1			
	93678	TTV-like mini virus		1		1		
	167758	TTV-like virus DXL1		10		10		
	37133	Tula virus	1	14	1	14		
	37347	Tupaia belangeri		1		1		
X	246437	Tupaia chinensis			1		1	
	63673	Turbo cornutus	2		2			
	11152	Turkey coronavirus	1		1			
	32644	unidentified		256		755		499
	237631	Ustilago maydis 521		2		2		
	10245	Vaccinia virus	5	493	9	493	4	
	10001973	Vaccinia virus Acambis 2000	5		8		3	
	332193	Vaccinia Virus Acambis 3000 MVA		20		20		
	126794	Vaccinia virus Ankara		24		127		103
	10001027	Vaccinia virus Connaught	1		1			
	10249	Vaccinia virus Copenhagen	31	803	31	815		12
	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		21		21		
	696871	Vaccinia virus Western Reserve		4		4		
	10254	Vaccinia virus WR	28	6316	28	6316		
	10247	Vaccinia virus WR 65-16		4		4		
	12870	Variola major virus		17		17		
	10000390	Variola major virus India-1967		1		1		
	53258	Variola minor virus		93		93		
	10255	Variola virus		249		249		
	587200	Variola virus human/India/Ind3/1967		4		4		
	11036	Venezuelan equine encephalitis virus	2	1	2	1		
	36382	Venezuelan equine encephalitis virus (strain 3880)		1		1		
	11037	Venezuelan equine encephalitis virus (strain TC-83)	24		24			
	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		10		10		
	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			
	150340	Vibrio antiquarius		15		15		
	666	Vibrio cholerae	38	90	38	90		
	592313	Vibrio cholerae 12129(1)		1		1		
	412966	Vibrio cholerae 1587		3		3		
	412614	Vibrio cholerae 2740-80		44		44		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	44104	Vibrio cholerae 569B	37		37			
	404974	Vibrio cholerae AM-19226		1		1		
	417400	Vibrio cholerae B33		5		5		
	412967	Vibrio cholerae MAK 757		9		9		
	345072	Vibrio cholerae MO10		1		1		
	417398	Vibrio cholerae MZO-2		2		2		
	412883	Vibrio cholerae MZO-3		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	3	1	3		
	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		2		2		
	345075	Vibrio cholerae V51		3		3		
	345076	Vibrio cholerae V52		32		32		
	670	Vibrio parahaemolyticus		57		57		
	563773	Vibrio parahaemolyticus AN-5034		4		4		
	419109	Vibrio parahaemolyticus AQ3810		38		38		
	627611	Vibrio parahaemolyticus K5030		22		22		
	223926	Vibrio parahaemolyticus RIMD 2210633	2	17	2	17		
	70203	Vibrio phage fs1		1		1		
X	671	Vibrio proteolyticus			1		1	
	314291	Vibrio splendidus 12B01		2		2		
	575788	Vibrio tasmaniensis LGP32		1		1		
	672	Vibrio vulnificus	1	66	1	66		
	216895	Vibrio vulnificus CMCP6		53		53		
	196600	Vibrio vulnificus YJ016		75		75		
	8704	Vipera ammodytes	1		1			
	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			
	3068	Volvox carteri f. nagariensis		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	50	415	50	429		14
	10000447	West Nile virus 3000.0259	2		2			
	10000971	West Nile virus NY-99	14	21	15	21	1	
	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			

NEW 2015	ORGANISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	406269	West Nile virus strain PTRoxo		12		12		
	11039	Western equine encephalitis virus		1		1		
	46919	Whitewater Arroyo mammarenavirus		349		349		
	10001617	Whitewater Arroyo virus strain AV9310135		1		1		
	163164	Wolbachia endosymbiont of Drosophila melanogaster		1		1		
	35269	Woodchuck hepatitis virus	4	6	4	6		
	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	13	8	1	1
	280	Xanthobacter autotrophicus		1		1		
	78245	Xanthobacter autotrophicus Py2		1		1		
X	29447	Xanthomonas albilineans				1		1
	8364	Xenopus (Silurana) tropicalis		2		2		
	8355	Xenopus laevis		3		3		
	132475	Yaba-like disease virus		3		3		
	11089	Yellow fever virus		1329		1329		
	11090	Yellow fever virus 17D		299		299		
	617102	Yellow fever virus 17D/Tiantan	4	5	4	5		
	31641	Yellow fever virus 1899/81		36		36		
	407141	Yellow fever virus isolate Ethiopia/Couma/1961		2		2		
	407134	Yellow fever virus strain Ghana/Asibi/1927		5		5		
X	161600	Yellow grouper nervous necrosis virus			1			1
	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		
	913028	Yersinia enterocolitica W22703		1		1		
	349966	Yersinia frederiksenii ATCC 33641		2		2		
	28152	Yersinia kristensenii		1		1		
	349967	Yersinia mollaretii ATCC 43969		3		3		
	632	Yersinia pestis	22	145	23	145	1	
	10000757	Yersinia pestis 195/P	5		5			
	349746	Yersinia pestis Angola		3		3		
	360102	Yersinia pestis Antiqua		36		36		
	373665	Yersinia pestis biovar Orientalis str. IP275		1		1		
	412420	Yersinia pestis CA88-4125		21		21		
	214092	Yersinia pestis CO92	4	22	4	22		
	375450	Yersinia pestis FV-1		2		2		
	10000756	Yersinia pestis KIM 5	21		21			
	187410	Yersinia pestis KIM10+		11		11		
	377628	Yersinia pestis Nepal516		135		135		
	386656	Yersinia pestis Pestoides F		2		2		
	633	Yersinia pseudotuberculosis		2		2		
	349747	Yersinia pseudotuberculosis IP 31758		9		9		
	273123	Yersinia pseudotuberculosis IP 32953		1		1		
	10001895	Yersinia pseudotuberculosis str. 32777		1		1		
	10001504	Yokenella regensburgei PCM 2476	1		1			
	10001505	Yokenella regensburgei PCM 2477	1		1			
	186538	Zaire ebolavirus	10	867	10	867		
	4577	Zea mays	3	1	3	1		
	34245	Zinnia violacea		1		1		

NEW 2015	ORGAN-ISM ID	SPECIES/STRAIN	B_14	T_14	B_15	T_15	D_B	D_T
	157914	Ziziphus mauritiana	4		4			
	12232	Zucchini yellow mosaic virus	1		1			

2 Website Features

There were three releases of the IEDB external website since the 2014 Annual Compendium was produced. The focus was converting the remaining IEDB 2.0 functionality to the IEDB 3.0 website and improving the speed of queries on the home page search. Release 3.1 (2 July 2015) included an updated Immunome Browser graphic interface with improved controls and export features and a new, integrated polling server to increase query performance. Release 3.2 (22 October 2015) featured speed improvements on the home page search and specialized searches. Release 3.3 (5 February 2016) introduced a revised molecule finder to use regional mappings for tree structure and searches.

In addition, there were two releases of the Analysis Resource – Release 2.14 on 11 November 2015 and Release 2.14.1 on 4 April 2016. Release 2.14 contained revisions to provide for a more consistent look and feel to the website and Release 2.14.1 introduced the Analysis Resource Labs page for beta versions of tools under development.

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

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

2.1 Home Page

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

The top box in the left column contains a welcome statement that briefly describes the content of the database. It also has a “Learn More” link that brings the user to a web page containing more information about the support and user help features available, about the data itself, and about the IEDB program. This page is described in detail in Section 2.6. The Summary Metrics are displayed in the bottom box of this column. These numbers are intended to be a gauge of the volume of data available in the system. The Summary Metrics provide the number of epitopes (peptidic and non-peptidic), assays (T cell, B cell, and MHC ligand assays), epitope source organisms, restricting MHC alleles, and references. A middle box may appear when there are special messages to convey to users. The text will appear in red. The middle column contains the initial search interface that is described in detail in Section 2.2.1. The rightmost column has links to the most frequently used tools in the Analysis Resource.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Home | Specialized Searches | Analysis Resource

Welcome

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

START YOUR SEARCH HERE

Epitope

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

Assay

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

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

Summary Metrics

Peptidic Epitopes	233,718
Non-Peptidic Epitopes	2,382
T Cell Assays	279,244
B Cell Assays	371,800
MHC Ligand Assays	491,172
Epitope Source Organisms	3,490
Restricting MHC Alleles	731
References	17,625

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, TAF)
- 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

Reset Search

Provide Feedback | Help Request | Solutions Center | Tool Licensing Information

Data Last Updated: April 17, 2016

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 3.3 Home page

2.2 Query

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

2.2.1 Perform a Home Page Search

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

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

The screenshot shows a search interface titled "START YOUR SEARCH HERE". It is divided into six main sections, each with a question mark icon:

- Epitope**: Includes radio buttons for "Any Epitopes", "Linear Epitope" (selected), "Discontinuous Epitopes", and "Non-peptidic Epitopes". A text field for "Exact M:" contains "SIINFEKL". A chemical structure of an amino acid is shown.
- Assay**: Includes checked checkboxes for "Positive Assays Only", "T Cell Assays", "B Cell Assays", and "MHC Ligand Assays". An icon of a pipette is shown.
- Antigen**: Includes text fields for "Organism" (containing "influenza, peanut") and "Antigen Name" (containing "core, capsid, myosin"). An icon of a protein structure is shown.
- MHC Restriction**: Includes radio buttons for "Any MHC Restriction" (selected), "MHC Class I", "MHC Class II", and "MHC Nonclassical". An icon of a hand holding a molecule is shown.
- Host**: Includes radio buttons for "Any Host" (selected), "Humans", "Rodents", "Non-human Primates", and "Other Common Hosts" (with a dropdown arrow). An icon of a person is shown.
- Disease**: Includes radio buttons for "Any Disease" (selected), "Infectious Disease", "Allergic Disease", "Autoimmune Disease", and "Transplant Disease". A caduceus icon is shown.

At the bottom, there are "Reset" and "Search" buttons.

Figure 2.2 Home page Simple Search

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

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

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

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

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

5 Records Found Page 1 of 1 25 Per Page

Go To Records Starting At 1200 Export Epitopes Results

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

2.2.2 Specialized Searches

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

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

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

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

[Use the Legacy Site](#) | [Help](#) | [More IEDB](#)

[Home](#) | [Specialized Searches](#) | [Analysis Resource](#)

Epitope Detailed Search

Reset Search

Epitope ?

Epitope ID

Structure Type - Any 1 ▼

Organism

Antigen Name

Epitope Referenc...

Epitope Structure Defines

Evidence Code for Sourc...

Epitope Name

Reference Start Position

Reference End Position

Reference Region

Comments

Data Location in Reference

Epitope Related ...

Related Object

Type - Any Type ▼

Organism

Antigen Name

Pending Filters ✖ Reference Type: 0

Epitopes
(413612)

Antigens
(25693)

Assays
(988554)

References
(16889)

Go To Records Starting At ↻ Export Epitopes Results ✕

413612 Records Found Page 1 of 16545 ▶▶ 25 Per Page

Details ▼	Epitope ▼	Antigen ▼	Organism ▼	# References ▼	# Assays ▼
123885	cardiolipin			323	1239
44920	NLVPMVAIV	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	223	562
113645	NEVGVYRSPFSSRVVHLYRNGK	Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	176	970
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	165	382
58560	SIINFEKL	Gal d 2	Gallus gallus (chicken)	142	367
112741	2,4-dinitrophenyl group			140	573
4602	ASNENMETM	Nucleoprotein	Influenza A virus	133	379
24786	HSLGKWLGHDPKF			115	781
112742	2,4,6-trinitrophenyl group			107	354
130649	alpha-Gal epitope			107	451
130694	1-O-(alpha-D-galactosyl)-N-hexacosanoylphosphatidylcholine			104	435
20788	GLCTLVAML	mRNA export factor ICP27 homolog	Human herpesvirus 4 (Epstein Barr virus)	103	227
6435	CINGVCWIV	Genome polyprotein	Hepatitis C virus	99	265
48237	PKYVKQNTLKLAT	Hemagglutinin	Influenza A virus	96	343
32208	KLVALGINAV	Genome polyprotein	Hepatitis C virus	86	225
61086	SSIEFARL	Envelope glycoprotein B	Human herpesvirus 1 (Herpes simplex virus type 1)	86	304
53112	RAHYNIVTF	Protein E7	Alphapapillomavirus 9	83	222
30001	KAVYNFATC	Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis virus	82	266
7493	DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA	Amyloid beta A4 protein	Homo sapiens (human)	81	301
6568	CLGGLLTMV	Latent membrane protein 2	Human herpesvirus 4 (Epstein Barr virus)	80	215
67436	TYQRTRALV	Nucleoprotein	Influenza A virus	80	181
16833	FLPSDFPFSV	Capsid protein	Hepatitis B virus	78	236
61151	SSELENFRAYV	Polymerase acidic protein	Influenza A virus	76	246
17516	FQPQNGQFI	Nucleoprotein	Lymphocytic choriomeningitis virus	75	198
16878	FLRGRAYGL	Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	74	166

Figure 2.4 Epitope Detail Search input screen

Epitope ?

Epitope ID

Structure Type - Any Epitopes

Organism

Antigen Name

Epitope Reference Details

Epitope Structure Defines

Evidence Code for Source...

Epitope Name

Reference Start Position to

Reference End Position to

Reference Region

Comments

Data Location in Reference

Epitope Related Object

Related Object

Type - Any Type

Organism

Antigen Name


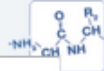


Figure 2.5 Epitope panel on the Specialized Search page expanded to show input fields

Epitope ? 

Epitope ID

Structure Type - Linear Epitopes ▼

Linear Sequence

Match

Modified Residue(s)

Modification(s)

Starting Position to

Ending Position to

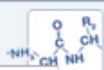
Organism

Antigen Name

Epitope Reference Details

Epitope Related Object

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

Epitope ? 

Epitope ID

Structure Type - Discontinuous Epitopes ▼

Discontinuous Residues

Modified Residue(s)

Modification(s)

Organism

Antigen Name

Epitope Reference Details

Epitope Related Object

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

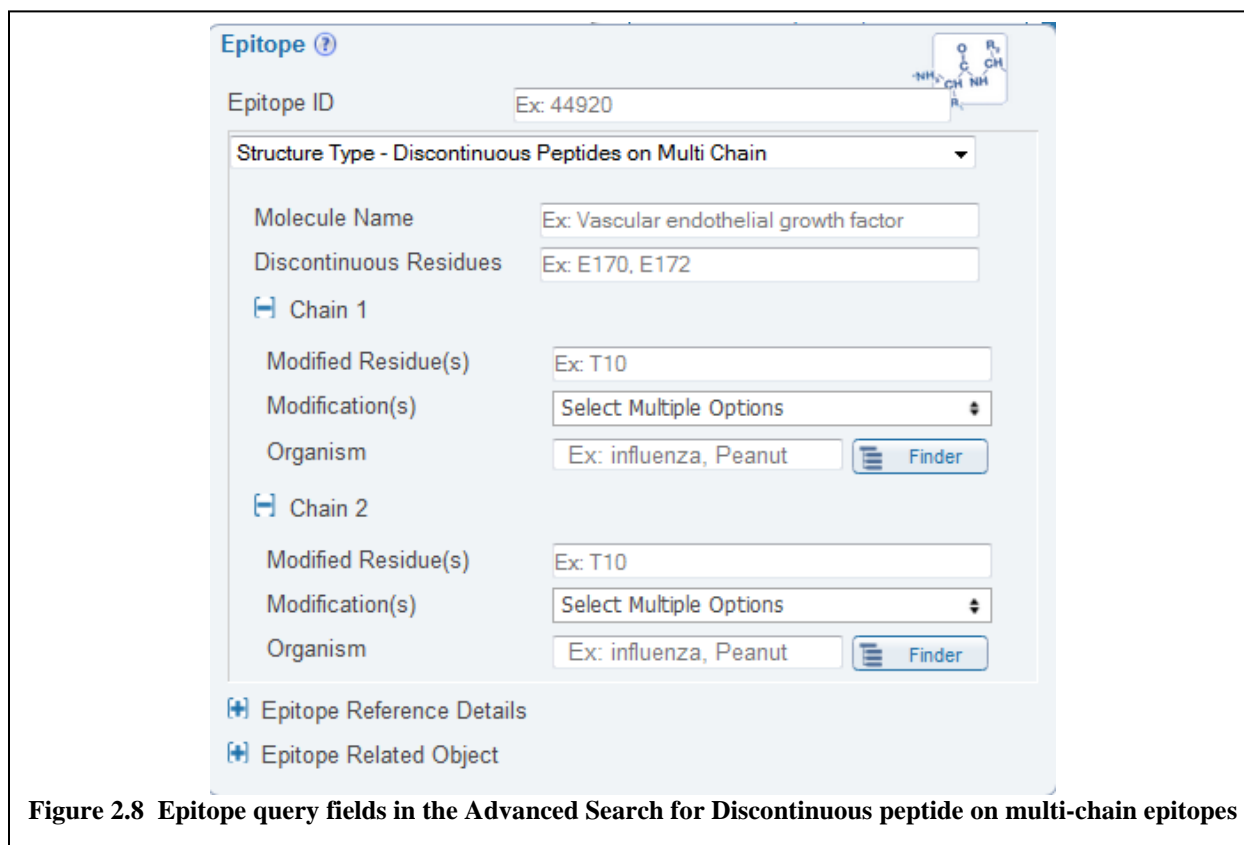


Figure 2.8 Epitope query fields in the Advanced Search for Discontinuous peptide on multi-chain epitopes

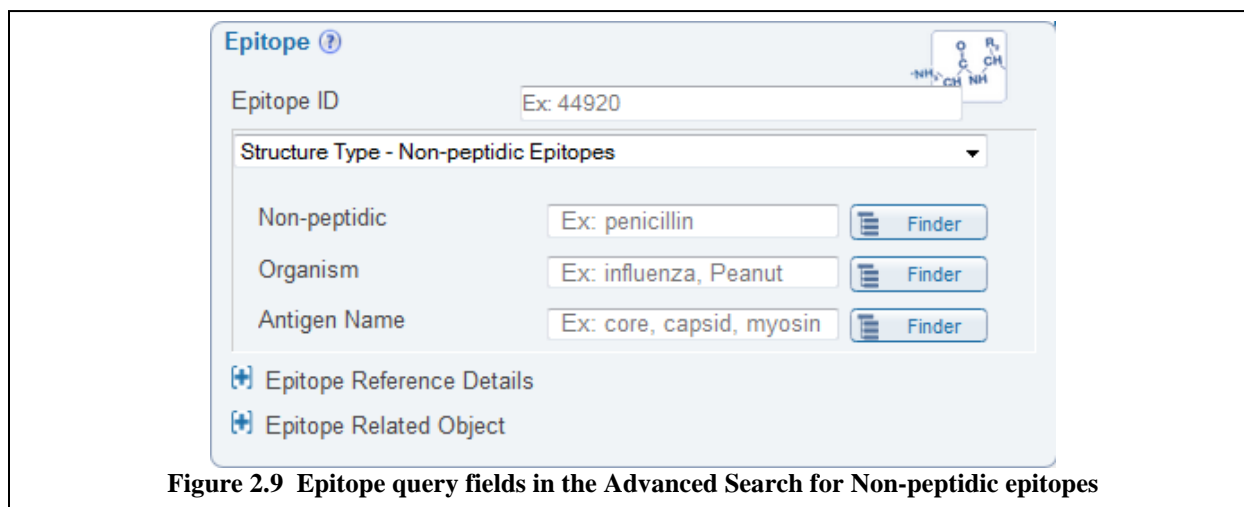


Figure 2.9 Epitope query fields in the Advanced Search for Non-peptidic epitopes

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

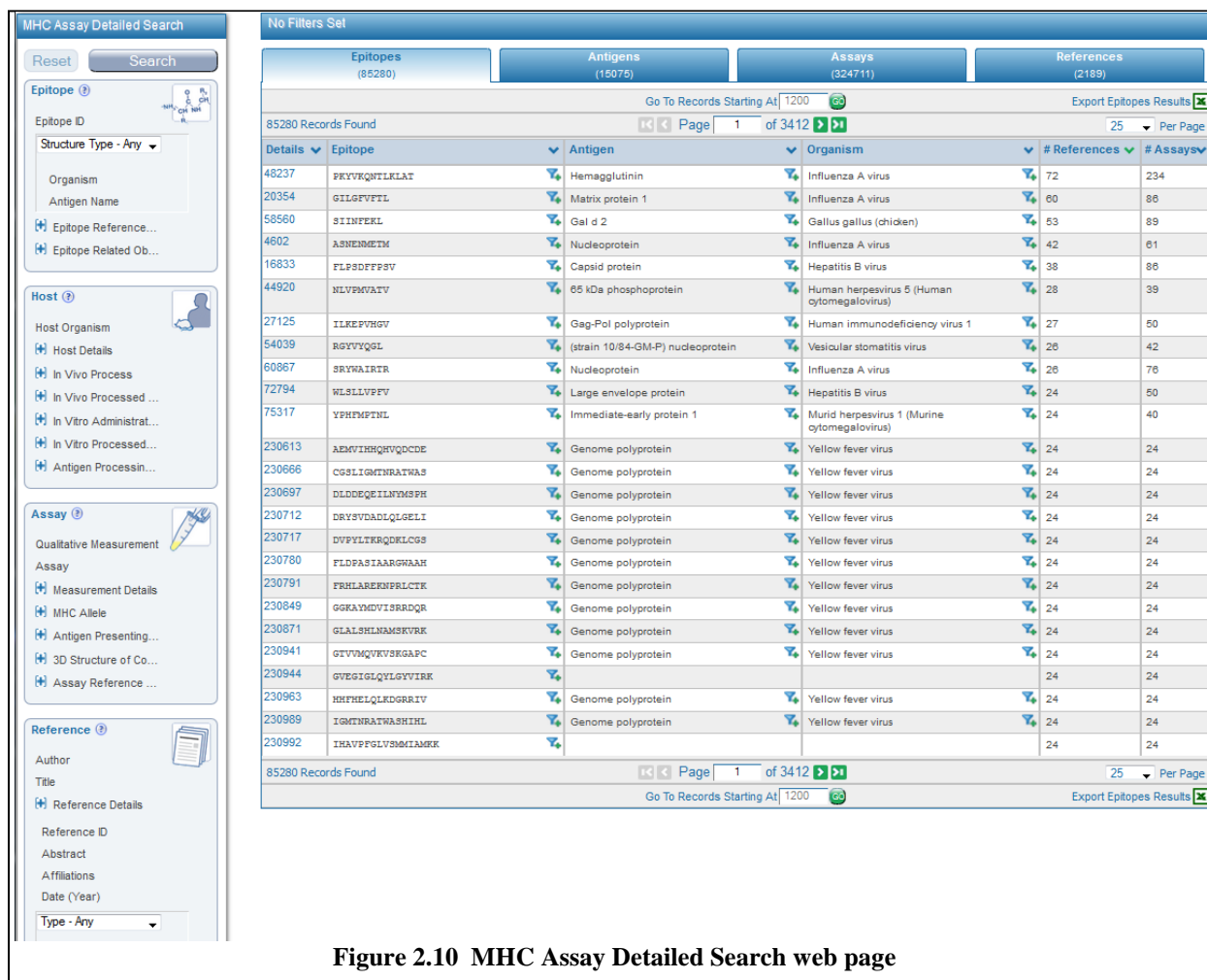


Figure 2.10 MHC Assay Detailed Search web page

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

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

The MHC Ligand assay category combines assays that were previously in the MHC Binding and MHC Ligand Elution assay categories. As such, the MHC Ligand category captures details relating to the in vitro interaction of the epitope with specific MHC molecules along with available Epitope-MHC complex structure details, that is the epitope's binding capacity to the MHC molecule. It also captures data related to epitopes that are naturally processed and presented on the surface of an antigen presenting cell. The MHC Ligand Elution subcategory differs from the MHC Binding subcategory in that for the former, antigen bound to the MHC molecule on the cell surface has been taken up and processed internally for presentation by the antigen presenting cell, where as for the latter, antigen in solution is bound to MHC molecules on the surface of the antigen presenting cells.

IDENTIFIER SEARCH

IEDB Identifiers

Epitope ID

Reference ID

Submission ID

Assay ID

External Identifiers

PubMed ID

PDB ID

ChEBI ID

Search

Figure 2.11 Identifier Search input screen

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

2.2.3 Search Results Page

The results of a search or query appear on the Results page (http://www.iedb.org/result_v3). An example is shown in Figure 2.12. The search criteria are listed in the Current Filters section above the results table. There are four tabs for the results. Figure 2.12 displays the Epitopes tab. Results are initially sorted by the number of assays, but the user can click on the column header to change the sort order. A second click will reverse the sort order of the selected column. The table includes the epitope structure description, the corresponding antigen, source organism, the number of references in which the epitope appears, and the number of assays (positive and negative) that reside in the database. Clicking on the Epitope ID number in the far left column will take the user to a Distinct Epitope detail page, as seen in Figure 2.13. The bottom section of the figure contains links to relevant tools in the Analysis Resource. Links can also appear to the Bioinformatics Resource Centers (BRC), such as the Influenza Research Database (IRD). The user can also refine the search results by clicking on the filter icon in the epitope, antigen, and organism fields.

Pending Filters

Reset Search

Epitope

- Any Epitopes
- Linear Epitope
- Discontinuous Epitopes
- Non-peptidic Epitopes

Antigen

Organism
Ex: influenza, peanut

Antigen Name
Ex: core, capsid, myosin

Assay

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

MHC Restriction

- Any MHC Restriction

Current Filters: Positive Assays Only

Epitopes (136124) | Antigens (18043) | Assays (401112) | References (16841)

Go To Records Starting At 1200 | Export Epitopes Results

136124 Records Found | Page 1 of 5445 | 25 Per Page

Details	Epitope	Antigen	Organism	# References	# Assays
123885	cardiolipin			318	1042
44920	NLVPMVATV	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	223	549
113645	MEVGWYRSPPFSRVVHLYRNGK	Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	174	905
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	163	369
58560	SIINFEKL	Gal d 2	Gallus gallus (chicken)	141	346
112741	2,4-dinitrophenyl group			138	474
4602	ASNENMETM	Nucleoprotein	Influenza A virus	129	352
24786	HSLGKWLGHPEDKF	Myelin proteolipid protein	Mus musculus (mouse)	111	685
130649	alpha-Gal epitope	Envelope glycoprotein	Murine leukemia virus	107	418
112742	2,4,6-trinitrophenyl group			105	312
130694	1-O-(alpha-D-galactosyl)-N-hexacosanoylphytyosphing osine			103	424
20788	GLCTLVAML	mRNA export factor ICP27 homolog	Human herpesvirus 4 (Epstein Barr virus)	100	219
6435	CINGVCWTV	Genome polyprotein	Hepatitis C virus	94	237
48237	PKYVKQITLKLAT	Hemagglutinin	Influenza A virus	91	305
61086	SSIEFARL	Envelope glycoprotein B	Human herpesvirus 1 (Herpes simplex virus type 1)	86	285

Figure 2.12 The Epitope tab of the search results page

Distinct Epitope	
Epitope ID	44920
Linear Sequence	NLVPMVATV
Source Organism	Human herpesvirus 5
Source Antigen	HCMVUL83

Related Information	
References	223 (Click for related results)
Bcell Assays	8 (Click for related results)
Tcell Assays	515 (Click for related results)
MHC Ligand Assays	39 (Click for related results)

Icon	Resource	Link
	IEDB-AR: MHC-I Processing	Predict MHC class I processing
	IEDB-AR: B cell scales	Predict B cell epitopes
	IEDB-AR: MHC-I	Predict MHC class I binding affinity

Figure 2.13 An example of the epitope detail page

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

Epitopes (136124)		Antigens (18043)		Assays (401112)		References (16841)	
Go To Records Starting At 1200 <input type="button" value="GO"/>				Export Antigens Results <input type="button" value="X"/>			
18043 Records Found				Page 1 of 722		25 Per Page	
Antigen	Organism	# Epitopes	# Assays	# References			
Genome polyprotein	Hepatitis C virus	4145	11805	540			
Hemagglutinin	Influenza A virus	1538	5108	531			
Nucleoprotein	Influenza A virus	500	2522	420			
Large envelope protein	Hepatitis B virus	640	2704	307			
Other Homo sapiens (human) protein	Homo sapiens (human)	1478	2304	302			
65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	313	1732	281			
Matrix protein 1	Influenza A virus	275	1266	276			
Amyloid beta A4 protein	Homo sapiens (human)	195	1583	262			
Gal d 2	Gallus gallus (chicken)	106	718	232			
Circumsporozoite (CS) protein	Plasmodium falciparum (malaria parasite P. falciparum)	357	1563	207			
Myelin basic protein	Homo sapiens (human)	367	1908	206			
Genome polyprotein	Dengue virus	6121	14122	205			
Protein E7	Alphapapillomavirus 9	212	1046	196			
Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	69	1107	188			
Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus	330	1670	174			
Envelope glycoprotein gp160	Human immunodeficiency virus 1	244	902	166			
Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	58	535	161			

Figure 2.14 The Antigens tab of the search results page

Current Filters: ✖ Positive Assays Only ✖ Antigen: Nucleoprotein

Epitopes (500)	Antigens (1)	Assays (2522)	References (420)	
Go To Records Starting At 1200 Go Export Antigens Results ✖				
1 Records Found ⏪ ⏩ Page 1 of 1 ⏪ ⏩ 25 Per Page				
Antigen	Organism	# Epitopes	# Assays	# References
Nucleoprotein ⏴ ⏵	Influenza A virus ⏴ ⏵	500	2522	420
1 Records Found ⏪ ⏩ Page 1 of 1 ⏪ ⏩ 25 Per Page				
Go To Records Starting At 1200 Go Export Antigens Results ✖				

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

The third tab on the results page is the Assays tab (Figure 2.16). Results are initially sorted by the Assay Description, but the user can click on the column header to change the sort order. The table contains three additional tabs, one each for the three assay categories – T cell, B cell, and MHC Ligand. The table for the T cell assays includes the assay ID, the reference, epitope, host organism, immunization, assay antigen, antigen epitope relation, MHC restriction, and assay description. The content of the B cell assay tab is the same except it omits the MHC restriction column. The MHC ligand assay tab contains fields for assay ID, reference, epitope, antigen processing, MHC restriction, assay description, and quantitative measure. Clicking on the Assay ID in the far left lane will take the user to an Assay Detail page. An example is given in Figure 2.17. The actual page contains additional fields below what is shown in the figure. The user can also refine the results further by clicking on the filter icon that is available in several of the fields, such as reference, epitope, and host.

Epitopes (136124)		Antigens (18043)		Assays (401112)		References (16841)		
T Cell Assays (109813)		B Cell Assays (104161)		MHC Ligand Assays (187138)				
Go To Records Starting At <input type="text" value="A,b"/> <input type="button" value="GO"/>						Export T Cell Assays Results <input type="button" value="X"/>		
109813 Records Found						Page 1 of 4393		
						25 Per Page		
ID	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	MHC Restriction	Assay Description
1244283	H M Vordermeier : Immunology 1993	LFAAFPSFA GLRPTF DTRLM 14 kDa antigen (21-40) Mycobacterium tuberculosis	Mus musculus C57BL/10	Administration in vivo with Mycobacterium tuberculosis H37Ra (Taxonomic Child)	LFAAFPSFAG LRPTF DTRLM 14 kDa antigen (21-40) Mycobacterium tuberculosis	Epitope	H-2-b class II	3H-thymidine proliferation Positive-High
1244288	H M Vordermeier : Immunology 1993	RDGQLTIKA ERTEQK DFDGRS 14 kDa antigen (71-91) Mycobacterium tuberculosis	Mus musculus C57BL/10	Administration in vivo with Mycobacterium tuberculosis H37Ra (Taxonomic Child)	RDGQLTIKA ERTEQK DFDGRS 14 kDa antigen (71-91) Mycobacterium tuberculosis	Epitope	H-2-b class II	3H-thymidine proliferation Positive-High
1481149	T Collen; J Immunol 1991	ETQIQRRQ HTDVSI MDRFVVPN LRGDLQV LAQKVART LP	Bos taurus Friesian	Administration in vivo with Foot-and-mouth disease virus (strain O1) (O1BFS) (Structurally Related) followed by restimulation in vitro	ETQIQRRQH TDVSI MDRFVVPNL RGDLQV LAQKVARTL P	Epitope	class II	3H-thymidine proliferation Positive-High

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

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

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

Epitope	
Epitope ID	35787
Chemical Type	Linear peptide
Linear Sequence	LFAAFPSFAGLRPTFDTRLM
Starting Position	21
Ending Position	40
Source Molecule Name	14 kDa antigen
Source Accession	61217071
Source Organism ID	1773
Source Organism	Mycobacterium tuberculosis

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

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



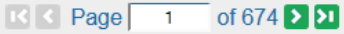








Go To Records Starting At 1200 							Export References Results 	
16841 Records Found							Page 1 of 674 	25 Per Page
Ref ID	PMID	Author	Title	Abstract	Date			
1028722 	25642819 	Richard W Birkinshaw; Daniel G Pellicci; Tan-Yun Cheng; Andrew N Keller; Maria Sandoval-Romero; Stephanie Gras; Annemieke de Jong; Adam P Uldrich; D Branch Moody; Dale I Godfrey; Jamie Rossjohn	$\alpha\beta$ T cell antigen receptor recognition of CD1a presenting self lipid ligands.	A central paradigm in T cell-mediated immunity is the simultaneous co-recognition of antigens and antigen-presenting molecules by the T cell antigen receptor (TCR). CD1a presents a broad repertoire ... more...	2015			
1028867 	25185583 	D Goedhals; J T Paweska; F J Burt	Identification of human linear B-cell epitope sites on the envelope glycoproteins of Crimean-Congo haemorrhagic fever virus.	A peptide library was used to screen for regions containing potential linear B-cell epitope sites in the glycoproteins and nucleoprotein of Crimean-Congo haemorrhagic fever virus (CCHFV) in an enzyme- ... more...	2015			
1028697 	25668439 	Hongquan Wan; Hua Yang; David A Shore; Rebecca J Garten; Laura Couzens; Jin Gao; Lianlian Jiang; Paul J Carney; Julie Villanueva; James Stevens; Maryna C Eichelberger	Structural characterization of a protective epitope spanning A(H1N1)pdm09 influenza virus neuraminidase monomers.	A(H1N1)pdm09 influenza A viruses predominated in the 2013-2014 USA influenza season, and although most of these viruses remain sensitive to Food and Drug Administration-approved neuraminidase (NA) inh ... more...	2015			
1028889 	25855295 	Hiroaki Tanabe; Yoshifumi Fujii; Miki Okada-Iwabu; Masato Iwabu; Yoshihiro Nakamura; Toshiaki Hosaka; Kanna Motoyama; Mariko Ikeda; Motoaki Wakiyama; Takaho Terada; Noboru Ohsawa; Masakatsu Hato; Satoshi Ogasawara; Tomoya Hino; Takeshi Murata; So Iwata; Kunio Hirata; Yoshiaki Kawano; Masaki Yamamoto; Tomomi Kimura-Someya; Mikako Shirouzu; Toshimasa Yamauchi; Takashi Kadowaki; Shige-yuki Yokoyama	Crystal structures of the human adiponectin receptors.	Adiponectin stimulation of its receptors, AdipoR1 and AdipoR2, increases the activities of 5' AMP-activated protein kinase (AMPK) and peroxisome proliferator-activated receptor (PPAR), respectively, t ... more...	2015			

Figure 2.18 The References tab of the search results page

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

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

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

Figure 2.19 An example of the Reference detail page

2.2.3.1 Peptide MHC Binding Motif Displays

A display of peptide MHC binding motif diagrams and amino acid binding charts for a subset of MHC allele records appears on the MHC Allele Details page. This page was migrated to IEDB 3.0 from the IEDB 2.x legacy website in 2015. The version for IEDB 3.0 will have the same functionality but the appearance will change slightly to be consistent with the design of the new website. Clicking on the allele name in the MHC Restriction column on the Assays tab for T Cells and MHC Ligand will bring the user to an MHC Allele Details page (Figure 2.20). As can be seen by the tabs in the binding motif display, the Peptide MHC Binding Motif diagrams on MHC Allele Information pages support diagrams for multiple lengths.

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

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

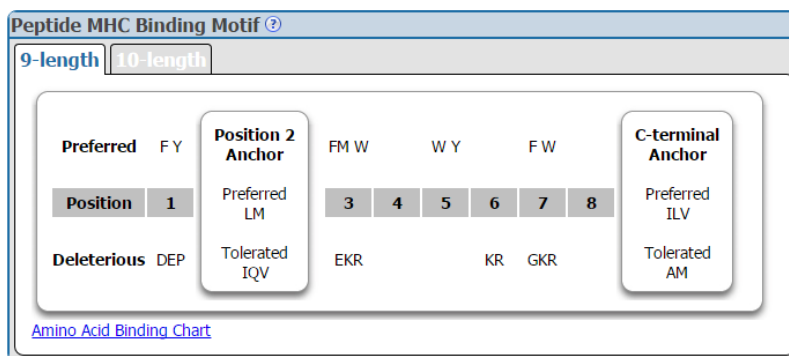


Figure 2.20 Sample MHC Allele Details page with Peptide MHC Binding Motif diagram for HLA-A*02:01. Note the link to the corresponding Amino Acid Binding Chart on the bottom left of the diagram

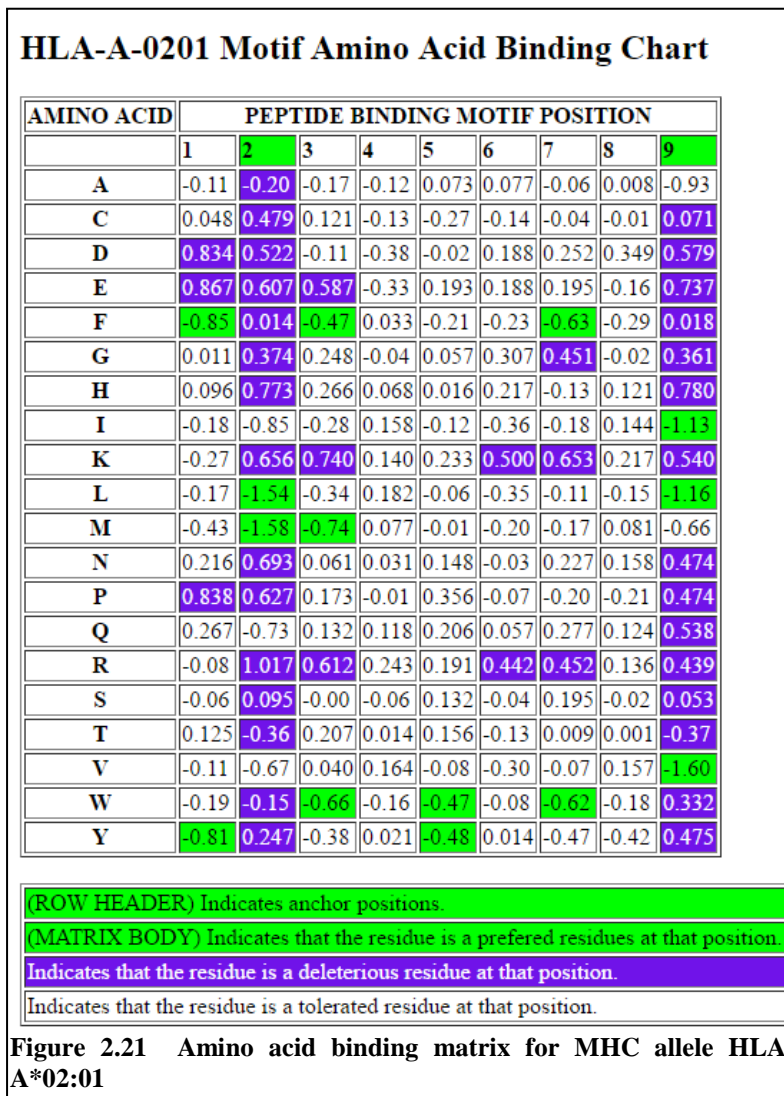
The Peptide MHC Binding Motif diagram summarizes the results of the amino acid binding for each position, which is shown in Figure 2.21. The amino acids are color-coded for each position, where green indicates the residue is preferred for binding, purple indicates it is deleterious for binding, and white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

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

For anchor position:

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

- The remaining residues are designated as deleterious



For non-anchor position:

- determine the median value of this position from corresponding column of the SMM matrix
- 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
- if a residue's value in this column of the SMM matrix is above 3 fold of the median value, designate this residue as preferred
- if a residue's value in this column of the SMM matrix is below 3 fold of the median value, designate this residue as deleterious

2.2.3.2 Immunome Browser

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

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



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

Each selected antigen is considered to be a target protein, and the tool by default maps and visualizes all epitopes in the query result that are from the source antigen which is the target protein or any of its taxonomic child. The mapping is done using the alignment between the source antigen and the target protein and matching the epitope positions in the source antigen with the residue positions in the target protein. By default, epitopes that were tested as negative for the correspondent query will be mapped as well, even if the user queried only for positive assays. Also, the epitopes that failed to satisfy the default mapping criteria won't be mapped and visualized. The Immunome Browser output for query criteria of T cell assays, linear epitopes, Hepatitis C virus, and human host is shown in Figure 2.23



Figure 2.23 Immunome Browser graphical output displaying assay results mapped onto a reference proteome by residue position

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

Results Returned: 3464 | Displaying: 3464 Display Graphed Residue Positions [Export Results](#)

Epitope ID	Epitope Sequence	Mapped Position	Identity	Subjects Tested	Subjects Responded	Assays Positive	Assays Negative	Response Freq.(95% CI)
42691	MSTNFKPQR	1-9	100%	3	0	0	1	0.00 (0.00:0.61)
42698	MSTNFKPQRKTKRNTNRR	1-18	100%	7	1	1	0	0.14 (0.01:0.50)
42673	MSTIIPKPKRQKTKRN	1-14	92%	60	3	1	0	0.05 (0.02:0.14)
42683	MSTNFKPKQKGNKRNT	1-15	86%	2	0	0	2	0.00 (0.00:0.76)
42682	MSTNFKPKQK	1-9	88%	4	0	0	2	0.00 (0.00:0.51)
42685	MSTNFKPKQKGNKRNTNRRPQ	1-20	90%	23	1	1	1	0.04 (0.00:0.18)
42679	MSTNFKPKFRKTKRN	1-15	85%	60	5	1	0	0.08 (0.04:0.18)
42696	MSTNFKPKRQKTKRNT	1-15	100%	1	0	0	1	0.00 (0.00:0.94)
42699	MSTNFKPKRQKTKRNTNRRPQ	1-20	100%	6	1	1	2	0.17 (0.01:0.56)
42681	MSTNFKPKQIKTKRNTNRR	1-19	94%	1	0	0	1	0.00 (0.00:0.94)

Figure 2.24 Immunome Browser tabular output.

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

2.2.4 Finders Overview

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

2.2.4.1 Allele Finder

The MHC Allele Finder facilitates the selection of one or more MHC alleles. The finder consists of four sections as shown in Figure 2.25. The top section lists the alleles that the user selects. The selections can be removed by clicking on the red X of an allele name or by clicking on the Reset button to delete all selected alleles. When the user has completed the selection process, the user needs to click the green Apply button. The middle left section of the finder contains the “Search By” panel. Users can search by allele name, source organism, and/or class (I, II, or non-classical). After the user supplies their search criteria and clicks the Search button, the system will filter the list of MHC alleles using the organism, class, and allele provided. The allele finder uses wild card characters by default on both ends of criteria entered into the allele field. The system then returns in the bottom “Search Results” panel a list of any alleles that contain the value in the name field and match the class selected. Users can click on the green + icon to select an allele. Users can also click on the yellow highlighter icon to highlight the allele in the allele tree in the middle right section of the finder. Alternatively, a user can browse the hierarchical allele tree. Clicking on a node in this tree will add the allele to the Current Selections section of the finder.

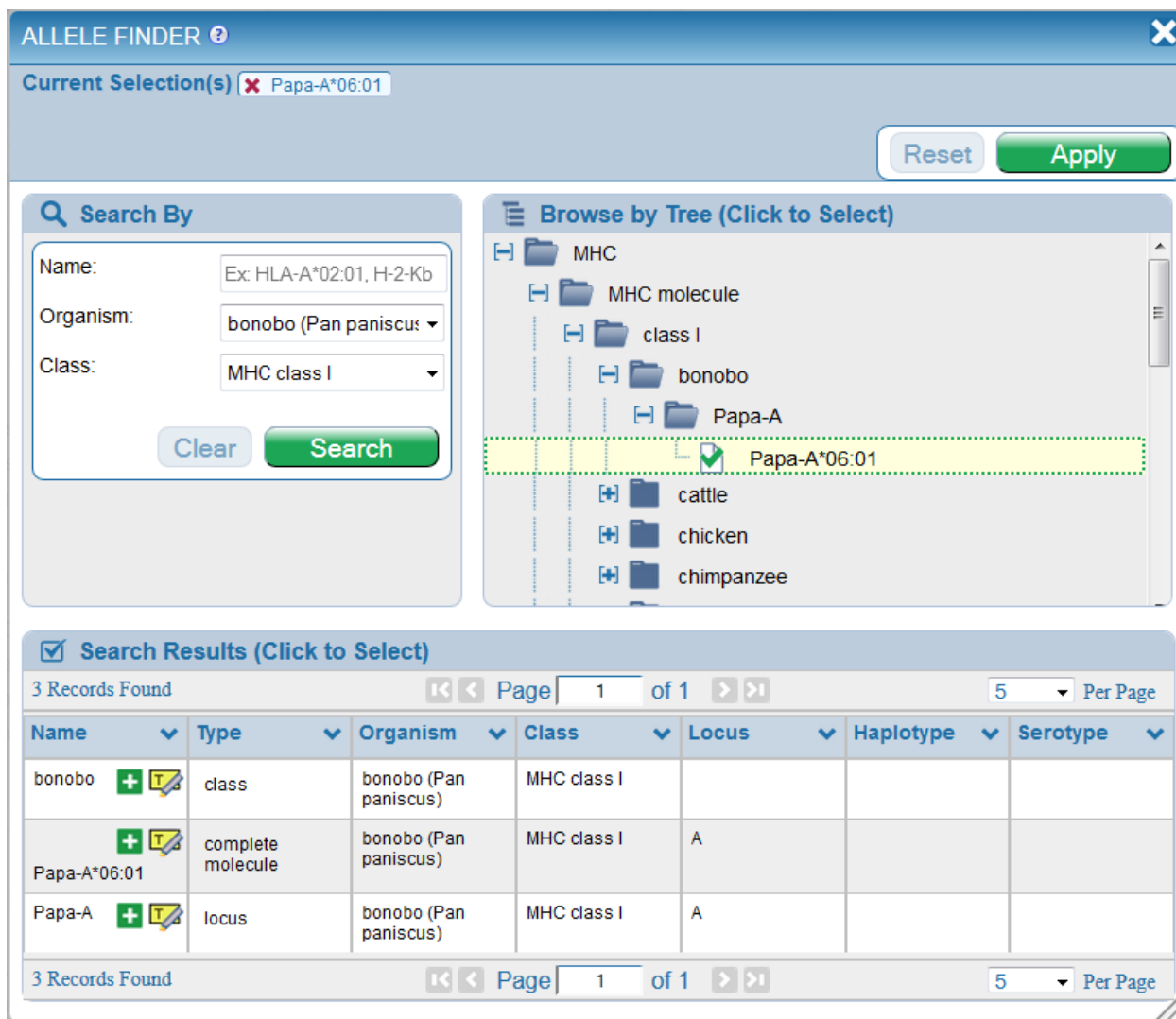


Figure 2.25 Allele Finder. Alleles are displayed in a tree structure and users can search by allele name, source organism, and MHC class (I, II, or non-classical)

2.2.4.2 Assay Finder

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

The Assay Finder is used to facilitate the selection of one or more assay types and lists all assay types in the selected assay category. The Assay Finder for T Cell, B cell, and MHC Ligand assays can be found in the Assay section on the left-hand side of the Results page and on their respective Specialized Search pages. These versions of the Assay Finder organize and display assays in a tree structure, as seen in Figure 2.26 for the T Cell assays. Users can also search for assays by their method/technique and by the characters within the assay's name. The figure shows the results for ELISA type assays for "CCL1/TCA-3 release". Users can click on the green + icon to select an assay. Users can also click on the yellow highlighter icon to highlight the assay in the assay tree in the middle right section of the finder, as is shown in the figure. Alternatively, a user can browse the hierarchical assay tree. Clicking on a node in this tree will add the assay to the Current Selections section of the finder.

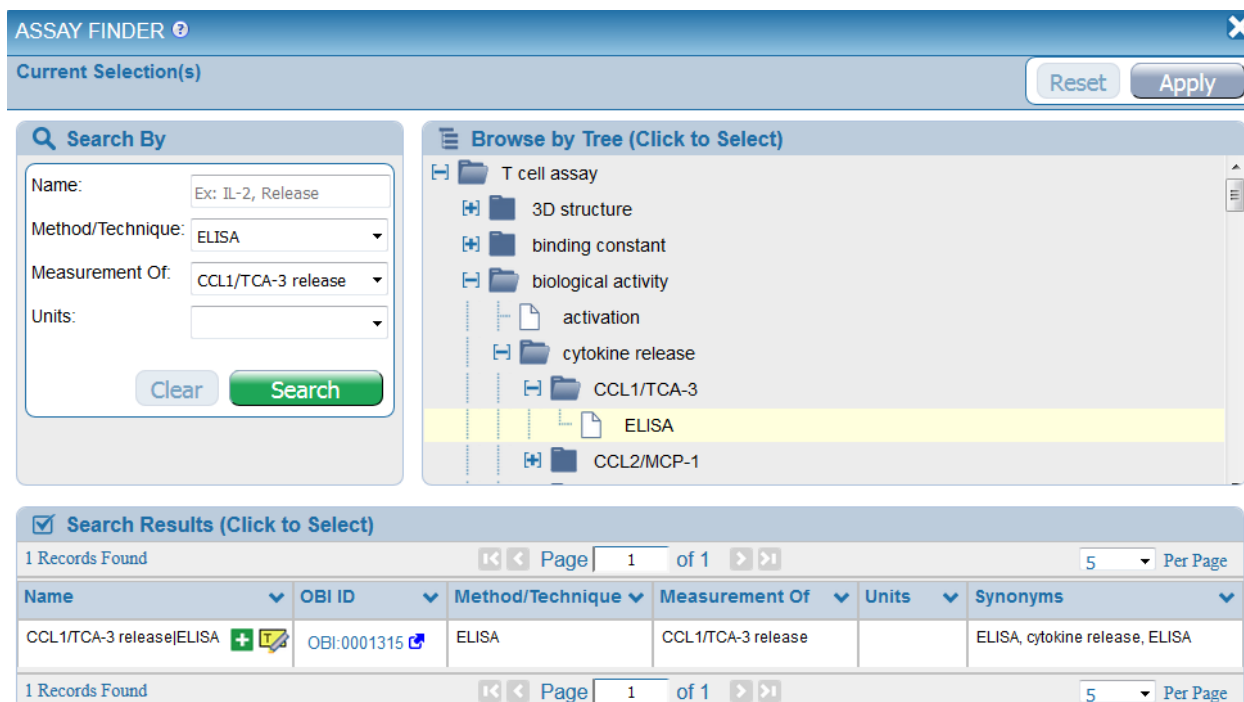


Figure 2.26 Assay Finder on the T Cell Advanced Search page. Assays are displayed in a tree structure and users can find displays by their method/technique and by the characters with which the assay name starts

2.2.4.3 Disease Finder

This query feature allows users to select a disease association based on the host disease state or status as captured in curation. Diseases are organized into a browsable tree structure. Upon the selection of host disease state/status, the system provides the user with a hierarchical *Disease Tree* that organizes the data at the highest level according to the five disease categories (Allergy, Autoimmunity, Infectious Disease, Additional Diseases by category, and Transplant-related Disease and Allo-reactivity) and then by the anatomical location of the disease (e.g. respiratory tract, gastrointestinal tract). In this way the user can either type in the disease name or synonym of interest, or navigate the Disease Tree by disease manifestation and physical location to see what is available. A node for healthy subjects is also included. The Disease Finder is fully functional for only Autoimmunity. The finder will be revised with an updated disease ontology and hierarchical tree during 2016 that will make it functional for the other disease categories. Infectious disease searches are best accommodated using the Organism Finder to specify the antigen.

Figure 2.27 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.

DISEASE FINDER

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

Reset Apply

Search By

Disease Name:

Disease ID:

ID Source:

Clear Search

Browse by Tree (Click to Select)

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

Search Results (Click to Select)

4 Records Found Page 1 of 1 5 Per Page

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

Figure 2.27 The disease finder is particularly helpful in specifying epitopes related to autoimmune diseases. In the example shown, diabetes is highlighted and selected.

2.2.4.4 Molecule Finder

The Molecule Finder is used to facilitate the selection of source antigens, immunogens, and epitopes. There are two versions of the Molecule Finder – one specifically for non-peptidic molecules found in the Epitope box in the results page, and another that includes peptidic and non-peptidic branches, found in the Antigen box in the results page. The former contains the structures curated by the Chemical Entities of Biological Interest (ChEBI) database. An example of the non-peptidic finder is shown in Figure 2.28.

NON-PEPTIDIC MOLECULE FINDER

Current Selection(s) x penicillin Reset Apply

Search By

Name:

Molecule ID:

Clear Search

Browse by Tree (Click to Select)

- [-] monobactam
- [-] oxacephem
- [-] penams
 - [-] penamcarboxylate
 - [-] penicillanic acid ester
 - [-] penicillanic acids
 - [-] 6-aminopenicillanic acid
 - [-] 6-formamidopenicillanic acid
 - [-] penicillin

Search Results (Click to Select)

19 Records Found Page 1 of 4 5 Per Page

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

Figure 2.28 The non-peptidic version of the Molecule Finder. This finder is accessed in the Epitope filter on the search results page.

With regard to the protein or peptidic branch of the Molecule Finder, individual GenPept proteins utilized by IEDB data are assigned to parent proteins from reference proteomes by sequence homology. These reference proteomes are graded by a star system described below that reflects the quality and completeness of each. An example of the star system and the protein tree can be seen in Figure 2.29.

The screenshot shows the MOLECULE FINDER interface. At the top, the current selection is 'Voltage-gated potassium channel' with two stars. Below this, there are two main sections: 'Search By' and 'Browse by Tree (Click to Select)'. The 'Search By' section has fields for Name (potassium channel), Molecule ID (Ex: P69710), and Source Organism (Ex: influenza, peanut). The 'Browse by Tree' section shows a hierarchical view of categories, with 'Voltage-gated potassium channel' selected and highlighted in yellow. Below these sections is a 'Search Results (Click to Select)' table showing 87 records found. The table has columns for Molecule Name, Synonyms, Database ID, and Organism Name. Three rows are visible, each representing a different type of potassium channel with its UniProt ID and organism (Homo sapiens).

Molecule Name	Synonyms	Database ID	Organism Name
ATP-sensitive inward rectifier potassium channel 1 ★★	Potassium channel, KCNJ11_HUMAN, Potassium channel, inwardly rectifying subfamily J member 1, ATP-regulated potassium channel ROM-K, inwardly rectifying subfamily J member 1, ATP-sensitive inward recti ...more...	UniProt [P48048]	Homo sapiens (human)
ATP-sensitive inward rectifier potassium channel 10 ★★	ATP-dependent inwardly rectifying potassium channel Kir4.1, ATP-sensitive inward rectifier potassium channel 10, inward rectifier K+ channel KIR1.2, Potassium channel, inwardly rectifying subfamily J ...more...	UniProt [P78508]	Homo sapiens (human)
ATP-sensitive inward rectifier potassium channel 11 ★★	Potassium channel, inwardly rectifying subfamily J member 11, Potassium channel, inwardly rectifying subfamily J member 11, inward rectifier K(+) channel Kir6.2, KCJ11_HUMAN, IKATP, ATP-sensitive inwa ...more...	UniProt [Q14654]	Homo sapiens (human)

Figure 2.29 An example of the protein branch of the Molecule Finder

Proteomes

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

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

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

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

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

Proteins

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

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

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

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

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

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

2.2.4.5 Organism Finder

The organism finder is used to facilitate the selection of a species or strain from the NCBI Taxonomy Database. The Organism finder allows the user to find species using their name, synonyms, or taxonomy identifier (assigned by NCBI). When the user performs a search, the system will display a tree structure. The user can search for a name or Organism ID in the "Search By" panel in the upper lefthand portion of the Finder. In the example shown in Figure 2.30, a search for "dengue" is performed, which results in 45 items being found. The user can select one or more of the items by clicking on the green "+" icon or clicking a branch in the tree. The user can also choose to highlight the item in the tree, as shown in the figure, by clicking the corresponding yellow highlighter icon. Synonyms for a selection are listed next to the organism name column in the search results table. When the Organism Finder is adjacent to a Host Organism field, only the source organisms for which data exist in the IEDB are displayed in the tree structure.

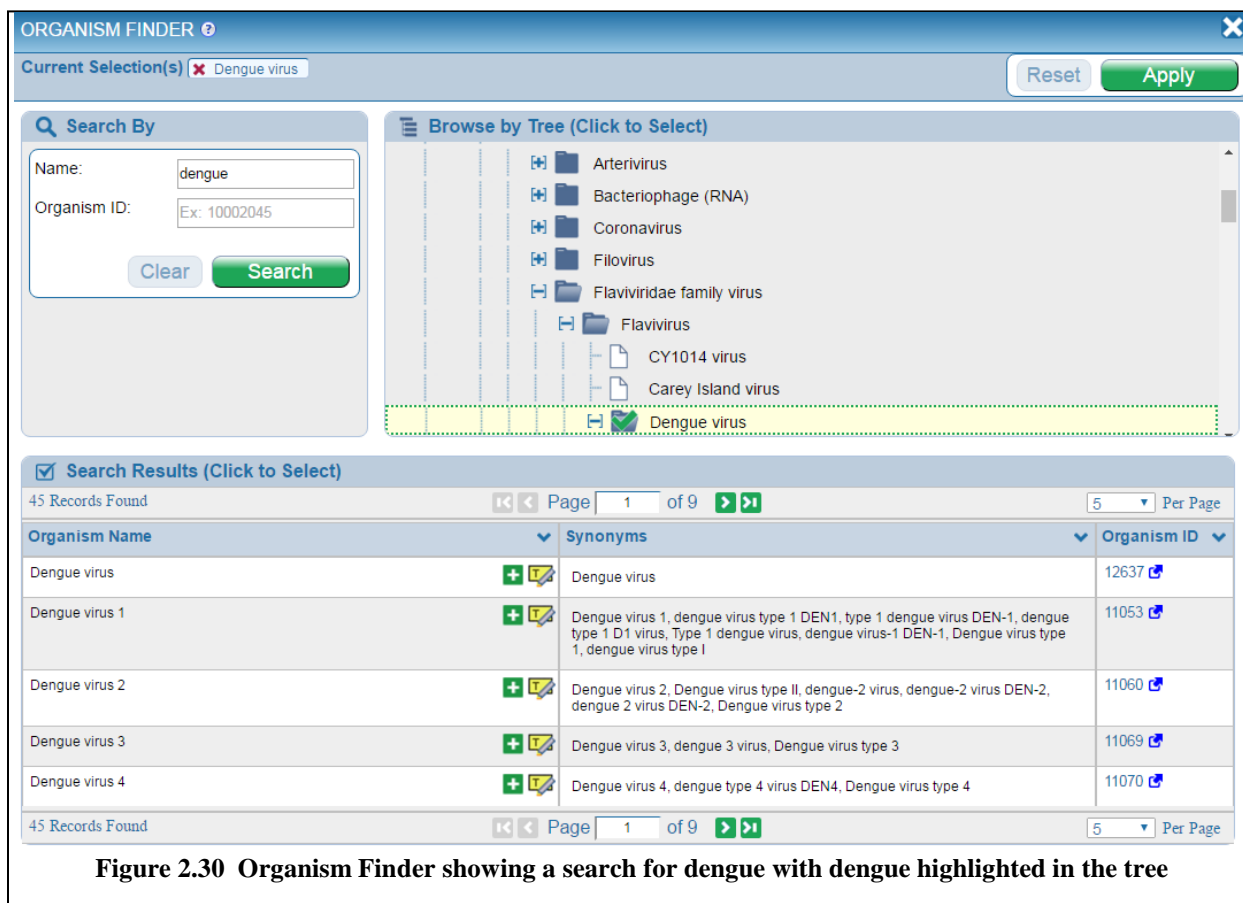


Figure 2.30 Organism Finder showing a search for dengue with dengue highlighted in the tree

2.2.4.6 Geolocation Finder

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

To use the Finder, simply navigate the tree by clicking open the continent of choice to find the country(ies) where study subjects were exposed to the immunogen tested in the immune epitope assays. Alternatively, one may use the "Search By" feature and type free text to search the tree. The Search By feature accepts synonyms as search criteria. Its use is shown in Figure 2.31 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.

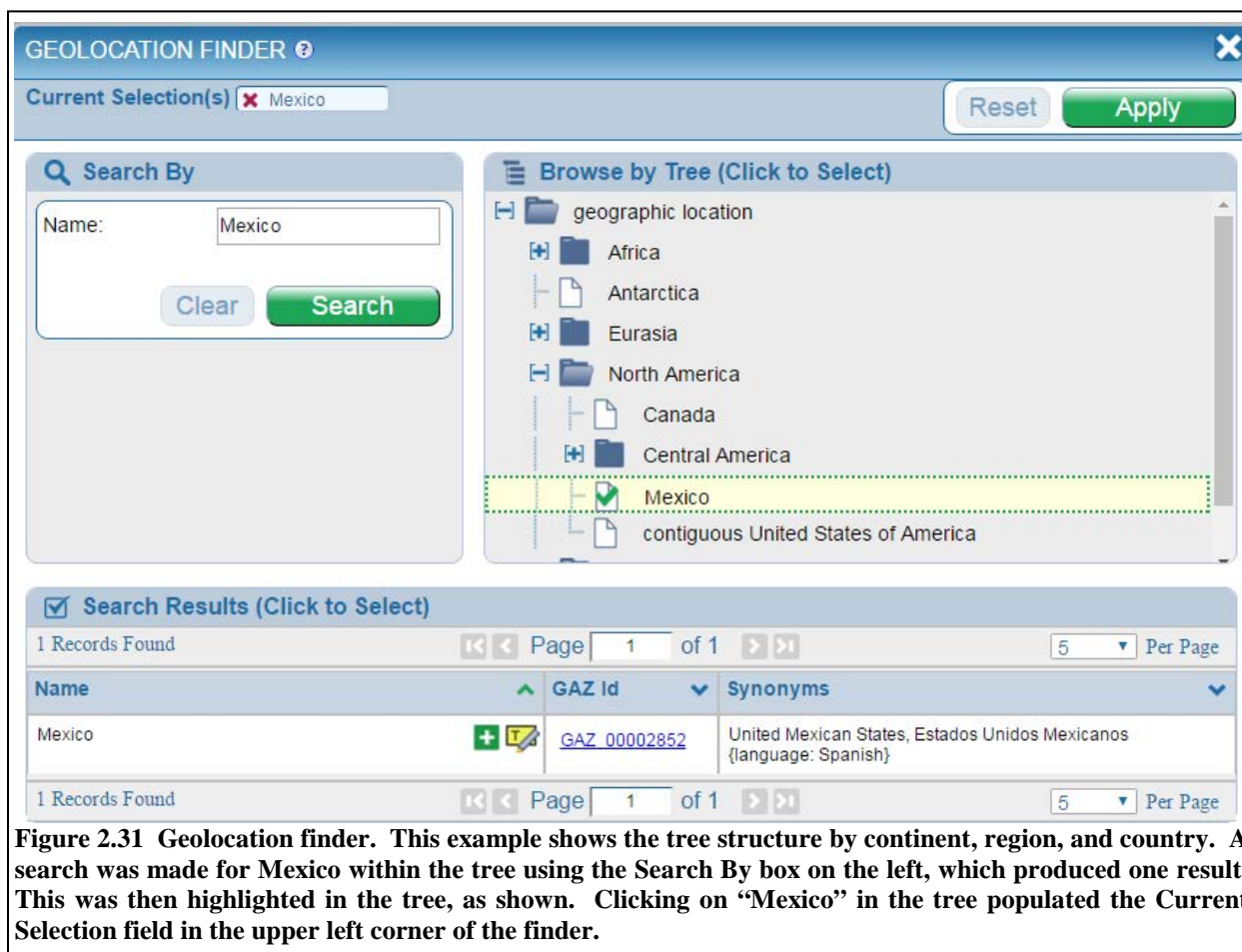


Figure 2.31 Geolocation finder. This example shows the tree structure by continent, region, and country. A search was made for Mexico within the tree using the Search By box on the left, which produced one result. This was then highlighted in the tree, as shown. Clicking on “Mexico” in the tree populated the Current Selection field in the upper left corner of the finder.

2.3 Tools

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

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

For prediction tools, it is important to differentiate between the **tool** making predictions, and the **method** used to generate that tool, given a set of training data. For example, the artificial neural network method or approach, when trained on a particular data set, will yield a prediction tool. As the ANN method is trained on different data sets, different corresponding prediction tools will result. In this way, the ANN

method can be used to develop an MHC class I prediction tool and a separate MHC class II prediction tool. These tools can be refined as more data are available for training. One benefit of the IEDB is that it allows implementing methods to automatically generate new prediction tools as the database grows.

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

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

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

2.3.1 T Cell Epitope Prediction

2.3.1.1 T Cell Epitopes - MHC binding prediction

The Analysis Resource provides tools for predicting peptide binding to MHC class I and II molecules. For class I binding predictions, users can select predictions performed with tools derived from nine different methods – IEDB Recommended, artificial neural network (ANN), stabilized matrix method (SMM), SMM with a peptide:MHC binding energy covariance matrix (SMMPMBEC), Scoring matrices derived from combinatorial peptide libraries (Comblib_Sidney2008), Consensus, NetMHCpan, PickPocket, and NetMHCcons. 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, 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 2.3.5.

2.3.1.1.1 Peptide Binding to MHC Class I Molecules

Users can select from nine different methods for predicting class I epitopes – ANN, SMM, SMMPMBEC, Comblib_Sidney2008, Consensus, NetMHCpan, NetMHCcons, PickPocket, 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 Lundegaard et al. (Nucleic Acids Res. 2008), 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 (Comlib_Sidney2008)

Comlib_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 Moutafsi 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; cattle; and pig. Predictions can be made for peptide sequences of 8 to 14 residues in length. All non 9mer predictions are made using approximations. Most HLA molecules have a strong preference for binding 9mers. The method has been trained on over 150,000 peptide/MHC interactions. Further information about the method can be found in Hoof I et al. Immunogenetics 2009 and Nielsen M et al. PLoS ONE 2007.

PickPocket

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

NetMHCcons

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

IEDB Recommended

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

2.3.1.1.2 Peptide Binding to MHC Class II Molecules

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

SMM-align

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

Sturniolo

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

Combinatorial Library

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

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

Consensus

The consensus method was developed by the IEDB team by exploiting features of three aforementioned methods. The Consensus method uses NN-align, SMM-align, and the combinatorial peptide scanning library. When the scanning library is not available for an allele, the Sturniolo method is used instead. A paper describing the original method was published by Wang et al. (*PLoS Comput Biol*, 2008), and a subsequent paper was published by Wang et al. (*BMC Bioinformatics*, 2010).

The datasets used in assessing the performance of the ARB, SMM-align, and Sturniolo methods and in developing the Consensus method, as described in Wang et al. (2008), can be found at <http://tools.iedb.org/main/datasets/>. 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).

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 all three human MHC class II isotypes- HLA-DR, HLA-DP, and HLA-DQ, in addition to mouse H-2-I molecules. A paper describing the method was published by Nielsen et al. in *PLoS Computational Biology*, 2008, and a paper describing the latest version 3.0 was published by Karosiene et al., in *Immunogenetics*, 2013.

IEDB Recommended

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

2.3.1.2 T Cell Epitopes – MHC I Processing Prediction

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

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

The proteasomal cleavage predictions evaluate how efficiently a peptide or its N-terminally prolonged precursors can be liberated from its source protein. The TAP transport predictions evaluate how efficiently a peptide or its N-terminal prolonged precursors are transported into the ER by TAP (Peters et al., Immunol, 2003). When this information is taken together and combined with MHC class I binding predictions, the tool yields a prediction of the efficiency with which a peptide is presented on the cell surface. The methods available are ANN, SMM, ARB, SMMPMBEC, Comlib_Sidney2008, NetMHCpan, PickPocket, NetMHCcons, and IEDB Recommended, which are described in Section 2.3.1.1.1.

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

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

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

NetCTL predicts CTL epitopes in protein sequences integrating prediction of peptide MHC binding, proteasomal C terminal cleavage and TAP transport efficiency. The method is described in detail in Larsen et al. (Eur J Immunol., 2005). NetCTLpan is an update to the original NetCTL server that allows for prediction of CTL epitope with restriction to any MHC molecules of known protein sequence (Stranzl et al., Immunogenetics, 2010).

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

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

2.3.1.3 T cell class I pMHC immunogenicity predictor

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

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

2.3.2 B Cell Epitope Prediction

2.3.2.1 Prediction of linear epitopes from protein sequence

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

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

BepiPred combines the predictions of a hidden Markov model and the propensity scale of Parker et al. It is described in Larsen et al. (Immunome Research, 2006).

2.3.2.2 DiscoTope - Prediction of epitopes from protein structure

DiscoTope was augmented in 2013 to include include version 2.0 as well as version 1.1. DiscoTope is designed specifically to predict discontinuous epitopes. It uses protein three-dimensional structural data

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

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

2.3.2.3 ElliPro - Epitope prediction based upon structural protrusion

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

2.3.2.4 Prediction of ImmunoGlobulin Structure (PIGS)

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

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

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

2.3.3 Epitope Analysis Tools

2.3.3.1 Population coverage

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

epitope sets. Accordingly, epitope-based vaccines or diagnostics can be designed to maximize population coverage, while minimizing complexity (that is, the number of different epitopes included in the diagnostic or vaccine), and also minimizing the variability of coverage obtained or projected in different ethnic groups.

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

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

2.3.3.2 Epitope conservancy

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

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

2.3.3.3 Epitope Cluster Analysis

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

2.3.3.4 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. Users can also input their own conformational epitopes and map them to protein structures. This feature is documented on the "Example 5" tab of the homology mapping web page. The 3D visualization is currently being updated to JSmol, a server side visualization package. The original EpitopeViewer uses a Java application. The migration to a server side application is motivated by the enhanced security features of modern web browsers that have made it difficult to spawn the Viewer.

2.3.3.5 Computational Methods for Mapping Mimotopes to Protein Antigens

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

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

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

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

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

2.3.4 IEDB Analysis Resource Labs

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

Two tools are currently available on the Labs web page:

RATE (Restrictor Analysis Tool for Epitopes): is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles.

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

2.3.5 Benchmark references and data sets

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

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

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

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

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

For the B cell predictions, the references are:

- Kringelum JV, Nielsen M, Padkjær SB, Lund O. Structural analysis of B-cell epitopes in antibody:protein complexes. *Mol Immunol*. 2013 Jan;53(1-2):24-34. doi: 10.1016/j.molimm.2012.06.001. Epub 2012 Jul 10. PubMed PMID: 22784991; PubMed Central PMCID: PMC3461403
- Kringelum JV, Lundegaard C, Lund O, Nielsen M. Reliable B cell epitope predictions: impacts of method development and improved benchmarking. *PLoS Comput Biol*. 2012;8(12):e1002829. doi: 10.1371/journal.pcbi.1002829. Epub 2012 Dec 27. PubMed PMID: 23300419; PubMed Central PMCID: PMC3531324.
- Rubinstein ND, Mayrose I, Martz E, Pupko T. Epitopia: a web-server for predicting B-cell epitopes. *BMC Bioinformatics*. 2009 Sep 14;10:287. doi: 10.1186/1471-2105-10-287. PubMed PMID: 19751513; PubMed Central PMCID: PMC2751785.

- Liang S, Zheng D, Standley DM, Yao B, Zacharias M, Zhang C. EPSVR and EPMeta: prediction of antigenic epitopes using support vector regression and multiple server results. *BMC Bioinformatics*. 2010 Jul 16;11:381. doi: 10.1186/1471-2105-11-381. PubMed PMID: 20637083; PubMed Central PMCID: PMC2910724.
- Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. *BMC Struct Biol*. 2007 Oct 2;7(1):64. PMID: 17910770

2.3.6 Other Ways to Access Tools

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

The Download tab takes the user to the IEDB Tools Download web page. For users from non-commercial organizations with batch processing needs, the MHC class I and II binding prediction tools, linear B cell epitope prediction tool, ElliPro, the epitope cluster analysis tool, and the MHC class I immunogenicity tool (added in 2015) are available as standalone scripts for download. These command line tools are kept in sync with the web tools and should therefore produce the same results as clicking through the web interface. They are freely available to non-profit/academic users through an open source license.

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

2.4 Help Overview

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

2.4.1 Support

The IEDB Solutions Center is the primary resource for information on using the website's features. The user can submit help requests, check on the status of requests, browse and search the knowledge base and forums, and link to help documentation, such as the Curation Manual. In order to submit 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.

The Solutions Center has extensive documentation organized in forums that address a variety of topics, including the epitope analysis and prediction tools, submitting data to the IEDB, querying the database,

and general announcements and updates. The Solutions Center is also the repository for the Annual Compendia, the list of meta-analyses and other papers published by the IEDB team, release notes for the main website and the Analysis Resource, and the IEDB quarterly newsletters, which were replaced in 2012 with topics in the News and Noteworthy forum. In addition, written and video tutorials, including the presentations from the 2015 IEDB User Workshop can be found there.

2.4.2 Help Request

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

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

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

2.4.3 Provide Feedback

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

2.4.4 Video Tutorials

There is a link to the IEDB video tutorials under the Help menu at the top of each web page. This link takes the user to the “How-to Videos” article in the Solutions Center in the Tutorials and Reference Materials folder. Most of the videos are edited versions of live presentations made at the 2015 IEDB User Workshop held in October 2015 at the NIAID facility in Rockville, Maryland. The videos are list in Table 2.1. An overview of the resource and information regarding the data structure and curation are presented first. The next category address the query and reporting features. Videos for all the tools in the Analysis Resource are presented next. Some videos for the legacy website have been retained because users can still access that website for some time to come, and because many of the concepts described within them can be applied to the redesigned website.

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

Table 2.1 Available IEDB video tutorials

2.5 More IEDB

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

2.5.1 Database Export

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

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

In addition to the XML export, the contents of the IEDB are exported weekly as a MySQL Structure Query Language (SQL) database. The database export page contains the complete database export in two formats, a single SQL script (iedb_public.sql.gz), and a TAR archive of MyISAM binary tables (iedb_public.tar.gz). Both export formats are generated from a 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 compressed file that contains an XML for each reference. The corresponding XSD files are also available for download.

Select compilations of data are available for download from the Database Export web page in CSV format in the section titled CSV Metric Exports. Users can download these files to conveniently obtain all the information in the IEDB for specific categories. Files are available for all epitopes, antigens, T cell assays, B cell assays, MHC ligand assays, and references. Separate files for source organism and non-peptidic epitopes were dropped in 2015, along with the compact format files. In addition to the files available on the Database Export web page, comma separated values (CSV) file exports are available on-demand from all list pages and list tabs throughout the site.

Information about our database export features can be found in our [developer's forum](#).

XML Database Export	
Complete Database Export	130MB
iedbAccessionList.zip	35kB
MhcAlleleNameList.zip	21kB
OrganismList.zip	23MB
AssayTypeList.zip	5kB

IEDB Schema	
Curation.xsd (Primary IEDB schema)	46kB
CurationSimpleTypes.xsd	151kB
iedbPDBViewerSchema.xsd	7kB
iedbAccessionList.xsd	909B
MhcAlleleNameList.xsd	1kB
OrganismList.xsd	751B
AssayTypeList.xsd	771B

MySQL Database Export	
SQL Statement Export	175MB
MyISAM Binary Export	322MB

Physical Entity Relationship Diagram	
iedb_public_erd.pdf	25kB

CSV Metric Exports	
epitope_full_v3.zip	15MB
antigen_full_v3.zip	755kB
tcell_full_v3.zip	15MB
bcell_full_v3.zip	19MB
mhc_ligand_full.zip	17MB
reference_full_v3.zip	9MB

[Archived Versions](#)

Figure 2.32 IEDB Database Export web page

2.5.2 Meta-Analyses

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

2.5.3 Citing the IEDB

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

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

1. The IEDB website should be cited using the URL: www.iedb.org
2. The journal reference for the IEDB was updated after the release of IEDB 3.0. The IEDB should be cited as:

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

2.5.4 Release Notes

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

2.5.5 Links to External Sources

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

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

2.6 Learn More

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

IMMUNE EPIOTOPE DATABASE AND ANALYSIS RESOURCE

Home | Specialized Searches | Analysis Resource | More IEDB

News and Updates

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

Support

- Ask a question or submit an idea
- Browse support topics
- Watch how to videos
- Get help with common searches
- Browse links to epitope resources

About the Data

Export all or part of the IEDB
Meta-analyses
Read about the data fields
See how the data is entered
Learn about the IEDB ontology

About Us

- Citation guidelines
- IEDB publications
- Acknowledgments
- Terms of use
- Compendia & newsletters

Latest Release Notes

IEDB 3.3 Release Notes (5 February 2015)
The redesigned IEDB website version 3.3.0 was deployed as the new production site on February 2015. Release highlights include:

IEDB Analysis Resource v2.13 release notes
v2.13 - February 2015
MHC I/II binding & processing

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

IEDB Analysis Resource v2.12 release notes
v2.12 - July 2014
NEW Tool added!

- Prediction of Immunoglobulin Structures...

IEDB v2.13.0 release notes
This topic contains the release notes for IEC version 2.13.0.

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

[View Previous Release Notes >>](#)

[Provide Feedback](#) | [Help Request](#) | [Solutions Center](#)

Data Last Updated: March 01, 2015

Figure 2.33 The Learn More page, accessed from the Welcome message in the upper left corner of the IEDB home page

2.6.1 Support

Each link is briefly described below.

Ask a question or submit an idea

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

Browse support topics

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

Watch how to videos

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

Get help with common searches

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

Browse links to epitope resources

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

2.6.2 About the Data

Each link is briefly described below.

Export all or part of the IEDB

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

Meta-analyses

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

Read about the data fields

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

See how the data is entered

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

Learn about the IEDB ontology

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

2.6.3 About Us

Citation Guidelines

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

IEDB Publications

A list of publications relevant to the IEDB can be found on the Publications page. They have been grouped into four categories – General IEDB, Epitope Meta-analyses, Analysis Resource, and Curation. This list is updated with each new release of the main website. A list of IEDB related publications can also be found in the Publications folder in the IEDB Solutions Center at <http://help.iedb.org/forums/95858-Publications>.

Acknowledgements

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

Terms of Use

The Terms of Use page is a collection of statements that outline the conditions related to using the IEDB system. The Terms of use includes our privacy notice, copyright information, and various disclaimers.

The IEDB privacy policy describes what user information is collected, the circumstances for collecting it, and how it is used. Personal information about users is not collected unless the users choose to provide it.

Compendia and newsletters

A variety of IEDB reference materials can be found on http://www.iedb.org/documents_v3.php. 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. The IEDB quarterly newsletter archive is also found on this page. The newsletters ceased production in mid-2011 to be replaced by the New and Noteworthy forum in the IEDB Solutions Center. Summaries of these articles can be seen in the News and Updates section on the Learn More page.

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 ten 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 2015, 12 articles were published, seven in 2014, ten in 2013, six were published in 2012, three in 2011, nine in 2010, seven in 2009, nine in 2008, twelve in 2007, five in 2006, six in 2005, and one in 2004. In all, the team has written 87 scientific articles about the IEDB in the last 11 years.

3.1.1 2015

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

10. Andreatta M, Nielsen M. *Gapped sequence alignment using artificial neural networks: application to the MHC class I system*. *Bioinformatics*. 2015 Oct 29. pii: btv639. [Epub ahead of print] PubMed PMID: 26515819
11. Sette A, Paul S, Vaughan K, Peters B. *The Use of the Immune Epitope Database to Study Autoimmune Epitope Data Related to Alopecia Areata*. *J Investig Dermatol Symp Proc*. 2015 Nov;17(2):36-41. doi: 10.1038/jidsymp.2015.39. Review. PubMed PMID: 26551944
12. Vita R, Vasilevsky N, Bandrowski A, Haendel M, Sette A, Peters B. *Reproducibility and Conflicts in Immune Epitope Data*. *Immunology*. 2015 Dec 17. doi: 10.1111/imm.12566. [Epub ahead of print] PubMed PMID: 26678806

3.1.2 2014

13. Ponomarenko J, Vaughan K, Sette A, Maurer-Stroh S. Conservancy of mAb Epitopes in Ebola virus Glycoproteins of Previous and 2014 Outbreaks. *PLOS Currents Outbreaks*. 2014 Nov 3. Edition 1.
14. Vaughan K, Peters B, Mallone R, von Herrath M, Roep BO, Sette A. Navigating diabetes-related immune epitope data: resources and tools provided by the Immune Epitope Database (IEDB). *Immunome Res*. 2013;9(1). doi: 10.4172/1745-7580.1000063. PubMed PMID: 25140192; PubMed Central PMCID: PMC4134942.
15. Vaughan K, Seymour E, Peters B, Sette A. Substantial gaps in knowledge of Bordetella pertussis antibody and T cell epitopes relevant for natural immunity and vaccine efficacy. *Hum Immunol*. 2014 May;75(5):440-451. doi: 10.1016/j.humimm.2014.02.013. Epub 2014 Feb 12. Review. PubMed PMID: 24530743.
16. Trolle T, Nielsen M. NetTepi: an integrated method for the prediction of T cell epitopes. *Immunogenetics*. 2014 May 27. [Epub ahead of print] PubMed PMID: 24863339
17. Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B. Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. *BMC Bioinformatics*. 2014 Jul 14;15:241. doi: 10.1186/1471-2105-15-241. PubMed PMID: 25017736; PubMed Central PMCID: PMC4111843.
18. Shirai H, Prades C, Vita R, Marcatili P, Popovic B, Xu J, Overington JP, Hirayama K, Soga S, Tsunoyama K, Clark D, Lefranc MP, Ikeda K. Antibody informatics for drug discovery. *Biochim Biophys Acta*. 2014 Nov;1844(11):2002-2015. doi: 10.1016/j.bbapap.2014.07.006. Epub 2014 Aug 8. Review. PubMed PMID: 25110827.
19. Vita R, Overton JA, Greenbaum JA, Ponomarenko J, Clark JD, Cantrell JR, Wheeler DK, Gabbard JL, Hix D, Sette A, Peters B. The immune epitope database (IEDB) 3.0. *Nucleic Acids Res*. 2014 Oct 9. pii: gku938. [Epub ahead of print] PubMed PMID: 25300482.

3.1.3 2013

20. 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.
21. Vita R, Overton JA, Greenbaum JA, Sette A; OBI consortium, Peters B. Query enhancement through the practical application of ontology: the IEDB and OBI. *J Biomed Semantics*. 2013 Apr 15;4 Suppl 1:S6. doi: 10.1186/2041-1480-4-S1-S6. Epub 2013 Apr 15. PubMed PMID: 23734660; PubMed Central PMCID: PMC3633001.

22. Jessen LE, Hoof I, Lund O, Nielsen M. SigniSite: Identification of residue-level genotype-phenotype correlations in protein multiple sequence alignments. *Nucleic Acids Res.* 2013 Jul 1;41(Web Server issue):W286-91. doi: 10.1093/nar/gkt497. Epub 2013 Jun 12. PMID: 23761454; PMCID: PMC3692133
23. Jørgensen KW, Rasmussen M, Buus S, Nielsen M. NetMHCstab - predicting stability of peptide:MHC-I complexes; impacts for CTL epitope discovery. *Immunology.* 2013 Aug 8. doi: 10.1111/imm.12160. PubMed PMID: 23927693; PubMed Central PMCID: PMC3893846
24. Schubert B, Lund O, Nielsen M. Evaluation of peptide selection approaches for epitope-based vaccine design. *Tissue Antigens.* 2013 Oct;82(4):243-51. doi: 10.1111/tan.12199. PubMed PMID: 24461003
25. Karosiene E, Rasmussen M, Blicher T, Lund O, Buus S, Nielsen M. NetMHCIIpan-3.0, a common pan-specific MHC class II prediction method including all three human MHC class II isotypes, HLA-DR, HLA-DP and HLA-DQ. *Immunogenetics.* 2013 Oct;65(10):711-24. doi: 10.1007/s00251-013-0720-y. Epub 2013 Jul 31. PubMed PMID: 23900783.
26. Vaughan K, Peters B, O'Connor KC, Martin R, Sette A. A molecular view of multiple sclerosis and experimental autoimmune encephalitis: What can we learn from the epitope data? *J Neuroimmunol.* 2013 Dec 12. pii: S0165-5728(13)00340-8. doi: 10.1016/j.jneuroim.2013.12.009. PubMed PMID: 24365494.
27. Paul S, Kolla RV, Sidney J, Weiskopf D, Fleri W, Kim Y, Peters B, Sette A. Evaluating the immunogenicity of protein drugs by applying in vitro MHC binding data and the immune epitope database and analysis resource. *Clin Dev Immunol.* 2013;2013:467852. doi: 10.1155/2013/467852. Epub 2013 Oct 8. PubMed PMID: 24222776; PubMed Central PMCID: PMC3816028.
28. Calis JJ, Maybeno M, Greenbaum JA, Weiskopf D, De Silva AD, Sette A, Kesmir C, Peters B. Properties of MHC class I presented peptides that enhance immunogenicity. *PLoS Comput Biol.* 2013 Oct;9(10):e1003266. doi: 10.1371/journal.pcbi.1003266. Epub 2013 Oct 24. PubMed PMID: 24204222; PubMed Central PMCID: PMC3808449.
29. Paul S, Weiskopf D, Angelo MA, Sidney J, Peters B, Sette A. HLA Class I Alleles Are Associated with Peptide-Binding Repertoires of Different Size, Affinity, and Immunogenicity. *J Immunol.* 2013 Dec 15;191(12):5831-9. doi: 10.4049/jimmunol.1302101. Epub 2013 Nov 4. PubMed PMID: 24190657; PubMed Central PMCID: PMC3872965.

3.1.4 2012

30. Kim Y, Ponomarenko J, Zhu Z, Tamang D, Wang P, Greenbaum J, Lundegaard C, Sette A, Lund O, Bourne PE, Nielsen M, Peters B. Immune epitope database analysis resource. *Nucleic Acids Res.* 2012 Jul;40 (Web Server issue):W525-30. Epub 2012 May 18. PubMed PMID: 22610854.
31. Kim Y, Vaughan K, Greenbaum J, Peters B, Law M, Sette A. A Meta-Analysis of the Existing Knowledge of Immunoreactivity against Hepatitis C Virus (HCV). *PLoS One.* 2012;7(5):e38028. Epub 2012 May 31. PubMed PMID: 22675428; PubMed Central PMCID: PMC3364976.
32. 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

33. Salimi N, Fleri W, Peters B, Sette A. The Immune Epitope Database: A Historical Retrospective of the First Decade. *Immunology*. 2012 Jun 8. doi:10.1111/j.1365-2567.2012.03611.x. [Epub ahead of print] PubMed PMID: 22681406.
34. Vaughan K, Kim Y, Sette A. A comparison of epitope repertoires associated with myasthenia gravis in humans and nonhuman hosts. *Autoimmune Dis*. 2012;2012:403915. doi: 10.1155/2012/403915. Epub 2012 Dec 2. PubMed PMID: 23243503; PubMed Central PMCID: PMC3518085.
35. Vaughan K, Peters B, Larche M, Pomes A, Broide D, Sette A. Strategies to Query and Display Allergy-Derived Epitope Data from the Immune Epitope Database. *Int Arch Allergy Immunol*. 2012 Nov 21;160(4):334-345. [Epub ahead of print] PubMed PMID: 23172234.

3.1.5 2011

36. Seymour E., Damle R., Sette A., Peters B. (2011). "Cost sensitive hierarchical document classification to triage PubMed abstracts for manual curation." *BMC Bioinformatics* 12(1): 482. [Epub ahead of print]. PMID: 22182279.
37. Vaughan K, Greenbaum J, Kim Y, Vita R, Chung J, Peters B, Broide D, Goodman R, Grey H, Sette A. Towards defining molecular determinants recognized by adaptive immunity in allergic disease: an inventory of the available data. *J Allergy (Cairo)*. 2010;2010:628026. Epub 2011 Feb 13. PubMed PMID: 21403821
38. Vita R, Peters B, Josephs Z, de Matos P, Ennis M, Turner S, Steinbeck C, Seymour E, Zarebski L, Sette A. (2011). "A Model for Collaborative Curation, The IEDB and ChEBI Curation of Non-peptidic Epitopes." *Immunome Res*. 2011 Apr 1;7(1):1-8. PubMed PMID: 21897450

3.1.6 2010

39. Brinkman RR, Courtot M, Derom D, Fostel JM, He Y, Lord P, Malone J, Parkinson H, Peters B, Rocca-Serra P, Ruttenger A, Sansone SA, Soldatova LN, Stoeckert CJ Jr, Turner JA, Zheng J; OBI consortium. Modeling biomedical experimental processes with OBI. *J Biomed Semantics*. 2010 Jun 22;1 Suppl 1:S7. PubMed PMID: 20626927
40. Diehl AD, Augustine AD, Blake JA, Cowell LG, Gold ES, Gondré-Lewis TA, Masci AM, Meehan TF, Morel PA, Nijnik A, Peters B, Pulendran B, Scheuermann RH, Yao QA, Zand MS, Mungall CJ. "Hematopoietic cell types: Prototype for a revised cell ontology. *J Biomed Inform*. 2010 Feb 1. [Epub ahead of print] PMID: 20123131
41. Kim Y, Sette A, Peters B. Applications for T-cell epitope queries and tools in the Immune Epitope Database and Analysis Resource. *J Immunol Methods*. 2010 Oct 31. [Epub ahead of print] PubMed PMID: 21047510.
42. Nielsen M, Lund O, Buus S, Lundegaard C. MHC class II epitope predictive algorithms. *Immunology*. 2010 Jul;130(3):319-28. Epub 2010 Apr 12. Review. PubMed PMID: 20408898;
43. Ponomarenko J, Papangelopoulos N, Zajonc DM, Peters B, Sette A, Bourne PE. IEDB-3D: structural data within the immune epitope database. *Nucleic Acids Res*. 2010 Oct 28. [Epub ahead of print] PubMed PMID: 21030437.
44. Salimi N, Fleri W, Peters B, Sette A. Design and utilization of epitope-based databases and predictive tools. *Immunogenetics*. 2010 Apr;62(4):185-96. Epub 2010 Mar 6. Review. PubMed PMID: 20213141; PubMed Central PMCID: PMC2843836.
45. Vaughan K, Greenbaum J, Blythe M, Peters B, Sette A. Meta-analysis of all immune epitope data in the Flavivirus genus: inventory of current immune epitope data status in the context of virus

immunity and immunopathology. *Viral Immunol.* 2010 Jun;23(3):259-84. PubMed PMID: 20565291; PubMed Central PMCID: PMC2942863.

46. 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.
47. Zhang H, Wang P, Papangelopoulos N, Xu Y, Sette A, Bourne PE, Lund O, Ponomarenko J, Nielsen M, Peters B. Limitations of Ab initio predictions of peptide binding to MHC class II molecules. *PLoS One.* 2010 Feb 17;5(2):e9272. PubMed PMID: 20174654; PubMed Central PMCID: PMC2822856.

3.1.7 2009

48. Davies V, Vaughan K, Damle R, Peters B, Sette A. Classification of the universe of immune epitope literature: representation and knowledge gaps. *PLoS One.* 2009 Sep 14;4(9):e6948. PubMed PMID: 19774228;
49. Greenbaum JA, Kotturi MF, Kim Y, Oseroff C, Vaughan K, Salimi N, Vita R, Ponomarenko J, Scheuermann RH, Sette A, Peters B. Pre-existing immunity against swine-origin H1N1 influenza viruses in the general human population. *Proc Natl Acad Sci U S A.* 2009 Dec 1;106(48):20365-70. Epub 2009 Nov 16. PubMed PMID: 19918065; PubMed Central PMCID: PMC2777968.
50. Hoof I, Peters B, Sidney J, Pedersen LE, Sette A, Lund O, Buus S, Nielsen M, NetMHCpan, a method for MHC class I binding prediction beyond humans. *Immunogenetics.* 2009 Jan;61(1):1-13. PMID: 19002680
51. 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.
52. Vaughan K, Blythe M, Greenbaum J, Zhang Q, Peters B, Doolan DL, Sette A, Meta-analysis of immune epitope data for all Plasmodia: overview and applications for malarial immunobiology and vaccine-related issues. *Parasite Immunol.* 2009 Feb;31(2):78-97. [PMID: 19149776]
53. Vita R, Zarebski L, Greenbaum JA, Emami H, Hoof I, Salimi N, Damle R, Sette A, Peters B. The Immune Epitope Database 2.0. *Nucleic Acids Res.* 2009 Nov 11. [Epub ahead of print] PubMed PMID: 19906713.
54. Zhang H, Lund O, Nielsen M. The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: Application to MHC-peptide binding. *Bioinformatics.* 2009 Mar 17. PMID: 19297351

3.1.8 2008

55. Lundegaard C., K. Lamberth, M. Harndahl, S. Buus, O. Lund, M. Nielsen. (2008). "NetMHC-3.0: accurate web accessible predictions of human, mouse and monkey MHC class I affinities for peptides of length 8-11." *Nucleic Acids Res.* 2008 36:W509-12. PMID: 18996943
56. Nielsen, M., C. Lundegaard, T. Blicher, B. Peters, A. Sette, S. Justesen, S. Buus, O. Lund. (2008). "Quantitative Predictions of Peptide Binding to Any HLA-DR Molecule of Known Sequence: NetMHCIIpan." *PLoS Computational Biology* 4(7). PMID: 18604266
57. Ponomarenko J, H. H. Bui, W. Li, N. Fusseder, P. E. Bourne, A. Sette, B. Peters. (2008). "ElliPro: a new structure-based tool for the prediction of antibody epitopes." *BMC Bioinformatics*, 9(514). PMID: 19055730

58. Ponomarenko J. V., M. H. C. van Regenmortel (2008) "B-cell epitope prediction." *Structural Bioinformatics*, Ed: Bourne PE, Gu J. Wiley-Liss; 2 edition.
59. Rapin N., I. Hoof, O. Lund, M. Nielsen. (2008). "MHC motif viewer." *Immunogenetics*. 60(12): 759-65. PMID: 18766337
60. Vita R., B. Peters, A. Sette. (2008). "The Curation Guidelines of the Immune Epitope Database and Analysis Resource." *Cytometry A* 73(11): 1066-1070. PMID: 18688821
61. 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
62. Zarebski L. M., K. Vaughan, J. Sidney, B. Peters, H. Grey, K. D. Janda, A. Casadevall, A. Sette. (2008). "Analysis of epitope information related to *Bacillus anthracis* and *Clostridium botulinum*." *Expert Rev Vaccines* 7(1): 55-74. PMID: 18251694
63. Zhang, Q., P. Wang, et al. (2008). "Immune epitope database analysis resource (IEDB-AR)." *Nucleic Acids Research* 36: W513-W518. PMID: 18515843

3.1.9 2007

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

73. Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. *BMC Struct Biol.* 2007 Oct 2;7(1):64. PMID: 17910770
74. Sette A, Peters B., Immune epitope mapping in the post-genomic era: lessons for vaccine development. *Curr Opin Immunol.* 2007 Feb;19(1):106-10. PMID: 17113275
75. Wang P, Morgan AA, Zhang Q, Sette A, Peters B. Automating document classification for the Immune Epitope Database. *BMC Bioinformatics.* 2007 Jul 26;8:269. PMID: 17655769

3.1.10 2006

76. Bui HH, Sidney J, Dinh K, Southwood S, Newman MJ, Sette A. Predicting population coverage of T-cell epitope-based diagnostics and vaccines. *BMC Bioinformatics.* 2006 Mar 17;7(1):153. PMID: 16545123
77. 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
78. Salimi N, R. Vita. (2006). "The biocurator: connecting and enhancing scientific data". *PLoS Comput Biol* 2(10) :e125. PMID: 17069454
79. Sette, A., H. H. Bui, S. Buus, W. Fleri, R. Kubo, O. Lund, D. Nemazee, J. V. Ponomarenko, M. Sathiamurthy, S. Stewart, S. Way, S. S. Wilson, B. Peters. (2006). "The Immune Epitope Database and Analysis Resource." *Pattern Recognition in Bioinformatics: International Workshop, Hong Kong, China, August 20, 2006 : Proceedings, Springer, Jagath C. Rajapakse, Limsoon Wong, Raj Acharya (Eds).* ISBN: 3540374469 9783540374466
80. Vita R, K. Vaughan, L. Zarebski, N. Salimi, W. Fleri, H. Grey, M. Sathiamurthy, J. Mokili, H. H. Bui, P. E. Bourne, J. V. Ponomarenko, R. de Castro Jr, R. K. Chan, J. Sidney, S. S. Wilson, S. Stewart, S. Way, B. Peters, A. Sette. (2006) "Curation of complex, context-dependent immunological data." *BMC Bioinformatics.* 12(7): 341. PMID: 16836764

3.1.11 2005

81. Bui HH, Sidney J, Peters B, Sathiamurthy M, Sinichi A, Purton KA, Mothé BR, Chisari FV, Watkins DI, Sette A. Automated generation and evaluation of specific MHC binding predictive tools: ARB matrix applications. *Immunogenetics.* 2005 Jun;57(5):304-14. Epub 2005 May 3. PMID: 15868141
82. Peters B, Sette A. Generating quantitative models describing the sequence specificity of biological processes with the stabilized matrix method. *BMC Bioinformatics.* 2005 May 31;6:132. PMID: 15927070
83. Peters, B., J. Sidney, P. Bourne, H. H. Bui, S. Buus, G. Doh, W. Fleri, M. Kronenberg, R.Kubo, O. Lund, D. Nemazee, J. V. Ponomarenko, M. Sathiamurthy, S. Schoenberger, S. Stewart, P. Surko, S. Way, S. Wilson, A. Sette. (2005). "The design and implementation of the immune epitope database and analysis resource." *Immunogenetics* 57(5): 326-336. PMID: 15895191
84. Peters, B., J. Sidney, P. Bourne, H. H. Bui, S. Buus, G. Doh, W. Fleri, M. Kronenberg, R.Kubo, O. Lund, D. Nemazee, J. V. Ponomarenko, M. Sathiamurthy, S. Schoenberger, S. Stewart, P. Surko, S. Way, S. Wilson, A. Sette. (2005). "The Immune Epitope Database and Analysis Resource: From Vision to Blueprint." *PLoS Biology* 3(3). PMID: 15760272
85. Sathiamurthy, M., B. Peters, H. H. Bui, J. Sidney, J. Mokili, S. S. Wilson, W. Fleri, D. McGuinness, P. Bourne, A. Sette. (2005). "An ontology for immune epitopes: application to the

design of a broad scope database of immune reactivities." *Immunome Res* 1(2): 1745-7580. PMID: 16305755

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

3.1.12 2004

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

3.2 Publications Citing the IEDB in 2014

In 2015, 462 references cited at least one of the 87 papers written by the IEDB team over the past eleven years. This represents an increase of 33 citations over 2014. The citation list was compiled by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the 87 papers. The list excludes self-citations by the 87 IEDB papers. This total may increase over time since these databases may not include references published late in 2015.

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* (2014) paper, and thus is listed under General IEDB and has an [AR, G] to indicate the Analysis Resource citation. Any paper that has "General" as one of its categories has been listed in the General category below. All papers having "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, 532 references cited at least one of the 87 papers written by the IEDB team in the past eleven years. The "General" category IEDB papers were cited 165 times in 2015. The Analysis Resource papers received 255 citations. The Curation category papers received 5. The meta-analysis papers received 37. There may be an overlap in citations among these categories.

Adhering to the hierarchy, 462 references cited at least one of the 87 papers written by the IEDB team in the past eleven years. The "General" category IEDB papers were cited 165 times in 2015. The Analysis Resource papers received 255 citations. The Curation category papers received 5. The meta-analysis papers received 37. The hierarchical list is presented below.

3.2.1 General IEDB

1. Abeyruwan, S.W. (2015). "Learnable knowledge for autonomous agents." http://scholarlyrepository.miami.edu/oa_dissertations/1462/. [Thesis]. [G]
2. Abts, K.C., Ivy, J.A., and DeWoody, J. (2015). "Immunomics of the koala (*Phascolarctos cinereus*)." *Immunogenetics* 67(5-6): 305-321. [G]
3. Abualrous, E.T., Saini, S.K., Ramnarayan, V.R., Ilca, F.T., Zacharias, M., and Springer, S. (2015). "The carboxy terminus of the ligand peptide determines the stability of the MHC Class I molecule H-2K(b): A combined molecular dynamics and experimental study." *PLOS One* 10(8): e0135421. doi: 10.1371/journal.pone.0135421. [G]

4. Afzal, M., Khurshid, S., Khalid, R., Paracha, R.Z., Khan, I.H., and Akhtar, M. (2015). "Fusion of selected regions of mycobacterial antigens for enhancing sensitivity in serodiagnosis of tuberculosis." *Journal of Microbiological Methods* 115: 104-111. [G]
5. Ali, M.T. and Islam, M.O. (2015). "A highly conserved GEQYQQLR epitope has been identified in the nucleoprotein of Ebola virus by using an in silico approach." *Advances in Bioinformatics* 2015: 278197. doi: 10.1155/2015/278197. [G, AR]
6. Allen, J., de Beaumont, W., Galescu, L., and Teng, C.M. (2015). "Complex event extraction using DRUM." *ACL-IJCNLP 2015 Workshop on Biomedical Natural Language Processing*: 1-11. [G]
7. Angelova, M., Charoentong, P., Hackl, H., Fischer, M.L., Snajder, R., Krogsdam, A.M., Waldner, M., Bindea, G., Mlecnik, B., Galon, J., and Trajanoski, Z. (2015). "Characterization of the immunophenotypes and antigenomes of colorectal cancers reveals distinct tumor escape mechanisms and novel targets for immunotherapy." *Genome Biol* 16: 64. doi: 10.1186/s13059-015-0620-6. [G, AR]
8. Anugraha, G., Madhumathi, J., Prince, P., Prita, P., Khatri, V., Amdare, N., Reddy, M., V, and Kaliraj, P. (2015). "Chimeric epitope vaccine from multistage antigens for Lymphatic filariasis." *Scandinavian Journal of Immunology* 82(4): 380-389. [G]
9. Axelsson-Robertson, R., Ju, J.H., Kim, H.Y., Zumla, A., and Maeurer, M. (2015). "Mycobacterium tuberculosis-specific and MHC class I-restricted CD8+T-cells exhibit a stem cell precursor-like phenotype in patients with active pulmonary tuberculosis." *International Journal of Infectious Diseases* 32: 13-22. [G]
10. Axelsson-Robertson, R., Rao, M., Loxton, A.G., Walzl, G., Bates, M., Zumla, A., and Maeurer, M. (2015). "Frequency of Mycobacterium tuberculosis-specific CD8+T-cells in the course of anti-tuberculosis treatment." *International Journal of Infectious Diseases* 32: 23-29. [G]
11. Backert, L. and Kohlbacher, O. (2015). "Immunoinformatics and epitope prediction in the age of genomic medicine." *Genome Medicine* 7: 119. doi: 10.1186/s13073-015-0245-0. [G, AR]
12. Baharia, R.K., Tandon, R., Sharma, T., Suthar, M.K., Das, S., Siddiqi, M.I., Saxena, J.K., Sunder, S., and Dube, A. (2015). "Recombinant NAD-dependent SIR-2 protein of *Leishmania donovani*: Immunobiochemical characterization as a potential vaccine against visceral Leishmaniasis." *PLOS Neglected Tropical Diseases* 9(3): e0003557. doi: 10.1371/journal.pntd.0003557. [G, AR]
13. Balkhi, M.Y., Ma, Q., Ahmad, S., and Junghans, R.P. (2015). "T cell exhaustion and Interleukin 2 downregulation." *Cytokine* 71(2): 339-347. [G, AR]
14. Barton, A., Duvauferrier, R., and Burgun, A. (2015). "Formalization of indicators of diagnostic performance in a realist ontology." *International Conference on Biomedical Ontology 2015*. [G]
15. Bastian, F.B., Chibucos, M.C., Gaudet, P., Giglio, M., Holliday, G.L., Huang, H., Lewis, S.E., Niknejad, A., Orchard, S., Poux, S., Skunca, N., and Robinson-Rechavi, M. (2015). "The confidence information ontology: A step towards a standard for asserting confidence in annotations." *Database-the Journal of Biological Databases and Curation* 2015: bav043. doi: 10.1093/database/bav043. [G]
16. Batrancourt, B., Dojat, M., Gibaud, B., and Kassel, G. (2015). "A multilayer ontology of instruments for neurological, behavioral and cognitive assessments." *Neuroinformatics* 13(1): 93-110. [G]
17. Belhajjame, K., Zhao, J., Garijo, D., Gamble, M., Hettne, K., Palma, R., Mina, E., Corcho, O., Gomez-Perez, J.M., Bechhofer, S., Klyne, G., and Goble, C. (2015). "Using a suite of ontologies for preserving workflow-centric research objects." *Journal of Web Semantics* 32: 16-42. [G]

18. Bolton, E. (2015). "Reporting biological assay screening results for maximum impact." *Drug Discovery Today: Technologies* 14: 31-36. [G]
19. Bona, J., Kohn, G., and Ruttenberg, A. (2015). "Ontology-driven patient history questionnaires." *American Medical Informatics Association 2015 Annual Symposium*. [G]
20. Bujotzek, A., Lipsmeier, F., Harris, S.F., Benz, J., Kuglstatter, A., and Georges, G. (2015). "VH-VL orientation prediction for antibody humanization candidate selection: A case study." *mAbs*. doi: 10.1080/19420862.2015.1117720. [G]
21. Calis, J.J., Reinink, P., Keller, C., Kloetzel, P.M., and Kesmir, C. (2015). "Role of peptide processing predictions in T cell epitope identification: Contribution of different prediction programs." *Immunogenetics* 67(2): 85-93. [G]
22. Caoili, S.E. (2015). "An integrative structure-based framework for predicting biological effects mediated by anti-peptide antibodies." *Journal of Immunological Methods* 427: 19-29. [G, AR]
23. Capone, G., Fasano, C., Lucchese, G., Calabro, M., and Kanduc, D. (2015). "EBV-associated cancer and autoimmunity: Searching for therapies." *Vaccines* 3(1): 74-89. [G]
24. Caron, E., Kowalewski, D.J., Koh, C.C., Sturm, T., Schuster, H., and Aebersold, R. (2015). "Analysis of major histocompatibility complex (MHC) immunopeptidomes using mass spectrometry." *Molecular & Cellular Proteomics* 14(12): 3105-3117. [G, AR]
25. Carrillo-Vazquez, J.P., Correa-Basurto, J., Garcia-Machorro, J., Campos-Rodriguez, R., Moreau, V., Rosas-Trigueros, J.L., Reyes-Lopez, C.A., Rojas-Lopez, M., and Zamorano-Carrillo, A. (2015). "A continuous peptide epitope reacting with pandemic influenza AH1N1 predicted by bioinformatic approaches." *Journal of Molecular Recognition* 28(9): 553-564. [G, AR]
26. Ceusters, W., Nasri-Heir, C., Alnaas, D., Cairns, B., Michelotti, A., and Ohrbach, R. (2015). "Perspectives on next steps in classification of oro-facial pain - part 3: Biomarkers of chronic oro-facial pain - from research to clinic." *Journal of Oral Rehabilitation* 42(12): 956-966. [G]
27. Chailyan, A. and Marcatili, P. (2015). "Structural characterization of peptide antibodies." *Peptide Antibodies: Methods and Protocols* 1348: 205-214. [G]
28. Cheung, N.J., Xu, Z.K., Ding, X.M., and Shen, H.B. (2015). "Modeling nonlinear dynamic biological systems with human-readable fuzzy rules optimized by convergent heterogeneous particle swarm." *European Journal of Operational Research* 247(2): 349-358. [G]
29. Chowell, D., Krishna, S., Becker, P.D., Cocita, C., Shu, J., Tan, X., Greenberg, P.D., Klavinskis, L.S., Blattman, J.N., and Anderson, K.S. (2015). "TCR contact residue hydrophobicity is a hallmark of immunogenic CD8(+) T cell epitopes." *Proceedings of the National Academy of Sciences of the United States of America* 112(14): E1754-E1762. [G, AR, MA]
30. Comber, J.D. and Bamezai, A. (2015). "Gold nanoparticles (AuNPs): A new frontier in vaccine delivery." *Journal of Nanomedicine & Biotherapeutic Discovery* 5: e139. doi: 10.4172/2155-983X.1000e139. [G]
31. Cortes-Ciriano, I., Ul Ain, Q., Subramanian, V., Lenselink, E.B., Mendez-Lucio, O., IJzerman, A.P., Wohlfahrt, G., Prusis, P., Malliavin, T.E., van Westen, G.J., and Bender, A. (2015). "Polypharmacology modelling using proteochemometrics (PCM): Recent methodological developments, applications to target families, and future prospects." *MedChemComm* 6(1): 24-50. [G]
32. Coscolla, M., Copin, R., Sutherland, J., Gehre, F., de Jong, B., Owolabi, O., Mbayo, G., Giardina, F., Ernst, J.D., and Gagneux, S. (2015). "M. tuberculosis T cell epitope analysis reveals paucity of

- antigenic variation and identifies rare variable TB antigens." *Cell Host & Microbe* 18(5): 538-548. [G, AR, MA]
33. Courtot, M., Meskas, J., Diehl, A.D., Droumeva, R., Gottardo, R., Jalali, A., Taghiyar, M.J., Maecker, H.T., McCoy, J., Ruttenberg, A., Scheuermann, R.H., and Brinkman, R.R. (2015). "flowCL: Ontology-based cell population labelling in flow cytometry." *Bioinformatics* 31(8): 1337-1339. [G]
 34. Cox, K.S., Tang, A., Chen, Z., Horton, M.S., Yan, H., Wang, X.M., Dubey, S.A., DiStefano, D.J., Ettenger, A., Fong, R.H., Doranz, B.J., Casimiro, D.R., and Vora, K.A. (2015). "Rapid isolation of dengue-neutralizing antibodies from single cell-sorted human antigen-specific memory B-cell cultures." *mAbs*. doi: 10.1080/19420862.2015.1109757. [G]
 35. Davidson, E., Bryan, C., Fong, R.H., Barnes, T., Pfaff, J.M., Mabila, M., Rucker, J.B., and Doranz, B.J. (2015). "Mechanism of binding to Ebola virus glycoprotein by the ZMapp, ZMAB, and MB-003 cocktail antibodies." *Journal of Virology* 89(21): 10982-10992. [G, MA]
 36. Deans, A.R., Lewis, S.E., Huala, E., Anzaldo, S.S., Ashburner, M., Balhoff, J.P., Blackburn, D.C., Blake, J.A., Burleigh, J.G., Charet, B., ... Mabee, P. (2015). "Finding our way through phenotypes." *PLOS Biol* 13(1): e1002033. doi:10.1371/journal.pbio.1002033. [G]
 37. Desrichard, A., Snyder, A., and Chan, T.A. (2015). "Cancer neoantigens and applications for immunotherapy." *Clinical Cancer Research*. doi: 10.1158/1078-0432.CCR-14-3175. [G]
 38. Dimitrov, I. and Doytchinova, I. (2015). "Peptide binding prediction to five most frequent HLA-DQ proteins - a proteochemometric approach." *Molecular Informatics* 34(6-7): 467-476. [G, AR]
 39. dos Santos, E.J.M., McCabe, A., Gonzalez-Galarza, F.F., Jones, A.R., and Middleton, D. (2015). "Allele Frequencies Net Database: Improvements for storage of individual genotypes and analysis of existing data." *Human Immunology* pii: S0198-8859(15)00566-2. doi: 10.1016/j.humimm.2015.11.013. [G]
 40. Dowling, C.P., Johnson, S., Jurrus, E., and Baker, N.A. (2015). "An ISA-Tab specification for protein titration data exchange." *arxiv.org/abs/1511.06431*. [Thesis]. [G]
 41. Duarte, A., Queiroz, A.T., Tosta, R., Carvalho, A.M., Barbosa, C.H., Bellio, M., de Oliveira, C.I., and Barral-Netto, M. (2015). "Prediction of CD8+ epitopes in *Leishmania braziliensis* proteins using EPIBOT: In silico search and in vivo validation." *PLOS One* 10(4): e0124786. doi: 10.1371/journal.pone.0124786. [G]
 42. Dunbar, J. and Deane, C.M. (2015). "ANARCI: Antigen receptor numbering and receptor classification." *Bioinformatics*. doi: 10.1093/bioinformatics/btv552. Epub 2015 Sep 30. [G]
 43. Eng, L.P., Tan, T.W., and Tong, J.C. (2015). "Building MHC class II epitope predictor using machine learning approaches." *Computational Peptidology* 1268: 67-73. [G, AR]
 44. Ethier, J., Curcin, V., Barton, A., McGilchrist, M., Bastiaens, H., Andreasson, A., Rossiter, J., Zhao, L., Arvanitis, T., Taweel, A., Delaney, B., and Burgun, A. (2015). "Clinical data integration model core interoperability ontology for research using primary care data." *Methods of Information in Medicine* 54(1): 16-23. [G]
 45. Farhadi, T., Nezafat, N., Ghasemi, Y., Karimi, Z., Hemmati, S., and Erfani, N. (2015). "Designing of complex multi-epitope peptide vaccine based on Omgs of *Klebsiella pneumoniae*: An in silico approach." *International Journal of Peptide Research and Therapeutics* 21(3): 325-341. [G, AR]

46. Farrell, D. and Gordon, S.V. (2015). "Epitopemap: A web application for integrated whole proteome epitope prediction." *BMC Bioinformatics* 16: 221. doi: 10.1186/s12859-015-0659-0. **[G, AR]**
47. Foulger, R.E., Osumi-Sutherland, D., McIntosh, B.K., Hulo, C., Masson, P., Poux, S., Le Mercier, P., and Lomax, J. (2015). "Representing virus-host interactions and other multi-organism processes in the Gene Ontology." *BMC Microbiology* 15: 146. doi: 10.1186/s12866-015-0481-x. **[G]**
48. Fuchs, J.E., Wellenzohn, B., Weskamp, N., and Liedl, K.R. (2015). "Matched peptides: Tuning matched molecular pair analysis for biopharmaceutical applications." *Journal of Chemical Information and Modeling* 55(11): 2315-2323. **[G, AR]**
49. Gastelum-Avina, P., Velazquez, C., Espitia, C., Lares-Villa, F., and Garibay-Escobar, A. (2015). "A PE_PGRS33 protein of *Mycobacterium tuberculosis*: An ideal target for future tuberculosis vaccine design." *Expert Review of Vaccines* 14(5): 699-711. **[G]**
50. Geibel, P., Trautwein, M., Erdur, H., Zimmermann, L., Jegzentis, K., Bengner, M., Nolte, C.H., and Tolxdorff, T. (2015). "Ontology-based information extraction: Identifying eligible patients for clinical trials in neurology." *Journal on Data Semantics* 4(2): 133-147. **[G]**
51. Geng, S., Chang, H., Qin, W., Lv, M., Li, Y., Feng, J., and Shen, B. (2015). "A novel anti-TNF scFv constructed with human antibody frameworks and antagonistic peptides." *Immunologic Research* 62(3): 377-385. **[G, AR]**
52. Georgieva, M.V., Yahya, G., Codo, L., Ortiz, R., Teixido, L., Claros, J., Jara, R., Jara, M., Iborra, A., Gelpi, J.L.,...Aldea, M. (2015). "Inntags: Small self-structured epitopes for innocuous protein tagging." *Nature Methods* 12(10): 955-958. **[G]**
53. Gilchuk, P., Hill, T.M., Wilson, J.T., and Joyce, S. (2015). "Discovering protective CD8 T cell epitopes -- no single immunologic property predicts it!" *Current Opinion in Immunology* 34: 43-51. **[G, AR]**
54. Goedhals, D., Paweska, J., and Burt, F. (2015). "Identification of human linear B-cell epitope sites on the envelope glycoproteins of Crimean-Congo haemorrhagic fever virus." *Epidemiology and Infection* 143(7): 1451-1456. **[G]**
55. Gonzalez, C., Alvarez, P.J., Rodriguez-Serrano, F., Velez, C., Rama, A., Aranega, A.E., and Prados, J.C. (2015). "Computer tools and collaborative translational research in the life sciences: The further advance of genomics and proteomics." *European Journal of Anatomy* 19(2): 131-137. **[G]**
56. Grifoni, A., Montesano, C., Colizzi, V., and Amicosante, M. (2015). "Key role of human leukocyte antigen in modulating human immunodeficiency virus progression: An overview of the possible applications." *World Journal of Virology* 4(2): 124-133. **[G, AR]**
57. Grifoni, A., Patronov, A., Montesano, C., Colizzi, V., and Amicosante, M. (2015). "Structural differences in KIR3DL1 and LILRB1 interaction with HLA-B and the loading peptide polymorphisms: In silico evidences." *Computational Biology Journal* 2015. doi:10.1155/2015/427217. **[G]**
58. Gubin, M.M., Artyomov, M.N., Mardis, E.R., and Schreiber, R.D. (2015). "Tumor neoantigens: Building a framework for personalized cancer immunotherapy." *Journal of Clinical Investigation* 125(9): 3413-3421. **[G, AR]**
59. Gupta, S.K., Jaitly, T., Schmitz, U., Schuler, G., Wolkenhauer, O., and Vera, J. (2015). "Personalized cancer immunotherapy using Systems Medicine approaches." *Briefings in Bioinformatics* pii: bbv046. doi: 10.1093/bib/bbv046. **[G, AR]**

60. Gutierrez, J.B., Harb, O.S., Zheng, J., Tisch, D.J., Charlebois, E.D., Stoeckert, C.J., and Sullivan, S.A. (2015). "A framework for global collaborative data management for malaria research." *American Journal of Tropical Medicine and Hygiene* 93(3): 124-132. [G]
61. Habibi, M., Bakhshi, P.K., and Aghdam, R. (2015). "LRC: A new algorithm for prediction of conformational B-cell epitopes using statistical approach and clustering method." *Journal of Immunological Methods* 427: 51-57. [G, AR]
62. Hamilton, J.A., Li, J., Wu, Q., Yang, P., Luo, B., Li, H., Bradley, J.E., Taylor, J.J., Randall, T.D., Mountz, J.D., and Hsu, H.C. (2015). "General approach for tetramer-based identification of autoantigen-reactive B cells: Characterization of La- and snRNP-Reactive B cells in autoimmune BXD2 mice." *Journal of Immunology* 194(10): 5022-5034. [G, AR]
63. Hart, G.R. and Ferguson, A.L. (2015). "Empirical fitness models for hepatitis C virus immunogen design." *Physical Biology* 12(6): 066006. doi: 10.1088/1478-3975/12/6/066006. [G]
64. Hassan, C. (2015). "New strategies in identification and quantification of minor histocompatibility antigens." <https://openaccess.leidenuniv.nl/handle/1887/35349>. [Thesis]. [G]
65. Hastings, J., Jeliazkova, N., Owen, G., Tsiliki, G., Munteanu, C.R., Steinbeck, C., and Willighagen, E. (2015). "eNanoMapper: Harnessing ontologies to enable data integration for nanomaterial risk assessment." *Journal of Biomedical Semantics* 6: 10. doi: 10.1186/s13326-015-0005-5. [G]
66. He, B., Chai, G., Duan, Y., Yan, Z., Qiu, L., Zhang, H., Liu, Z., He, Q., Han, K., and Ru, B. (2015). "BDB: Biopanning Data Bank." *Nucleic Acids Research*. doi: 10.1093/nar/gkv1100. [G]
67. Hinz, D., Oseroff, C., Pham, J., Sidney, J., Peters, B., and Sette, A. (2015). "Definition of a pool of epitopes that recapitulates the T cell reactivity against major house dust mite allergens." *Clinical and Experimental Allergy* 45(10): 1601-1612. [G]
68. Horvati, K., Bosze, S., Gideon, H.P., Bacsa, B., Szabo, T.G., Goliath, R., Rangaka, M.X., Hudecz, F., Wilkinson, R.J., and Wilkinson, K.A. (2015). "Population tailored modification of tuberculosis specific interferon-gamma release assay." *Journal of Infection*. doi: 10.1016/j.jinf.2015.10.012. [G, AR]
69. Hsu, W., Gonzalez, N.R., Chien, A., Villablanca, J., Pajukanta, P., Vinuela, F., and Bui, A.A. (2015). "An integrated, ontology-driven approach to constructing observational databases for research." *Journal of Biomedical Informatics* 55: 132-142. [G]
70. Huang, W.L., Tsai, M.J., Hsu, K.T., Wang, J.R., Chen, Y.H., and Ho, S.Y. (2015). "Prediction of linear B-cell epitopes of hepatitis C virus for vaccine development." *BMC Medical Genomics* 8(Suppl 4): S3. doi: 10.1186/1755-8794-8-S4-S3. [G, AR]
71. Jezek, P. and Moucek, R. (2015). "Semantic framework for mapping object-oriented model to semantic web languages." *Frontiers in Neuroinformatics* 9: 3. doi: 10.3389/fninf.2015.00003. [G]
72. Kametani, Y., Miyamoto, A., Tsuda, B., and Tokuda, Y. (2015). "B cell epitope-based vaccination therapy." *Antibodies* 4(3): 225-239. [G]
73. Kamisetty, H., Ghosh, B., Langmead, C.J., and Bailey-Kellogg, C. (2015). "Learning sequence determinants of protein: protein interaction specificity with sparse graphical models." *Journal of Computational Biology* 22(6): 474-486. [G, AR]
74. Kanduc, D., Fasano, C., Capone, G., Delfino, A.P., Calabro, M., and Polimeno, L. (2015). "Applying the concept of peptide uniqueness to anti-polio vaccination." *Journal of Immunology Research* 2015: 541282. doi: 10.1155/2015/541282. [G]

75. Karadeniz, I., Hur, J., He, Y., and Ozgur, A. (2015). "Literature mining and ontology based analysis of host-Brucella gene-gene interaction network." *Frontiers in Microbiology* 6: 1386. doi: 10.3389/fmicb.2015.01386. [G]
76. Knight, R., Dolton, G., Kronenberg-Versteeg, D., Eichmann, M., Zhao, M., Huang, G., Beck, K., Cole, D., Sewell, A., Skowera, A., and Peakman, M. (2015). "A distinct immunogenic region of glutamic acid decarboxylase 65 is naturally processed and presented by human islet cells to cytotoxic CD8 T cells." *Clinical and Experimental Immunology* 179(1): 100-107. [G]
77. Konopka, B.M. (2015). "Biomedical ontologies - A review." *Biocybernetics and Biomedical Engineering* 35(2): 75-86. [G]
78. Kozlova, E.E., Viart, B.T., de Avila, R.A., Felicori, L.F., and Chavez-Olortegui, C. (2015). "Classification epitopes in groups based on their protein family." *BMC Bioinformatics* 16(Suppl 19): S7. doi: 10.1186/1471-2105-16-S19-S7. [G, AR]
79. Kshirsagar, M. (2015). "Combine and conquer: methods for multitask learning in biology and language." https://www.lti.cs.cmu.edu/sites/default/files/meghana_kshirsagar_combine_and_conquer_methods_for_multitask_learning_in_biology_and_language.pdf. [Thesis]. [G]
80. Kui, X., Guan, Y., Zhou, Y., Yan, S., Zhang, L., Li, H., and Sun, M. (2015). "Progress on adenovirus-vectored universal influenza vaccines." *Human Vaccines & Immunotherapeutics* 11(5): 1209-1222. [G, C]
81. Kuksa, P.P., Min, M.R., Dugar, R., and Gerstein, M. (2015). "High-order neural networks and kernel methods for peptide-MHC binding prediction." *Bioinformatics* 31(22): 3600-3607. [G, AR]
82. Laing, K.J., Russell, R.M., Dong, L., Schmid, D., Stern, M., Magaret, A., Haas, J.G., Johnston, C., Wald, A., and Koelle, D.M. (2015). "Zoster vaccination increases the breadth of CD4(+) T cells responsive to varicella zoster virus." *Journal of Infectious Diseases* 212(7): 1022-1031. [G]
83. Lee, A.J., Das, S.R., Wang, W., Fitzgerald, T., Pickett, B.E., Aevermann, B.D., Topham, D.J., Falsey, A.R., and Scheuermann, R.H. (2015). "Diversifying selection analysis predicts antigenic evolution of 2009 pandemic H1N1 influenza A virus in humans." *Journal of Virology* 89(10): 5427-5440. [G, AR]
84. Lefranc, M.P., Giudicelli, V., Duroux, P., Jabado-Michaloud, J., Folch, G., Aouinti, S., Carillon, E., Duvergey, H., Houles, A., Paysan-Lafosse, T., Hadi-Saljoqi, S., Sasorith, S., Lefranc, G., and Kossida, S. (2015). "IMGT®, the international ImMunoGeneTics information system® 25 years on." *Nucleic Acids Research* 43(Database issue): D413-D422. doi: 10.1093/nar/gku1056. [G]
85. Lei, J., Osen, W., Gardyan, A., Hotz-Wagenblatt, A., Wei, G., Gissmann, L., Eichmuller, S., and Lochelt, M. (2015). "Replication-competent foamy virus vaccine vectors as novel epitope scaffolds for immunotherapy." *PLOS One* 10(9): e0138458. doi: 10.1371/journal.pone.0138458. [G]
86. Levin, A.M., Adrianto, I., Datta, I., Iannuzzi, M.C., Trudeau, S., Li, J., Drake, W.P., Montgomery, C., and Rybicki, B.A. (2015). "Association of HLA-DRB1 with sarcoidosis susceptibility and progression in African Americans." *American Journal of Respiratory Cell and Molecular Biology* 53(2): 206-216. [G, AR]
87. Li, B., Zheng, X., Hu, C., and Cao, Y. (2015). "Human papillomavirus genome-wide identification of T-cell epitopes for peptide vaccine development against cervical cancer: An integration of computational analysis and experimental assay." *Journal of Computational Biology* 22(10): 962-974. [G]

88. Lian, Y., Huang, Z.C., Ge, M., and Pan, X.M. (2015). "An improved method for predicting linear B-cell epitope using deep maxout networks." *Biomedical and Environmental Sciences* 28(6): 460-463. [G]
89. Lin, Y., Xiang, Z., and He, Y. (2015). "Ontology-based representation and analysis of host-Brucella interactions." *Journal of Biomedical Semantics* 6: 37. doi: 10.1186/s13326-015-0036-y. [G]
90. Lucchese, G., Capone, G., and Kanduc, D. (2015). "H1N1 versus H5N1 hemagglutinins: A possible differential immunologic impact on neurodevelopment." *Neurology, Psychiatry and Brain Research* 21(1): 39-50. [G]
91. Luo, H., Du, T., Zhou, P., Yang, L., Mei, H., Ng, H., Zhang, W., Shu, M., Tong, W., Shi, L., Mendrick, D.L., and Hong, H. (2015). "Molecular docking to identify associations between drugs and class I human leukocyte antigens for predicting idiosyncratic drug reactions." *Combinatorial Chemistry & High Throughput Screening* 18(3): 296-304. [G]
92. Luo, H., Ye, H., Ng, H.W., Shi, L., Tong, W., Mattes, W., Mendrick, D., and Hong, H. (2015). "Understanding and predicting binding between human leukocyte antigens (HLAs) and peptides by network analysis." *BMC Bioinformatics* 16(Suppl 13): S9. doi: 10.1186/1471-2105-16-S13-S9. [G, AR]
93. Luo, H., Ye, H., Ng, H.W., Shi, L., Tong, W., Mendrick, D.L., and Hong, H. (2015). "Machine learning methods for predicting HLA-peptide binding activity." *Bioinformatics and Biology Insights* 9(Suppl 3): 21-29. [G, AR]
94. Machkovech, H.M., Bedford, T., Suchard, M.A., and Bloom, J.D. (2015). "Positive selection in CD8(+) T-cell epitopes of influenza virus nucleoprotein revealed by a comparative analysis of human and swine viral lineages." *Journal of Virology* 89(22): 11275-11283. [G]
95. Malladi, V.S., Erickson, D.T., Podduturi, N.R., Rowe, L.D., Chan, E.T., Davidson, J.M., Hitz, B.C., Ho, M., Lee, B.T., Miyasato, S., ... Hong, E.L. (2015). "Ontology application and use at the ENCODE DCC." *Database (Oxford)* pii: bav010. doi: 10.1093/database/bav010. [G]
96. Maman, Y., Hershberg, U., and Louzoun, Y. (2015). "Viral CD8 T cell epitope nucleotide composition shows evidence of short- and long-term evolutionary strategies." *Immunogenetics* 67(1): 15-24. [G]
97. Marillet, S., Lefranc, M.P., Boudinot, P., and Cazals, F. (2015). "Dissecting interfaces of antibody-antigen complexes: From ligand specific features to binding affinity predictions." RR-8770, Inria Sophia Antipolis. 2015: 61. <https://hal.inria.fr/hal-01191462>. [Research Report]. [G]
98. Mazor, R., Crown, D., Addissie, S., Jang, Y., Kaplan, G., and Pastan, I. (2015). "Elimination of murine and human T-cell epitopes in recombinant immunotoxin eliminates neutralizing and anti-drug antibodies in vivo." *Cellular & Molecular Immunology*. doi: 10.1038/cmi.2015.91. [G, AR]
99. Mendes, M.F., Antunes, D.A., Rigo, M.M., Sinigaglia, M., and Vieira, G.F. (2015). "Improved structural method for T-cell cross-reactivity prediction." *Molecular Immunology* 67(2): 303-310. [G, AR]
100. Meyer, A.G. and Wilke, C.O. (2015). "Geometric constraints dominate the antigenic evolution of influenza H3N2 hemagglutinin." *PLOS Pathogens* 11(5): e1004940. doi: 10.1371/journal.ppat.1004940. [G, MA]
101. Meysman, P., Ogunjimi, B., Naulaerts, S., Beutels, P., Van Tendeloo, V., and Laukens, K. (2015). "Varicella-zoster virus-derived major histocompatibility complex class I-restricted

- peptide affinity is a determining factor in the HLA risk profile for the development of postherpetic neuralgia." *Journal of Virology* 89(2): 962-969. [G, AR]
102. Minkiewicz, P., Darewicz, M., Iwaniak, A., Sokolowska, J., Starowicz, P., Bucholska, J., and Hryniewicz, M. (2015). "Common amino acid subsequences in a universal proteome-relevance for food science." *International Journal of Molecular Sciences* 16(9): 20748-20773. [G]
 103. Minkiewicz, P., Sokolowska, J., and Darewicz, M. (2015). "The occurrence of sequences identical with epitopes from the allergen Pen a 1.0102 among food and non-food proteins." *Polish Journal of Food and Nutrition Sciences* 65(1): 21-29. [G]
 104. Mitraka, E. and Schriml, L.M. (2015). "2015 Disease Ontology update: DO's expanded curation activities to connect disease-related data." *International Conference on Biomedical Ontology Biocuration 2015*. *biocuration2015.big.ac.cn/pdf/0426/Workshop5-Elvira%20Mitraka.pdf*. [G]
 105. Mohn, K.G.I., Cox, R.J., Tunheim, G., Berdal, J.E., Hauge, A.G., Jul-Larsen, A., Norwegian Pandemic Group, Peters, B., Oftung, F., Jonassen, C.M., and Mjaaland, S. (2015). "Immune responses in acute and convalescent patients with mild, moderate and severe disease during the 2009 influenza pandemic in Norway." *PLOS One* 10(11): e0143281. doi: 10.1371/journal.pone.0143281. [G, AR]
 106. Moise, L., Gutierrez, A., Kibria, F., Martin, R., Tassone, R., Liu, R., Terry, F., Martin, B., and De Groot, A.S. (2015). "iVAX: An integrated toolkit for the selection and optimization of antigens and the design of epitope-driven vaccines." *Human Vaccines & Immunotherapeutics* 11(9): 2312-2321. [G]
 107. Molero-Abraham, M., Glutting, J.P., Flower, D.R., Lafuente, E.M., and Reche, P.A. (2015). "EPIPOX: Immunoinformatic characterization of the shared T-cell epitome between variola virus and related pathogenic orthopoxviruses." *Journal of Immunology Research* 2015: 738020. doi: 10.1155/2015/738020. [G]
 108. Monterrubio-Lopez, G.P., Gonzalez Y-Merchand, J.A., and Ribas-Aparicio, R.M. (2015). "Identification of novel potential vaccine candidates against tuberculosis based on reverse vaccinology." *Biomed Research International* 2015: 483150. doi: 10.1155/2015/483150. [G]
 109. Mortier, M.C., Jongert, E., Mettens, P., and Ruelle, J.L. (2015). "Sequence conservation analysis and in silico human leukocyte antigen-peptide binding predictions for the Mtb72F and M72 tuberculosis candidate vaccine antigens." *BMC Immunology* 16: 63. doi: 10.1186/s12865-015-0119-7. [G, AR, MA]
 110. Mukherjee, S., Warwicker, J., and Chandra, N. (2015). "Deciphering complex patterns of class-I HLA-peptide cross-reactivity via hierarchical grouping." *Immunology and Cell Biology* 93(6): 522-532. [G, AR]
 111. Mukonyora, M. (2015). "A review of important discontinuous B-cell epitope prediction tools." *Journal of Clinical & Cellular Immunology* 6: 358. doi:10.4172/2155-9899.1000358. [G, AR]
 112. Nagpal, G., Gupta, S., Chaudhary, K., Dhanda, S.K., Prakash, S., and Raghava, G.P. (2015). "VaccineDA: Prediction, design and genome-wide screening of oligodeoxynucleotide-based vaccine adjuvants." *Scientific Reports* 5: 12478. doi: 10.1038/srep12478. [G, AR]
 113. Nayak, A., Pattabiraman, N., Fadra, N., Goldman, R., Pond, S.L., and Mazumder, R. (2015). "Structure-function analysis of hepatitis C virus envelope glycoproteins E1 and E2." *Journal of Biomolecular Structure & Dynamics* 33(8): 1682-1694. [G]
 114. Nayak, K., Jing, L., Russell, R.M., Davies, D., Hermanson, G., Molina, D.M., Liang, X., Sherman, D.R., Kwok, W.W., Yang, J., Kenneth, J., Ahamed, S.F., Chandele, A., Murali-

- Krishna, K., and Koelle, D.M. (2015). "Identification of novel Mycobacterium tuberculosis CD4 T-cell antigens via high throughput proteome screening." *Tuberculosis* 95(3): 275-287. [G]
115. Neal, M.L., Carlson, B.E., Thompson, C.T., James, R.C., Kim, K.G., Tran, K., Crampin, E.J., Cook, D.L., and Gennari, J.H. (2015). "Semantics-based composition of integrated cardiomyocyte models motivated by real-world use cases." *PLOS One* 10(12): e0145621. doi: 10.1371/journal.pone.0145621. [G]
116. Nielsen, M. and Marcatili, P. (2015). "Prediction of antibody epitopes." *Peptide Antibodies: Methods and Protocols* 1348: 23-32. [G, AR]
117. Nithichanon, A., Rinchai, D., Gori, A., Lassaux, P., Peri, C., Conchillio-Sole, O., Ferrer-Navarro, M., Gourlay, L.J., Nardini, M., Vila, J., ... and Lertmemonkolchai, G. (2015). "Sequence-and structure-based immunoreactive epitope discovery for Burkholderia pseudomallei flagellin." *PLOS Negl Trop Dis* 9(7): e0003917. doi: 10.1371/journal.pntd.0003917. [G, AR]
118. Olsen, L.R., Sun, J., Simon, C., Zhang, G.L., and Brusic, V. (2015). "Genomics in vaccine development." *Post-Genomic Approaches in Drug and Vaccine Development* 5: 179-203. [G, AR]
119. Oyarzun, P. and Kobe, B. (2015). "Computer-aided design of T-cell epitope-based vaccines: Addressing population coverage." *International Journal of Immunogenetics* 42(5): 313-321. [G, AR]
120. Piras, C., Soggiu, A., Greco, V., Alloggio, I., Bonizzi, L., and Roncada, P. (2015). "Peptidomics in veterinary science: Focus on bovine paratuberculosis." *Peptidomics* 2(1). doi: 10.1515/ped-2015-0001. [G]
121. Prabdi-Sing, N., Blackard, J.T., Puren, A.J., Mahomed, A., Abuelhassan, W., Mahlangu, J., Vermeulen, M., and Bowyer, S.M. (2015). "Naturally occurring resistance mutations within the core and NS5B regions in Hepatitis C genotypes, particularly genotype 5a, in South Africa." *Antiviral Research* 127: 90-98. doi: 10.1016/j.antiviral.2015.11.011. [G]
122. Prickett, S., Rolland, J., and O'Hehir, R. (2015). "Immunoregulatory T cell epitope peptides: The new frontier in allergy therapy." *Clinical and Experimental Allergy* 45(6): 1015-1026. [G, MA]
123. Pritchard, A.L., Hastie, M.L., Neller, M., Gorman, J.J., Schmidt, C.W., and Hayward, N.K. (2015). "Exploration of peptides bound to MHC class I molecules in melanoma." *Pigment Cell & Melanoma Research* 28(3): 281-294. doi: 10.1111/pcmr.12357. [G, AR]
124. Pyysalo, S., Ohta, T., Rak, R., Rowley, A., Chun, H.W., Jung, S.J., Choi, S.P., Tsujii, J., and Ananiadou, S. (2015). "Overview of the cancer genetics and pathway curation tasks of BioNLP Shared Task 2013." *BMC Bioinformatics* 16(Suppl 10): S2. doi: 10.1186/1471-2105-16-S10-S2. [G]
125. Rao, X., Hoof, I., van Baarle, D., Kesmir, C., and Textor, J. (2015). "HLA preferences for conserved epitopes: A potential mechanism for hepatitis C clearance." *Frontiers in Immunology* 6: 552. doi: 10.3389/fimmu.2015.00552. [G, AR]
126. Reguzova, A., Antonets, D., Karpenko, L., Ilyichev, A., Maksyutov, R., and Bazhan, S. (2015). "Design and evaluation of optimized artificial HIV-1 poly-T cell-epitope immunogens." *PLOS One* 10(3): e0116412. doi: 10.1371/journal.pone.0116412. [G]
127. Reverdatto, S., Burz, D.S., and Shekhtman, A. (2015). "Peptide aptamers: Development and applications." *Current Topics in Medicinal Chemistry* 15(12): 1082-1101. [G]

128. Rigo, M.c.M., Antunes, D.A., de Freitas, M.V., de Almeida Mendes, M.F., Meira, L., Sinigaglia, M., and Vieira, G.F. (2015). "DockTope: A Web-based tool for automated pMHC-I modelling." *Scientific Reports* 5: 18413. doi: 10.1038/srep18413. [G]
129. Rocca-Serra, P., Walls, R., Parnell, J., Gallery, R., Zheng, J., Sansone, S.A., and Gonzalez-Beltran, A. (2015). "Modeling a microbial community and biodiversity assay with OBO Foundry ontologies: The interoperability gains of a modular approach." *Database (Oxford)* pii: bau132. doi: 10.1093/database/bau132. [G]
130. Romano, E. and Romero, P. (2015). "The therapeutic promise of disrupting the PD-1/PD-L1 immune checkpoint in cancer: Unleashing the CD8 T cell mediated anti-tumor activity results in significant, unprecedented clinical efficacy in various solid tumors." *Journal for Immunotherapy of Cancer* 3: 15. doi: 10.1186/s40425-015-0059-z. [G, AR]
131. Rosendahl Huber, S.K. (2015). "Immune responses to conserved influenza epitopes: lessons for peptide vaccination strategies." <http://hdl.handle.net/1887/36510>. [Thesis]. [G]
132. Saini, S.K., Schuster, H., Ramnarayan, V.R., Rammensee, H.G., Stevanovic, S., and Springer, S. (2015). "Dipeptides catalyze rapid peptide exchange on MHC class I molecules." *Proceedings of the National Academy of Sciences of the United States of America* 112(1): 202-207. [G]
133. Saravanan, V. and Gautham, N. (2015). "Harnessing computational biology for exact linear B-cell epitope prediction: A novel amino acid composition-based feature descriptor." *Omics-A Journal of Integrative Biology* 19(10): 648-658. [G, AR]
134. Sarkar, T., Das, S., De, A., Nandy, P., Chattopadhyay, S., Chawla-Sarkar, M., and Nandy, A. (2015). "H7N9 influenza outbreak in China 2013: In silico analyses of conserved segments of the hemagglutinin as a basis for the selection of peptide vaccine targets." *Computational Biology and Chemistry* 59: 8-15. [G, AR]
135. Schriml, L.M. and Mitraka, E. (2015). "The Disease Ontology: Fostering interoperability between biological and clinical human disease-related data." *Mammalian Genome* 26(9-10): 584-589. [G]
136. Schubert, B., Brachvogel, H.P., Jurges, C., and Kohlbacher, O. (2015). "EpiToolKit--a web-based workbench for vaccine design." *Bioinformatics* 31(13): 2211-2213. [G]
137. Shawky, H., Maghraby, A.S., Solliman, M.E.-D., El-Mokadem, M.T., Sherif, M.M., Arafa, A., and Bahgat, M.M. (2015). "Expression, immunogenicity and diagnostic value of envelope proteins from an Egyptian hepatitis C virus isolate." *Archives of Virology* 160(4): 945-958. [G]
138. Shen, K., Shen, L., Wang, J., Jiang, Z., and Shen, B. (2015). "Understanding amino acid mutations in hepatitis B virus proteins for rational design of vaccines and drugs." *Advances in Protein Chemistry and Structural Biology* 99: 131-153. [G, AR]
139. Shepherd, A.J., Skelton, S., Sansom, C.E., Gomez, K., Moss, D.S., and Hart, D.P. (2015). "A large-scale computational study of inhibitor risk in non-severe haemophilia A." *British Journal of Haematology* 168(3): 413-420. [G, AR]
140. Simon, C., Kudahl, U.J., Sun, J., Olsen, L.R., Zhang, G.L., Reinherz, E.L., and Brusica, V. (2015). "FluKB: A knowledge-based system for influenza vaccine target discovery and analysis of the immunological properties of influenza viruses." *Journal of Immunology Research* 2015: 380975. doi: 10.1155/2015/380975. [G, AR]
141. Singh, S.P. and Mishra, B.N. (2015). "Major histocompatibility complex linked databases and prediction tools for designing vaccines." *Human Immunology* pii: S0198-8859(15)00565-0. doi: 10.1016/j.humimm.2015.11.012. [G, AR]

142. Singh, S.P., Verma, V., and Mishra, B.N. (2015). "Characterization of Plasmodium falciparum proteome at asexual blood stages for screening of effective vaccine candidates: An immunoinformatics approach." *Immunology and Immunogenetics Insights* 7: 21-30. doi: 10.4137/III.S24755. [G, AR]
143. Smith, B., Arabandi, S., Brochhausen, M., Calhoun, M., Ciccarese, P., Doyle, S., Gibaud, B., Goldberg, I., Kahn Jr, C.E., and Overton, J. (2015). "Biomedical imaging ontologies: A survey and proposal for future work." *Journal of Pathology Informatics* 6: 37. doi: 10.4103/2153-3539.159214. [G]
144. Snyder, A. and Chan, T.A. (2015). "Immunogenic peptide discovery in cancer genomes." *Current Opinion in Genetics & Development* 30: 7-16. [G, AR]
145. Spreckelsen, C., Schmithausen, D., Roeder, P., Schmidt, R., Dahl, E., Geisler, S., and Kabino, K. (2015). "Model-based approach for optimizing the storage management of bio-repositories." *Simulation Modelling Practice and Theory* 53: 74-87. [G]
146. Subramanian, S.L., Kitchen, R.R., Alexander, R., Carter, B.S., Cheung, K.H., Laurent, L.C., Pico, A., Roberts, L.R., Roth, M.E., Rozowsky, J.S., Su, A.I., Gerstein, M.B., and Milosavljevic, A. (2015). "Integration of extracellular RNA profiling data using metadata, biomedical ontologies and Linked Data technologies." *Journal of Extracellular Vesicles* 4: 27497. doi: 10.3402/jev.v4.27497. [G]
147. Tahvildari, D. (2015). "Semantic support for recording laboratory experimental metadata: A study in food chemistry." *The Semantic Web. Latest Advances and New Domains. Lecture Notes in Computer Science* 9088: 783-794. [G]
148. Tang, Q., Nie, F., Kang, J., Ding, H., Zhou, P., and Huang, J. (2015). "NIEluter: Predicting peptides eluted from HLA class I molecules." *Journal of Immunological Methods* 422: 22-27. [G, AR]
149. Thessen, A.E., Bunkers, D.E., Buttigieg, P.L., Cooper, L.D., Dahdul, W.M., Domisch, S., Franz, N.M., Jaiswal, P., Lawrence-Dill, C.J., Midford, P.E., Mungall, C.J., Ramirez, M.J., Specht, C.D., Vogt, L., Vos, R.A., Walls, R.L., White, J.W., Zhang, G., Deans, A.R., Huala, E., Lewis, S.E., and Mabee, P.M. (2015). "Emerging semantics to link phenotype and environment." *PeerJ* 3: e1470. doi: 10.7717/peerj.1470. [G]
150. Thibault, J., Roe, D., Eilbeck, K., Cheatham, T., and Facelli, J. (2015). "Development of an informatics infrastructure for data exchange of biomolecular simulations: Architecture, data models and ontology." *SAR and QSAR in Environmental Research* 26(7-9): 577-593. [G]
151. Tong, C., Xiao, B., Cheng, S., Li, W., Liao, X., Luo, S., and Hao, W. (2015). "Generation and identification of peptide-based monoclonal antibodies against vacuolar proton pyrophosphatase of *Toxoplasma gondii*." *Monoclonal Antibodies in Immunodiagnosis and Immunotherapy* 34(3): 191-200. [G]
152. Tsuda, B., Kametani, Y., Miyamoto, A., Miyako, H., Kumaki, N., Ogiy, R., Oshitanai, R., Terao, M., Morioka, T., and Niikura, N. (2015). "The effect of peptide treatment on the HLA-binding and antibody production in peripheral blood mononuclear cells obtained from Japanese breast cancer patients." *Journal of Vaccines and Vaccination* 6: 270. doi:10.4172/2157-7560.1000270. [G]
153. Turner, J.A., Pasquerello, D., Turner, M.D., Keator, D.B., Alpert, K., King, M., Landis, D., Calhoun, V.D., Potkin, S.G., and Tallis, M. (2015). "Terminology development towards harmonizing multiple clinical neuroimaging research repositories." *Data Integration in the Life Sciences. Lecture Notes in Computer Science* 9162: 104-117. [G]

154. Tyagi, N., Farnell, E.J., Fitzsimmons, C.M., Ryan, S., Tukahebwa, E., Maizels, R.M., Dunne, D.W., Thornton, J.M., and Furnham, N. (2015). "Comparisons of allergenic and metazoan parasite proteins: Allergy the price of immunity." *PLOS Comput Biol* 11(10): e1004546. doi: 10.1371/journal.pcbi.1004546. [G, AR]
155. Uciteli, A. and Kirsten, T. (2015). "Ontology-based retrieval of scientific data in LIFE." *BTW Workshops*: 109-114. [G]
156. Valentini, D., Ferrara, G., Advani, R., Hallander, H.O., and Maeurer, M.J. (2015). "Serum reactome induced by *Bordetella pertussis* infection and pertussis vaccines: Qualitative differences in serum antibody recognition patterns revealed by peptide microarray analysis." *BMC Immunology* 16: 40. doi: 10.1186/s12865-015-0090-3. [G]
157. van Deutekom, H.W. and Kesmir, C. (2015). "Zooming into the binding groove of HLA molecules: Which positions and which substitutions change peptide binding most?" *Immunogenetics* 67(8): 425-436. [G, AR]
158. Vanek, J. and Moucek, R. (2015). "On data and metadata formats for electrophysiological experiments." *IEEE 13th International Scientific Conference on Informatics*: 290-295. [G]
159. Verma, S. and Prabhakar, Y.S. (2015). "Target based drug design - a reality in virtual sphere." *Current Medicinal Chemistry* 22(13): 1603-1630. [G, AR]
160. Villena, J. Zelaya, H., Rojas-Caro, S., Alvarez, S., Garcia, A., Kitazawa, H., Rodriguez-Jorge, O., Santana, M. A., Laino, J.,...Salcido-Ochoa, R. (2015). "Recent trends in immunology." S. Ahmad Mir (Ed). *SM Online Publishers LLC*. [G]
161. Wang, Q.H., Gao, X.Y., Lou, X.L., Yao, L., Zhang, Z.X., Zhang, X.H., Xia, Y.H., Liu, B.B., and Zhang, L.L. (2015). "Genome-wide screening of human papillomavirus-specific CTL epitopes presented by HLA-A alleles in cervical cancer." *International Journal of Peptide Research and Therapeutics*: 1-8. doi: 10.1007/s10989-015-9480-x. [G, AR]
162. Xiang, Z., Zheng, J., Lin, Y., and He, Y. (2015). "Ontorat: Automatic generation of new ontology terms, annotations, and axioms based on ontology design patterns." *Journal of Biomedical Semantics* 6: 4. doi: 10.1186/2041-1480-6-4. [G]
163. Xu, G.J., Kula, T., Xu, Q., Li, M.Z., Vernon, S.D., Ndung'u, T., Ruxrungtham, K., Sanchez, J., Brander, C., Chung, R.T., O'Connor, K.C., Walker, B., Larman, H., and Elledge, S.J. (2015). "Viral immunology. Comprehensive serological profiling of human populations using a synthetic human virome." *Science* 348(6239): aaa0698. doi: 10.1126/science.aaa0698. [G]
164. Xu, G.J. (2015). "Comprehensive approaches to identifying the targets of natural and synthetic antibodies using microarray DNA synthesis and high-throughput sequencing." <http://nrs.harvard.edu/urn-3:HUL.InstRepos:23845497>. [Thesis]. [G]
165. Zhang, W., Niu, Y., Zou, H., Luo, L., Liu, Q., and Wu, W. (2015). "Accurate prediction of immunogenic T-cell epitopes from epitope sequences using the genetic algorithm-based ensemble learning." *PLOS One* 10(5): e0128194. doi: 10.1371/journal.pone.0128194. [G, AR]

3.2.2 Analysis Resource

1. Acevedo-Saenz, L., Ochoa, R., Rugeles, M.T., Olaya-Garcia, P., Velilla-Hernandez, P.A., and Diaz, F.J. (2015). "Selection pressure in CD8(+) T-cell epitopes in the pol gene of HIV-1 infected individuals in Colombia. A bioinformatic approach." *Viruses-Basel* 7(3): 1313-1331. [AR]

2. Achinko, D. and Dormer, A. (2015). "Epitope specificity and protein signaling interactions driving epidemic occurrences of Ebola disease." *F1000Research* 4: 166. doi: 10.12688/f1000research.6515.1. [AR]
3. Ahmed, S.S., Volkmuth, W., Duca, J., Corti, L., Pallaoro, M., Pezzicoli, A., Karle, A., Rigat, F., Rappuoli, R., Narasimhan, V., Julkunen, I., Vuorela, A., Vaarala, O., Nohynek, H., Pasini, F.L., Montomoli, E., Trombetta, C., Adams, C.M., Rothbard, J., and Steinman, L. (2015). "Antibodies to influenza nucleoprotein cross-react with human hypocretin receptor 2." *Science Translational Medicine* 7(294): 294ra105. doi: 10.1126/scitranslmed.aab2354. [AR]
4. Ali, M.T., Morshed, M.M., and Hassan, F. (2015). "A computational approach for designing a universal epitope-based peptide vaccine against Nipah virus." *Interdisciplinary Sciences-Computational Life Sciences* 7(2): 177-185. [AR]
5. Amat-ur-Rasool, H., Saghir, A., and Idrees, M. (2015). "Computational prediction and analysis of envelop glycoprotein epitopes of DENV-2 and DENV-3 Pakistani isolates: A first step towards dengue vaccine development." *PLOS One* 10(3): e0119854. doi: 10.1371/journal.pone.0119854. [AR]
6. Anderson, D., Fakiola, M., Hales, B., Pennell, C., Thomas, W., and Blackwell, J. (2015). "Genome-wide association study of IgG1 responses to the choline-binding protein PspC of *Streptococcus pneumoniae*." *Genes and Immunity* 16(5): 289-296. [AR]
7. Andrick, B.J., Schwab, A.I., Cauley, B., O'Donnell, L.A., and Meng, W.S. (2015). "Predicting hemagglutinin MHC-II ligand analogues in anti-TNF α biologics: Implications for immunogenicity of pharmaceutical proteins." *PLOS One* 10(8): e0135451. doi: 10.1371/journal.pone.0135451. [AR, MA]
8. Anum, D., Kusi, K.A., Ganeshan, H., Hollingdale, M.R., Ofori, M.F., Koram, K.A., Gyan, B.A., du-Amankwah, S., Badji, E., Huang, J., Belmonte, M., Banania, G.J., Kwofie, T.B., Villasante, E., Dodoo, D., and Sedegah, M. (2015). "Measuring naturally acquired ex vivo IFN-gamma responses to *Plasmodium falciparum* cell-traversal protein for ookinetes and sporozoites (CeTOS) in Ghanaian adults." *Malaria Journal* 14: 20. doi: 10.1186/s12936-014-0539-5. [AR]
9. Asgari, S., Mirzahoseini, H., Karimipour, M., and Ebrahim-Habibi, A. (2015). "Structural and dynamic insight into hirudin epitopes-HLA-DRB1 0101 complexes and their modified peptide ligands: A molecular dynamic simulation study." *Tropical Journal of Pharmaceutical Research* 14(12): 2171-2178. [AR]
10. Asgari, S., Mirzahoseini, H., Karimipour, M., Rahimi, H., and Ebrahim-Habibi, A. (2015). "Rational design of stable and functional hirudin III mutants with lower antigenicity." *Biologicals* 43(6): 479-491. [AR]
11. Ataie, N., Xiang, J., Cheng, N., Brea, E.J., Lu, W., Scheinberg, D.A., Liu, C., and Ng, H.L. (2015). "Structure of a TCR-mimic antibody with target predicts pharmacogenetics." *Journal of Molecular Biology* 428(1):194-205. doi: 10.1016/j.jmb.2015.12.002. Epub 2015 Dec 11. [AR]
12. Aumentado-Armstrong, T.T., Istrate, B., and Murgita, R.A. (2015). "Algorithmic approaches to protein-protein interaction site prediction." *Algorithms for Molecular Biology* 10: 7. doi: 10.1186/s13015-015-0033-9. [AR]
13. Barrett, C.L., DeBoever, C., Jepsen, K., Saenz, C.C., Carson, D.A., and Frazer, K.A. (2015). "Systematic transcriptome analysis reveals tumor-specific isoforms for ovarian cancer diagnosis and therapy." *Proceedings of the National Academy of Sciences of the United States of America* 112(23): E3050-E3057. [AR]

14. Bassani-Sternberg, M., Pletscher-Frankild, S., Jensen, L.J., and Mann, M. (2015). "Mass spectrometry of human leukocyte antigen class I peptidomes reveals strong effects of protein abundance and turnover on antigen presentation." *Molecular & Cellular Proteomics* 14(3): 658-673. [AR, MA]
15. Becerra-Artiles, A., Dominguez-Amorocho, O., Stern, L.J., and Calvo-Calle, J. (2015). "A simple proteomics-based approach to identification of immunodominant antigens from a complex pathogen: Application to the CD4 T cell response against human herpesvirus 6B." *PLOS One* 10(11): e0142871. doi: 10.1371/journal.pone.0142871. [AR]
16. Behloul, N., Wen, J., Dai, X., Dong, C., and Meng, J. (2015). "Antigenic composition and immunoreactivity differences between HEV recombinant capsid proteins generated from different genotypes." *Infection Genetics and Evolution* 34: 211-220. [AR]
17. Bergmann, T., Moore, C., Sidney, J., Miller, D., Tallmadge, R., Harman, R.M., Oseroff, C., Wriston, A., Shabanowitz, J., Hunt, D.F., Osterrieder, N., Peters, B., Antczak, D.F., and Sette, A. (2015). "The common equine class I molecule Eqca-1*00101 (ELA-A3.1) is characterized by narrow peptide binding and T cell epitope repertoires." *Immunogenetics* 67(11-12): 675-689. [AR]
18. Bergseng, E., Dorum, S., Arntzen, M.O., Nielsen, M., Nygard, S., Buus, S., de Souza, G.A., and Sollid, L.M. (2015). "Different binding motifs of the celiac disease-associated HLA molecules DQ2.5, DQ2.2, and DQ7.5 revealed by relative quantitative proteomics of endogenous peptide repertoires." *Immunogenetics* 67(2): 73-84. [AR]
19. Blankenstein, T., Leisegang, M., Uckert, W., and Schreiber, H. (2015). "Targeting cancer-specific mutations by T cell receptor gene therapy." *Current Opinion in Immunology* 33: 112-119. [AR]
20. Bossini-Castillo, L., Lopez-Isac, E., Mayes, M.D., and Martin, J. (2015). "Genetics of systemic sclerosis." *Seminars in Immunopathology* 37(5): 443-451. [AR]
21. Brown, S., Majikes, J., Martinez, A., Giron, T.M., Fennell, H., Samano, E.C., and LaBean, T.H. (2015). "An easy-to-prepare mini-scaffold for DNA origami." *Nanoscale* 7(40): 16621-16624. [AR]
22. Bruffaerts, N., Pedersen, L.E., Vandermeulen, G., Preat, V., Stockhofe-Zurwieden, N., Huygen, K., and Romano, M. (2015). "Increased B and T cell responses in M-bovis bacille Calmette-Guerin vaccinated pigs co-immunized with plasmid DNA encoding a prototype tuberculosis antigen." *PLOS One* 10(7): e0132288. doi: 10.1371/journal.pone.0132288. [AR]
23. Buch, D.R., Souza, F.N., Meissner, G.O., Morgon, A.M., Gremski, L.H., Ferrer, V.r.P., Trevisan-Silva, D., Matsubara, F.H., Boia-Ferreira, M., and Sade, Y.B. (2015). "Brown spider (*Loxosceles* genus) venom toxins: Evaluation of biological conservation by immune cross-reactivity." *Toxicon* 108: 154-166. [AR]
24. Bunse, L., Schumacher, T., Sahm, F., Pusch, S., Oezen, I., Rauschenbach, K., Gonzalez, M., Solecki, G., Osswald, M., Capper, D., Wiestler, B., Winkler, F., Herold-Mende, C., von Deimling, A., Wick, W., and Platten, M. (2015). "Proximity ligation assay evaluates IDH1(R132H) presentation in gliomas." *Journal of Clinical Investigation* 125(2): 593-606. [AR]
25. Burkovitz, A. and Ofran, Y. (2015). "Understanding differences between synthetic and natural antibodies can help improve antibody engineering." *mAbs* 8(2):278-87. doi: 10.1080/19420862.2015.1123365. Epub 2015 Dec 14. [AR]
26. Burns, J.C., Touma, R., Song, Y., Padilla, R.L., Tremoulet, A.H., Sidney, J., Sette, A., and Franco, A. (2015). "Fine specificities of natural regulatory T cells after IVIG therapy in patients with Kawasaki disease." *Autoimmunity* 48(3): 181-188. [AR]

27. Buus, S., Andreatta, M., Stryhn, A., Rasmussen, M., Karosiene, E., and Nielsen, M. (2015). "Prediction of peptide-MHC class II binding affinity with improved binding core identification; implications for the interpretation of T cell cross-reactivity." 6th Argentinian Conference on Bioinformatics and Computational Biology. <http://lidecc.cs.uns.edu.ar/cab2c2015/proceedings/handle/1234/59>. [AR]
28. Cabrera-Mora, M., Fonseca, J.A., Singh, B., Oliveira-Ferreira, J., Lima-Junior Jda C., Calvo-Calle, J.M., and Moreno, A. (2015). "Induction of multifunctional broadly reactive T cell responses by a Plasmodium vivax circumsporozoite protein recombinant chimera." *Infection and Immunity* 83(9): 3749-3761. [AR]
29. Calderon-Gonzalez, R., Frande-Cabanes, E., Tobes, R., Pareja, E., Alaez-Alvarez, L., and Alvarez-Dominguez, C. (2015). "A dendritic cell-targeted vaccine loaded with glyceraldehyde-3-phosphate dehydrogenase peptides proposed for individuals at high risk of Listeriosis." *Journal of Vaccines and Vaccination* 6: 266. doi: 10.4172/2157-7560.1000266. [AR]
30. Calderon-Gonzalez, R., Tobes, R., Pareja, E., Frande-Cabanes, E., Petrovsky, N., and Alvarez-Dominguez, C. (2015). "Identification and characterisation of T-cell epitopes for incorporation into dendritic cell-delivered Listeria vaccines." *Journal of Immunological Methods* 424: 111-119. [AR]
31. Capello, M., Caorsi, C., Hernandez, P.J.B., Dametto, E., Bertinetto, F.E., Magistroni, P., Rendine, S., Amoroso, A., and Novelli, F. (2015). "Phosphorylated alpha-enolase induces autoantibodies in HLA-DR8 pancreatic cancer patients and triggers HLA-DR8 restricted T-cell activation." *Immunology Letters* 167(1): 11-16. [AR]
32. Cardona, N.I., Moncada, D.M., and Gomez-Marin, J.E. (2015). "A rational approach to select immunogenic peptides that induce IFN- γ response against Toxoplasma gondii in human leukocytes." *Immunobiology* 220(12): 1337-1342. [AR]
33. Carmona, S.J., Nielsen, M., Schafer-Nielsen, C., Mucci, J., Altcheh, J., Balouz, V., Tekiel, V., Frasch, A.C., Campetella, O., Buscaglia, C.A., and Agueero, F. (2015). "Towards high-throughput immunomics for infectious diseases: Use of next-generation peptide microarrays for rapid discovery and mapping of antigenic determinants." *Molecular & Cellular Proteomics* 14(7): 1871-1884. [AR]
34. Caron, E., Espona, L., Kowalewski, D.J., Schuster, H., Ternette, N., Alpizar, A., Schittenhelm, R.B., Ramarathinam, S.H., Arlehamn, C.S.L., Koh, C.C., Gillet, L.C., Rabsteyn, A., Navarro, P., Kim, S., Lam, H., Sturm, T., Marcilla, M., Sette, A., Campbell, D.S., Deutsch, E.W., Moritz, R.L., Purcell, A.W., Rammensee, H.G., Stevanovic, S., and Aebbersold, R. (2015). "An open-source computational and data resource to analyze digital maps of immunopeptidomes." *Elife* 4. doi: 10.7554/eLife.07661. [AR]
35. Carpenter, C., Sidney, J., Kolla, R., Nayak, K., Tomiyama, H., Tomiyama, C., Padilla, O.A., Rozot, V., Ahamed, S.F., Ponte, C., Rolla, V., Antas, P.R., Chandele, A., Kenneth, J., Laxmi, S., Makgotlho, E., Vanini, V., Ippolito, G., Kazanova, A.S., Panteleev, A.V., Hanekom, W., Mayanja-Kizza, H., Lewinsohn, D., Saito, M., McElrath, M., Boom, W., Goletti, D., Gilman, R., Lyadova, I.V., Scriba, T.J., Kallas, E.G., Murali-Krishna, K., Sette, A., and Arlehamn, C.S.L. (2015). "A side-by-side comparison of T cell reactivity to fifty-nine Mycobacterium tuberculosis antigens in diverse populations from five continents." *Tuberculosis* 95(6): 713-721. [AR]
36. Carreno, B.M., Magrini, V., Becker-Hapak, M., Kaabinejadian, S., Hundal, J., Petti, A.A., Ly, A., Lie, W.R., Hildebrand, W.H., Mardis, E.R., and Linette, G.P. (2015). "A dendritic cell vaccine increases the breadth and diversity of melanoma neoantigen-specific T cells." *Science* 348(6236): 803-808. [AR]

37. Carvalho, R.V., van den Heuvel, J., Kleijn, J., and Verbeek, F.J. (2015). "Coupling of petri net models of the mycobacterial infection process and innate immune response." *Computation* 3(2): 150-176. [AR]
38. Chappell, P., Meziane, E.K., Harrison, M., Magiera, L., Hermann, C., Mears, L., Wrobel, A.G., Durant, C., Nielsen, L.L., Buus, S., Ternette, N., Mwangi, W., Butter, C., Nair, V., Ahyee, T., Duggleby, R., Madrigal, A., Roversi, P., Lea, S.M., and Kaufman, J. (2015). "Expression levels of MHC class I molecules are inversely correlated with promiscuity of peptide binding." *Elife* 4: e05345. doi: 10.7554/eLife.05345. [AR]
39. Cheloha, R.W., Sullivan, J.A., Wang, T., Sand, J.M., Sidney, J., Sette, A., Cook, M.E., Suresh, M., and Gellman, S.H. (2015). "Consequences of periodic α -to- β (3) residue replacement for immunological recognition of peptide epitopes." *ACS Chemical Biology* 10(3): 844-854. [AR]
40. Cherryholmes, G.A., Stanton, S.E., and Disis, M.L. (2015). "Current methods of epitope identification for cancer vaccine design." *Vaccine* 33(51): 7408-7414. [AR]
41. Choudhury, N.J., Kiyotani, K., Yap, K.L., Campanile, A., Antic, T., Yew, P.Y., Steinberg, G., Park, J.H., Nakamura, Y., and O'Donnell, P.H. (2015). "Low T-cell receptor diversity, high clonal mutation burden, and high neoantigen load as predictors of clinical outcome in muscle-invasive bladder cancer." *European Urology Focus* pii: S2405-4569(15)00144-3. doi: 10.1016/j.euf.2015.09.007. [AR]
42. Cohen, C.J., Gartner, J.J., Horovitz-Fried, M., Shamalov, K., Trebska-McGowan, K., Bliskovsky, V.V., Parkhurst, M.R., Ankri, C., Prickett, T., Crystal, J.S., Li, Y.F., El-Gamil, M., Rosenberg, S.A., and Robbins, P.F. (2015). "Isolation of neoantigen-specific T cells from tumor and peripheral lymphocytes." *Journal of Clinical Investigation* 125(10): 3981-3991. [AR]
43. Constans, M., Ssemadaali, M., Kolyvushko, O., and Ramamoorthy, S. (2015). "Antigenic determinants of possible vaccine escape by porcine circovirus subtype 2b viruses." *Bioinformatics and Biology Insights* 9: 1-12. [AR]
44. Cortes, A. and Coral, J. (2015). "The use of planar electromagnetic fields to explain coupling between HLA-II molecules and peptides." *Acta Bioquimica Clinica Latinoamericana* 49(2): 221-228. [AR]
45. Costa, A.I., Koning, D., Ladell, K., McLaren, J.E., Grady, B.P., X, Schellens, I.M., van Ham, P., Nijhuis, M., Borghans, J.A., Kesmir, C., Price, D.A., and van Baarle, D. (2015). "Complex T-cell receptor repertoire dynamics underlie the CD8(+) T-cell response to HIV-1." *Journal of Virology* 89(1): 110-119. [AR]
46. Cousens, L.P., Moise, L., and De Groot, A.S. (2015). "Novel methods for addressing immunogenicity of therapeutic enzymes." *Biobetters. AAPS Advances in the Pharmaceutical Sciences Series* 19: 63-77. [AR]
47. Creaney, J., Ma, S., Sneddon, S.A., Tourigny, M.R., Dick, I.M., Leon, J.S., Khong, A., Fisher, S.A., Lake, R.A., Lesterhuis, W., Nowak, A.K., Leary, S., Watson, M.W., and Robinson, B.W. (2015). "Strong spontaneous tumor neoantigen responses induced by a natural human carcinogen." *Oncoimmunology* 4(7): e1011492. [AR]
48. Crossey, E., Fritze, K., Narum, D.L., Peabody, D.S., and Chackerian, B. (2015). "Identification of an immunogenic mimic of a conserved epitope on the Plasmodium falciparum blood stage antigen AMA1 using virus-like particle (VLP) peptide display." *PLOS One* 10(7): e0132560. doi: 10.1371/journal.pone.0132560. [AR]
49. Crowley, J.T., Drouin, E.E., Pianta, A., Strle, K., Wang, Q., Costello, C.E., and Steere, A.C. (2015). "A highly expressed human protein, apolipoprotein B-100, serves as an autoantigen in a

- subgroup of patients with Lyme disease." *Journal of Infectious Diseases* 212(11): 1841-1850. [AR]
50. Dargel, C., Bassani-Sternberg, M., Hasreiter, J., Zani, F., Bockmann, J.H., Thiele, F., Bohne, F., Wisskirchen, K., Wilde, S., and Sprinzl, M.F. (2015). "T cells engineered to express a T-cell receptor specific for glypican-3 to recognize and kill hepatoma cells in vitro and in mice." *Gastroenterology* 149(4): 1042-1052. [AR]
 51. Deehan, M., Garces, S., Kramer, D., Baker, M.P., Rat, D., Roettger, Y., and Kromminga, A. (2015). "Managing unwanted immunogenicity of biologicals." *Autoimmunity Reviews* 14(7): 569-574. [AR]
 52. Diken, M., Kreiter, S., Kloke, B., and Sahin, U. (2015). "Current developments in actively personalized cancer vaccination with a focus on RNA as the drug format." *Progress in Tumor Research* 42: 44-54. [AR]
 53. Dikhit, M.R., Kumar, S., Vijaymahantesh, Sahoo, B.R., Mansuri, R., Amit, A., Ansari, M., Sahoo, G.C., Bimal, S., and Das, P. (2015). "Computational elucidation of potential antigenic CTL epitopes in Ebola virus." *Infection Genetics and Evolution* 36: 369-375. [AR]
 54. Dillon, M.B.C., Schulten, V., Oseroff, C., Paul, S., Dullanty, L.M., Frazier, A., Belles, X., Piulachs, M., Visness, C., and Bacharier, L. (2015). "Different Bla-g T cell antigens dominate responses in asthma versus rhinitis subjects." *Clinical & Experimental Allergy* 45(12): 1856-1867. [AR]
 55. Dinga, J.N., Wamalwa, M., Njimoh, D.L., Njahira, M.N., Djikeng, A., Skilton, R., Titanji, V.P.K., and Pelle, R. (2015). "TpUB05, a homologue of the immunodominant Plasmodium falciparum protein UB05, is a marker of protective immune responses in cattle experimentally vaccinated against East Coast Fever." *PLOS One* 10(6): e0128040. doi: 10.1371/journal.pone.0128040. [AR]
 56. Doritchamou, J., Sabbagh, A., Jespersen, J.S., Renard, E., Salanti, A., Nielsen, M.A., Deloron, P., and Ndam, N.T. (2015). "Identification of a major dimorphic region in the functionally critical N-terminal ID1 domain of VAR2CSA." *PLOS One* 10(9): e0137695. doi: 10.1371/journal.pone.0137695. [AR]
 57. Drillon, G., Audit, B., Argoul, F., and Arneodo, A. (2015). "Ubiquitous human 'master' origins of replication are encoded in the DNA sequence via a local enrichment in nucleosome excluding energy barriers." *Journal of Physics: Condensed Matter* 27(6): 064102. doi: 10.1088/0953-8984/27/6/064102. [AR]
 58. Du, H., Shi, L., Chen, P., Yang, W., Xun, Y., Yang, C., Zhao, L., Zhou, Y., and Chen, G. (2015). "Prohibitin is involved in patients with IgG4 related disease." *PLOS One* 10(5): e0125331. doi: 10.1371/journal.pone.0125331. [AR]
 59. Ebadi, M., Reddy, N.M., and Rezaei, N. (2015). "Immunopathology and immunotherapy of Non-Hodgkin Lymphoma." *Cancer Immunology*: 135-183. [AR]
 60. Edlefsen, P.T., Rolland, M., Hertz, T., Tovanabuttra, S., Gartland, A.J., deCamp, A.C., Magaret, C.A., Ahmed, H., Gottardo, R., Juraska, M., McCoy, C., Larsen, B.B., Sanders-Buell, E., Carrico, C., Menis, S., Bose, M., Arroyo, M.A., O'Connell, R.J., Nitayaphan, S., Pitisuttithum, P., Kaewkungwal, J., Rerks-Ngarm, S., Robb, M.L., Kirys, T., Georgiev, I.S., Kwong, P.D., Scheffler, K., Pond, S.L., Carlson, J.M., Michael, N.L., Schief, W.R., Mullins, J.I., Kim, J.H., and Gilbert, P.B. (2015). "Comprehensive sieve analysis of breakthrough HIV-1 sequences in the RV144 vaccine efficacy trial." *PLOS Computational Biology* 11(2): e1003973. doi: 10.1371/journal.pcbi.1003973. [AR]

61. Erdmann, N., Du, V.Y., Carlson, J., Schaefer, M., Jureka, A., Sterrett, S., Yue, L., Dileria, D., Lakhi, S., Tang, J., Sidney, J., Gilmour, J., Allen, S., Hunter, E., Heath, S., Bansal, A., and Goepfert, P.A. (2015). "HLA class-II associated HIV polymorphisms predict escape from CD4+T cell responses." *PLOS Pathogens* 11(8): e1005111. doi: 10.1371/journal.ppat.1005111. [AR]
62. Fan, W., Tang, Q., Shen, C., Qin, D., Lu, C., and Yan, Q. (2015). "Preparation and characterization of polyclonal antibody against Kaposi's sarcoma-associated herpesvirus lytic gene encoding RTA." *Folia Microbiologica* 60(6): 473-481. [AR]
63. Fenoy, E. and Nielsen, M. (2015). "Development and comparison of stability and affinity based networks." 6th Argentinian Conference on Bioinformatics and Computational Biology. <http://lidecc.cs.uns.edu.ar/cab2c2015/proceedings/handle/1234/13>. [AR]
64. Fischer, A. and Rybicki, B.A. (2015). "Granuloma genes in sarcoidosis: What is new?" *Current Opinion in Pulmonary Medicine* 21(5): 510-516. [AR]
65. Fomsgaard, A. (2015). "Therapeutic HIV peptide vaccine." *Peptide Antibodies: Methods and Protocols* 351-357. [AR]
66. Formanova, P., Cerny, J., Bolfikova, B.C., Valdes, J.J., Kozlova, I., Dzhioev, Y., and Ruzek, D. (2015). "Full genome sequences and molecular characterization of tick-borne encephalitis virus strains isolated from human patients." *Ticks and Tick-Borne Diseases* 6(1): 38-46. [AR]
67. Forouharmehr, A. and Nassiry, M.R. (2015). "B and T-cell epitopes prediction of the P40 antigen for developing mycoplasma agalactiae vaccine using bioinformatic tools." *Genetics in the 3rd Millennium* 13(1): 3954-3961. <http://eprints.hums.ac.ir/3864/>. [AR]
68. Forsdyke, D.R. (2015). "Lymphocyte repertoire selection and intracellular self/non-self-discrimination: Historical overview." *Immunology and Cell Biology* 93(3): 297-304. [AR]
69. Frosig, T.M. (2015). "Elucidating the immunological effects of 5-Azacytidine treatment in patients with myelodysplastic syndrome and identifying new conditional ligands and T-cell epitopes of relevance in melanoma." *Danish Medical Journal* 62(8): B5144. [AR]
70. Frosig, T.M., Lyngaa, R., Met, O., Larsen, S.K., Donia, M., Svane, I.M., Straten, P.T., and Hadrup, S.R. (2015). "Broadening the repertoire of melanoma-associated T-cell epitopes." *Cancer Immunology Immunotherapy* 64(5): 609-620. [AR]
71. Frosig, T.M., Yap, J., Seremet, T., Lyngaa, R., Svane, I.M., Straten, P.T., Heemskerk, M.H., Grotenbreg, G.M., and Hadrup, S.R. (2015). "Design and validation of conditional ligands for HLA-B*08:01, HLA-B*15:01, HLA-B*35:01, and HLA-B*44:05." *Cytometry Part A* 87A (10): 967-975. [AR]
72. Futami, J., Nonomura, H., Kido, M., Niidoi, N., Fujieda, N., Hosoi, A., Fujita, K., Mandai, K., Atago, Y., Kinoshita, R., Honjo, T., Matsushita, H., Uenaka, A., Nakayama, E., and Kakimi, K. (2015). "Sensitive multiplexed quantitative analysis of autoantibodies to cancer antigens with chemically S-cationized full-length and water-soluble denatured proteins." *Bioconjugate Chemistry* 26(10): 2076-2084. [AR]
73. Galaine, J., Borg, C., Godet, Y., and Adotevi, O. (2015). "Interest of tumor-specific CD4 T helper 1 cells for therapeutic anticancer vaccine." *Vaccines* 3(3): 490-502. [AR]
74. Gama, S.P.G. (2015). "The clinical relevance of drug immunogenicity." <http://hdl.handle.net/10451/17949>. [Thesis]. [AR]
75. Garstka, M.A., Fish, A., Celie, P.H., Joosten, R.P., Janssen, G.M., Berlin, I., Hoppes, R., Stadnik, M., Janssen, L., Ovaa, H., van Veelen, P.A., Perrakis, A., and Neefjes, J. (2015). "The first step of

- peptide selection in antigen presentation by MHC class I molecules." *Proceedings of the National Academy of Sciences of the United States of America* 112(5): 1505-1510. [AR]
76. Geneugelijk, K., Hoenger, G., van Deutekom, H., Thus, K., Kesmir, C., Hoesli, I., Schaub, S., and Spierings, E. (2015). "Predicted indirectly recognizable HLA epitopes presented by HLA-DRB1 are related to HLA antibody formation during pregnancy." *American Journal of Transplantation* 15(12): 3112-3122. [AR]
 77. Goodswen, S.J., Barratt, J.L., Kennedy, P.J., and Ellis, J.T. (2015). "Improving the gene structure annotation of the apicomplexan parasite *Neospora caninum* fulfils a vital requirement towards an in silico-derived vaccine." *International Journal for Parasitology* 45(5): 305-318. [AR]
 78. Granados, D.P., Laumont, C.M., Thibault, P., and Perreault, C. (2015). "The nature of self for T cells - a systems-level perspective." *Current Opinion in Immunology* 34: 1-8. [AR]
 79. Grundtman, C., Jakic, B., Buszko, M., Onestingel, E., Almanzar, G., Demetz, E., Dietrich, H., Cappellano, G., and Wick, G. (2015). "Mycobacterial heat shock protein 65 (mbHSP65)-induced atherosclerosis: Preventive oral tolerization and definition of atheroprotective and atherogenic mbHSP65 peptides." *Atherosclerosis* 242(1): 303-310. [AR]
 80. Gupta, S., Kapoor, P., Chaudhary, K., Gautam, A., Kumar, R., and Raghava, G.P. (2015). "Peptide toxicity prediction." *Methods in Molecular Biology* 1268: 143-157. doi: 10.1007/978-1-4939-2285-7_7. [AR]
 81. Gutierrez, A.H., Martin, W.D., Bailey-Kellogg, C., Terry, F., Moise, L., and De Groot, A.S. (2015). "Development and validation of an epitope prediction tool for swine (PigMatrix) based on the pocket profile method." *BMC Bioinformatics* 16: 290. doi: 10.1186/s12859-015-0724-8. [AR]
 82. Haase, K., Raffegerst, S., Schendel, D.J., and Frishman, D. (2015). "Expitope: A web server for epitope expression." *Bioinformatics* 31(11): 1854-1856. [AR]
 83. Hasan, M., Khan, M., Datta, A., Mazumder, M., and Hossain, M.U. (2015). "A comprehensive immunoinformatics and target site study revealed the corner-stone toward Chikungunya virus treatment." *Molecular Immunology* 65(1): 189-204. [AR]
 84. He, L., De Groot, A.S., and Bailey-Kellogg, C. (2015). "Hit-and-run, hit-and-stay, and commensal bacteria present different peptide content when viewed from the perspective of the T cell." *Vaccine* 33(48): 6922-6929. [AR]
 85. He, Y. and Tao, A. (2015). "Bioinformatics methods to predict allergen epitopes." *Translational Bioinformatics series. Allergy Bioinformatics*: 223-238. [AR]
 86. Hinz, D., Seumois, G.g., Gholami, A.M., Greenbaum, J.A., Lane, J., White, B., Broide, D.H., Schulten, V., Sidney, J., and Bakhru, P. (2015). "Lack of allergy to timothy grass pollen is not a passive phenomenon but associated with allergen-specific modulation of immune reactivity." *Clinical & Experimental Allergy*. doi: 10.1111/cea.12692. [AR]
 87. Hirayama, M., Tomita, Y., Yuno, A., Tsukamoto, H., Senju, S., Imamura, Y., bu Sayem, M., Irie, A., Yoshitake, Y., and Fukuma, D. (2015). "An oncofetal antigen, IMP-3-derived long peptides induce immune responses of both helper T cells and CTLs." *Oncoimmunology*. doi: 10.1080/2162402X.2015.1123368. [AR]
 88. Hoelzemer, A., Thobakgale, C.F., Cruz, C.A., Garcia-Beltran, W.F., Carlson, J.M., van Teijlingen, N.H., Mann, J.K., Jaggernath, M., Kang, S.g., Koerner, C., Chung, A.W., Schafer, J.L., Evans, D.T., Alter, G., Walker, B.D., Goulder, P.J., Carrington, M., Hartmann, P., Pertel, T., Zhou, R., Ndung'u, T., and Altfeld, M. (2015). "Selection of an HLA-C*03:04-restricted HIV-1 p24 gag sequence variant is associated with viral escape from KIR2DL3+natural killer cells: Data

- from an observational cohort in South Africa." *PLOS Medicine* 12(11): e1001900; discussion e1001900. doi: 10.1371/journal.pmed.1001900. [AR]
89. Holtappels, R., Lemmermann, N.A., Thomas, D., Renzaho, A., and Reddehase, M.J. (2015). "Identification of an atypical CD8 T cell epitope encoded by murine cytomegalovirus ORF-M54 gaining dominance after deletion of the immunodominant antiviral CD8 T cell specificities." *Medical Microbiology and Immunology* 204(3): 317-326. [AR]
 90. Houen, G. (2015). "Peptide antibodies: Past, present, and future." *Methods in Molecular Biology* 1348: 1-6. doi: 10.1007/978-1-4939-2999-3_1. [AR]
 91. Howitt, B.E., Shukla, S.A., Sholl, L.M., Ritterhouse, L.L., Watkins, J.C., Rodig, S., Stover, E., Strickland, K.C., D'Andrea, A.D., Wu, C.J., Matulonis, U., and Konstantinopoulos, P. (2015). "Association of polymerase e-mutated and microsatellite-unstable endometrial cancers with neoantigen load, number of tumor-infiltrating lymphocytes, and expression of PD-1 and PD-L1." *JAMA Oncology* 1(9): 1319-1323. [AR]
 92. Hui, D.J., Edmonson, S.C., Podsakoff, G.M., Pien, G.C., Ivanciu, L., Camire, R.M., Ertl, H., Mingozi, F., High, K.A., and Basner-Tschakarjan, E. (2015). "AAV capsid CD8+ T-cell epitopes are highly conserved across AAV serotypes." *Molecular Therapy. Methods & Clinical Development* 2: 15029. doi: 10.1038/mtm.2015.29. [AR]
 93. Hussain, M., Idrees, M., and Afzal, S. (2015). "Development of global consensus of dengue virus envelope glycoprotein for epitopes based vaccine design." *Current Computer-Aided Drug Design* 11(1): 84-97. [AR]
 94. Hutahaeen, S. (2015). "Production of antibody IgY anti-c-Myc in chicken eggs." *KnE Life Sciences* 2(1): 330-335. [AR]
 95. Ilyas, S. and Yang, J.C. (2015). "Landscape of tumor antigens in T cell immunotherapy." *Journal of Immunology* 195(11): 5117-5122. [AR]
 96. Ip, P.P., Nijman, H.W., and Daemen, T. (2015). "Epitope prediction assays combined with validation assays strongly narrows down putative cytotoxic T lymphocyte epitopes." *Vaccines* 3(2): 203-220. [AR]
 97. Ivanova, E.A., Bobryshev, Y.V., and Orekhov, A.N. (2015). "Intimal pericytes as the second line of immune defence in atherosclerosis." *World Journal of Cardiology* 7(10): 583-593. [AR]
 98. Jafarpour, S., Ayat, H., and Ahadi, A.M. (2015). "Design and antigenic epitopes prediction of a new trial recombinant multiepitopic rotaviral vaccine: In silico analyses." *Viral Immunology* 28(6): 325-330. [AR]
 99. Jahn, L., Hombrink, P., Hassan, C., Kester, M.G., van der Steen, D.M., Hagedoorn, R.S., Falkenburg, J., van Veelen, P.A., and Heemskerk, M.H. (2015). "Therapeutic targeting of the BCR-associated protein CD79b in a TCR-based approach is hampered by aberrant expression of CD79b." *Blood* 125(6): 949-958. [AR]
 100. Jozwik, A., Habibi, M.S., Paras, A., Zhu, J., Guvenel, A., Dhariwal, J., Almond, M., Wong, E.H., Sykes, A., Maybeno, M., Del Rosario, J., Trujillo-Torrallbo, M.B., Mallia, P., Sidney, J., Peters, B., Kon, O.M., Sette, A., Johnston, S.L., Openshaw, P.J., and Chiu, C. (2015). "RSV-specific airway resident memory CD8+T cells and differential disease severity after experimental human infection." *Nature Communications* 6: 10224. doi: 10.1038/ncomms10224. [AR]
 101. Jun, S.R., Leuze, M.R., Nookaew, I., Uberbacher, E.C., Land, M., Zhang, Q., Wanchai, V., Chai, J., Nielsen, M., Trolle, T., Lund, O., Buzard, G.S., Pedersen, T.D., Wassenaar, T.M., and Ussery, D.W. (2015). "Ebola virus comparative genomics." *FEMS Microbiology Reviews* 39(5): 764-778. [AR]

102. Kanduc, D. (2015). "Measles virus hemagglutinin epitopes are potential hotspots for crossreactions with immunodeficiency-related proteins." *Future Microbiology* 10(4): 503-515. [AR]
103. Karasaki, T., Nagayama, K., Kawashima, M., Hiyama, N., Murayama, T., Kuwano, H., Nitadori, J.i., Anraku, M., Sato, M., Miyai, M., ...Nakajima, J. (2015). "Identification of individual cancer-specific somatic mutations for neoantigen-based immunotherapy of lung cancer." *Journal of Thoracic Oncology*. doi: 10.1016/j.jtho.2015.11.006. Epub 2015 Dec 29. [AR]
104. Kaufman, J. (2015). "What chickens would tell you about the evolution of antigen processing and presentation." *Current Opinion in Immunology* 34: 35-42. [AR]
105. Khalili, S., Rahbar, M.R., Dezfulian, M.H., and Jahangiri, A. (2015). "In silico analyses of Wilms' tumor protein to designing a novel multi-epitope DNA vaccine against cancer." *Journal of Theoretical Biology* 379: 66-78. [AR]
106. Khan, M., Hossain, M., Rakib-Uz-Zaman, S., and Morshed, M. (2015). "Epitope-based peptide vaccine design and target site depiction against Ebola viruses: An immunoinformatics study." *Scandinavian Journal of Immunology* 82(1): 25-34. [AR]
107. Kitzmueller, C., Zulehner, N., Roulias, A., Briza, P., Ferreira, F., Fae, I., Fischer, G.F., and Bohle, B. (2015). "Correlation of sensitizing capacity and T-cell recognition within the Bet v 1 family." *Journal of Allergy and Clinical Immunology* 136(1): 151-158. [AR]
108. Knapp, B. and Deane, C.M. (2015). "T-cell receptor binding affects the dynamics of the peptide/MHC-I complex." *Journal of Chemical Information and Modeling*. doi: 10.1021/acs.jcim.5b00511. Epub 2015 Dec 29. [AR]
109. Kori, P., Sajjan, S.S., and Madagi, S.B. (2015). "In silico prediction of epitopes for Chikungunya viral strains." *Journal of Pharmaceutical Investigation* 45(6): 579-591. [AR]
110. Kowalsky, C.A., Faber, M.S., Nath, A., Dann, H.E., Kelly, V.W., Liu, L., Shanker, P., Wagner, E.K., Maynard, J.A., Chan, C., and Whitehead, T.A. (2015). "Rapid fine conformational epitope mapping using comprehensive mutagenesis and deep sequencing." *Journal of Biological Chemistry* 290(44): 26457-26470. [AR]
111. Kuan, C.W. (2015). "Investigation of the effect of genetic polymorphism on the selection of antigenic peptides in major histocompatibility complexes." <http://hdl.handle.net/2429/52349>. [Thesis]. [AR]
112. Kuiper, J., Rothova, A., de Boer, J., and Radstake, T. (2015). "The immunopathogenesis of birdshot chorioretinopathy; a bird of many feathers." *Progress in Retinal and Eye Research* 44: 99-110. [AR]
113. Kulkarni, A., Shinde, P., Kothari, S., Warke, R., Chowdhary, A., and Deshmukh, R.A. (2015). "A novel tetravalent recombinant envelope domain III vaccine against dengue: An in silico approach." *International Journal of Pharmaceutical Sciences and Research* 6(6): 2441-2450. [AR]
114. Kumar, A., Baycin-Hizal, D., Wolozny, D., Pedersen, L.E., Lewis, N.E., Heffner, K., Chaerkady, R., Cole, R.N., Shiloach, J., Zhang, H., Bowen, M.A., and Betenbaugh, M.J. (2015). "Elucidation of the CHO super-ome (CHO-SO) by proteoinformatics." *Journal of Proteome Research* 14(11): 4687-4703. [AR]
115. Kumar, S.R., Prabakaran, M., Raj, K.V.A., He, F., and Kwang, J. (2015). "Amino acid substitutions improve the immunogenicity of H7N7HA protein and protect mice against lethal H7N7 viral challenge." *PLOS One* 10(6): e0128940. doi: 10.1371/journal.pone.0128940. [AR]

116. Kumar, V., Damodharan, S., Pandaranayaka, E.P., Madathiparambil, M.G., and Tennyson, J. (2015). "Molecular modeling and in-silico engineering of Cardamom mosaic virus coat protein for the presentation of immunogenic epitopes of *Leptospira* LipL32." *Journal of Biomolecular Structure and Dynamics*. doi: 10.1080/07391102.2015.1009491. Epub 2015 Feb 18. [AR]
117. Kuzelova, K., Brodska, B., Fuchs, O., Dobrovolna, M., Soukup, P., and Cetkovsky, P. (2015). "Altered HLA class I profile associated with type A/D nucleophosmin mutation points to possible anti-nucleophosmin immune response in acute myeloid leukemia." *PLOS One* 10(5): e0127637. doi: 10.1371/journal.pone.0127637. [AR]
118. Land, M., Hauser, L., Jun, S.R., Nookaew, I., Leuze, M.R., Ahn, T.H., Karpinets, T., Lund, O., Kora, G., Wassenaar, T., Poudel, S., and Ussery, D.W. (2015). "Insights from 20 years of bacterial genome sequencing." *Functional & Integrative Genomics* 15(2): 141-161. [AR]
119. Lau, Q., Yasukochi, Y., and Satta, Y. (2015). "A limit to the divergent allele advantage model supported by variable pathogen recognition across HLA-DRB1 allele lineages." *Tissue Antigens* 86(5): 343-352. [AR]
120. Le, D., Uram, J., Wang, H., Bartlett, B., Kemberling, H., Eyring, A., Skora, A., Luber, B., Azad, N., Laheru, D., Biedrzycki, B., Donehower, R., Zaheer, A., Fisher, G., Crocenzi, T., Lee, J., Duffy, S., Goldberg, R., de la Chapelle, A., Koshiji, M., Bhajee, F., Huebner, T., Hruban, R., Wood, L., Cuka, N., Pardoll, D., Papadopoulos, N., Kinzler, K., Zhou, S., Cornish, T., Taube, J., Anders, R., Eshleman, J., Vogelstein, B., and Diaz, L. (2015). "PD-1 blockade in tumors with mismatch-repair deficiency." *New England Journal of Medicine* 372(26): 2509-2520. [AR]
121. Liljeroos, L., Malito, E., Ferlenghi, I., and Bottomley, M.J. (2015). "Structural and computational biology in the design of immunogenic vaccine antigens." *Journal of Immunology Research* 2015: 156241. doi: 10.1155/2015/156241. [AR]
122. Lin, T.Y., Su, Y.H., and Chuang, C.k. (2015). "PTD-J domain acts as an antigen carrier for cell mediated immunity." *Journal of Immunotherapy Applications* 2: 1. doi.org/10.7243/2055-2394-2-1. [AR]
123. Liu, T., Zhang, Y., Liu, Y., Wang, Y., Jia, H., Kang, M., Luo, X., Caballero, D., Gonzalez, J., Sherwood, L., Nunez, V., Wang, D., Woods, A., Schultz, P.G., and Wang, F. (2015). "Functional human antibody CDR fusions as long-acting therapeutic endocrine agonists." *Proceedings of the National Academy of Sciences of the United States of America* 112(5): 1356-1361. [AR]
124. Lohia, N. and Baranwal, M. (2015). "Identification of conserved peptides comprising multiple T cell epitopes of matrix 1 protein in H1N1 influenza virus." *Viral Immunology* 28(10): 570-579. [AR]
125. Longley, R.J., Halbroth, B.R., Ewer, K.J., Hill, A.V., and Spencer, A.J. (2015). "Identification of immunodominant responses to the *Plasmodium falciparum* antigens PfUIS3, PflSA1 and PflSAP2 in multiple strains of mice." *PLOS One* 10(12): e0144515. doi: 10.1371/journal.pone.0144515. [AR]
126. Longley, R.J., Hill, A.V., and Spencer, A.J. (2015). "Malaria vaccines: Identifying *Plasmodium falciparum* liver-stage targets." *Frontiers in Microbiology* 6: 965. doi: 10.3389/fmicb.2015.00965. [AR]
127. Longo, V., Costa, M.A., Cibella, F., Cuttitta, G., La Grutta, S., and Colombo, P. (2015). "Multiple IgE recognition on the major allergen of the *Parietaria* pollen Par j 2." *Molecular Immunology* 63(2): 412-419. [AR]
128. Lorenz, F.K., Wilde, S., Voigt, K., Kieback, E., Mosetter, B., Schendel, D.J., and Uckert, W. (2015). "Codon optimization of the human papillomavirus E7 oncogene induces a CD8(+) T cell

- response to a cryptic epitope not harbored by wild-type E7." *PLOS One* 10(3): e0121633. doi: 10.1371/journal.pone.0121633. [AR]
129. Lugo, J.S. and Cadavid, L.F. (2015). "Patterns of MHC-G-Like and MHC-B Diversification in New World monkeys." *PLOS One* 10(6): e0131343. doi: 10.1371/journal.pone.0131343. [AR]
 130. Luthra, A., Anand, A., Hawley, K.L., LeDoyt, M., La Vake, C.J., Caimano, M.J., Cruz, A.R., Salazar, J.C., and Radolf, J.D. (2015). "A homology model reveals novel structural features and an immunodominant surface loop/opsonic target in the *Treponema pallidum* BamA ortholog TP_0326." *Journal of Bacteriology* 197(11): 1906-1920. [AR]
 131. Maheshwari, K., Wozniak, J.M., Armstrong, T.G., Katz, D.S., Binkowski, T. A., Zhong, X., Heinonen, O., Karpeyev, D., and Wilde, M. (2015). "Porting ordinary applications to Blue Gene/Q Supercomputers." e-Science, 2015 IEEE 11th International Conference. doi: 10.1109/eScience.2015.8. [AR]
 132. Mahida, N., Blythe, M., Davies, M.N, Doytchinova, I.A., and Flower, D.R. (2015). "Toward the computer-aided discovery and design of epitope ensemble vaccines." *Post-Genomic Approaches in Drug and Vaccine Development* 205-244. [Book chapter]. [AR]
 133. Malito, E., Carfi, A., and Bottomley, M.J. (2015). "Protein crystallography in vaccine research and development." *International Journal of Molecular Sciences* 16(6): 13106-13140. [AR]
 134. Marani, M.M., Costa, J., Mafra, I., Oliveira, M.B., Camperi, S.A., and de Souza Almeida Leite, J.R. (2015). "In silico peptide prediction for antibody generation to recognize 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) in genetically modified organisms." *Biopolymers* 104(2): 91-100. [AR]
 135. Marquez, E.A. and Kane, K.P. (2015). "Identities of P2 and P3 residues of H-2K(b)-bound peptides determine mouse Ly49C recognition." *PLOS One* 10(7): e0131308. doi: 10.1371/journal.pone.0131308. [AR]
 136. Matsuo, H., Yokooji, T., and Taogoshi, T. (2015). "Common food allergens and their IgE-binding epitopes." *Allergology International* 64(4): 332-343. [AR]
 137. Mattapallil, M.J., Silver, P.B., Cortes, L.M., Leger, A.J.S., Jittayasothon, Y., Kielczewski, J.L., Moon, J.J., Chan, C.C., and Caspi, R.R. (2015). "Characterization of a new epitope of IRBP that induces moderate to severe uveoretinitis in mice with H-2b haplotype hIRBP651-670: A novel uveitogenic epitope." *Investigative Ophthalmology & Visual Science* 56(9): 5439-5449. [AR]
 138. Mazor, R., Crown, D., Addissie, S., Jang, Y., Kaplan, G., and Pastan, I. (2015). "Elimination of murine and human T-cell epitopes in recombinant immunotoxin eliminates neutralizing and anti-drug antibodies in vivo." *Cellular & Molecular Immunology*. doi: 10.1038/cmi.2015.91. [AR]
 139. McCluskie, M.J., Thorn, J., Gervais, D.P., Stead, D.R., Zhang, N., Benoit, M., Cartier, J., Kim, I.J., Bhattacharya, K., and Finneman, J.I. (2015). "Anti-nicotine vaccines: Comparison of adjuvanted CRM 197 and Qb-VLP conjugate formulations for immunogenicity and function in non-human primates." *International Immunopharmacology* 29(2): 663-671. [AR]
 140. Moroni, E., Paladino, A., and Colombo, G. (2015). "The dynamics of drug discovery." *Current Topics in Medicinal Chemistry* 15(20): 2043-2055. [AR]
 141. Mothe, B.R., Arlehamn, C.S.L., Dow, C., Dillon, M.B., Wiseman, R.W., Bohn, P., Karl, J., Golden, N.A., Gilpin, T., Foreman, T.W., Rodgers, M.A., Mehra, S., Scriba, T.J., Flynn, J.L., Kaushal, D., O'Connor, D.H., and Sette, A. (2015). "The TB-specific CD4(+) T cell immune repertoire in both cynomolgus and rhesus macaques largely overlap with humans." *Tuberculosis* 95(6): 722-735. [AR]

142. Moyle, P.M. (2015). "Progress in vaccine development." *Current Protocols in Microbiology* 36: 18.1.1-26. doi: 10.1002/9780471729259.mc1801s36. [AR]
143. Mukherjee, G., Chaparro, R.J., Schloss, J., Smith, C., Bando, C.D., and DiLorenzo, T.P. (2015). "Glucagon-reactive islet-infiltrating CD8 T cells in NOD mice." *Immunology* 144(4): 631-640. [AR]
144. Musvosvi, M.N. (2015). "Systems analysis of the CD4 T cell response induced by the novel subunit tuberculosis vaccine, H1: IC31." <https://open.uct.ac.za/handle/11427/16724>. [Thesis]. [AR]
145. Nanda Kumar, Y., Jeyakodi, G., Gunasekaran, K., and Jambulingam, P. (2015). "Computational screening and characterization of putative vaccine candidates of *Plasmodium vivax*." *Journal of Biomolecular Structure and Dynamics* 1-15. [Epub ahead of print]. [AR]
146. Navalkar, K.A., Johnston, S.A., and Stafford, P. (2015). "Peptide based diagnostics: Are random-sequence peptides more useful than tiling proteome sequences?" *Journal of Immunological Methods* 417:10-21. [AR]
147. Nazeri, S., Mehri, A.A., Djadid, N.D., and Zakeri, S. (2015). "A comparative study on worldwide genetic diversity and population structure analysis of *Plasmodium vivax* thrombospondin-related adhesive protein (PvTRAP) and its implications for the vivax vaccine design." *Infection Genetics and Evolution* 36: 410-423. [AR]
148. Nguyen, H.N., Steede, N.K., Robinson, J.E., and Landry, S.J. (2015). "Conformational instability governed by disulfide bonds partitions the dominant from subdominant helper T-cell responses specific for HIV-1 envelope glycoprotein gp120." *Vaccine* 33(25): 2887-2896. [AR]
149. Nielsen, J.S., Sedgwick, C., Shahid, A., Zong, Z., Brumme, Z.L., Yu, S., Liu, L., Kroeger, D.R., Treon, S.P., and Connors, J.M. (2015). "Toward personalized lymphoma immunotherapy: Identification of common driver mutations recognized by patient CD8+ T cells." *Clinical Cancer Research*. doi: 10.1158/1078-0432.CCR-15-2023. [Epub ahead of print]. [AR]
150. Nishimura, Y., Tomita, Y., Yuno, A., Yoshitake, Y., and Shinohara, M. (2015). "Cancer immunotherapy using novel tumor-associated antigenic peptides identified by genome-wide cDNA microarray analyses." *Cancer Science* 106(5): 505-511. [AR]
151. Oany, A. (2015). "Identification of highly conserved regions in L-segment of Crimean-Congo hemorrhagic fever virus and immunoinformatic prediction about potential novel vaccine." *Advances and Applications in Bioinformatics and Chemistry* 8: 1-10. doi: 10.2147/AABC.S75250. [AR]
152. Oany, A.R., Sharmin, T., Chowdhury, A.S., Jyoti, T.P., and Hasan, M.A. (2015). "Highly conserved regions in Ebola virus RNA dependent RNA polymerase may be act as a universal novel peptide vaccine target: A computational approach." *In Silico Pharmacology* 3(1): 1-13. [AR]
153. Obrezanova, O., Arnell, A., de la Cuesta, R.G., Berthelot, M.E., Gallagher, T.R., Zurdo, J., and Stallwood, Y. (2015). "Aggregation risk prediction for antibodies and its application to biotherapeutic development." *mAbs* 7(2): 352-363. [AR]
154. Okiyama, N., Hasegawa, H., Oida, T., Hirata, S., Yokozeki, H., Fujimoto, M., Miyasaka, N., and Kohsaka, H. (2015). "Experimental myositis inducible with transfer of dendritic cells presenting a skeletal muscle C protein-derived CD8 epitope peptide." *International Immunology* 27(7): 327-332. [AR]

155. Okoniewska, K.M., Okoniewski, J., and Grabowski, T. (2015). "Relationship between tregitopes structure and binding with major histocompatibility complex class I." *Drug Research*. doi: 10.1055/s-0035-1564117. [Epub ahead of print]. [AR]
156. Olsen, L.R., Simon, C., Kudahl, U.J., Bagger, F.O., Winther, O., Reinherz, E.L., Zhang, G.L., and Brusic, V. (2015). "A computational method for identification of vaccine targets from protein regions of conserved human leukocyte antigen binding." *BMC Medical Genomics* 8(Suppl 4): S1. doi: 10.1186/1755-8794-8-S4-S1. [AR]
157. Ondieki, M.C., Nyaribari, M.C., Ejekwumadu, N.J., and Nyakangö, M.J. (2015). "Design of a recombinant hepatitis B vaccine based on stably binding HLA-I peptides." *Biomolecular Research & Therapeutics* 4: 120. [AR]
158. Overgaard, N.H., Frosig, T.M., Welner, S., Rasmussen, M., Ilsoe, M., Sorensen, M.R., Andersen, M.H., Buus, S., and Jungersen, G. (2015). "Establishing the pig as a large animal model for vaccine development against human cancer." *Frontiers in Genetics* 6: 286. doi: 10.3389/fgene.2015.00286. [AR]
159. Oyarzun, P., Ellis, J.J., Gonzalez-Galarza, F.F., Jones, A.R., Middleton, D., Boden, M., and Kobe, B. (2015). "A bioinformatics tool for epitope-based vaccine design that accounts for human ethnic diversity: Application to emerging infectious diseases." *Vaccine* 33(10): 1267-1273. [AR]
160. Pandya, M., Rasmussen, M., Hansen, A., Nielsen, M., Buus, S., Golde, W., and Barlow, J. (2015). "A modern approach for epitope prediction: Identification of foot-and-mouth disease virus peptides binding bovine leukocyte antigen (BoLA) class I molecules." *Immunogenetics* 67(11-12): 691-703. [AR]
161. Pappalardo, F., Flower, D., Russo, G., Pennisi, M., and Motta, S. (2015). "Computational modelling approaches to vaccinology." *Pharmacological Research* 92: 40-45. [AR]
162. Pedersen, L.E., Rasmussen, M., Harndahl, M., Nielsen, M., Buus, S., and Jungersen, G. (2015). "A combined prediction strategy increases identification of peptides bound with high affinity and stability to porcine MHC class I molecules SLA-1* 04: 01, SLA-2* 04: 01, and SLA-3* 04: 01." *Immunogenetics* 1-9. [AR]
163. Peri, C., Sole, O.C., Corrada, D., Gori, A., Daura, X., and Colombo, G. (2015). "Prediction of antigenic B and T cell epitopes via energy decomposition analysis: Description of the web-based prediction tool BEPPE." *Methods in Molecular Biology* 1348: 13-22. doi: 10.1007/978-1-4939-2999-3_3. [AR]
164. Pfafferott, K., Deshpande, P., McKinnon, E., Merani, S., Lucas, A., Heckerman, D., Mallal, S., John, M., Gaudieri, S., and Lucas, M. (2015). "Anti-hepatitis C virus T-cell immunity in the context of multiple exposures to the virus." *PLOS One* 10(6): e0130420. doi: 10.1371/journal.pone.0130420. [AR]
165. Poh, C.L., Kirk, K., Chua, H.N., and Grollo, L. (2015). "Enterovirus-specific anti-peptide antibodies." *Methods in Molecular Biology* 1348: 341-350. doi: 10.1007/978-1-4939-2999-3_29. [AR]
166. Polyakova, A., Kuznetsova, K., and Moshkovskii, S. (2015). "Proteogenomics meets cancer immunology: Mass spectrometric discovery and analysis of neoantigens." *Expert Review of Proteomics* 12(5): 533-541. [AR]
167. Poorinmohammad, N. and Mohabatkar, H. (2015). "Homology modeling and conformational epitope prediction of envelope protein of Alkhumra haemorrhagic fever virus." *Journal of Arthropod-Borne Diseases* 9(1): 116-124. [AR]

168. Pratheek, B., Suryawanshi, A.R., Chattopadhyay, S., and Chattopadhyay, S. (2015). "In silico analysis of MHC-I restricted epitopes of Chikungunya virus proteins: Implication in understanding anti-CHIKV CD8(+) T cell response and advancement of epitope based immunotherapy for CHIKV infection." *Infection Genetics and Evolution* 31: 118-126. [AR]
169. Pratt, K.P. (2015). "Engineering less immunogenic and antigenic FVIII proteins." *Cellular Immunology* 301:12-7. doi: 10.1016/j.cellimm.2015.10.008. [Epub 2015 Nov 2]. [AR]
170. Pritchard, A.L., Burel, J.G., Neller, M.A., Hayward, N.K., Lopez, J., Fatho, M., Lennerz, V., Woelfel, T., and Schmidt, C.W. (2015). "Exome sequencing to predict neoantigens in melanoma." *Cancer Immunology Research* 3(9): 992-998. [AR]
171. Rahman, K., Chowdhury, E.U., Poudel, A., Ruettger, A., Sachse, K., and Kaltenboeck, B. (2015). "Defining species-specific immunodominant B cell epitopes for molecular serology of Chlamydia species." *Clinical and Vaccine Immunology* 22(5): 539-552. [AR]
172. Ramya, L. and Pulicherla, K.K. (2015). "Studies on deimmunization of antileukaemic L-asparaginase to have reduced clinical immunogenicity - an in silico approach." *Pathology & Oncology Research* 21(4): 909-920. [AR]
173. Rana, A. and Akhter, Y. (2015). "A multi-subunit based, thermodynamically stable model vaccine using combined immunoinformatics and protein structure based approach." *Immunobiology* 221(4): 544-557. doi: 10.1016/j.imbio.2015.12.004. [Epub 2015 Dec 9]. [AR]
174. Rana, A., Rub, A., and Akhter, Y. (2015). "Proteome-wide B and T cell epitope repertoires in outer membrane proteins of Mycobacterium avium subsp paratuberculosis have vaccine and diagnostic relevance: A holistic approach." *Journal of Molecular Recognition* 28(8): 506-520. [AR]
175. Ranjbar, M.M., Nabian, S., Ahmadi, N.A., Ghorban, K., Sazmand, A., Dadmanesh, M., and Hekmatimoghaddam, S.H. (2015). "Immunoinformatics and similarity analysis of house dust mite tropomyosin." *Novelty in Biomedicine* 3(4): 161-170. [AR]
176. Ratto-Kim, S., de Souza, M.S., Currier, J.R., Karasavvas, N., Sidney, J., Rolland, M., Valencia-Micolta, A., Madnote, S., Sette, A., Nitayaphan, S., Pitisuttathum, P., Kaewkungwal, J., Rerks-Ngarm, S., O'Connell, R., Michael, N., Robb, M.L., Marovich, M., and Kim, J.H. (2015). "Identification of immunodominant CD4-restricted epitopes co-located with antibody binding sites in individuals vaccinated with ALVAC-HIV and AIDSVAX B/E." *PLOS One*: 10(2):e0115582. doi: 10.1371/journal.pone.0115582. [AR] ca
177. Razzaq, B.A., Scalora, A., Koparde, V.N., Meier, J., Mahmood, M., Salman, S., Jameson-Lee, M., Serrano, M.G., Sheth, N., and Voelkner, M. (2015). "Dynamical system modeling to simulate donor T cell response to whole exome sequencing-derived recipient peptides demonstrates different alloreactivity potential in HLA-matched and mismatched donor-recipient pairs." *Biology of Blood and Marrow Transplantation* pii: S1083-8791(15)01860-1. doi: 10.1016/j.bbmt.2015.11.1103. [AR]
178. Ren, J., Liu, Q., Ellis, J., and Li, J. (2015). "Positive-unlabeled learning for the prediction of conformational B-cell epitopes." *BMC Bioinformatics* 16(Suppl 18): S12. doi: 10.1186/1471-2105-16-S18-S12. [AR]
179. Ren, J., Wang, X., Zhu, L., Hu, Z., Gao, Q., Yang, P., Li, X., Wang, J., Shen, X., Fry, E.E., Rao, Z., and Stuart, D.I. (2015). "Structures of coxsackievirus A16 capsids with native antigenicity: Implications for particle expansion, receptor binding, and immunogenicity." *Journal of Virology* 89(20): 10500-10511. [AR]

180. Richards, K.A., Nayak, J., Chaves, F.A., DiPiazza, A., Knowlden, Z.A., Alam, S., Treanor, J.J., and Sant, A.J. (2015). "Seasonal influenza can poise hosts for CD4 T-cell immunity to H7N9 avian influenza." *Journal of Infectious Diseases* 212(1): 86-94. [AR]
181. Rizvi, N.A., Hellmann, M.D., Snyder, A., Kvistborg, P., Makarov, V., Havel, J.J., Lee, W., Yuan, J., Wong, P., Ho, T.S., Miller, M.L., Rekhtman, N., Moreira, A.L., Ibrahim, F., Bruggeman, C., Gasmir, B., Zappasodi, R., Maeda, Y., Sander, C., Garon, E.B., Merghoub, T., Wolchok, J.D., Schumacher, T.N., and Chan, T.A. (2015). "Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer." *Science* 348(6230): 124-128. [AR]
182. Ronka, A.L., Kinnunen, T.T., Goudet, A., Rytkonen-Nissinen, M.A., Sairanen, J., Kailaanmaki, A.H., Randell, J.T., Maillere, B., and Virtanen, T.I. (2015). "Characterization of human memory CD4(+) T-cell responses to the dog allergen Can f 4." *Journal of Allergy and Clinical Immunology* 136(4): 1047-1054. e10. doi: 10.1016/j.jaci.2015.02.025. [AR]
183. Rooney, M.S., Shukla, S.A., Wu, C.J., Getz, G., and Hacohen, N. (2015). "Molecular and genetic properties of tumors associated with local immune cytolytic activity." *Cell* 160(1-2): 48-61. [AR]
184. Sabbaghian, E., Roodbari, F., Rafiei, A., and Amani, J. (2015). "In silico design of a multimeric polytope as a highly immunogenic DNA vaccine against human cytomegalovirus." *Journal of Applied Biotechnology Reports* 1(4): 143-153. [AR]
185. Sachdeva, N. (2015). "Epitope specific T cells in type 1 diabetes: From detection to immunotherapy." *Immunoendocrinology* 2: e760. doi: 10.14800/ie.760. [AR]
186. Sahu, T.K., Rao, A., Meher, P.K., Sahoo, B.C., Gupta, S., and Rai, A. (2015). "Computational prediction of MHC class I epitopes for most common viral diseases in cattle (*Bos taurus*)." *Indian Journal of Biochemistry & Biophysics* 52(1): 34-44. [AR]
187. Saini, S., Hamasaki-Katagiri, N., Pandey, G., Yanover, C., Guelcher, C., Simhadri, V., Dandekar, S., Guerrero, M., Kimchi-Sarfaty, C., and Sauna, Z. (2015). "Genetic determinants of immunogenicity to factor IX during the treatment of haemophilia B." *Haemophilia* 21(2): 210-218. [AR]
188. Salvat, R.S., Choi, Y., Bishop, A., Bailey-Kellogg, C., and Griswold, K.E. (2015). "Protein deimmunization via structure-based design enables efficient epitope deletion at high mutational loads." *Biotechnology and Bioengineering* 112(7): 1306-1318. [AR]
189. Salvat, R.S., Parker, A.S., Choi, Y., Bailey-Kellogg, C., and Griswold, K.E. (2015). "Mapping the pareto optimal design space for a functionally deimmunized biotherapeutic candidate." *PLOS Computational Biology* 11(1): e1003988. doi: 10.1371/journal.pcbi.1003988. [AR]
190. Samal, H.B., Prava, J., Suar, M., and Mahapatra, R.K. (2015). "Comparative genomics study of *Salmonella typhimurium* LT2 for the identification of putative therapeutic candidates." *Journal of Theoretical Biology* 369: 67-79. [AR]
191. Santos, E.J.M., McCabe, A., Gonzalez-Galarza, F.F., Jones, A.R., and Middleton, D. (2015). "Allele Frequencies Net Database: Improvements for storage of individual genotypes and analysis of existing data." *Human Immunology* pii: S0198-8859(15)00566-2. doi: 10.1016/j.humimm.2015.11.013. [AR]
192. Sauna, Z.E., Lozier, J.N., Kasper, C.K., Yanover, C., Nichols, T., and Howard, T.E. (2015). "The intron-22-inverted F8 locus permits factor VIII synthesis: Explanation for low inhibitor risk and a role for pharmacogenomics." *Blood* 125(2): 223-228. [AR]
193. Scalia, C.R., Gendusa, R., Basciu, M., Riva, L., Tusa, L., Musaro, A., Veronese, S., Formenti, A., D'Angelo, D., Ronzio, A.G., Cattoretto, G., and Bolognesi, M.M. (2015). "Epitope recognition in

- the human-pig comparison model on fixed and embedded material." *Journal of Histochemistry & Cytochemistry* 63(10): 805-822. [AR]
194. Schellens, I.M., Hoof, I., Meiring, H.D., Spijkers, S.N., Poelen, M.C., van Gaans-van den Brink, J., van der Poel, K., Costa, A.I., van Els, C.A., van Baarle, D., and Kesmir, C. (2015). "Comprehensive analysis of the naturally processed peptide repertoire: Differences between HLA-A and B in the immunopeptidome." *PLOS One* 10(9): e0136417. doi: 10.1371/journal.pone.0136417. [AR]
 195. Schellens, I.M., Meiring, H.D., Hoof, I., Spijkers, S.N., Poelen, M.C., van Gaans-van den Brink, J., Costa, A.I., Vennema, H., Kesmir, C., van Baarle, D., and van Els, C.A. (2015). "Measles virus epitope presentation by HLA: Novel insights into epitope selection, dominance, and microvariation." *Frontiers in Immunology* 6: 546. doi: 10.3389/fimmu.2015.00546. [AR]
 196. Schmiedel, J.r.M., Klemm, S.L., Zheng, Y., Sahay, A., Bluthgen, N., Marks, D.S., and van Oudenaarden, A. (2015). "Gene Expression. MicroRNA control of protein expression noise." *Science* 348(6230): 128-132. [AR]
 197. Scholtalbers, J., Boegel, S., Bukur, T., Byl, M., Goerges, S., Sorn, P., Loewer, M., Sahin, U., and Castle, J.C. (2015). "TCLP: An online cancer cell line catalogue integrating HLA type, predicted neo-epitopes, virus and gene expression." *Genome Medicine* 7: 118. doi: 10.1186/s13073-015-0240-5. [AR]
 198. Schumacher, T.N. and Schreiber, R.D. (2015). "Neoantigens in cancer immunotherapy." *Science* 348(6230): 69-74. [AR]
 199. Sefid, F., Rasooli, I., Jahangiri, A., and Bazmara, H. (2015). "Functional exposed amino acids of BauA as potential immunogen against *Acinetobacter baumannii*." *Acta Biotheoretica* 63(2): 129-149. [AR]
 200. Sekhavati, M.H., Heravi, R.M., Tahmoorespur, M., Yousefi, S., bbassi-Dalooi, T., and Akbari, R. (2015). "Cloning, molecular analysis and epitopes prediction of a new chaperone GroEL *Brucella melitensis* antigen." *Iranian Journal of Basic Medical Sciences* 18(5): 499-505. [AR]
 201. Sela-Culang, I., Ashkenazi, S., Peters, B., and Ofran, Y. (2015). "PEASE: Predicting B-cell epitopes utilizing antibody sequence." *Bioinformatics* 31(8): 1313-1315. [AR]
 202. Shah, M.N.A., Barua, P., and Khan, M.K. (2015). "Immunoinformatics aided prediction of cytotoxic T cell epitope of respiratory syncytial virus." *Biores Comm* 1(2): 99-104. [AR]
 203. Shahangian, S.S., Sajedi, R.H., Hasannia, S., Jalili, S., Mohammadi, M., Taghdir, M., Shali, A., Mansouri, K., and Sariri, R. (2015). "A conformation-based phage-display panning to screen neutralizing anti-VEGF VHHs with VEGFR2 mimicry behavior." *International Journal of Biological Macromolecules* 77: 222-234. [AR]
 204. Shahid, A., Olvera, A., Anmole, G., Kuang, X.T., Cotton, L.A., Plana, M., Brander, C., Brockman, M.A., and Brumme, Z.L. (2015). "Consequences of HLA-B*13-associated escape mutations on HIV-1 replication and Nef function." *Journal of Virology* 89(22): 11557-11571. [AR]
 205. Shahid, N., Tahir, S., Rao, A.Q., Hassan, S., Khan, A., Latif, A., Au Khan, M., Tabassum, B., Shahid, A.A., Zafar, A.U., and Husnain, T. (2015). "Escherichia coli expression of NDV fusion protein gene and determination of its antigenic epitopes." *Biologia* 70(12): 1553-1564. [AR]
 206. Shao, H., Lin, Y., Wang, T., Ou, Y., Shen, H., Tao, C., Wu, F., Zhang, W., Bo, H., Wang, H., and Huang, S. (2015). "Identification of peptide-specific TCR genes by in vitro peptide stimulation and CDR3 length polymorphism analysis." *Cancer Letters* 363(1): 83-91. [AR]

207. Shi, J., Sun, J., Wu, M., Hu, N., Li, J., Li, Y., Wang, H., and Hu, Y. (2015). "Inferring protective CD8(+) T-cell epitopes for NS5 protein of four serotypes of dengue virus Chinese isolates based on HLA-A, -B and -C allelic distribution: Implications for epitope-based universal vaccine design." *PLOS One* 10(9): e0138729. doi: 10.1371/journal.pone.0138729. [AR]
208. Shi, J., Zhang, J., Li, S., Sun, J., Teng, Y., Wu, M., Li, J., Li, Y., Hu, N., Wang, H., and Hu, Y. (2015). "Epitope-based vaccine target screening against highly pathogenic MERS-CoV: An in silico approach applied to emerging infectious diseases." *PLOS One* 10(12): e0144475. doi: 10.1371/journal.pone.0144475. [AR]
209. Skora, A.D., Douglass, J., Hwang, M.S., Tam, A.J., Blosser, R.L., Gabelli, S.B., Cao, J., Diaz, L.A., Papadopoulos, N., Kinzler, K.W., Vogelstein, B., and Zhou, S. (2015). "Generation of MANAbodies specific to HLA-restricted epitopes encoded by somatically mutated genes." *Proceedings of the National Academy of Sciences of the United States of America* 112(32): 9967-9972. [AR]
210. Soellner, J. (2015). "Computational peptide vaccinology." *Computational Peptidology* 1268: 291-312. [AR]
211. Sofron, A., Ritz, D., Neri, D., and Fugmann, T. (2015). "High-resolution analysis of the murine MHC class II immunopeptidome." *European Journal of Immunology*. doi: 10.1002/eji.201545930. [Epub 2015 Nov 17]. [AR]
212. Solanki, K., Yadav, J., Singh, R., and Verma, S.R. (2015). "Prediction of epitope and host organism for generation of antibodies against human toll-like receptor 5 protein." *Molecular Enzymology and Drug Targets* 1 (2:5): 1-6. [AR]
213. Soni, D.K., Nath, A., and Dubey, S.K. (2015). "Evaluation and use of in silico structure based epitope prediction for listeriolysin O of *Listeria monocytogenes*." *Indian Journal of Biotechnology* 14(2): 160-166. [AR]
214. Soria-Guerra, R.E., Nieto-Gomez, R., Govea-Alonso, D.O., and Rosales-Mendoza, S. (2015). "An overview of bioinformatics tools for epitope prediction: Implications on vaccine development." *Journal of Biomedical Informatics* 53: 405-414. [AR]
215. Sun, P., Ju, H., Zhang, B., Gu, Y., Liu, B., Huang, Y., Zhang, H., and Li, Y. (2015). "Conformational B-cell epitope prediction method based on antigen preprocessing and mimotopes analysis." *BioMed Research International* 2015: 257030. doi: 10.1155/2015/257030. [AR]
216. Taffon, S., Kondili, L.A., Giuseppetti, R., Ciccaglione, A.R., Pulimanti, B., Attili, A.F., Rapicetta, M., and D'Ugo, E. (2015). "Woodchuck hepatitis virus core gene deletions and proliferative responses of peripheral blood mononuclear cells stimulated by an immunodominant epitope: A viral immune escape in the woodchuck model of chronic hepatitis B?" *Archives of Virology* 160(4): 1065-1073. [AR]
217. Taherkhani, R. and Farshadpour, F. (2015). "A new strategy for development of hepatitis E vaccine: Epitope-based vaccines." *Pathogen & Infectious Disease* 1(1): e933. doi: 10.14800/pid.933. [AR]
218. Tang, B., Zhou, W., Du, J., He, Y., and Li, Y. (2015). "Identification of human leukemia antigen A*0201-restricted epitopes derived from epidermal growth factor pathway substrate number 8." *Molecular Medicine Reports* 12(2): 1741-1752. [AR]
219. Teh-Poot, C., Tzec-Arjona, E., Martinez-Vega, P., Jesus Ramirez-Sierra, M., Rosado-Vallado, M., and Dumonteil, E. (2015). "From genome screening to creation of vaccine against

- Trypanosoma cruzi by use of immunoinformatics." *Journal of Infectious Diseases* 211(2): 258-266. [AR]
220. Ternette, N., Block, P.D., Sanchez-Bernabeu, A., Borthwick, N., Pappalardo, E., Abdul-Jawad, S., Ondondo, B., Charles, P.D., Dorrell, L., Kessler, B.M., and Hanke, T. (2015). "Early kinetics of the HLA class I-associated peptidome of MVA.HIVconsv-infected cells." *Journal of Virology* 89(11): 5760-5771. [AR]
221. Terry, F.E., Moise, L., Martin, R.F., Torres, M., Pilotte, N., Williams, S.A., and De Groot, A.S. (2015). "Time for T? Immunoinformatics addresses vaccine design for neglected tropical and emerging infectious diseases." *Expert Review of Vaccines* 14(1): 21-35. [AR]
222. Textoris-Taube, K., Keller, C., Liepe, J., Henklein, P., Sidney, J., Sette, A., Kloetzel, P.M., and Mishto, M. (2015). "The T210M substitution in the HLA-a*02:01 gp100 epitope strongly affects overall proteasomal cleavage site usage and antigen processing." *Journal of Biological Chemistry* 290(51): 30417-30428. [AR]
223. Trajanoski, Z., Maccalli, C., Mennonna, D., Casorati, G., Parmiani, G., and Dellabona, P. (2015). "SOMATICALLY MUTATED TUMOR ANTIGENS IN THE QUEST FOR A MORE EFFICACIOUS PATIENT-ORIENTED IMMUNOTHERAPY OF CANCER." *Cancer Immunology, Immunotherapy* 64(1): 99-104. [AR]
224. Tran, E., Ahmadzadeh, M., Lu, Y.C., Gros, A., Turcotte, S., Robbins, P.F., Gartner, J.J., Zheng, Z., Li, Y.F., and Ray, S. (2015). "Immunogenicity of somatic mutations in human gastrointestinal cancers." *Science* 350(6266): 1387-1390. [AR]
225. Tschärke, D.C., Croft, N.P., Doherty, P.C., and La Gruta, N.L. (2015). "Sizing up the key determinants of the CD8(+) T cell response." *Nature Reviews Immunology* 15(11): 705-716. [AR]
226. Tshabalala, M., Mellet, J., and Pepper, M.S. (2015). "Human leukocyte antigen diversity: A Southern African perspective." *Journal of Immunology Research* 2015: 746151. doi: 10.1155/2015/746151. [AR]
227. Uslan, V. and Seker, H. (2015). "The quantitative prediction of HLA-B* 2705 peptide binding affinities using Support Vector Regression to gain insights into its role for the spondyloarthropathies." *Engineering in Medicine and Biology Society (EMBC), 2015 37th Annual International Conference of the IEEE: 7651-7654.* [AR]
228. Valdivia-Olarte, H., Requena, D., Ramirez, M., Saravia, L.E., Izquierdo, R., Falconi-Agapito, F., Zavaleta, M., Best, I., Fernandez-Diaz, M., and Zimic, M. (2015). "Design of a predicted MHC restricted short peptide immunodiagnostic and vaccine candidate for fowl adenovirus C in chicken infection." *Bioinformatics* 11(10): 460-465. [AR]
229. Van Allen, E.M., Miao, D., Schilling, B., Shukla, S.A., Blank, C., Zimmer, L., Sucker, A., Hillen, U., Foppen, M.H.G., and Goldinger, S.M. (2015). "Genomic correlates of response to CTLA-4 blockade in metastatic melanoma." *Science* 350(6257): 207-211. [AR]
230. van Gool, I.C., Eggink, F.A., Freeman-Mills, L., Stelloo, E., Marchi, E., de Bruyn, M., Palles, C., Nout, R.A., de Kroon, C.D., Osse, E.M., Klenerman, P., Creutzberg, C.L., Tomlinson, I.P., Smit, V.T., Nijman, H.W., Bosse, T., and Church, D.N. (2015). "POLE proofreading mutations elicit an antitumor immune response in endometrial cancer." *Clinical Cancer Research* 21(14): 3347-3355. [AR]
231. Vanchinathan, H.P., Marfurt, A., Robelin, C.A., Kossmann, D., and Krause, A. (2015). "Discovering valuable items from massive data." *Proceedings of the 21th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining: 1195-1204.* [AR]

232. Vera, J., Gupta, S.K., Wolkenhauer, O., and Schuler, G. (2015). "Envisioning the application of systems biology in cancer immunology." *Cancer Immunology*: 429-449. [Book chapter]. 2015. [AR]
233. Viana de Carvalho, R. (2015). "Computational modeling of mycobacterium infection and innate immune response in zebrafish." <https://openaccess.leidenuniv.nl/handle/1887/35896>. [Thesis]. [AR]
234. Walton, S., Slender, A., Pizutto, S., Mounsey, K., Opresecu, F., Thomas, W., Hales, B., and Currie, B. (2015). "Analysis of IgE binding patterns to house dust mite allergens in scabies-endemic communities: Insights for both diseases." *Clinical and Experimental Allergy* 45(12): 1868-1872. [AR]
235. Walz, S., Stickel, J.S., Kowalewski, D.J., Schuster, H., Weisel, K., Backert, L., Kahn, S., Nelde, A., Stroh, T., Handel, M., Kohlbacher, O., Kanz, L., Salih, H.R., Rammensee, H.G., and Stevanovic, S. (2015). "The antigenic landscape of multiple myeloma: Mass spectrometry (re) defines targets for T-cell-based immunotherapy." *Blood* 126(10): 1203-1213. [AR]
236. Wan, S., Knapp, B., Wright, D.W., Deane, C.M., and Coveney, P.V. (2015). "Rapid, precise, and reproducible prediction of peptide-MHC binding affinities from molecular dynamics that correlate well with experiment." *Journal of Chemical Theory and Computation* 11(7): 3346-3356. [AR]
237. Wang, Y., Zhou, P., Lin, Y., Shu, M., Hu, Y., Xia, Q., and Lin, Z. (2015). "Quantitative prediction of class I MHC/epitope binding affinity using QSAR modeling derived from amino acid structural information." *Combinatorial Chemistry & High Throughput Screening* 18(1): 75-82. [AR]
238. Wayengera, M. (2015). "Multiple protein-domain conservation architecture as a non-deterministic confounder of linear B cell epitopes." *African Journal of Biotechnology* 14(32): 2526-2531. [AR]
239. Weiskopf, D., Angelo, M.A., Bangs, D.J., Sidney, J., Paul, S., Peters, B., de Silva, A.D., Lindow, J.C., Diehl, S.A., Whitehead, S., Durbin, A., Kirkpatrick, B., and Sette, A. (2015). "The human CD8(+) T cell responses induced by a live attenuated tetravalent dengue vaccine are directed against highly conserved epitopes." *Journal of Virology* 89(1): 120-128. [AR]
240. Weiskopf, D., Bangs, D.J., Sidney, J., Kolla, R.V., de Silva, A.D., de Silva, A.M., Crotty, S., Peters, B., and Sette, A. (2015). "Dengue virus infection elicits highly polarized CX3CR1(+) cytotoxic CD4(+) T cells associated with protective immunity." *Proceedings of the National Academy of Sciences of the United States of America* 112(31): E4256-E4263. [AR]
241. Weiskopf, D., Cerpas, C., Angelo, M.A., Bangs, D.J., Sidney, J., Paul, S., Peters, B., Sanches, F.P., Silvera, C.G., Costa, P.R., Kallas, E.G., Gresh, L., de Silva, A.D., Balmaseda, A., Harris, E., and Sette, A. (2015). "Human CD8(+) T-cell responses against the 4 dengue virus serotypes are associated with distinct patterns of protein targets." *Journal of Infectious Diseases* 212(11): 1743-1751. [AR]
242. Woodfolk, J.A., Glesner, J., Wright, P.W., Kepley, C.L., Li, M., Himly, M., Muehling, L.M., Gustchina, A., Wlodawer, A., and Chapman, M.D. (2015). "Antigenic determinants of the bilobal cockroach allergen Bla g 2." *Journal of Biological Chemistry*. doi: 10.1074/jbc.M115.702324. Epub 2015 Dec 7. [AR]
243. Xiang, S.D., Gao, Q., Wilson, K.L., Heyerick, A., and Plebanski, M. (2015). "Mapping T and B cell epitopes in sperm protein 17 to support the development of an ovarian cancer vaccine." *Vaccine* 33(44): 5950-5959. [AR]

244. Xu, Y., Jin, Y., Liu, L., Zhang, X., Chen, Y., and Wei, J. (2015). "Study of circulating IgG antibodies to peptide antigens derived from BIRC5 and MYC in cervical cancer." *FEBS Open Bio* 5: 198-201. [AR]
245. Yang, X., Gao, M., Chen, G., Pierce, B.G., Lu, J., Weng, N.p., and Mariuzza, R.A. (2015). "Structural basis for clonal diversity of the public T cell response to a dominant human cytomegalovirus epitope." *Journal of Biological Chemistry* 290(48): 29106-29119. [AR]
246. Yin, L., Chen, X., Tiwari, A., Vicini, P., and Hickling, T.P. (2015). "The role of aggregates of therapeutic protein products in immunogenicity: An evaluation by mathematical modeling." *Journal of Immunology Research* 2015: 401956. doi: 10.1155/2015/401956. Epub 2015 Nov 22. [AR]
247. Yin, L., Chen, X., Vicini, P., Rup, B., and Hickling, T.P. (2015). "Therapeutic outcomes, assessments, risk factors, and mitigation efforts of immunogenicity of therapeutic protein products." *Cellular Immunology* 295(2): 118-126. [AR]
248. Yousefi, S., Tahmoorespur, M., and Sekhavati, M.H. (2015). "B and T-cell epitope prediction of the OMP25 antigen for developing *Brucella melitensis* vaccines for sheep." *Iranian Journal of Applied Animal Science* 5(3): 629-638. [AR, MA]
249. Yu, S., Zhang, H., Yao, D., Liu, W., Wang, X., Chen, X., Wei, Y., Zhang, Z., Wang, J., Yu, L., Sun, H., Wu, Z., Yu, Y., Song, B., Ma, J., Tong, C., and Cui, Y. (2015). "Identification of CD4(+) T-cell epitopes on iron-regulated surface determinant B of *Staphylococcus aureus*." *Microbial Pathogenesis* 89: 108-113. [AR]
250. Zhang, X., Yu, B., Jin, Y., Lei, M., Zhang, X., Duan, Z., Lin, Y., Megson, I.L., and Wei, J. (2015). "A study of IgG antibodies to the ApoB protein in non-ST segment elevation acute coronary syndrome." *Scandinavian Cardiovascular Journal* 49(3): 136-141. [AR]
251. Zhang, Y., Zou, H., Wang, Y., Caballero, D., Gonzalez, J., Chao, E., Welzel, G., Shen, W., Wang, D., Schultz, P.G., and Wang, F. (2015). "Rational design of a humanized glucagon-like peptide-1 receptor agonist antibody." *Angewandte Chemie-International Edition* 54(7): 2126-2130. [AR]
252. Zhao, H., Verma, D., Li, W., Choi, Y., Ndong, C., Fiering, S.N., Bailey-Kellogg, C., and Griswold, K.E. (2015). "Depletion of T cell epitopes in lysostaphin mitigates anti-drug antibody response and enhances antibacterial efficacy in vivo." *Chemistry & Biology* 22(5): 629-639. [AR]
253. Zhao, Y., Huang, X., Li, D., Qiu, L., and Sun, Q. (2015). "Prediction of secondary structure and B cell epitope of glycoprotein of ebolavirus." *Chinese Journal of Biologicals* 28(1): 30-34. [AR]
254. Zheng, W., Ruan, J., Hu, G., Wang, K., Hanlon, M., and Gao, J. (2015). "Analysis of conformational B-cell epitopes in the antibody-antigen complex using the depth function and the convex hull." *PLOS One* 10(8): e0134835. doi: 10.1371/journal.pone.0134835. [AR]
255. Zilberberg, J., Feinman, R., and Korngold, R. (2015). "Strategies for the identification of T cell-recognized tumor antigens in hematological malignancies for improved graft-versus-tumor responses after allogeneic blood and marrow transplantation." *Biology of Blood and Marrow Transplantation* 21(6): 1000-1007. [AR]

3.2.3 Curation

1. Huang, H. (2015). "Domain knowledge and data quality perceptions in genome curation work." *Journal of Documentation* 71(1): 116-142. [C]

2. Huang, H., Jorgensen, C., and Stvilia, B. (2015). "Genomics data curation roles, skills and perception of data quality." *Library & Information Science Research* 37(1): 10-20. [C]
3. Rodriguez-Esteban, R. (2015). "Biocuration with insufficient resources and fixed timelines." *Database-the Journal of Biological Databases and Curation* pii: bav116. doi: 10.1093/database/bav116. [C]
4. Taylor, B.D. and Rotenstreich, S. (2015). "Towards automating inter-organizational workflow semantic resolution." 2015 IEEE International Conference on Services Computing (SCC): 777-781. [C]
5. Teng, F., Yu, L., Bian, Y., Sun, J., Wu, J., Ling, C., Yang, L., Wang, Y., and Cui, Y. (2015). "In silico structural analysis of group 3,6 and 9 allergens from *Dermatophagoides farinae*." *Molecular Medicine Reports* 11(5): 3559-3564. [C]

3.2.4 Epitope Meta-Analyses

1. Adisasmitho, W., Hunter, B.M., Krumkamp, R., Latief, K., Rudge, J.W., Hanvoravongchai, P., and Coker, R.J. (2015). "Pandemic influenza and health system resource gaps in Bali: An analysis through a resource transmission dynamics model." *Asia-Pacific Journal of Public Health* 27(2): NP713-NP733. [MA]
2. Ambati, A.S. (2015). "Influenza specific T-and B-cell responses in immunosuppressed patients." <http://hdl.handle.net/10616/44577>. [Thesis]. [MA]
3. Ambati, A., Valentini, D., Montomoli, E., Lapini, G., Biuso, F., Wenschuh, H., Magalhaes, I., and Maeurer, M. (2015). "H1N1 viral proteome peptide microarray predicts individuals at risk for H1N1 infection and segregates infection versus Pandemrix® vaccination." *Immunology* 145(3): 357-366. [MA]
4. Barbosa, V.C., Donangelo, R., and Souza, S.R. (2015). "Quasispecies dynamics on a network of interacting genotypes and idiotypes: Formulation of the model." *Journal of Statistical Mechanics-Theory and Experiment* arXiv: 1311.4857v1 (q-bio.PE). [MA]
5. Bird, N.L., Olson, M.R., Hurt, A.C., Oshansky, C.M., Oh, D.Y., Reading, P.C., Chua, B.Y., Sun, Y., Tang, L., Handel, A., Jackson, D.C., Turner, S.J., Thomas, P.G., and Kedzierska, K. (2015). "Oseltamivir prophylaxis reduces inflammation and facilitates establishment of cross-strain protective T cell memory to influenza viruses." *PLOS One* 10(6): e0129768. doi: 10.1371/journal.pone.0129768. [MA]
6. Boyce, T.G. and Virk, A. (2015). "While waiting for better pertussis vaccines, let's use the ones we have." *Journal of Infectious Diseases* 211(7): 1196-1197. [MA]
7. Brummelman, J., Wilk, M.M., Han, W.G., van Els, C.A., and Mills, K.H. (2015). "Roads to the development of improved pertussis vaccines paved by immunology." *Pathogens and Disease* 73(8): ftv067. doi: 10.1093/femspd/ftv067. [MA]
8. Coughlan, L. and Lambe, T. (2015). "Measuring cellular immunity to influenza: Methods of detection, applications and challenges." *Vaccines* 3(2): 293-319. [MA]
9. Cruz-Oliveira, C., Freire, J.M., Conceicao, T.M., Higa, L.M., Castanho, M.A., and Da Poian, A.T. (2015). "Receptors and routes of dengue virus entry into the host cells." *FEMS Microbiology Reviews* 39(2): 155-170. [MA]
10. Curtidor, H., Patarroyo, M.E., and Patarroyo, M.A. (2015). "Recent advances in the development of a chemically synthesised anti-malarial vaccine." *Expert Opinion on Biological Therapy* 15(11): 1567-1581. [MA]

11. Desheva, Y.A., Smolonogina, T.A., Donina, S.A., and Rudenko, L.G. (2015). "Serum strain-specific or cross-reactive neuraminidase inhibiting antibodies against pandemic A/California/07/2009 (H1N1) influenza in healthy volunteers." *BMC Research Notes* 8: 136. doi: 10.1186/s13104-015-1086-z. [MA]
12. Gonzalez-Gonzalez, E., Alvarez, M.M.s., Marquez-Ipina, A.R., Trujillo-de Santiago, G., Rodriguez-Martinez, L.M., Annabi, N., and Khademhosseini, A. (2015). "Anti-Ebola therapies based on monoclonal antibodies: Current state and challenges ahead." *Critical Reviews in Biotechnology*: 1-16. [MA]
13. Hunsawong, T., Sunintaboon, P., Warit, S., Thaisomboonsuk, B., Jarman, R.G., Yoon, I.K., Ubol, S., and Fernandez, S. (2015). "A novel dengue virus serotype-2 nanovaccine induces robust humoral and cell-mediated immunity in mice." *Vaccine* 33(14): 1702-1710. [MA]
14. Jiang, Y., Liu, H., Li, M., Li, G., Pang, H., Dou, X., Zhao, X., and Wan, K. (2015). "Single nucleotide polymorphism in Ag85 genes of Mycobacterium tuberculosis complex: Analysis of 178 clinical isolates from China and 13 BCG strains." *International Journal of Medical Sciences* 12(2): 126-134. [MA]
15. Jiang, Y., Liu, H., Wang, X., Li, G., Qiu, Y., Dou, X., and Wan, K. (2015). "Conserved hypothetical protein Rv1977 in Mycobacterium tuberculosis strains contains sequence polymorphisms and might be involved in ongoing immune evasion." *International Journal of Clinical and Experimental Pathology* 8(6): 6891-6900. [MA]
16. Kong, L., Kadam, R.U., Giang, E., Ruwona, T.B., Nieusma, T., Culhane, J.C., Stanfield, R.L., Dawson, P.E., Wilson, I.A., and Law, M. (2015). "Structure of Hepatitis C virus envelope glycoprotein E1 antigenic site 314-324 in complex with antibody IGH526." *Journal of Molecular Biology* 427(16): 2617-2628. [MA]
17. Lartey, S., Pathirana, R.D., Zhou, F., Jul-Larsen, A., Montomoli, E., Wood, J., and Cox, R.J. (2015). "Single dose vaccination of the ASO3-adjuvanted A (H1N1)pdm09 monovalent vaccine in health care workers elicits homologous and cross-reactive cellular and humoral responses to H1N1 strains." *Human Vaccines & Immunotherapeutics* 11(7): 1654-1662. [MA]
18. Laskowski, M., Xiao, Y., Charland, N., and Moghadas, S. (2015). "Strategies for early vaccination during novel influenza outbreaks." *Scientific Reports* 5: 18062. doi:10.1038/srep18062. [MA]
19. Laurie, K.L., Guarnaccia, T.A., Carolan, L.A., Yan, A.W., Aban, M., Petrie, S., Cao, P., Heffernan, J.M., McVernon, J., Mosse, J., Kelso, A., McCaw, J.M., and Barr, I.G. (2015). "Interval between infections and viral hierarchy are determinants of viral interference following influenza virus infection in a ferret model." *Journal of Infectious Diseases* 212(11): 1701-1710. [MA]
20. Li, X., Chen, L., Zhu, Y., Yu, X., Cao, J., Wang, R., Lv, X., He, J., Guo, A., and Huang, H. (2015). "Genomic analysis of a Mycobacterium bovis bacillus Calmette-Guerin strain isolated from an adult patient with pulmonary tuberculosis." *PLOS One* 10(4): e0122403. doi: 10.1371/journal.pone.0122403. [MA]
21. Liu, B., Shi, D., Chang, S., Gong, X., Yu, Y., Sun, Z., and Wu, J. (2015). "Characterization and immunological activity of different forms of recombinant secreted Hc of botulinum neurotoxin serotype B products expressed in yeast." *Scientific Reports* 5:7678. doi: 10.1038/srep07678. [MA]
22. Losikoff, P.T., Mishra, S., Terry, F., Gutierrez, A., Ardito, M.T., Fast, L., Nevola, M., Martin, W.D., Bailey-Kellogg, C., De Groot, A.S., and Gregory, S.H. (2015). "HCV epitope, homologous

- to multiple human protein sequences, induces a regulatory T cell response in infected patients." *Journal of Hepatology* 62(1): 48-55. [MA]
23. Lynch, G.W., Portelli, S.S., Wong, S.W., Costa, M.R., Lemgruber, A.P.M., Williamson, P., Sullivan, J.S., Booy, R., and Church, B. (2015). "Imaging of high and low resolution Ebola envelope GP structures composited with in silico models of difficult-to-resolve sections." *Journal of Molecular and Genetic Medicine* 7: 186. doi:10.4172/1747-0862.1000186. [MA]
 24. Nunes-Alves, C., Booty, M.G., Carpenter, S.M., Rothchild, A.C., Martin, C.J., Desjardins, D., Steblenko, K., Kloverpris, H.N., Madansein, R., Ramsuran, D., Leslie, A., Correia-Neves, M., and Behar, S.M. (2015). "Human and murine clonal CD8+T cell expansions arise during tuberculosis because of TCR selection." *PLOS Pathogens* 11(5): e1004849. doi: 10.1371/journal.ppat.1004849. [MA]
 25. Reiber, H., Kruse-Sauter, H., and Quentin, C.D. (2015). "Antibody patterns vary arbitrarily between cerebrospinal fluid and aqueous humor of the individual multiple sclerosis patient: Specificity-independent pathological B cell function." *Journal of Neuroimmunology* 278: 247-254. [MA]
 26. Rothman, A.L., Currier, J.R., Friberg, H.L., and Mathew, A. (2015). "Analysis of cell-mediated immune responses in support of dengue vaccine development efforts." *Vaccine* 33(50): 7083-7090. [MA]
 27. Sahu, G.P. and Dhar, J. (2015). "Dynamics of an SEQIHRS epidemic model with media coverage, quarantine and isolation in a community with pre-existing immunity." *Journal of Mathematical Analysis and Applications* 421(2): 1651-1672. [MA]
 28. Samy, R.P. and Lim, L.H. (2015). "DAMPs and influenza virus infection in ageing." *Ageing Research Reviews* 24: 83-97. [MA]
 29. Schippers, T. (2015). "Functional characterization of the potential immune evasion proteins pUL49, 5 and p012 of Marek's disease virus (MDV)." http://www.diss.fu-berlin.de/diss/receive/FUDISS_thesis_000000098929. [Thesis]. [MA]
 30. Sridhar, S. (2015). "Clinical development of Ebola vaccines." *Therapeutic Advances in Vaccines* 3(5-6): 125-138. [MA]
 31. Steinman, L. (2015). "The re-emergence of antigen-specific tolerance as a potential therapy for MS." *Multiple Sclerosis Journal* 21(10): 1223-1238. [MA]
 32. van Nierop, G.P., Janssen, M., Mitterreiter, J.G., van de Vijver, D.A., de Swart, R.L., Haagsmans, B.L., Verjans, G.M., and Hintzen, R.Q. (2015). "Intrathecal CD4+ and CD8+ T-cell responses to endogenously synthesized candidate disease-associated human autoantigens in multiple sclerosis patients." *European Journal of Immunology*. doi: 10.1002/eji.201545921. Epub 2015 Nov 9. [MA]
 33. Wang, J., Hilchey, S.P., Hyrien, O., Huertas, N., Perry, S., Ramanunnair, M., Bucher, D., and Zand, M.S. (2015). "Multi-dimensional measurement of antibody-mediated heterosubtypic immunity to influenza." *PLOS One* 10(6): e0129858. doi: 10.1371/journal.pone.0129858. [MA]
 34. Weinberg, A., Muresan, P., Richardson, K.M., Fenton, T., Dominguez, T., Bloom, A., Watts, D., Abzug, M.J., Nachman, S.A., and Levin, M.J. (2015). "Determinants of vaccine immunogenicity in HIV-infected pregnant women: Analysis of B and T cell responses to pandemic H1N1 monovalent vaccine." *PLOS One* 10(4): e0122431. doi: 10.1371/journal.pone.0122431. [MA]
 35. Yadav, S.K., Mindur, J.E., Ito, K., and Dhib-Jalbut, S. (2015). "Advances in the immunopathogenesis of multiple sclerosis." *Current Opinion in Neurology* 28(3): 206-219. [MA]

36. Yu, Y., Shi, D., Liu, S., Gong, Z.W., Wang, S., and Sun, Z. (2015). "Production and evaluation of a recombinant subunit vaccine against botulinum neurotoxin serotype B using a 293E expression system." *Human Vaccines & Immunotherapeutics* 11(2): 468-473. [MA]
37. Zinder, D. (2015). "Phylodynamic patterns in pathogen ecology and evolution." <http://hdl.handle.net/2027.42/113494>. [Thesis]. [MA]

4 References

- Beaver JE, Bourne PE, Ponomarenko JV. EpitopeViewer: a Java application for the visualization and analysis of immune epitopes in the Immune Epitope Database and Analysis Resource (IEDB). *Immunome Res.* 2007 Feb 21;3:3. PMID: 17313688
- Bui HH, Sidney J, Peters B, Sathiamurthy M, Sinichi A, Purton KA, Mothe BR, Chisari FV, Watkins DI, Sette A. Automated generation and evaluation of specific MHC binding predictive tools: ARB matrix applications. *Immunogenetics.* 2005 Jun;57(5):304-14. Epub 2005 May 3.
- Bui HH, Sidney J, Dinh K, Southwood S, Newman MJ, Sette A. Predicting population coverage of T-cell epitope-based diagnostics and vaccines. *BMC Bioinformatics.* 2006 Mar 17;7(1):153. PMID: 16545123
- Bui HH, Sidney J, Li W, Fusseder N, Sette A. Development of an epitope conservancy analysis tool to facilitate the design of epitope-based diagnostics and vaccines. *BMC Bioinformatics.* 2007 Sep 26;8(1):361. PMID: 17897458
- Calis JJ, Maybeno M, Greenbaum JA, Weiskopf D, De Silva AD, Sette A, Keşmir C, Peters B. Properties of MHC class I presented peptides that enhance immunogenicity. *PLoS Comput Biol.* 2013 Oct;9(10):e1003266. doi:10.1371/journal.pcbi.1003266. Epub 2013 Oct 24. PubMed PMID: 24204222; PubMed Central PMCID: PMC3808449.
- Chou P, Fasman G. Prediction of the secondary structure of proteins from their amino acid sequence. *Adv Enzymol Relat Areas Mol Biol.* 1978;45–148. PMID: 364941
- Emini E, Hughes J, Perlow D, Boger J. Induction of hepatitis A virus-neutralizing antibody by a virus specific synthetic peptide. *J Virol.* 1985;55:836–839. PMID: 2991600
- Giguère S, Drouin A, Lacoste A, Marchand M, Corbeil J, Laviolette F. MHC-NP: predicting peptides naturally processed by the MHC. *J Immunol Methods.* 2013 Dec 31;400-401:30-6. doi: 10.1016/j.jim.2013.10.003. Epub 2013 Oct 18. PubMed PMID: 24144535.
- González-Galarza FF, Takeshita LY, Santos EJ, Kempson F, Maia MH, da Silva AL, Teles e Silva AL, Ghattaoraya GS, Alfirovic A, Jones AR, Middleton D. Allele frequency net 2015 update: new features for HLA epitopes, KIR and disease and HLA adverse drug reaction associations. *Nucleic Acids Res.* 2015 Jan;43(Database issue):D784-8. doi: 10.1093/nar/gku1166. Epub 2014 Nov 20. PubMed PMID: 25414323; PubMed Central PMCID: PMC4383964
- Haste Andersen P, Nielsen M, Lund O. Prediction of residues in discontinuous B-cell epitopes using protein 3D structures. *Protein Sci.* 2006 Nov;15(11):2558-67. Epub 2006 Sep 25. PMID: 17001032
- Hoof I, Peters B, Sidney J, Pedersen LE, Sette A, Lund O, Buus S, Nielsen M, NetMHCpan, a method for MHC class I binding prediction beyond humans. *Immunogenetics.* 2009 Jan;61(1):1-13. PMID: 19002680
- Karosiene E, Lundegaard C, Lund O and Nielsen M. 2012. NetMHCcons: a consensus method for the major histocompatibility complex class I predictions. *Immunogenetics* **64(3)**:177-186. [PMID: 22009319](#)
- Karosiene E1, Rasmussen M, Blicher T, Lund O, Buus S, Nielsen M. 2013. NetMHCIIpan-3.0, a common pan-specific MHC class II prediction method including all three human MHC class II isotypes, HLA-DR, HLA-DP and HLA-DQ. *Immunogenetics* **65(10)**:711. PMID: 23900783
- Karplus PA, Schulz GE. Prediction of chain flexibility in proteins. *Naturwissenschaften.* 1985. 72:212-213.

- Keşmir C, Nussbaum AK, Schild H, Detours V, Brunak S. Prediction of proteasome cleavage motifs by neural networks. *Protein Eng.* 2002 Apr;15(4):287-96. PMID: 11983929
- Kim Y, Ponomarenko J, Zhu Z, Tamang D, Wang P, Greenbaum J, Lundegaard C, Sette A, Lund O, Bourne PE, Nielsen M, Peters B. Immune epitope database analysis resource. *Nucleic Acids Res.* 2012 Jul;40(Web Server issue):W525-30. doi: 10.1093/nar/gks438. Epub 2012 May 18. PubMed PMID: 22610854; PubMed Central PMCID: PMC3394288
- Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B. Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. *BMC Bioinformatics.* 2014 Jul 14;15:241. doi: 10.1186/1471-2105-15-241. PubMed PMID: 25017736; PubMed Central PMCID: PMC4111843
- Kim Y, Sidney J, Pinilla C, Sette A, Peters B. Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior. *BMC Bioinformatics.* 2009 Nov 30;10:394. PMID: 19948066
- Kolaskar AS, Tongaonkar PC. A semi-empirical method for prediction of antigenic determinants on protein antigens. *FEBS Lett.* 1990 Dec 10;276(1-2):172-4. PMID: 1702393
- Kringelum JV, Lundegaard C, Lund O, Nielsen M. Reliable B cell epitope predictions: impacts of method development and improved benchmarking. *PLoS Comput Biol.* 2012;8(12):e1002829. doi: 10.1371/journal.pcbi.1002829. Epub 2012 Dec 27. PubMed PMID: 23300419; PubMed Central PMCID: PMC3531324.
- Kringelum JV, Nielsen M, Padkjær SB, Lund O. Structural analysis of B-cell epitopes in antibody:protein complexes. *Mol Immunol.* 2013 Jan;53(1-2):24-34. doi: 10.1016/j.molimm.2012.06.001. Epub 2012 Jul 10. PubMed PMID: 22784991; PubMed Central PMCID: PMC3461403
- Larsen JE, Lund O, Nielsen M. Improved method for predicting linear B-cell epitopes. *Immunome Res.* 2006 Apr 24;2:2. PMID: 16635264
- Larsen MV, Lundegaard C, Lamberth K, Buus S, Brunak S, Lund O, Nielsen M. An integrative approach to CTL epitope prediction: a combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions. *Eur J Immunol.* 2005 Aug;35(8):2295-303. PMID: 15997466
- Liang S, Zheng D, Standley DM, Yao B, Zacharias M, Zhang C. EPSVR and EPMeta: prediction of antigenic epitopes using support vector regression and multiple server results. *BMC Bioinformatics.* 2010 Jul 16;11:381. doi: 10.1186/1471-2105-11-381. PubMed PMID: 20637083; PubMed Central PMCID: PMC2910724.
- Lundegaard C, Lamberth K, Harndahl M, Buus S, Lund O, Nielsen M. NetMHC-3.0: accurate web accessible predictions of human, mouse and monkey MHC class I affinities for peptides of length 8-11. *Nucleic Acids Res.* 2008 Jul 1;36(Web Server issue):W509-12. doi: 10.1093/nar/gkn202. Epub 2008 May 7. PubMed PMID: 18463140; PubMed Central PMCID: PMC2447772
- Marcatili P, Rosi A, Tramontano A., 2008. PIGS: automatic prediction of antibody structures. *Bioinformatics* 24(17):1953-4. PMID: 18641403
- Moutaftsi M, Peters B, Pasquetto V, Tschärke DC, Sidney J, Bui HH, Grey H, Sette A. A consensus epitope prediction approach identifies the breadth of murine T(CD8+)-cell responses to vaccinia virus. *Nat Biotechnol.* 2006 Jul;24(7):817-9. PMID: 16767078
- Nielsen M, Lund O. NN-align. An artificial neural network-based alignment algorithm for MHC class II peptide binding prediction. *BMC Bioinformatics.* 2009 Sep 18;10:296. doi: 10.1186/1471-2105-10-296. PubMed PMID: 19765293; PubMed Central PMCID: PMC2753847

- Nielsen M, Lundegaard C, Blicher T, Lamberth K, Harndahl M, Justesen S, Roder G, Peters B, Sette A, Lund O, Buus S. 2007. NetMHCpan, a method for quantitative predictions of peptide binding to any HLA-A and -B locus protein of known sequence. *PLoS ONE* 2:e796. PMID: 17726526
- Nielsen M, Lundegaard C, Blicher T, Peters B, Sette A, Justesen S, Buus S, and Lund O. 2008. Quantitative predictions of peptide binding to any HLA-DR molecule of known sequence: NetMHCIIpan. *PLoS Comput Biol.*4(7)e1000107. PMID: 18604266
- Nielsen M, Lundegaard C, Lund O. Prediction of MHC class II binding affinity using SMM-align, a novel stabilization matrix alignment method. *BMC Bioinformatics.* 2007 Jul 4;8:238. PMID: 17608956
- Nielsen M, Lundegaard C, Worning P, Lauemoller SL, Lamberth K, Buus S, Brunak S, Lund O., Reliable prediction of T-cell epitopes using neural networks with novel sequence representations, *Protein Sci.* 2003 May;12(5):1007-17
- Parker J, Guo D, Hodges R. New hydrophilicity scale derived from High-Performance Liquid Chromatography peptide retention data: correlation of predicted surface residues with antigenicity and X-ray-derived accessible sites. *Biochemistry.* 1986;25:5425–5432. PMID: 2430611
- Peters B, Sidney J, Bourne P, Bui HH, Buus S, Doh G, Fleri W, Kronenberg M, Kubo R, Lund O, Nemazee D, Ponomarenko JV, Sathiamurthy M, Schoenberger S, Stewart S, Surko P, Way S, Wilson S, Sette A. The immune epitope database and analysis resource: from vision to blueprint. *PLoS Biol.* 2005 Mar;3(3):e91. PMID: 15760272.
- Peters B, 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
- Peters B, Sette A., "Generating quantitative models describing the sequence specificity of biological processes with the stabilized matrix method." *BMC Bioinformatics* 2005 May 31;6(1):132
- Peters B, Bulik S, Tampe R, Van Endert PM, Holzhutter HG. Identifying MHC class I epitopes by predicting the TAP transport efficiency of epitope precursors. *J Immunol.* 2003 Aug 15;171(4):1741-9.
- Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. *BMC Struct Biol.* 2007 Oct 2;7(1):64. PMID: 17910770
- Ponomarenko J, H. H. Bui, W. Li, N. Fusseder, P. E. Bourne, A. Sette, B. Peters. (2008). "ElliPro: a new structure-based tool for the prediction of antibody epitopes." *BMC Bioinformatics*, 9(514). PMID: 19055730
- Rubinstein ND, Mayrose I, Martz E, Pupko T. EpiToPIA: a web-server for predicting B-cell epitopes. *BMC Bioinformatics.* 2009 Sep 14;10:287. doi: 10.1186/1471-2105-10-287. PubMed PMID: 19751513; PubMed Central PMCID: PMC2751785.
- Sidney J, Assarsson E, Moore C, Ngo S, Pinilla C, Sette A, Peters B. Quantitative peptide binding motifs for 19 human and mouse MHC class I molecules derived using positional scanning combinatorial peptide libraries. *Immunome Res.* 2008 Jan 25;4:2. PMID: 18221540
- Stranzl T, Larsen MV, Lundegaard C, Nielsen M. NetCTLpan: pan-specific MHC class I pathway epitope predictions. *Immunogenetics.* 2010 Jun;62(6):357-68. Epub 2010 Apr 9. PubMed PMID: 20379710; PubMed Central PMCID: PMC2875469
- Sturniolo T, Bono E, Ding J, Radrizzani L, Tuereci O, Sahin U, Braxenthaler M, Gallazzi F, Protti MP, Sinigaglia F, Hammer J. Generation of tissue-specific and promiscuous HLA ligand databases

- using DNA microarrays and virtual HLA class II matrices. *Nat Biotechnol.* 1999 Jun;17(6):555-61. PMID: 10385319
- Tenzer S, Peters B, Bulik S, Schoor O, Lemmel C, Schatz MM, Kloetzel PM, Rammensee HG, Schild H, Holzhutter HG. Modeling the MHC class I pathway by combining predictions of proteasomal cleavage, TAP transport and MHC class I binding. *Cell Mol Life Sci.* 2005 May;62(9):1025-37.
- Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M. Automated benchmarking of peptide-MHC class I binding predictions. *Bioinformatics.* 2015 Jul 1;31(13):2174-81. doi: 10.1093/bioinformatics/btv123. Epub 2015 Feb 25. PubMed PMID: 25717196; PubMed Central PMCID: PMC4481849.
- Vita R, Overton JA, Greenbaum JA, Ponomarenko J, Clark JD, Cantrell JR, Wheeler DK, Gabbard JL, Hix D, Sette A, Peters B. The immune epitope database (IEDB) 3.0. *Nucleic Acids Res.* 2014 Oct 9. pii: gku938. [Epub ahead of print] PubMed PMID: [25300482](https://pubmed.ncbi.nlm.nih.gov/25300482/).
- Wang, P., J. Sidney, C. Dow, B. Mothe, A. Sette, B. Peters. (2008). "A Systematic Assessment of MHC Class II Peptide Binding Predictions and Evaluation of a Consensus Approach." *PLoS Computational Biology* 4(4). PMID: 18389056
- Wang P, Sidney J, Kim Y, Sette A, Lund O, Nielsen M, Peters B. 2010. Peptide binding predictions for HLA DR, DP and DQ molecules. *BMC Bioinformatics.* 11:568
- Zhang H, Lund O, Nielsen M. The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: Application to MHC-peptide binding. *Bioinformatics.* 2009 Mar 17. PMID: 19297351