

Contract No. HHSN266200400006C

Immune Epitope Database and Analysis Program

2008 Annual IEDB Compendium

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February 2009

Table of Contents

Table of Contents	i
Introduction	1
1 Antibody and T Cell Epitopes	2
2 What's New in IEDB 2.0?	38
2.1 Browsing, querying, reporting, and tools	38
2.2 Ontology and data structure revisions	41
2.3 Finder functions	41
2.4 Field changes relating to the epitope, immunization procedures and adoptive transfer	42
2.4.1 Epitope	42
2.4.2 Immunization procedures	43
2.4.3 Adoptive transfer	47
2.4.4 Changes relating to the fields describing the various types of assays used to characterize epitopes	48
2.4.5 T cell	50
2.4.6 B cell	50
2.4.7 MHC ligand elution	51
3 Website Features	53
3.1 Home Page	53
3.2 Browse	54
3.2.1 Browse Records by MHC Allele	54
3.2.2 Browse Records by Source Organism	55
3.3 Query	58
3.3.1 Perform a Keyword Search	58
3.3.2 Perform a Home Page Search	59
3.3.3 Detailed Query	60
3.3.4 Search Results Summary	63
3.3.4.1 Download Query Results	70
3.3.4.2 Accessing the EpitopeViewer	70
3.3.5 Finders Overview	71
3.3.5.1 Allele Finder	71
3.3.5.2 Assay Finder	72
3.3.5.3 Disease Finder	72
3.3.5.4 Molecule Finder	73
3.3.5.5 Organism Finder	74
3.4 Tools	75
3.4.1 T Cell Epitope Prediction	76
3.4.1.1 T Cell Epitopes - MHC binding prediction	76
3.4.1.1.1 Peptide Binding to MHC Class I Molecules	76
3.4.1.1.1.1 MHC Class I Binding Prediction Resource	77
3.4.1.1.2 Peptide Binding to MHC Class II Molecules	78
3.4.1.2 T Cell Epitopes – MHC I Processing Prediction	78

3.4.1.2.1	Proteasomal cleavage/TAP transport/MHC class I combined predictor	78
3.4.1.2.2	Neural network based prediction of proteasomal cleavage sites (NetChop) and T cell epitopes (NetCTL)	79
3.4.2	B Cell Epitope Prediction	79
3.4.2.1	Prediction of linear epitopes from protein sequence	79
3.4.2.2	DiscoTope - Prediction of epitopes from protein structure	80
3.4.2.3	ElliPro - Epitope prediction based upon structural protrusion	80
3.4.3	Epitope Analysis Tools	80
3.4.3.1	Population coverage	80
3.4.3.2	Epitope conservancy	81
3.4.3.3	Epitope Cluster Analysis	81
3.4.3.4	Homology Mapping Tool and EpitopeViewer	82
3.5	Support Overview	83
3.5.1	Solutions Center	83
3.5.2	Provide Feedback	83
3.5.3	Help Request	83
3.5.4	Data Field Descriptions	84
3.6	More IEDB	84
3.6.1	Acknowledgements	84
3.6.2	Citing the IEDB	84
3.6.3	Database Export	84
3.6.4	Documents	85
3.6.5	Links to External Sources	85
3.6.6	Patent List	86
3.6.7	Terms of Use	86
3.6.8	Publications	86
4	Scientific Publications	87
4.1	Publications of the IEDB team by Year	87
4.1.1	2008	87
4.1.2	2007	88
4.1.3	2006	89
4.1.4	2005	89
4.1.5	2004	89
4.2	Publications Citing the IEDB in 2008	89
4.3	Publications Citing the IEDB in 2007	97
5	References	102

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 fourth Annual Compendium of the Immune Epitope Database and Analysis Resource consists of four sections. The first section contains a list of the antibody and T cell epitope information in the database as of 14 January 2009. The second section lists the many new features and changes found in IEDB 2.0, a major database and website revision implemented during 2008. The third section describes the features of the IEDB 2.0 website. The fourth section lists the scientific publications in 2008 and 2007 for which the IEDB played a contributory role.

Since the publication of last year's 2007 Annual Compendium, the quantity of data available in the IEDB has increased significantly with the addition of over 1500 fully curated references. By the end of the year, curation of data relating to NIAID Category A, B, and C priority pathogens, NIAID Emerging and Re-emerging infectious diseases, Malaria, Hepatitis B, Clostridium tetani, Leishmania, Candida albicans, and herpesvirus was current through 30 September 2008.

1 Antibody and T Cell Epitopes

Many new references and many new pathogens were added to the IEDB in 2008, 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 2007 and 2008. Of the 1402 species/strains listed, 326 were added in 2008. 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. Although the curation of autoimmune epitopes has not been a priority to date, they have entered the IEDB as a result of importing large epitope datasets and of curating them when they appear in priority infectious disease references.

In the table below, the leftmost column labeled "New 2008" indicates with an "X" if epitopes for the species/strain was added to the IEDB in 2008. 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. The columns labeled "B-07", "T-07", "B-08", and "T-08" indicate the cumulative number of distinct B cell and T cell epitopes in the database at the end of 2007 and 2008, respectively. The two rightmost columns display the differences in the B and T cell epitope counts from 2007 to 2008. The changes in B and T cell epitope counts are shown in red. In 2008, the number of B cell epitopes increased by 3681, from 10,102 to 13,783, and the number of T cell epitopes increased by 3368, from 20,817 to 24,185.

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

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	5755	Acanthamoeba castellanii	14	1	14	1		
	228399	Actinobacillus pleuropneumoniae serovar 1 str. 4074	2		2			
X	209841	Actinobacillus pleuropneumoniae serovar 7			1		1	
X	10804	Adeno-associated virus - 2			14	5	14	5
X	202813	Adeno-associated virus - 8				3		3
	10508	Adenoviridae	3	2	3	2		
X	4494	Aegilops markgrafii				1		1
X	117204	African horse sickness virus 3			21		21	
	714	Aggregatibacter actinomycetemcomitans		4		4		
X	5039	Ajellomyces dermatitidis				1		1
X	10000828	Ajellomyces dermatitidis ATCC 60636				1		1
	11791	AKR (endogenous) murine leukemia virus		1		2		1
	11790	AKT8 murine leukemia virus		1		1		
X	10783	Aleutian mink disease parvovirus (STRAIN G)			3		3	
	28314	Aleutian mink disease virus	1		1			
	5599	Alternaria alternata	1		1			
	4212	Ambrosia artemisiifolia	1	2	1	2		
	4215	Ambrosia elatior		4	9	12	9	8
	4214	Ambrosia trifida		3		6		3
	171929	Anacardium occidentale	27		27			
X	769	Anaplasma centrale				1		1
	770	Anaplasma marginale	14	1	14	13		12
	10000760	Anaplasma marginale South Idaho		2		2		
	320483	Anaplasma marginale str. Florida		27		39		12
	234826	Anaplasma marginale str. St. Maries		1		1		
X	212042	Anaplasma phagocytophilum HZ			21		21	
	46607	Andes virus	1		1			
	10000553	Andes virus CHI-7913	49		53		4	
X	70175	Androctonus australis hector			6		6	
X	6269	Anisakis simplex			1		1	
	7460	Apis mellifera	3	85	9	87	6	2
	4045	Apium graveolens		1		14		13
	3702	Arabidopsis thaliana		2		2		
	3818	Arachis hypogaea	39	26	63	26	24	
X	10000980	Arcanobacterium pyogenes Strain 42			4		4	
X	3704	Armoracia rusticana			1		1	
X	6661	Artemia franciscana			1		1	
	4220	Artemisia vulgaris		18	1	18	1	
X	76803	Arteriviridae			4		4	
	5085	Aspergillus fumigatus	25	6	26	17	1	11
	5064	Aspergillus restrictus	1		1			
	11861	Avian erythroblastosis virus	1		1			
	172851	Avian hepatitis E virus	7		10		3	
X	11127	Avian infectious bronchitis virus (strain M41)			4		4	

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	231428	Avian infectious bronchitis virus (strain Vic S)			11	8	11	8
X	38171	Avian reovirus strain S1133			2		2	
	195700	Avian rotavirus PO-13	4		6		2	
	5866	Babesia bigemina		3		3		
	5865	Babesia bovis		2		2		
X	1000382	Babesia bovis Mexico			1		1	
	1000383	Babesia bovis Mexico Mo7		10	1	33	1	23
	5868	Babesia microti	2		2			
	120505	Baboon cytomegalovirus		1		1		
	196403	Baboon endogenous virus		1	1	1	1	
X	11764	Baboon endogenous virus strain M7			1		1	
X	1390	Bacillus amyloliquefaciens				2		2
	1392	Bacillus anthracis	22	43	33	44	11	1
	260799	Bacillus anthracis str. Sterne	5		5			
	1000291	Bacillus anthracis str. Sterne 34F2	1		1			
	1396	Bacillus cereus		2	1	2	1	
X	1467	Bacillus lentus				1		1
	1402	Bacillus licheniformis		5		9		4
X	1404	Bacillus megaterium				1		1
X	1428	Bacillus thuringiensis			2		2	
X	1435	Bacillus thuringiensis serovar san diego				2		2
X	2	Bacteria			2		2	
	63673	Batillus cornutus	2		2			
	37962	Bayou virus	1		1			
X	12260	Bean pod mottle virus			2		2	
	31715	Bean-pod mottle virus (strain Kentucky G7)		1	9	1	9	
X	31721	Beet necrotic yellow vein virus			8		8	
X	12161	Beet yellows virus			5		5	
X	3645	Bertholletia excelsa			7	24	7	24
	3505	Betula pendula	10	101	13	180	3	79
	10629	BK polyomavirus		3		12		9
X	65743	Blackcurrant reversion virus			2		2	
X	6973	Blattella germanica				15		15
X	40697	Blomia tropicalis			5		5	
X	40051	Bluetongue virus			6		6	
X	10904	Bluetongue virus (serotype 1 / isolate Australia)			7		7	
X	33717	Bluetongue virus (serotype 13 / isolate USA)			1		1	
X	33718	Bluetongue virus (serotype 17 / isolate USA)			4		4	
X	10906	Bluetongue virus 10			3		3	
	271108	Bombyx mori NPV	2		2			
	518	Bordetella bronchiseptica		1		1		
	520	Bordetella pertussis	10	3	75	15	65	12
	12455	Borna disease virus	8	2	8	4		2
	29518	Borrelia afzelii		1		1		
	390236	Borrelia afzelii PKo	2		2			

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	139	Borrelia burgdorferi	39	34	39	34		
	1000902	Borrelia burgdorferi ZS7	2	45	2	45		
	224326	Borrelia burgdorferi B31	63		66		3	
X	10001091	Borrelia burgdorferi BEP4			1		1	
	10000675	Borrelia burgdorferi CA12		6		6		
	64895	Borrelia burgdorferi group	3		3			
	10000677	Borrelia burgdorferi N40	4		4			
	412419	Borrelia duttonii Ly	7		7			
	29519	Borrelia garinii	2		2			
	10000530	Borrelia garinii IP90	3		3			
	9913	Bos taurus	164	75	222	90	58	15
X	8722	Bothrops asper			1		1	
X	11128	Bovine coronavirus			6		6	
	12064	Bovine enterovirus	13		13			
X	12065	Bovine enterovirus (STRAIN VG-5-27)			6		6	
	10000472	Bovine ephemeral fever virus BB7721	2		2			
	10320	Bovine herpesvirus 1	4	1	4	1		
	10000404	Bovine herpesvirus 1 Lam	1		1			
	263683	Bovine herpesvirus 5 strain TX89	2		2			
	79889	Bovine herpesvirus type 1.1	1		1			
	10323	Bovine herpesvirus type 1.1 (strain Cooper)	8	18	8	18		
	10324	Bovine herpesvirus type 1.1 (strain P8-2)	1		1			
X	11901	Bovine leukemia virus			25	12	25	12
	10562	Bovine papillomavirus - 4	3	3	3	3		
	10559	Bovine papillomavirus type 1	1		1			
	11215	Bovine parainfluenza virus 3		1		1		
	11246	Bovine respiratory syncytial virus	1		2	1	1	1
X	11249	Bovine respiratory syncytial virus (strain RB94)			3		3	
X	82824	Bovine respiratory syncytial virus strain snook				75		75
	10927	Bovine rotavirus	2		7		5	
X	10933	Bovine rotavirus (strain RF)			2		2	
X	129818	Bovine rotavirus RF			11		11	
X	11099	Bovine viral diarrhea virus 1			1	11	1	11
X	11100	Bovine viral diarrhea virus 1-NADL			3	3	3	3
X	54315	Bovine viral diarrhea virus 2			1		1	
X	82470	Bovine viral diarrhea virus strain Oregon C24V			5		5	
	158474	Bovine viral diarrhea virus strain Trangie Y546	1		1			
	3707	Brassica juncea	9		9			
	235	Brucella abortus	3	3	3	3		
	35802	Brucella abortus 1	2		2			
	29459	Brucella melitensis	3	16	3	16		
	224914	Brucella melitensis 16M	7		7			
	236	Brucella ovis	2		2			
	29461	Brucella suis		2		2		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	89462	Bubalus bubalis		1		1		
X	8616	Bungarus multicinctus			5		5	
	350702	Burkholderia cenocepacia PC184		1		1		
	13373	Burkholderia mallei		1		1		
	243160	Burkholderia mallei ATCC 23344		1		1		
	6239	Caenorhabditis elegans		4		4		
	32019	Campylobacter fetus subsp. fetus	3		3			
	197	Campylobacter jejuni		5		5		
X	192222	Campylobacter jejuni subsp. jejuni NCTC 11168			10		10	
	5476	Candida albicans	82	32	83	55	1	23
	10000335	Candida albicans A-9 (serotype B)	1		1			
	10000337	Candida albicans KIT 1113	1		1			
	10000338	Candida albicans LGH1095 (serotype B)	1		1			
	10000339	Candida albicans serotype A	1		1			
	5480	Candida parapsilosis	1		1			
	292348	Canine calicivirus (strain 48)	2		2			
	11232	Canine distemper virus		1		1		
	11233	Canine distemper virus strain Onderstepoort	6		6			
	35258	Canine oral papillomavirus		25		25		
	10788	Canine parvovirus	2		8		6	
	9615	Canis familiaris		58		58		
	11662	Caprine arthritis encephalitis virus (STRAIN G63)	6		6			
X	11660	Caprine arthritis-encephalitis virus			10	1	10	1
X	7957	Carassius auratus			3		3	
X	6878	Centruroides noxius			6		6	
	10325	Cercopithecine herpesvirus 1	1		1			
	45455	Cercopithecine herpesvirus 15		18		18		
	47929	Cercopithecine herpesvirus 8		67		67		
	13415	Chamaecypris obtusa		27		28		1
X	12618	Chicken anemia virus			3		3	
X	310542	Chimpanzee adenovirus			2		2	
	7154	Chironomus thummi	2	3	2	3		
	7155	Chironomus thummi thummi	8	27	8	27		
	810	Chlamydia	8		9		1	
X	243161	Chlamydia muridarum Nigg				14		14
	813	Chlamydia trachomatis	12	21	31	42	19	21
	315277	Chlamydia trachomatis A/HAR-13	5	1	6	1	1	
X	10000858	Chlamydia trachomatis B/Jali-20/OT			2		2	
	10000762	Chlamydia trachomatis B/Tw-5/OT	5		5			
X	10000804	Chlamydia trachomatis Serovar B			3		3	
	10000763	Chlamydia trachomatis Serovar C	1		2		1	
	10000764	Chlamydia trachomatis Serovar E	1	1	2	1	1	
	10000765	Chlamydia trachomatis Serovar H	1		1			
	10000766	Chlamydia trachomatis Serovar I	1		1			
	10000767	Chlamydia trachomatis serovar K	1		9		8	

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	10000853	Chlamydia trachomatis Serovar L1	15		17	1	2	1
X	10000768	Chlamydia trachomatis Serovar L2			4	4	4	4
	10000769	Chlamydia trachomatis Serovar L3	1		1			
	204428	Chlamydiae	1		1			
	83555	Chlamydomphila abortus	3		3			
	10000559	Chlamydomphila abortus B-577	11		11			
	83558	Chlamydomphila pneumoniae		17		25		8
X	115713	Chlamydomphila pneumoniae CWL029				48		48
X	10000852	Chlamydomphila pneumoniae Kajaani 6				7		7
	182082	Chlamydomphila pneumoniae TW-183		9		9		
	83554	Chlamydomphila psittaci	65		72		7	
	9534	Chlorocebus aethiops		1		1		
X	12162	Citrus tristeza virus			1		1	
	11096	Classical swine fever virus	1	1	3	1	2	
	358769	Classical swine fever virus - Alfort/187	1		2		1	
X	11098	Classical swine fever virus - Brescia			4		4	
X	10001025	Classical swine fever virus Glentorf				26		26
	10000451	Classical swine fever virus Shimen	9		16		7	
	36911	Clavispora lusitaniae	2		2			
	214432	Cloning vector pscFvCA-E8VHd		1		1		
	1491	Clostridium botulinum	83	52	121	52	38	
	36826	Clostridium botulinum A	44		44			
	10000302	Clostridium botulinum A Kyoto-F	1		1			
	441771	Clostridium botulinum A str. Hall	42		42			
	10000301	Clostridium botulinum A str. Hall hyper	3		3			
	10000295	Clostridium botulinum B 111	2		2			
	10000303	Clostridium botulinum B Lammana	1		1			
	10000305	Clostridium botulinum B Okra	3		3			
	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	2		2			
	10000299	Clostridium botulinum E Beluga	2		2			
	10000903	Clostridium botulinum E Iwanei	5		5			
	36831	Clostridium botulinum F	2		2			
	10000304	Clostridium botulinum F NCTC 10281	1		1			
	1496	Clostridium difficile	15		15			
	10000307	Clostridium difficile BART'S W1	1		1			
	1502	Clostridium perfringens	2		7		5	
	107819	Clostridium perfringens D	1		1			
	195102	Clostridium perfringens str. 13		1		1		
	1513	Clostridium tetani	74	169	75	224	1	55
	5501	Coccidioides immitis		1		1		
	199306	Coccidioides posadasii		2		2		
	9014	Colinus virginianus		2		2		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	8932	Columba livia		7		8		1
	13451	Corylus avellana	2	27	2	27		
	1717	Corynebacterium diphtheriae	1	9	2	10	1	1
	152794	Corynebacterium efficiens		1		1		
	1718	Corynebacterium glutamicum		17		17		
X	12264	Cowpea mosaic virus				1		1
	10243	Cowpox virus		4		7		3
	10000571	Cowpox virus (Brighton Red) White-pock		1		1		
	777	Coxiella burnetii		8		8		
	103903	Coxsackievirus B3 (strain Nancy)	13	30	13	30		
X	103905	Coxsackievirus B4 (strain E2)			5	41	5	41
	103906	Coxsackievirus B4 (strain JVB / Benschooten / New York/51)		73		76		3
X	8732	Crotalus durissus terrificus			2		2	
	3369	Cryptomeria japonica	6	14	20	170	14	156
	5807	Cryptosporidium parvum		4		4		
	3656	Cucumis melo	12		12			
	28909	Cynodon dactylon	1		1	23		23
	10358	Cytomegalovirus		32		32		
	7955	Danio rerio		1		1		
	4039	Daucus carota		1		1		
	243164	Dehalococcoides ethenogenes 195		1		1		
X	12637	Dengue virus				1		1
	11052	Dengue virus group	1		1			
	11053	Dengue virus type 1	1	11	2	11	1	
X	10000965	Dengue virus type 1 FGA/89			1		1	
	10000440	Dengue virus type 1 Hawaii		10		10		
	11059	Dengue virus type 1 Nauru/West Pac/1974	1		1			
	33741	Dengue virus type 1 Singapore/S275/1990		2		2		
	11060	Dengue virus type 2	41	42	44	62	3	20
	31635	Dengue virus type 2 16681-PDK53		2		2		
	11064	Dengue virus type 2 Jamaica/1409/1983	261	10	261	10		
	11066	Dengue virus type 2 Puerto Rico/PR159-S1/1969	5		30		25	
	10000441	Dengue virus type 2 Sri Lanka	1	1	1	1		
	31634	Dengue virus type 2 Thailand/16681/84		50	9	50	9	
	11065	Dengue virus type 2 Thailand/NGS-C/1944	7	10	8	10	1	
	11069	Dengue virus type 3		39		39		
	10000442	Dengue virus type 3 CH53489		7		7		
	11070	Dengue virus type 4	5	29	5	30		1
	408871	Dengue virus type 4 Dominica/814669/1981		4	1	4	1	
	6954	Dermatophagoides farinae	4		11	36	7	36
	6956	Dermatophagoides pteronyssinus	10	30	44	97	34	67
	7227	Drosophila melanogaster	2	1	2	1		
	12639	Duck hepatitis B virus	189	20	189	20		
	10000466	Duvenhage virus 6		2		2		
	10000439	Eastern equine encephalitis virus SV	8		8			

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	205488	Ebola virus sp.		1		1		
	6210	Echinococcus granulosus	2		19		17	
X	99586	Echis ocellatus			5		5	
	31705	Echovirus 11 (strain Gregory)		1		1		
	12643	Ectromelia virus		2		2		
	779	Ehrlichia ruminantium	3		3			
X	5802	Eimeria tenella			4		4	
X	12104	Encephalomyocarditis virus				1		1
	5759	Entamoeba histolytica	27		27			
	10000352	Entamoeba histolytica YS-27	1		1			
X	12340	Enterobacteria phage 933J			1		1	
	10710	Enterobacteria phage lambda		3		4		1
X	10754	Enterobacteria phage P22			5		5	
	10665	Enterobacteria phage T4	5	20	5	20		
X	12022	Enterobacterio phage MS2			1		1	
X	12059	Enterovirus				9		9
X	150846	Enterovirus 5865/sin/000009			2		2	
	82830	Epstein-barr virus strain ag876	1	1	1	1		
	10326	Equid herpesvirus 1	2		5		3	
	10000525	Equid herpesvirus 2 16V	1		1			
	10000526	Equid herpesvirus 2 5FN	1		1			
	10000524	Equid herpesvirus 2 691	1		1			
	10000391	Equid herpesvirus 2 ER32	1		1			
	10000527	Equid herpesvirus 2 FIN60	1		1			
	10331	Equid herpesvirus 4	5		5			
	10000405	Equid herpesvirus 4 TH20	2		2			
	82831	Equid herpesvirus type 2 strain 86/87	1		1			
	11047	Equine arteritis virus	2		2			
	11665	Equine infectious anemia virus	2	39	33	78	31	39
	11670	Equine infectious anemia virus (CLONE 1369)		1		1		
	11671	Equine infectious anemia virus (STRAIN WSU5)		6		16		10
	10000499	Equine infectious anemia virus PV		1		2		1
X	10000835	Equine rhinitis A virus 393/76			4		4	
	9796	Equus caballus	1	42	1	43		1
	562	Escherichia coli	26	22	111	22	85	
	10000727	Escherichia coli 180/C3	1		1			
	37762	Escherichia coli B	1		1			
	10000728	Escherichia coli B B/r CM6		1		1		
	316401	Escherichia coli ETEC H10407	62	31	62	31		
	83333	Escherichia coli K12		7	3	7	3	
	168807	Escherichia coli O127:H6	1		1			
	83334	Escherichia coli O157:H7		16	2	16	2	
	10000733	Escherichia coli O5:K4:H4	1		1			
	217992	Escherichia coli O6		6		6		
	10000734	Escherichia coli O65:K-:H-	1		1			

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	2759	Eukaryota	1		1			
X	6958	Euroglyphus maynei				10		10
	420521	Expression vector pNIC-NHT-CF	1		1			
	3617	Fagopyrum esculentum	28		28			
X	6690	Farfantepenaeus aztecus			11		11	
	46835	Fasciola gigantica	2		2			
	6192	Fasciola hepatica	12	11	24	11	12	
	11978	Feline calicivirus	4		4			
	11981	Feline calicivirus (STRAIN F9)	2		2			
	11980	Feline calicivirus (STRAIN JAPANESE F4)	6		6			
	11673	Feline immunodeficiency virus		28		28		
X	11674	Feline immunodeficiency virus (isolate Petaluma)			2	3	2	3
X	33734	Feline infectious peritonitis virus (strain 79-1146)			4		4	
	9685	Felis catus	11	24	18	26	7	2
	4606	Festuca arundinacea	1		1			
	12110	Foot-and-mouth disease virus	2		10	1	8	1
X	10000991	Foot-and-mouth disease virus - type A (strain A22 Iraq)			5		5	
X	10000989	Foot-and-mouth disease virus - type A (strain A22)			8	6	8	6
X	110195	Foot-and-mouth disease virus - type Asia 1			2	2	2	2
X	10000995	Foot-and-mouth disease virus - type Asia 1 Pakistan			1		1	
X	12116	Foot-and-mouth disease virus - type C			3		3	
	12118	Foot-and-mouth disease virus - type O	1		3	2	2	2
X	10000801	Foot-and-mouth disease virus - type O (O/SKR/2002)			1		1	
X	10000856	Foot-and-mouth disease virus - type O isolate O/UKG/35/2001				13		13
X	10000992	Foot-and-mouth disease virus - type SAT 1 (Strain Bot 1/68)			1		1	
X	10000993	Foot-and-mouth disease virus - type SAT 2 (Strain Ken 3/57)			1		1	
X	10001000	Foot-and-mouth disease virus - type SAT 2 (strain Rho 1/48)			4		4	
X	10000994	Foot-and-mouth disease virus - type SAT 3 (Strain Bec 1/65)			1		1	
X	12112	Foot-and-mouth disease virus (strain A10-61)			8		8	
	12114	Foot-and-mouth disease virus (strain A12)	1		17		16	
X	12115	Foot-and-mouth disease virus (strain A24 Cruzeiro)			1		1	
X	12113	Foot-and-mouth disease virus (strain A5)			3		3	
X	12117	Foot-and-mouth disease virus (strain C3 Indaial)			1		1	
	73482	Foot-and-mouth disease virus (strain O1)	4	1	16	1	12	

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	10000820	Foot-and-mouth disease virus (strain O1) (O/Taiwan/1/97)			1		1	
X	10000964	Foot-and-mouth disease virus (strain O1) (O1 Brugge)			2		2	
	10000516	Foot-and-mouth disease virus (strain O1) (O1 Campos)	1	1	6	5	5	4
	10000513	Foot-and-mouth disease virus (strain O1) (O1 Kaufbeuren)	4		37	8	33	8
X	10000514	Foot-and-mouth disease virus (strain O1) (O1BFS 1860)			8		8	
X	10000515	Foot-and-mouth disease virus (strain O1) (O1BFS)			3		3	
X	10000556	Foot-and-mouth disease virus (strain O1) Kaufbeuren			26	11	26	11
	161727	Foot-and-mouth disease virus A10Holland	2	2	11	14	9	12
X	12121	Foot-and-mouth disease virus C1			1		1	
X	10000840	Foot-and-mouth disease virus C1 Brescia It/64			2		2	
X	10000836	Foot-and-mouth disease virus C1 CS8			22	24	22	24
X	46290	Foot-and-mouth disease virus C3			3	1	3	1
X	10001039	Foot-and-mouth disease virus C3 (strain Resendne-Br/55)			1		1	
	244367	Foot-and-mouth disease virus C-S8c1		1	9	1	9	
	13067	Forficula		2		2		
	31621	Four Corners hantavirus	2		2			
	263	Francisella tularensis		4		4		
	376619	Francisella tularensis subsp. holarctica LVS		3		3		
	177416	Francisella tularensis subsp. tularensis SCHU S4		89		89		
	11795	Friend murine leukemia virus		2		4		2
	11797	Friend murine leukemia virus (ISOLATE FB29)		1		1		
	8053	Gadus callarias	10		10			
	9031	Gallus gallus	48	50	65	103	17	53
X	11824	Gardner-Arnstein feline leukemia oncovirus B			1		1	
	54290	GB virus C	1		5		4	
	1422	Geobacillus stearothermophilus	1		1			
	5741	Giardia intestinalis		3		3		
	184922	Giardia lamblia ATCC 50803		41		41		
	3847	Glycine max	60	1	68	1	8	
	9595	Gorilla gorilla gorilla		4		4		
X	55951	Grapevine leafroll-associated virus 3			1		1	
X	35288	Grapevine virus A			19		19	
	45219	Guanarito virus		9		9		
	114727	H1N1 subtype	1		1			
X	102793	H5N1 subtype				16		16
	727	Haemophilus influenzae	1	32	10	45	9	13

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	10001055	Haemophilus influenzae 6U			1		1	
X	281310	Haemophilus influenzae 86-028NP			1		1	
X	10001053	Haemophilus influenzae MinnA			8		8	
X	10000833	Haemophilus influenzae NTHi 1128			6		6	
X	10001042	Haemophilus influenzae NTHi 1479			11	4	11	4
X	10000807	Haemophilus influenzae NTHi UC19			2	2	2	2
X	10000860	Haemophilus influenzae Serotype B			3		3	
	10000861	Haemophilus influenzae Variant d1	18		18			
	6454	Haliotis rufescens	1		1			
	11599	Hantaan virus	2	6	2	6		
	11602	Hantaan virus 76-118	9	5	11	8	2	3
	13557	Hapalemur griseus		1		1		
	4232	Helianthus annuus	18		18			
	32025	Helicobacter hepaticus		1		1		
X	235279	Helicobacter hepaticus ATCC 51449			2		2	
	210	Helicobacter pylori	26	3	26	3		
	85962	Helicobacter pylori 26695	13		13			
	10000718	Helicobacter pylori J223	2		2			
	102617	Helicobacter pylori SS1	1		1			
	10000720	Helicobacter pylori UA948	2		2			
	10000721	Helicobacter pylori UA955	1		1			
	63330	Hendra virus	7		7			
	11102	Hepacivirus		3		3		
	10404	Hepadnaviridae		1		1		
	12092	Hepatitis A virus	22	8	22	8		
	12098	Hepatitis A virus (STRAIN HM-175)	86	2	86	2		
	10407	Hepatitis B virus	179	404	182	424	3	20
	10411	Hepatitis B virus (STRAIN ALPHA1)		20		20		
	10414	Hepatitis B virus (STRAIN LSH / CHIMPANZEE ISOLATE)		2		2		
	31512	Hepatitis B virus (subtype ADR / mutant)		1		1		
	10409	Hepatitis B virus (SUBTYPE ADR4)	1	11	1	11		
	10410	Hepatitis B virus (SUBTYPE ADW / STRAIN 991)	2	2	2	2		
	10412	Hepatitis B virus (SUBTYPE ADW / STRAIN INDONESIA/PIDW420)		2		2		
	10413	Hepatitis B virus (SUBTYPE ADW / STRAIN JAPAN/PJDW233)		4		4		
	45410	Hepatitis b virus (subtype ADW4 / strain brazil / isolate w4b)		6		6		
	12513	Hepatitis B virus 2		1		1		
	10000433	Hepatitis B virus genotype B	1		1			
	10000434	Hepatitis B virus genotype C	3		3			
	10000435	Hepatitis B virus genotype D	1		1			
	31511	Hepatitis B virus subtype AD	3	3	3	3		
	106820	Hepatitis B virus subtype ADR	16	25	16	25		
	106821	Hepatitis B virus subtype ADW	17	60	17	60		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	10415	Hepatitis B virus subtype ADW strain OKINAWA/PODW282		4		4		
	10408	Hepatitis B virus subtype ADW2	68	58	70	59	2	1
	10419	Hepatitis B virus subtype ADYW		35		35		
	10000436	Hepatitis B virus subtype AY	7		7			
	10000437	Hepatitis B virus subtype AYR		1		1		
	10418	Hepatitis B virus subtype AYW	30	164	31	164	1	
	391647	Hepatitis B virus subtype AYW2	6		6			
	391646	Hepatitis B virus subtype AYW3	1		1			
	391650	Hepatitis B virus subtype AYW4	1		1			
	11103	Hepatitis C virus	563	690	603	704	40	14
	11104	Hepatitis C virus (isolate 1)	21	210	35	216	14	6
	356391	Hepatitis C virus (isolate 6a33)		5		5		
	356413	Hepatitis C virus (isolate BEBE1)		10		10		
	11105	Hepatitis C virus (isolate BK)	3	43	3	43		
	333284	Hepatitis C virus (isolate Con1)	3	5	3	5		
	356419	Hepatitis C virus (isolate EUH1480)		4		4		
	329389	Hepatitis C virus (isolate Glasgow)	2	1	2	1		
	11108	Hepatitis C virus (isolate H)	128	81	128	81		
	63746	Hepatitis C virus (isolate H77)	29	149	31	149	2	
	356410	Hepatitis C virus (isolate HC-G9)	2	1	2	1		
	11113	Hepatitis C virus (isolate HC-J6)	2	2	2	2		
	11115	Hepatitis C virus (isolate HC-J8)	2	1	2	1		
	11110	Hepatitis C virus (isolate HCT18)	1		1			
	356416	Hepatitis C virus (isolate HCV-K3a/650)		14		14		
	31644	Hepatitis C virus (isolate HCV-KF)	1	1	1	1		
	356386	Hepatitis C virus (isolate India)		1		1		
	11116	Hepatitis C virus (isolate Japanese)	6	42	6	42		
	356411	Hepatitis C virus (isolate JFH-1)		1	2	1	2	
	356417	Hepatitis C virus (isolate JK049)		5		5		
	356415	Hepatitis C virus (isolate NZL1)	1	1	1	1		
	31645	Hepatitis C virus (isolate Taiwan)	3	19	3	19		
	356421	Hepatitis C virus (isolate Th580)		4		4		
	357355	Hepatitis C virus (isolate Tr Kj)		3		3		
	356424	Hepatitis C virus (isolate VN004)		1		1		
	41856	Hepatitis C virus genotype 1	2	28	2	28		
	40271	Hepatitis C virus genotype 2	41		41			
	356114	Hepatitis C virus genotype 3	114	3	114	3		
X	33745	Hepatitis C virus genotype 4				1		1
	421877	Hepatitis C virus isolate HC-J1		26		26		
	31646	Hepatitis C virus subtype 1a	139	235	142	236	3	1
	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	523	143	523	146		3
	10000456	Hepatitis C virus subtype 1b AD78	71		71			

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	1000968	Hepatitis C virus subtype 1b isolate BE-11			3		3	
	31649	Hepatitis C virus subtype 2a	78	21	78	21		
	31650	Hepatitis C virus subtype 2b	100	3	100	3		
	356426	Hepatitis C virus subtype 3a	2	3	2	3		
	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		
	12475	Hepatitis delta virus	41	2	45	2	4	
	10000522	Hepatitis delta virus (isolate TW2667)		5		5		
	12461	Hepatitis E virus	128	27	131	27	3	
	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		1	6		6
X	39113	Hepatitis GB virus B				4		4
	28300	Heron hepatitis B virus		1		1		
	10299	Herpes simplex virus (type 1 / strain 17)	44	12	44	22		10
	10301	Herpes simplex virus (type 1 / strain Angelotti)		1		1		
	10304	Herpes simplex virus (type 1 / strain F)	12	5	12	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)	5		5			
	10292	Herpesviridae	5	1	5	1		
	3981	Hevea brasiliensis	32	42	43	42	11	
	11583	HoJo virus		1		1		
	29679	Holcus lanatus	6		14		8	
	9606	Homo sapiens	310	1201	349	1232	39	31
	10515	Human adenovirus 2	2	1	22	5	20	4
	28285	Human adenovirus 5		1	17	22	17	21
	129951	Human adenovirus C		1		1		
X	343462	Human adenovirus type 11p			7		7	
	28282	Human adenovirus type 12		1		1		
X	45659	Human adenovirus type 3				1		1
	28284	Human adenovirus type 40		1		1		
	11137	Human coronavirus 229E		2		2		
X	12067	Human coxsackievirus A9			7		7	
X	12071	Human coxsackievirus B1			4		4	
	12072	Human coxsackievirus B3	1	2	7	9	6	7
X	12073	Human coxsackievirus B4			4	2	4	2
X	11827	Human endogenous retrovirus			1	1	1	1
	39054	Human enterovirus 71	2		2			
X	138950	Human enterovirus C			1		1	
	208726	Human hepatitis A virus	3		4		1	
	10298	Human herpesvirus 1	122	65	127	65	5	
	10000394	Human herpesvirus 1 103/65	1		1			
	10000396	Human herpesvirus 1 McIntyre		1		1		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	10000398	Human herpesvirus 1 NS	1		1			
	10306	Human herpesvirus 1 strain KOS	17	4	17	4		
	10310	Human herpesvirus 2	38	36	38	38		2
X	10312	Human herpesvirus 2 strain 186				1		1
	10313	Human herpesvirus 2 strain 333		4		4		
	10315	Human herpesvirus 2 strain HG52		14		14		
	10335	Human herpesvirus 3	3	59	4	62	1	3
X	10338	Human herpesvirus 3 (strain Dumas)				28		28
	10000406	Human herpesvirus 3 H-551	26	15	26	15		
	10376	Human herpesvirus 4	53	269	61	278	8	9
	10377	Human herpesvirus 4 (strain B95-8)	28	172	37	174	9	2
	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	1	8	1	8		
	12509	Human herpesvirus 4 type 2	1	1	1	1		
	10000427	Human herpesvirus 4 type A		5		5		
	10359	Human herpesvirus 5	72	320	75	324	3	4
	10360	Human herpesvirus 5 strain AD169	26	196	27	244	1	48
	10363	Human herpesvirus 5 strain Towne	1	21	4	21	3	
	10368	Human herpesvirus 6	2	1	2	1		
	10369	Human herpesvirus 6 (strain GS)	2		2			
	10370	Human herpesvirus 6 (strain Uganda-1102)	1	1	1	1		
	32604	Human herpesvirus 6B	1	1	1	1		
	10000535	Human herpesvirus 6B HST	1		1			
	10372	Human herpesvirus 7	2		2			
	57278	Human herpesvirus 7 strain JI		1		1		
	37296	Human herpesvirus 8	26	125	26	125		
	12721	Human immunodeficiency virus		10	1	11	1	1
	11676	Human immunodeficiency virus 1	3	86	4	100	1	14
	10000500	Human immunodeficiency virus 1 IIIB		2		2		
	11709	Human immunodeficiency virus 2		4		5		1
	11685	Human immunodeficiency virus type 1 (ARV2/SF2 ISOLATE)		43		43		
	11678	Human immunodeficiency virus type 1 (BH10 ISOLATE)		15		16		1
	11686	Human immunodeficiency virus type 1 (BRU ISOLATE)	1	3	1	3		
	11687	Human immunodeficiency virus type 1 (CDC-451 ISOLATE)		3		3		
	11679	Human immunodeficiency virus type 1 (CLONE 12)		5		5		
	11689	Human immunodeficiency virus type 1 (ELI ISOLATE)		3		3		
	11706	Human immunodeficiency virus type 1 (HXB2 ISOLATE)		12		12		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	362651	Human immunodeficiency virus type 1 (isolate YU2)		20		20		
	11694	Human immunodeficiency virus type 1 (JH3 ISOLATE)		3		3		
	11688	Human immunodeficiency virus type 1 (JRCSF ISOLATE)		35		35		
	11697	Human immunodeficiency virus type 1 (MAL ISOLATE)		6		6		
	11704	Human immunodeficiency virus type 1 (MFA ISOLATE)		2		2		
	11696	Human immunodeficiency virus type 1 (MN ISOLATE)		21		21		
	11695	Human immunodeficiency virus type 1 (NDK ISOLATE)		8		8		
	11698	Human immunodeficiency virus type 1 (NEW YORK-5 ISOLATE)		1		1		
	11699	Human immunodeficiency virus type 1 (OYI ISOLATE)		3		3		
	11701	Human immunodeficiency virus type 1 (RF/HAT ISOLATE)		23	1	23	1	
	11691	Human immunodeficiency virus type 1 (SF162 ISOLATE)		1		1		
	11690	Human immunodeficiency virus type 1 (SF33 ISOLATE)		2		2		
	11703	Human immunodeficiency virus type 1 (STRAIN UGANDAN / ISOLATE U455)		13		13		
	31678	Human immunodeficiency virus type 1 (WMJ1 isolate)		15		15		
	11705	Human immunodeficiency virus type 1 (WMJ2 ISOLATE)		1		1		
	11683	Human immunodeficiency virus type 1 (Z2/CDC-Z34 ISOLATE)		1		1		
	82834	Human immunodeficiency virus type 1 lw12.3 isolate		6		6		
	11714	Human immunodeficiency virus type 2 (ISOLATE BEN)		7		7		
	11715	Human immunodeficiency virus type 2 (ISOLATE CAM2)		1		1		
	11713	Human immunodeficiency virus type 2 (ISOLATE D194)		1		1		
	11716	Human immunodeficiency virus type 2 (ISOLATE D205,7)		1		1		
	11717	Human immunodeficiency virus type 2 (ISOLATE GHANA-1)		5		5		
	73484	Human immunodeficiency virus type 2 (isolate KR)		2		2		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	11718	Human immunodeficiency virus type 2 (ISOLATE SBLISY)		2		2		
X	162145	Human metapneumovirus				22		22
	10566	Human papillomavirus		2		2		
	334203	Human papillomavirus - 1		1		1		
	10580	Human papillomavirus type 11		5		5		
	333760	Human papillomavirus type 16		32	3	40	3	8
	333761	Human papillomavirus type 18		10		10		
	37112	Human papillomavirus type 29		1		1		
	10585	Human papillomavirus type 31		5		5		
	10586	Human papillomavirus type 33		3		3		
	10592	Human papillomavirus type 44		1		1		
	10593	Human papillomavirus type 45		2		2		
	10618	Human papillomavirus type 52		4		4		
	333765	Human papillomavirus type 53		1		1		
	10596	Human papillomavirus type 56		3		3		
	10598	Human papillomavirus type 58		3		3		
	10600	Human papillomavirus type 6b		1		1		
	36412	Human parainfluenza 1 virus (strains A1426 / 86-315 / 62M-753)		1		1		
X	11217	Human parainfluenza 3 virus (strain NIH 47885)			5		5	
X	12063	Human parechovirus 1			5		5	
	10798	Human parvovirus B19	90	39	90	44		5
	1000438	Human parvovirus B19 genotype 1	1		1			
X	12080	Human poliovirus 1			2	1	2	1
X	12081	Human poliovirus 1 Mahoney			38	9	38	9
	12082	Human poliovirus 1 strain Sabin	1		3		2	
X	10001028	Human poliovirus 2 (strain MEF-1)			1		1	
X	10001040	Human poliovirus 2 (strain Sabin)			2		2	
X	12086	Human poliovirus 3			3	2	3	2
X	10001086	Human poliovirus 3 (strain Sabin)			3		3	
	11250	Human respiratory syncytial virus	1	1	11	18	10	17
X	11255	Human respiratory syncytial virus (strain RSB6190)			6		6	
X	11256	Human respiratory syncytial virus (strain RSB6256)			10		10	
X	11252	Human respiratory syncytial virus (strain RSB642)			1		1	
	11251	Human respiratory syncytial virus (subgroup B / strain 18537)	1		2	1	1	1
	208893	Human respiratory syncytial virus A		1	1	2	1	1
X	10000960	Human respiratory syncytial virus A Mon/3/88			6		6	
	11260	Human respiratory syncytial virus A strain Long	9	4	65	7	56	3
	11259	Human respiratory syncytial virus A2	17	19	46	88	29	69
X	410078	Human respiratory syncytial virus S2			1		1	

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	12131	Human rhinovirus 14			9		9	
X	12130	Human rhinovirus 2			11		11	
X	1000987	Human rhinovirus 2 Vienna			5		5	
X	10950	Human rotavirus (SEROTYPE 2 / STRAIN DS1)			1		1	
X	36428	Human rotavirus 1				1		1
X	10941	Human rotavirus A			1	2	1	2
	10962	Human rotavirus serotype 1 / strain WA	2	4	8	4	6	
	10960	Human rotavirus strain St. Thomas 3		1		1		
	11927	Human T-cell lymphotropic virus type 1 (Caribbean isolate)		4		4		
X	10001004	Human T-cell lymphotropic virus type 1 (Caribbean isolate) (Strain HS35)			1		1	
X	11928	Human T-cell lymphotropic virus type 1 (isolate MT-2)			1		1	
	11926	Human T-cell lymphotropic virus type 1 (strain ATK)		3	25	3	25	
	11908	Human T-lymphotropic virus 1	25	52	127	94	102	42
	11909	Human T-lymphotropic virus 2	16	1	63	1	47	
	77644	IncQ plasmid pIE1120		1		1		
X	11120	Infectious bronchitis virus			1		1	
X	1000825	Infectious bronchitis virus Avian strain D207			11		11	
X	10995	Infectious bursal disease virus			11		11	
	11290	Infectious hematopoietic necrosis virus	8		8			
	11320	Influenza A virus	10	150	16	162	6	12
	387139	Influenza A virus (A/Aichi/2/1968(H3N2))	4	10	4	10		
	385576	Influenza A virus (A/Alaska/6/1977(H3N2))		1		1		
	383602	Influenza A virus (A/Anas acuta/Primorje/695/1976(H2N3))		10		10		
	135322	Influenza A virus (A/Ann Arbor/6/60(H2N2))		180		180		
	62446	Influenza A virus (A/Argentina/3779/94(H3N2))		1		1		
	385630	Influenza A virus (A/Bangkok/1/1979(H3N2))	1	4	1	4		
	11327	Influenza A virus (A/Beijing/11/56 (H1N1))		22		22		
	62450	Influenza A virus (A/Beijing/32/92(H3N2))		54		54		
	282811	Influenza A virus (A/Bilthoven/4791/81(H3N2))		2		3		1
	385587	Influenza A virus (A/budgerigar/Hokkaido/1/1977(H4N6))		4		4		
	36418	Influenza A virus (A/chicken/Brescia/1902(H7N7))		1		1		
	11384	Influenza A virus (A/chicken/FPV/Weybridge(H7N7))		1		1		
	97348	Influenza A virus (A/Chicken/Hong Kong/G23/97(H9N2))		1		1		
	385617	Influenza A virus (A/chicken/Pennsylvania/1370/1983(H5N2))	1		1			

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	197585	Influenza A virus (A/chicken/Shandong/6/96(H9N2))			1		1	
	380985	Influenza A virus (A/Chile/1/1983(H1N1))		1		1		
	62541	Influenza A virus (A/Christ Church/2/88(H3N2))		1		1		
	107493	Influenza A virus (A/Cordoba/3278/96(H3N2))		1		1		
	88295	Influenza A virus (A/duck/Alberta/35/76(H1N1))		2		2		
	383550	Influenza A virus (A/duck/England/1/1956(H11N6))		1		1		
	365080	Influenza A virus (A/duck/Guangxi/1793/2004(H5N1))		1		1		
	80266	Influenza A virus (A/Duck/Hokkaido/8/80 (H3N8))		6		6		
	210671	Influenza A virus (A/duck/Hong Kong/366/78(H9N2))		1		1		
	353253	Influenza A virus (A/duck/Novosibirsk/56/2005(H5N1))		2		2		
	385580	Influenza A virus (A/duck/Ukraine/1/1963(H3N8))	3		3			
	11375	Influenza A virus (A/Dunedin/4/73(H3N2))	2		2			
	380210	Influenza A virus (A/England/333/1980(H1N1))	1		1			
	221011	Influenza A virus (A/England/878/69(H3N2))	1	2	1	2		
	137578	Influenza A virus (A/England/939/69 x A/PR/8/34)		1		1		
X	387223	Influenza A virus (A/equine/Miami/1963(H3N8))			5		5	
	229411	Influenza A virus (A/Fort Monmouth/1/47-MA(H1N1))		6		6		
	260806	Influenza A virus (A/FPV/Dutch/27(H7N7))	1		1			
	382786	Influenza A virus (A/FPV/Rostock/1934(H7N1))	2	4	2	4		
	107558	Influenza A virus (A/France/75/97(H3N2))		1		1		
	31661	Influenza A virus (A/Harbin/1/88(H1N2))		4		4		
	144556	Influenza A virus (A/Hong Kong(H3N2))		15		15		
	108859	Influenza A virus (A/Hong Kong/1/68(H3N2))		2		2		
	130760	Influenza A virus (A/Hong Kong/1073/99(H9N2))	1		1			
	130763	Influenza A virus (A/Hong Kong/156/97(H5N1))		2		2		
	317652	Influenza A virus (A/Hong Kong/2/68(H3N2))		2		2		
	88104	Influenza A virus (A/Hong Kong/483/1997(H5N1))	1		1			
	220500	Influenza A virus (A/Japan/305/57(H2N2))	2	26	2	26		
X	203126	Influenza A virus (A/Kamata/14/91(H3N2))			1		1	
	11422	Influenza A virus (A/Kiev/59/79(H1N1))		1		1		
	220985	Influenza A virus (A/Korea/426/68(H2N2))		1		1		
	393557	Influenza A virus (A/Leningrad/1954/1(H1N1))		3		3		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	62559	Influenza A virus (A/Los_Angeles/(H3N2))	5		5			
	95888	Influenza A virus (A/mallard duck/PA/10218/84(H5N2))	1		1			
	220503	Influenza A virus (A/Memphis/1/71(H3N2))	19	11	19	11		
	79695	Influenza A virus (A/Memphis/1/71H-A/Bellamy/42N)		1		1		
	252233	Influenza A virus (A/Memphis/102/72(H3N2))		7		7		
	228928	Influenza A virus (A/Memphis/31/98(H3N2))	6		6			
	11440	Influenza A virus (A/Memphis/6/86(H3N2))	2		2			
	62488	Influenza A virus (A/Nanchang/58/1993(H3N2))		1		1		
	132841	Influenza A virus (A/Netherlands/785e/90(H3N2))		1		1		
X	381512	Influenza A virus (A/New Caledonia/20/1999(H1N1))				3		3
	335313	Influenza A virus (A/New York/364/2004(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		
	260805	Influenza A virus (A/NT/60/68/(H3N2))		60		61		1
	155917	Influenza A virus (A/NWS/33HA-A/tern/Australia/G70C/75NA(H1N9))	1		1			
	382820	Influenza A virus (A/NWS/G70C(H1N9))	1		1			
	62503	Influenza A virus (A/Ohio/3/95(H3N2))		1		1		
	223935	Influenza A virus (A/Okuda/57(H2N2))	1	9	1	9		
X	381513	Influenza A virus (A/Panama/2007/1999(H3N2))			10	1	10	1
	119209	Influenza A virus (A/Philippines/2/82(H3N2))	1		1			
	385624	Influenza A virus (A/Port Chalmers/1/1973(H3N2))	7	1	7	1		
	211044	Influenza A virus (A/Puerto Rico/8/34(H1N1))	17	323	18	327	1	4
	183764	Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))	7	58	7	58		
	106423	Influenza A virus (A/Quail/Hong Kong/AF157/92(H9N2))		1		1		
	221012	Influenza A virus (A/Rio/6/69(H3N2))		1		1		
	384493	Influenza A virus (A/seal/Mass/1/1980(H7N7))	1		1			
	62512	Influenza A virus (A/Shangdong/5/94(H3N2))		1		1		
X	380948	Influenza A virus (A/Shangdong/9/1993(H3N2))			12		12	
	63105	Influenza A virus (A/Shanghai/16/89(H3N2))		1		1		
	220949	Influenza A virus (A/Singapore/1/57(H2N2))	1		1			
	150154	Influenza A virus (A/swine/29/37 (H1N1))		2		2		
	169169	Influenza A virus (A/swine/Cotes d'Armor/1482/99(H1N1))		1		1		
	11498	Influenza A virus (A/swine/Hong Kong/126/82(H3N2))		1		1		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	219641	Influenza A virus (A/swine/Hong Kong/81/78(H3N2))		8		8		
	145307	Influenza A virus (A/swine/Hong Kong/9/98(H9N2))	2		2			
	11504	Influenza A virus (A/swine/Indiana/1726/88(H1N1))		1		1		
	300743	Influenza A virus (A/swine/Korea/S10/2004(H1N1))		1		1		
	300744	Influenza A virus (A/swine/Korea/S175/2004(H1N1))		1		1		
	186460	Influenza A virus (A/swine/New Jersey/11/76(H1N1))	1		1			
	11517	Influenza A virus (A/swine/Ukkel/1/84(H3N2))		1		1		
	82372	Influenza A virus (A/Sydney/05/97-like(H3N2))		1		1		
	384509	Influenza A virus (A/tern/Australia/G70C/1975(H11N9))	10		10			
	183796	Influenza A virus (A/Texas/1/77(H3N2))	2	12	2	12		
	380301	Influenza A virus (A/turkey/Ontario/7732/1966(H5N9))	5	6	5	6		
X	293054	Influenza A virus (A/Ty/ON/6213/66(H5N?))			1		1	
	381517	Influenza A virus (A/Udorn/307/1972(H3N2))		4		4		
	62596	Influenza A virus (A/USSR/26/(H3N2))		1		1		
	381516	Influenza A virus (A/USSR/90/1977(H1N1))	13	1	13	1		
	392809	Influenza A virus (A/Victoria/3/1975(H3N2))	43	8	43	8		
	284217	Influenza A virus (A/Viet Nam/1194/2004(H5N1))		2		4		2
X	284218	Influenza A virus (A/Viet Nam/1203/2004(H5N1))				50		50
	382832	Influenza A virus (A/VM113-V1(H1N1))	1		1			
	11484	Influenza A virus (A/whale/Maine/1/84(H13N9))	3		3			
	381518	Influenza A virus (A/Wilson-Smith/1933(H1N1))		108		108		
	382835	Influenza A virus (A/WSN/1933(H1N1))	4	1	4	1		
	63106	Influenza A virus (A/Wuhan/359/95(H3N2))	5		5			
X	273330	Influenza A virus (A/Wyoming/3/03(H3N2))				1		1
	132504	Influenza A virus (A/X-31(H3N2))	58	144	65	151	7	7
	380905	Influenza A virus (A/X-47(H3N2))	1	2	3	2	2	
	11408	Influenza A virus (STRAIN A/EQUINE/NEW MARKET/76)		1		1		
	41857	Influenza A virus H3N2	1	5	1	5		
X	1000865	Influenza A virus H3N2 (A/Kiev/301/94)			3		3	
	1000550	Influenza A virus H3N2 (A/Netherlands/9/03 (H3N2))		1		1		
	1000474	Influenza A virus H3N2 (A/Resvir-9 (H3N2))		10		10		
	11520	Influenza B virus	2	4	2	6		2
	11521	Influenza B virus (B/Ann Arbor/1/1986)		3		3		
X	206203	Influenza B virus (B/Hong Kong/330/2001)				7		7

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	184816	Influenza B virus (B/Kadoma/122/99)	2		2			
	256080	Influenza B virus (B/Kobe/1/2003)	1		1			
	107412	Influenza B virus (B/Lee/40)	5	3	5	3		
	11541	Influenza B virus (B/Oregon/5/80)	2		2			
	150127	Influenza B virus (B/Osaka/983/97-V3)	1		1			
	107418	Influenza B virus (B/Victoria/2/87)	2		2			
	11531	Influenza B virus (STRAIN B/HONG KONG/8/73)		1		1		
	11553	Influenza C virus (C/Ann Arbor/1/50)	9		9			
	197911	Influenzavirus A		5		5		
	9725	Inia geoffrensis		1		1		
	42097	Isla Vista virus	1		1			
	11072	Japanese encephalitis virus	7		18	13	11	13
	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		
X	11073	Japanese encephalitis virus strain SA-14			1	1	1	1
X	10632	JC polyomavirus				2		2
	51240	Juglans regia	5		5			
	11619	Junin virus		1		1		
	13101	Juniperus ashei	3		12		9	
	573	Klebsiella pneumoniae	15		15	1		1
	11077	Kunjin virus		1		1		
	11078	Kunjin virus (STRAIN MRM61C)		2		2		
	11577	La Crosse virus		1		1		
X	8753	Lachesis muta muta			21		21	
X	11048	Lactate dehydrogenase-elevating virus			13		13	
	33727	Lake Victoria marburgvirus - Musoke	4		4			
	33728	Lake Victoria marburgvirus - Popp	1		1			
	11620	Lassa virus	4	4	4	4		
	11621	Lassa virus GA391		10		10		
	11622	Lassa virus Josiah		66		66		
	5667	Leishmania aethiopica	16		16			
	5659	Leishmania amazonensis		1		2		1
	5660	Leishmania braziliensis	6		6			
	5661	Leishmania donovani	5	35	9	38	4	3
	44271	Leishmania donovani chagasi	2		2			
	99875	Leishmania donovani donovani	1		1			
	1000341	Leishmania donovani donovani 1S2D	1		1			
	5671	Leishmania infantum	92	1	93	1	1	
	1000345	Leishmania infantum LEM 75	14		14			
	5664	Leishmania major	13	99	13	113		14
	5665	Leishmania mexicana	1		1			
	5679	Leishmania panamensis	3	6	3	6		
	5682	Leishmania pifanoi		20		20		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	11049	Lelystad virus			20		20	
	36936	Lepidoglyphus destructor	5		5	10		10
X	267671	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130			11		11	
X	189518	Leptospira interrogans serovar Lai str. 56601			1		1	
X	10000814	Leptospira interrogans serovar Lai str. HY-1			1		1	
X	10000847	Leptospira sp. Akiyami A AUT10			1		1	
	1642	Listeria innocua	2	1	2	1		
	1639	Listeria monocytogenes	18	49	18	53		4
	393133	Listeria monocytogenes 10403S		4		4		
	10000308	Listeria monocytogenes ATCC 35967		1		1		
	10000309	Listeria monocytogenes ATCC 43251		2		2		
	169963	Listeria monocytogenes EGD-e	5	42	5	42		
	265669	Listeria monocytogenes str. 4b F2365		3		3		
	217686	Little cherry virus 1		1		1		
	4522	Lolium perenne	16	26	24	78	8	52
	36386	Louping ill virus (strain 31)	1		1			
	11623	Lymphocytic choriomeningitis virus	1	47	1	51		4
	11624	Lymphocytic choriomeningitis virus (strain Armstrong)		68		68		
	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)		42		45		3
	11625	Lymphocytic choriomeningitis virus (strain Pasteur)		2		2		
	11627	Lymphocytic choriomeningitis virus (strain WE)		10		11		1
	10000494	Lymphocytic choriomeningitis virus (strain WE) variant 8.7		1		1		
	10000495	Lymphocytic choriomeningitis virus (strain WE) WE CL1.2		1		1		
	10000490	Lymphocytic choriomeningitis virus A22.2b		1		1		
	10000491	Lymphocytic choriomeningitis virus Docile		2		2		
	9541	Macaca fascicularis		1		1		
	9544	Macaca mulatta		1		1		
	10373	Macaca mulatta cytomegalovirus		35		35		
X	12750	Maedi-Visna-like virus EV1			1		1	
	3750	Malus x domestica	1	1	24	1	23	
	40674	Mammalia	2	1	2	1		
	7130	Manduca sexta		2		3		1
	45201	Mannheimia haemolytica serotype 1	13		13			
	11234	Measles virus	3	14	50	30	47	16

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	10000462	Measles virus CAM/RB		1		1		
	11235	Measles virus strain Edmonston	89	98	164	131	75	33
	70146	Measles virus strain Edmonston-B		6		13		7
X	11236	Measles virus strain Halle				4		4
X	132487	Measles virus strain Schwarz			1	1	1	1
	12107	Mengo virus	1		1			
	10036	Mesocricetus auratus	27		28		1	
	11801	Moloney murine leukemia virus		1		2		1
	10244	Monkeypox virus	5		5			
	300180	Mopeia Lassa reassortant 29		1		1		
	11629	Mopeia virus		2		2		
X	480	Moraxella catarrhalis			7		7	
X	11757	Mouse mammary tumor virus				10		10
	11161	Mumps virus	3		3			
	11169	Mumps virus (STRAIN KILHAM)	1		1			
	11173	Mumps virus (STRAIN SBL-1)	3		3			
	10366	Murid herpesvirus 1		31		41		10
	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		12		12		
	10000536	Murid herpesvirus 4 G2.4		3		3		
	10000537	Murid herpesvirus 4 WUMS		2		2		
	69156	Murine cytomegalovirus (strain K181)	2	11	2	11		
	10367	Murine cytomegalovirus (strain Smith)		10		26		16
X	11138	Murine hepatitis virus				5		5
	12760	Murine hepatitis virus strain 4		1		1		
	11142	Murine hepatitis virus strain A59	1		26	2	25	2
	11144	Murine hepatitis virus strain JHM	2	6	4	11	2	5
X	11786	Murine leukemia virus				2		2
X	10634	Murine polyomavirus				14		14
X	10636	Murine polyomavirus strain A2				1		1
X	28327	Murine rotavirus				3		3
X	70865	Murine rotavirus EDIM				27		27
	11812	Murine sarcoma virus 3611	4		4			
X	44561	Murine type C retrovirus				1		1
	11079	Murray Valley encephalitis virus	12	4	12	4		
	301478	Murray valley encephalitis virus (strain MVE-1-51)	10	10	10	10		
	10090	Mus musculus	95	164	124	505	29	341
	10000000	Mus musculus BALB/c		2		2		
	10092	Mus musculus domesticus		12		12		
	4641	Musa acuminata		1		1		
	1763	Mycobacterium	4	7	4	7		
	1764	Mycobacterium avium	4	6	7	11	3	5
	10000313	Mycobacterium avium serovar 1	1		1			

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	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		
	10000320	Mycobacterium avium serovar 9	1		1			
X	1770	<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i>					1	1
	10000328	Mycobacterium avium subsp. <i>paratuberculosis</i> Strain Ben		1		1		
	1765	Mycobacterium bovis	41	76	41	76		
	233413	Mycobacterium bovis AF2122/97		49		49		
	10000322	Mycobacterium bovis AN5	9	28	9	28		
	33892	Mycobacterium bovis BCG	9	136	9	136		
X	410289	<i>Mycobacterium bovis</i> BCG str. Pasteur 1173P2			1		1	
	10000323	Mycobacterium bovis T/91/1378		6		6		
	1766	Mycobacterium fortuitum		1		1		
	144549	Mycobacterium fortuitum subsp. <i>fortuitum</i>		1		1		
	10000331	Mycobacterium gastris W471	1		1			
	1767	Mycobacterium intracellulare	1	1	1	1		
	1768	Mycobacterium kansasii	9	7	9	7		
	10000324	Mycobacterium kansasii ATCC 12478	1		1			
	10000325	Mycobacterium kansasii Subspecies IV		3		3		
	10000326	Mycobacterium kansasii Subspecies V		2		2		
	1769	Mycobacterium leprae	120	292	120	297		5
	272631	Mycobacterium leprae TN		5		5		
	43304	Mycobacterium peregrinum	2		2			
	1783	Mycobacterium scrofulaceum	4		4			
	1772	Mycobacterium smegmatis		3		3		
	1785	Mycobacterium sp.		2		2		
	1773	Mycobacterium tuberculosis	191	543	206	616	15	73
	10000329	Mycobacterium tuberculosis 103	1		1			
	83331	Mycobacterium tuberculosis CDC1551		16		16		
	10000330	Mycobacterium tuberculosis Erdman	15	97	15	97		
	419947	Mycobacterium tuberculosis H37Ra		4		4		
	83332	Mycobacterium tuberculosis H37Rv	20	320	20	320		
X	347257	<i>Mycoplasma agalactiae</i> PG2			3		3	
	28903	Mycoplasma bovis	21		21			
X	10001075	<i>Mycoplasma gallisepticum</i> strain S6			1		1	
	2097	Mycoplasma genitalium		1		1		
	2104	Mycoplasma pneumoniae	3	2	9	2	6	
	10000332	Mycoplasma pneumoniae FH	1		1			
	272634	Mycoplasma pneumoniae M129	2		9		7	
X	13618	<i>Myrmecia pilosula</i>			2		2	
	35670	Naja naja	2		2			
X	8654	<i>Naja nigricollis</i>			2		2	

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	8658	Naja pallida	1	1	1	1		
	485	Neisseria gonorrhoeae		9	17	10	17	1
X	1000984	Neisseria gonorrhoeae MS11			4		4	
	487	Neisseria meningitidis		1	12	18	12	17
X	272831	Neisseria meningitidis FAM18			1		1	
X	122586	Neisseria meningitidis MC58			1		1	
X	10001051	Neisseria meningitidis serogroup A Strain 8659			1		1	
X	491	Neisseria meningitidis serogroup B			1		1	
X	1000843	Neisseria meningitidis serogroup B H44/76			10		10	
X	10001003	Neisseria meningitidis serogroup B CU385			2		2	
X	10001050	Neisseria meningitidis serogroup B Strain 7967			1		1	
X	10000979	Neisseria meningitidis serogroup B Strain 8047			1		1	
X	10000972	Neisseria meningitidis serogroup B Strain B16.B6			1		1	
X	10001049	Neisseria meningitidis serogroup B Strain S3446			1		1	
X	10001044	Neisseria meningitidis serogroup C MC51			1		1	
X	29176	Neospora caninum			2	2	2	2
X	5141	Neurospora crassa			4		4	
X	11176	Newcastle disease virus			9		9	
X	11177	Newcastle disease virus (STRAIN AUSTRALIA-VICTORIA/32)			3		3	
X	11178	Newcastle disease virus (STRAIN BEAUDETTE C/45)			12		12	
X	11180	Newcastle disease virus (STRAIN D26/76)			4		4	
	4097	Nicotiana tabacum	1		1			
	121791	Nipah virus	4		4			
	122928	Norovirus genogroup 1	1		1			
	122929	Norovirus genogroup 2	1		2		1	
X	1000829	Norovirus genogroup 2 Mexico type strain 36			3		3	
	10000560	Norovirus genogroup 3 Bo/Jena/1980/DE	1		1			
	8996	Numida meleagris	1		1			
	4146	Olea europaea	1	14	1	14		
	42764	Oliveros virus		1		1		
X	6282	Onchocerca volvulus			3	5	3	5
	9733	Orcinus orca		1		1		
	784	Orientia tsutsugamushi	86		86			
	357244	Orientia tsutsugamushi Boryong	2		2			
	10000761	Orientia tsutsugamushi Karp	1		1			
	9986	Oryctolagus cuniculus		1		1		
X	28869	Ovine respiratory syncytial virus			1		1	
	9940	Ovis aries	67		68		1	
	9598	Pan troglodytes	4	1	4	1		
X	3469	Papaver somniferum			1		1	

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	61183	Papio sp.			1		1	
	121759	Paracoccidioides brasiliensis	2		4	14	2	14
	10000566	Paracoccidioides brasiliensis B339		8		8		
X	266	Paracoccus denitrificans			1		1	
	33127	Parietaria judaica	4	1	4	1		
	13187	Parietaria officinalis	2		2			
	747	Pasteurella multocida		8		8		
	10000759	Pasteurella multocida X-73	2		2			
X	1254	Pediococcus acidilactici			1		1	
	133894	Penaeus	2		2			
	5076	Penicillium chrysogenum	9		45		36	
	6978	Periplaneta americana	3		7		4	
	31604	Peste-des-petits-ruminants virus	9	1	9	1		
X	10001020	Peste-des-petits-ruminants virus (strain Nigeria 75/1)				1		1
	3885	Phaseolus vulgaris		1		1		
	15957	Phleum pratense	37	26	46	54	9	28
	9742	Phocoena phocoena		1		1		
X	72539	Physalis mottle virus			2		2	
	9755	Physeter catodon	1	26	1	26		
	11630	Pichinde virus		4		4		
	141833	Plasmid pIPO2T		2		2		
	5820	Plasmodium	5	5	5	8		3
	5821	Plasmodium berghei	11	41	11	44		3
	10000356	Plasmodium berghei NK65	2	2	2	2		
	5823	Plasmodium berghei strain ANKA	5		5			
	5824	Plasmodium brasilianum	2		2			
	5825	Plasmodium chabaudi	4	4	4	4		
	10000357	Plasmodium chabaudi adami DS	2	37	2	37		
	5827	Plasmodium cynomolgi	1		1			
	5833	Plasmodium falciparum	493	656	509	666	16	10
	5835	Plasmodium falciparum (isolate CAMP / Malaysia)	36	3	36	3		
	5836	Plasmodium falciparum (isolate CDC / Honduras)	1		1			
	5837	Plasmodium falciparum (isolate FC27 / Papua New Guinea)	37	45	40	45	3	
	5834	Plasmodium falciparum (isolate RO-33 / Ghana)	8	1	8	1		
	5848	Plasmodium falciparum (isolate WELLCOME)	23	26	23	26		
	10000358	Plasmodium falciparum 366		1		1		
	36329	Plasmodium falciparum 3D7	32	194	118	197	86	3
	57266	Plasmodium falciparum 7G8	38	50	38	50		
	10000363	Plasmodium falciparum Brazil-608	1	1	1	1		
	10000364	Plasmodium falciparum Clone PNG3		1		1		
	10000366	Plasmodium falciparum FCB-2	1		1			
	5838	Plasmodium falciparum FCR-3/Gambia	7		7			

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	10000371	Plasmodium falciparum Indochina I/CDC	32		32			
	10000373	Plasmodium falciparum ItG2G1		1		1		
	5839	Plasmodium falciparum K1/Thailand	15	19	15	19		
	5840	Plasmodium falciparum LE5		2		2		
	5841	Plasmodium falciparum Mad20/Papua New Guinea	7	20	8	20	1	
	5843	Plasmodium falciparum NF54	13	28	13	28		
	5842	Plasmodium falciparum NF7/Ghana	3		3			
	57270	Plasmodium falciparum Palo Alto/Uganda	14		14			
	10000375	Plasmodium falciparum RO71	1	1	1	1		
	5846	Plasmodium falciparum T4/Thailand	25		25			
X	10000816	Plasmodium falciparum T9/96			1	1	1	1
	10000376	Plasmodium falciparum UF-5	2		2			
	5857	Plasmodium fragile		4		4		
	5850	Plasmodium knowlesi	2	7	2	7		
	5851	Plasmodium knowlesi strain H	7	6	7	6		
	5852	Plasmodium knowlesi strain Nuri		3		3		
	5858	Plasmodium malariae	1		1			
	5854	Plasmodium reichenowi		3		3		
	35085	Plasmodium simiovale	1		1			
	5859	Plasmodium simium	2		2			
	31272	Plasmodium sp.	1		1			
	5855	Plasmodium vivax	56	139	56	139		
	31273	Plasmodium vivax (strain Belem)	6	34	6	34		
	10000378	Plasmodium vivax NK		2		2		
	126793	Plasmodium vivax Sal-1	1	1	3	1	2	
	10000862	Plasmodium vivax VK247	1		1			
	27990	Plasmodium vivax-like sp.	2		2			
	5861	Plasmodium yoelii	9	33	9	33		
	73239	Plasmodium yoelii yoelii	21	24	21	24		
	10000555	Plasmodium yoelii yoelii 265BY		1		1		
	352914	Plasmodium yoelii yoelii str. 17XNL	6	1	6	1		
	10000381	Plasmodium yoelii yoelii YM	1	5	1	5		
X	12211	Plum pox virus			1		1	
X	10001100	Plum pox virus (strain W)			6		6	
X	4754	Pneumocystis carinii			2		2	
X	263815	Pneumocystis murina			3		3	
X	270473	Pneumonia virus of mice J3666				6		6
X	11245	Pneumovirus			4		4	
	4545	Poa pratensis	21	17	21	17		
	138953	Poliovirus	1	3	4	3	3	
X	12088	Poliovirus type 3 (strains P3/LEON/37 AND P3/LEON 12A[1]B)			4		4	
	188763	Pongine herpesvirus 4		2		2		
X	46221	Porcine circovirus				49		49
X	133704	Porcine circovirus 1			5		5	
X	85708	Porcine circovirus 2			5		5	

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	194958	Porcine endogenous retrovirus A			2		2	
X	28295	Porcine epidemic diarrhea virus			1		1	
X	229032	Porcine epidemic diarrhea virus (strain CV777)			4		4	
	28344	Porcine respiratory and reproductive syndrome virus	7		22		15	
X	10000969	Porcine respiratory and reproductive syndrome virus 111/92			9		9	
	10000529	Porcine respiratory and reproductive syndrome virus CH-1a	5		6		1	
X	10000859	Porcine respiratory and reproductive syndrome virus JA142			1		1	
X	10000864	Porcine respiratory and reproductive syndrome virus MD-001			1		1	
X	10000888	Porcine respiratory and reproductive syndrome virus Olot/91			3		3	
X	10919	Porcine rotavirus (STRAIN YM)			1	1	1	1
X	101350	Porcine rotavirus strain A253			2		2	
	53179	Porcine rubulavirus	3		3			
X	11150	Porcine transmissible gastroenteritis coronavirus strain FS772/70			1		1	
	11151	Porcine transmissible gastroenteritis coronavirus strain Purdue	1		14		13	
	837	Porphyromonas gingivalis		1	14	11	14	10
X	10001079	Porphyromonas gingivalis 381			1		1	
X	10001081	Porphyromonas gingivalis HG66			2		2	
X	12216	Potato virus Y			1		1	
	11603	Prospect Hill virus	1		1			
	584	Proteus mirabilis	1		1			
X	10001006	Proteus mirabilis CFT322			1		1	
X	88086	Protobothrops elegans			7		7	
	300559	PRRSV VR2332	1		17		16	
X	36596	Prunus armeniaca			4		4	
	42229	Prunus avium		1	2	1	2	
X	3758	Prunus domestica			4		4	
	3760	Prunus persica	11		15		4	
	287	Pseudomonas aeruginosa	27	35	51	36	24	1
X	10001057	Pseudomonas aeruginosa CD4			1		1	
	10000723	Pseudomonas aeruginosa Immunotype 4	4		4			
X	10001058	Pseudomonas aeruginosa K122-4			1		1	
	10000817	Pseudomonas aeruginosa KB7	1		2		1	
	10000818	Pseudomonas aeruginosa P1	1		1			
X	10000725	Pseudomonas aeruginosa PAK			7	3	7	3
	10000815	Pseudomonas aeruginosa PAO	1		2	2	1	2
	294	Pseudomonas fluorescens		3		3		
	303	Pseudomonas putida		5	1	5	1	
	306	Pseudomonas sp.		1		1		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	74138	Pseudomonas sp. DJ-12		1		1		
	71238	Pseudomonas sp. G-179		1		1		
	159091	Pseudomonas sp. KIE171		1		1		
	237609	Pseudomonas sp. KL28		1		1		
	150396	Pseudomonas sp. MT-1		1		1		
	11604	Puumala virus	30	8	30	8		
	10000485	Puumala virus (STRAIN HALLNAS B1) Vranica/Hallnas	4		4			
	39002	Puumala virus (strain sotkamo/v-2969/81)	196		196			
	10000483	Puumala virus CG18-20	5		5			
X	10000484	Puumala virus Kazan			25	7	25	7
	10000507	Rabbit hemorrhagic disease virus Olot/89	1		1			
	11292	Rabies virus	4	7	5	8	1	1
	11293	Rabies virus (strain AVO1)		3		3		
	11294	Rabies virus (strain CVS-11)	1		1			
	11295	Rabies virus (strain ERA)	9	21	9	21		
	11296	Rabies virus (strain HEP-FLURY)	7	1	7	1		
	11298	Rabies virus (strain Nishigahara RCEH)	1		1			
	37132	Rabies virus (strain Ontario fox)	3		3			
	103929	Rabies virus (strain Pasteur / PV)	1	1	1	1		
	10000467	Rabies virus CVS	14		14			
	10000470	Rabies virus Flury LEP		1		1		
	10000471	Rabies virus RC-HL	4		4			
	10116	Rattus norvegicus	2	1	5	20	3	19
X	1646	Renibacterium salmoninarum			12		12	
	12814	Respiratory syncytial virus		3	3	3	3	
	129003	Reston ebolavirus - Reston	2		2			
	103930	Rhesus cytomegalovirus strain 68-1		5		5		
X	10969	Rhesus rotavirus			6		6	
	60189	Rhipicephalus decoloratus	4		4			
	43767	Rhodococcus equi	15		15			
	160061	Ricinus		1		1		
	3988	Ricinus communis	7	3	7	3		
	781	Rickettsia conorii		6		6		
	272944	Rickettsia conorii str. Malish 7		5		5		
	782	Rickettsia prowazekii		10		10		
	783	Rickettsia rickettsii		1		1		
	35793	Rickettsia sibirica		3		3		
	785	Rickettsia typhi		1		1		
	11588	Rift Valley fever virus	4		4			
	11589	Rift valley fever virus (STRAIN ZH-548 M12)		1		1		
	10000482	Rift Valley fever virus ZH501	2		2			
X	11241	Rinderpest virus			1	2	1	2
X	11243	Rinderpest virus (strain L)			6		6	
X	36409	Rinderpest virus (strain RBOK)			33	5	33	5
	10000465	Rinderpest virus LATC	3		3			

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	46920	Rio Mamore virus	1		1			
	37207	Rio Segundo virus	1		1			
	1	root	1	1	2	1	1	
	11032	Ross river virus (STRAIN T48)	3		3			
	10912	Rotavirus		1		1		
X	11886	Rous sarcoma virus				4		4
	11041	Rubella virus	34	41	46	57	12	16
X	11043	Rubella virus (strain M33)				10		10
	11045	Rubella virus (strain THERIEN)	1		1	29		29
X	11044	Rubella virus (vaccine strain RA27/3)				4		4
	45709	Sabia virus		11		11		
	4932	Saccharomyces cerevisiae	2	2	2	3		1
	10381	Saimiriine herpesvirus 2		1		1		
	590	Salmonella	1		1			
	29477	Salmonella enterica subsp. enterica serovar Essen	1		1			
	70803	Salmonella enterica subsp. enterica serovar Minnesota	1		1			
	596	Salmonella enterica subsp. enterica serovar Muenchen	1		1			
	599	Salmonella sp.	1		1			
	72590	Salmonella sp. 'group B'	2		2			
	601	Salmonella typhi	4	12	9	12	5	
	10000739	Salmonella typhi 620Ty	1		1			
	10000740	Salmonella typhi Ty21a		6		6		
	602	Salmonella typhimurium	1	33	9	35	8	2
	99287	Salmonella typhimurium LT2		1		1		
	10000738	Salmonella typhimurium PL5 (O9,12)	1		1			
	10000743	Salmonella typhimurium SL3261		4		4		
	10000746	Salmonella typhimurium TV119	1		1			
X	8015	Salmonidae			1		1	
	227859	SARS coronavirus	139	186	144	191	5	5
	228407	SARS coronavirus BJ01	25	28	25	28		
	228415	SARS coronavirus CUHK-W1	17		17			
	229992	SARS coronavirus Frankfurt 1	1		1			
	227984	SARS coronavirus Tor2	168	1957	171	1957	3	
	228330	SARS coronavirus Urbani	22	28	22	28		
	6182	Schistosoma japonicum		9	36	12	36	3
	6183	Schistosoma mansoni	1	12	26	22	25	10
	10000385	Schistosoma mansoni Puerto Rico	2	1	17	6	15	5
X	4550	Secale cereale			51		51	
	11033	Semliki forest virus	25		25			
	11191	Sendai virus		4		5		1
	11194	Sendai virus (strain Enders)		9	7	11	7	2
X	11196	Sendai virus (strain Harris)			2		2	
X	302272	Sendai virus (strain Ohita)			1		1	
	11198	Sendai virus (Z)		1		1		

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	11610	Seoul virus SR11	1		1			
	615	Serratia marcescens		1		1		
	4182	Sesamum indicum	11		11			
X	622	Shigella dysenteriae			5		5	
	1000748	Shigella dysenteriae serotype 1	2		2			
	1000749	Shigella dysenteriae serotype 1 114Sd	3		3			
	623	Shigella flexneri	75	3	75	3		
	41434	Shigella flexneri 1b	1		1			
	42897	Shigella flexneri 2a	26		26			
	1000750	Shigella flexneri 2b	1		1			
	424717	Shigella flexneri 3a	2		2			
	1000751	Shigella flexneri 4b	1		1			
	424718	Shigella flexneri 5a	2		2			
	1000752	Shigella flexneri 5b	1		1			
	1000754	Shigella flexneri X	1		1			
	424720	Shigella flexneri Y	3		3			
	624	Shigella sonnei		1		1		
X	92652	Shrimp white spot syndrome virus			3		3	
	11723	Simian immunodeficiency virus		152		152		
	11711	Simian immunodeficiency virus - mac		1		1		
	1000501	Simian immunodeficiency virus - mac - mac 239		279		279		
	1000502	Simian immunodeficiency virus - mac - mac 32H		7		7		
	1000503	Simian immunodeficiency virus - mac - mac BK28		3		3		
	1000504	Simian immunodeficiency virus - mac - mac F965		1		1		
	31682	Simian immunodeficiency virus - mac1A11		8		8		
	1000506	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		
	11735	Simian immunodeficiency virus (K6W ISOLATE)		72		72		
	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		
X	11942	Simian retrovirus 1			1		1	
X	10923	Simian rotavirus A/SA11			1		1	
X	37137	Simian rotavirus A/SA11-both			17		17	
	10633	Simian virus 40		8	5	19	5	11
X	11207	Simian virus 5				1		1

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	31608	Simian virus 5 (isolate canine/CPI+)			1		1	
	57667	Simian-Human immunodeficiency virus		1		1		
	37705	Sin Nombre virus	1	3	1	3		
	10000544	Sin Nombre virus NM H10		8	4	8	4	
X	3728	Sinapis alba			2		2	
X	11034	Sindbis virus			1		1	
X	254355	Small ruminant lentivirus			1		1	
	11780	Snyder-Theilen feline sarcoma virus	1		1			
X	11984	Southampton virus			1		1	
	2133	Spiroplasma citri		1		1		
	11081	St. Louis encephalitis virus (strain MS1-7)	9		9			
	1280	Staphylococcus aureus	81	26	84	31	3	5
	93062	Staphylococcus aureus subsp. aureus COL	17		17			
	282458	Staphylococcus aureus subsp. aureus MRSA252	40		40			
X	1317	Streptococcus downei			2		2	
	119602	Streptococcus dysgalactiae subsp. equisimilis	1		18		17	
X	1336	Streptococcus equi			17		17	
	1309	Streptococcus mutans	4	1	22	6	18	5
X	10000974	Streptococcus mutans GS-5				14		14
X	10000773	Streptococcus mutans MT 8148			1	9	1	9
X	10000813	Streptococcus mutans SJ			1	1	1	1
	1313	Streptococcus pneumoniae		2	9	2	9	
	1314	Streptococcus pyogenes	68	72	71	72	3	
	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	12		12			
	286636	Streptococcus pyogenes MGAS10394		1		1		
	10000782	Streptococcus pyogenes NS1	1		1			
	10000783	Streptococcus pyogenes NS14	1		1			
	10000784	Streptococcus pyogenes NS27	1		1			
	10000785	Streptococcus pyogenes NS5	1		1			
	10000786	Streptococcus pyogenes serotype M11	2		2			
	342023	Streptococcus pyogenes serotype M12	3		3			
	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	2	1	2	1		
	301448	Streptococcus pyogenes serotype M3	1		1			
	10000542	Streptococcus pyogenes serotype M3 D58	2		2			

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
	1000790	Streptococcus pyogenes serotype M30	1		1			
	404331	Streptococcus pyogenes serotype M4	2		2			
	1000791	Streptococcus pyogenes serotype M41	1		1			
	301452	Streptococcus pyogenes serotype M49	1		1			
	301449	Streptococcus pyogenes serotype M5	51	51	52	51	1	
	1000792	Streptococcus pyogenes serotype M52	1		1			
	1000793	Streptococcus pyogenes serotype M54	1		1			
	1000794	Streptococcus pyogenes serotype M55	1		1			
	1000795	Streptococcus pyogenes serotype M57	1		1			
	301450	Streptococcus pyogenes serotype M6	5	5	8	5	3	
	1000824	Streptococcus pyogenes serotype M6 strain D471	4		4			
	1000796	Streptococcus pyogenes serotype M60	1		1			
	1000797	Streptococcus pyogenes serotype M75	1		1			
	1000798	Streptococcus pyogenes serotype M8	1		1			
	410069	Streptococcus pyogenes serotype M80	1		1			
	160491	Streptococcus pyogenes str. Manfredo	3	17	3	17		
	246202	Streptococcus sobrinus 6715	4	4	4	4		
	36470	Streptococcus sp. 'group A'	13		16		3	
X	1307	Streptococcus suis			1		1	
X	1349	Streptococcus uberis			5		5	
	128949	Sudan ebolavirus - Maleo (1979)		1		1		
	10345	Suid herpesvirus 1	2	2	2	2		
	10349	Suid herpesvirus 1 (strain NIA-3)	4		4			
	33703	Suid herpesvirus 1 strain Kaplan	3		3			
	9823	Sus scrofa	4		4			
X	12076	Swine vesicular disease virus (STRAIN H/3 '76)			5		5	
X	10001002	Swine vesicular disease virus SPA/1/93			16		16	
	32630	synthetic construct		3		3		
	11631	Tacaribe virus		1		1		
	6202	Taenia		1		1		
X	6207	Taenia crassiceps			4		4	
X	1000802	Taenia crassiceps Strain ORF			3	3	3	3
X	6206	Taenia saginata			5		5	
X	6204	Taenia solium			9	3	9	3
X	5874	Theileria annulata			1		1	
X	5875	Theileria parva			28		28	
X	333668	Theileria parva strain Muguga				15		15
X	1000848	Theileria sergenti Type B1				1		1
X	1000849	Theileria sergenti Type B2				2		2
X	1000850	Theileria sergenti Type C				5		5
X	1000851	Theileria sergenti Type I				1		1
	12124	Theiler's encephalomyelitis virus		8		13		5
X	12125	Theiler's encephalomyelitis virus (STRAIN BEAN 8386)			16	23	16	23
X	12126	Theiler's encephalomyelitis virus (STRAIN			3	2	3	2

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
		DA)						
X	10000855	Theiler's murine encephalomyelitis virus (strain BeAn 8386) (variant M2)				1		1
X	204711	Theilovirus				1		1
X	10479	Thermoproteus tenax virus 1			1		1	
	271	Thermus aquaticus	1		1			
	11084	Tick-borne encephalitis virus	14	1	14	1		
	11087	Tick-borne encephalitis virus (STRAIN SOFJIN)	6		6			
	10000449	Tick-borne encephalitis virus (WESTERN SUBTYPE) - Neudoerfl	1		1			
X	6887	Tityus serrulatus			85		85	
X	12242	Tobacco mosaic virus			8		8	
X	12246	Tobacco mosaic virus (strain Dahlemense)			2		2	
	83192	Topografov virus	1		1			
	7787	Torpedo californica	4		8		4	
	7788	Torpedo marmorata		3		3		
	5811	Toxoplasma gondii	9	13	12	18	3	5
	10000353	Toxoplasma gondii 76K	5	5	5	5		
	10000354	Toxoplasma gondii BK	1	1	1	1		
	383379	Toxoplasma gondii RH	5	5	5	5		
	11149	Transmissible gastroenteritis virus	1		6		5	
	160	Treponema pallidum	4		5		1	
X	10001021	Treponema pallidum subsp. pallidum (strain Chicago)			18		18	
X	243276	Treponema pallidum subsp. pallidum str. Nichols			204	9	204	9
X	6334	Trichinella spiralis				1		1
X	5722	Trichomonas vaginalis			2		2	
X	5551	Trichophyton rubrum			2	27	2	27
X	3677	Trichosanthes kirilowii			1		1	
X	88087	Trimeresurus flavoviridis			3		3	
	4565	Triticum aestivum	21	142	134	183	113	41
	279889	Triticum aestivum var. arduini		4		4		
X	4567	Triticum turgidum subsp. durum				1		1
	5691	Trypanosoma brucei	4		4			
	5693	Trypanosoma cruzi	108	293	108	293		
	10000347	Trypanosoma cruzi Dm28c	1		1			
	353153	Trypanosoma cruzi strain CL Brener	2		2			
	37133	Tula virus	1		1			
	11309	unidentified influenza virus		10		10		
	38018	unidentified phage		1		1		
	10245	Vaccinia virus		124		132		8
	332193	Vaccinia Virus (strain Acambis 3000 MVA)		8		11		3
	10251	Vaccinia virus (strain IHD-J)	1		1			
	10248	Vaccinia virus (strain LC16M8)		4		4		
	126794	Vaccinia virus Ankara		10		11		1

NEW 2008	ORGAN-ISM ID	SPECIES STRAIN	B-07	T-07	B-08	T-08	Δ B	Δ T
X	10001027	Vaccinia virus Connaught			1		1	
	10249	Vaccinia virus Copenhagen		100		156		56
X	10001084	Vaccinia virus Modified Vaccinia Ankara virus				35		35
	10000388	Vaccinia virus NYCBH - Dryvax		16		29		13
	10253	Vaccinia virus Tian Tan		1		1		
	10254	Vaccinia virus WR	1	2998	6	3160	5	162
	12870	Variola major virus		2		11		9
	10000390	Variola major virus India-1967		1		1		
	10255	Variola virus		4		4		
	11037	Venezuelan equine encephalitis virus (strain TC-83)	21		21			
	11038	Venezuelan equine encephalitis virus (strain Trinidad donkey)	14		14			
	7742	Vertebrata	13	1	13	1		
	11277	Vesicular stomatitis Indiana virus		1		1		
	11276	Vesicular stomatitis virus		3		5		2
	11278	Vesicular stomatitis virus (serotype Indiana / strain Glasgow)		1		1		
	11285	Vesicular stomatitis virus (strain San Juan)		1		1		
X	7444	Vespa basalis			1		1	
	7454	Vespula vulgaris		36		36		
	666	Vibrio cholerae	30	34	31	34	1	
	44104	Vibrio cholerae 569B	30		30			
	127906	Vibrio cholerae O1	8		10		2	
	686	Vibrio cholerae O1 biovar eltor	3		3			
	10000567	Vibrio cholerae O1 serotype Inaba	4		4			
	10000568	Vibrio cholerae O1 serotype Ogawa	4		4			
	670	Vibrio parahaemolyticus		17		17		
	223926	Vibrio parahaemolyticus RIMD 2210633	2		2			
	672	Vibrio vulnificus		26		26		
	11288	Viral hemorrhagic septicemia virus (STRAIN 07-71)	1		1			
	3972	Viscum album	17		17			
X	11742	Visna lentivirus (strain 1514)			1		1	
X	11741	Visna/Maedi virus			5		5	
	74537	Vladivostok virus	1		1			
X	43141	Watermelon silver mottle virus			3		3	
	11082	West Nile virus	12	47	15	148	3	101
	10000447	West Nile virus 3000.0259	2		2			
X	10000971	West Nile virus NY-99			3	6	3	6
X	10001047	West Nile virus strain 2741			31		31	
	307044	West Nile virus strain 385-99	4	12	8	12	4	
	46919	Whitewater Arroyo virus		2		2		
X	4963	Williopsis saturnus var. mrakii			1		1	
	66077	Wolbachia sp. wMel		1		1		
	35269	Woodchuck hepatitis virus	5	2	5	2		
	10430	Woodchuck hepatitis virus 1	3		3			

NEW 2008	ORGAN- ISM ID	SPECIES STRAIN	B- 07	T-07	B- 08	T-08	Δ B	Δ T
	341946	Woodchuck hepatitis virus 2	4		4			
	10433	Woodchuck hepatitis virus 8		24		24		
	8355	Xenopus laevis		2		2		
	8364	Xenopus tropicalis		1		1		
	11090	Yellow fever virus 17D	1	9	1	86		77
	11091	Yellow fever virus Pasteur 17D-204	3		3			
	630	Yersinia enterocolitica	3	9	3	12		3
	632	Yersinia pestis	5	78	14	87	9	9
	10000757	Yersinia pestis 195/P	5		5			
	214092	Yersinia pestis CO92		4		4		
	10000756	Yersinia pestis KIM 5	21		21			
	186538	Zaire ebolavirus		21		21		
	128952	Zaire ebolavirus - Mayinga (Zaire, 1976)	11	7	13	7	2	
	34245	Zinnia elegans		1		1		
X	157914	Ziziphus mauritiana			4		4	

2 What's New in IEDB 2.0?

This section gives an overview of the extensive changes made to the IEDB in developing the latest version (2.0). In contrast to previous updates that introduced incremental changes, we have reviewed the entire set of IEDB functionality, and re-implemented most of it to incorporate major improvements requested by IEDB users. This includes a complete revision of the database schema and the query and reporting functionality.

2.1 Browsing, querying, reporting, and tools

Major changes have been made to the home page, browse and query functionality, query reporting features, accessing tools, and submitting data ,as outlined below.

Improved home page layout and functionality

- Most commonly used search options are directly available on the home page.
- Help, support, forums, and feedback are centralized.
- Multiple summary metrics on the available data are provided and link directly to corresponding reports.
- Menu items and links on the homepage are grouped into logical categories.

Browse and query functionality

- Browsing by MHC Allele now groups alleles by source organism, MHC class, and locus.
- Browsing by epitope source organism now aggregates data at higher taxonomic levels (e.g. all epitopes from bacteria).
- Detailed specialized queries are available, making all fields in the database searchable on a single page. Less commonly used fields are initially collapsed into logical subcategories, as shown below.

The screenshot displays the 'T Cell Search' interface with a navigation bar at the top containing 'home', 'browse', 'search', 'tools', 'support', and 'more iedb'. The main content is organized into several expandable sections:

- Reference**
 - Epitope**
 - Type: [dropdown]
 - Source Molecule: [input] **Molecule Finder**
 - Source Organism: [input] **Organism Finder**
 - Epitope Reference Details
 - Epitope Related Object
- Immunization**
 - Host Organism: [input] **Organism Finder**
 - Host Details
 - 1st In Vivo Process: may or may not MUST MUST NOT be present in search results.
 - 1st Immunogen: may or may not MUST MUST NOT be present in search results.
 - 2nd In Vivo Process: may or may not MUST MUST NOT be present in search results.
 - 2nd Immunogen: may or may not MUST MUST NOT be present in search results.
 - In Vitro Administration: may or may not MUST MUST NOT be present in search results.
 - In Vitro Immunogen: may or may not MUST MUST NOT be present in search results.
 - Immunization Comments
 - Adoptive Transfer: may or may not MUST MUST NOT be present in search results.
- T Cell Assay**
 - Qualitative Measurement: [dropdown with 'Positive', 'Positive-Low']
 - Assay Type: [input] **Assay Finder**
 - Measurement Details
 - Effector Cells
 - Assayed TCR Molecule
 - Antigen Presenting Cells
 - MHC Allele**
 - MHC Allele Name: [input] **Allele Finder**
 - MHC Evidence Code: [dropdown with 'Cited reference', 'MHC binding assay', 'T cell assay -Single MHC type present', 'T cell assay -MHC subset identification']
 - Antigen
 - 3D Structure of Complex
 - Assay Reference Details

Figure 2.1 The advanced query of Version 1.0 has been replaced by specialized queries, such as this T Cell Search interface

Reporting functionality

- Assays relating to the same epitope structure that are reported in different references are grouped together into a summary view of the epitope, as shown below. Similar summary views of all assays and epitopes relating to a given source organism or MHC allele are also available.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Home | Browse | Query | Tools | Support

Epitope Information

Distinct Epitope

Epitope ID:	19861
Linear Sequence:	GILGFVFTL
Source Antigen:	Matrix protein 1 (7 more)
Source Organism:	Influenza A virus (6 more)

Source (12) | Reference (72) | MHC Binding (31) | T Cell Assay (113) | MHC Ligand Elution (1) | Links (3)

12 items found, displaying 1 to 12 (Click the column headers to adjust the sorting)

Source Accession ↑	Source Antigen	Source Organism	Links
138817	Matrix protein 1	Influenza A virus	Homology Mapping
138817	Matrix protein 1	Influenza A virus (A/Puerto Rico/8/34(H1N1))	Homology Mapping
138817	Matrix protein 1	Influenza A virus H3N2 (A/Resvir-9 (H3N2))	Homology Mapping
145112687	matrix protein 1	Influenza A virus	Homology Mapping
145112687	matrix protein 1	H5N1 subtype	Homology Mapping
27596998	matrix protein M1	Influenza A virus	Homology Mapping
27596998	matrix protein M1	Influenza A virus (A/Puerto Rico/8/34(H1N1))	Homology Mapping
50234640	matrix protein 1	Influenza A virus (A/Viet Nam/1194/2004(H5N1))	Homology Mapping
549378	Matrix protein 1	Influenza A virus	Homology Mapping
60458	M1 protein	Influenza A virus (A/WSN/1933(H1N1))	Homology Mapping
81972310	M1	Influenza A virus (A/X-31(H3N2))	Homology Mapping
P36347	Matrix protein 1	Influenza A virus	Homology Mapping

12 items found, displaying 1 to 12

Figure 2.2 The new epitope summary page lets users access source, reference, and assay information on tabs

- In table views of the data, which list multiple assays side by side, the information from groups of database fields is collapsed into a narrative that is easier to view compared to a sparsely populated table with many columns. This was implemented for the immunization narrative and the object descriptions.
- Naming conventions have been updated throughout the site for increased consistency and to improve the data representation.

Tool enhancements

- Separate tabs give direct access to tools.
- External tool providers can plug in to the tool/database connection directly, similar to the links provided on PubMed sites.

Data submission tool

We provide an additional avenue for direct submission of data from external users in a spreadsheet format (<http://submission.iedb.org>). Previously data submission was only possible in an XML format. While that option is still available, we found that it imposes difficulties on the average immunologist. Contact submission-support@iedb.org to register for access to the IEDB submission tool.

2.2 Ontology and data structure revisions

The IEDB's ontology, the Ontology of Immune Epitopes (ONTIE), has been completely revised and is now built upon the Ontology of Biomedical Investigations (OBI, <http://obi-ontology.org>). This integration into a larger ontology effort promises enhanced ability to connect data from the IEDB with other resources storing experimental information. All data captured by the IEDB were evaluated to determine how they should be represented in ontological terms. The figure below gives a high level overview of the ontology.

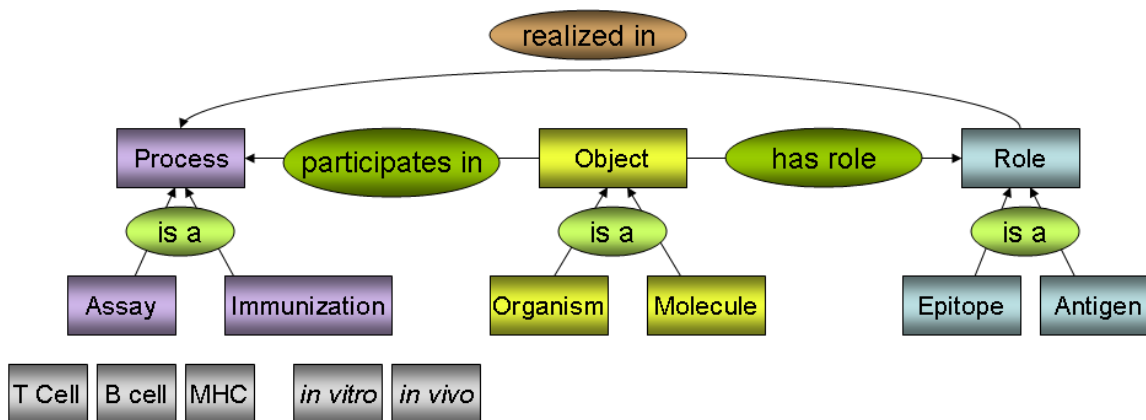


Figure 2.3 High-level overview of the new IEDB Ontology of Immune Epitopes (ONTIE)

As a result of this endeavor, the database has been restructured, and the resulting database structure is easier to update and maintain over time. Specifically, instead of having individual database tables for epitopes, antigens, immunogens and so forth, a single table is utilized to capture all types of objects. These are referenced from the process table (one for each assay), and assigned a specific role in the assay, such as antigen or immunogen. All immunization procedures and assays now exist as distinct processes that occur either *in vivo* or *in vitro* and have defined participants playing defined roles.

2.3 Finder functions

The database incorporates finder applications to assist in searching for MHC Alleles and Organisms utilizing standard nomenclature. While intended to be helpful, the original IEDB finders were cumbersome in that the end user was required to precisely enter the term of interest. In order to expand the search capabilities and to be more user friendly, the finders were enhanced as follows:

MHC Allele Finder

- Updated nomenclature
- Redundant entries removed
- Molecule sequences added when available
- New searchable fields added: synonym and organism
- New data provided: restriction level, haplotype, locus, and serotype

Organism Finder

- All curated organism data is mapped to the NCBI taxonomy whenever possible
- The NCBI tree was supplemented with IEDB organisms such as laboratory strains of mice and viral isolates
- Synonyms added to aid in search
- Common selections updated to be more relevant and extensive

2.4 Field changes relating to the epitope, immunization procedures and adoptive transfer

Many sections and field titles of the database have been restructured and renamed. Additionally, new fields have been added to allow the IEDB to capture additional information:

2.4.1 Epitope

The table below lists the enhancements that have been made to the fields describing the epitope structure. Note that the epitope is now presented as an object and new fields have been added to describe a second object to which the epitope is an analog or mimic, when applicable.

Table 2.1 Enhancements made in IEDB 2.0 to the fields describing epitope structure

1.0 Field Name	Change	2.0 Field Name	Note
	New field	Epitope Location	Displays the figure, table or text where the epitope structure was defined in the curated manuscript
Epitope Source Starting Position	Renamed	Reference Starting Position	Refers to the positions as listed in the reference
Epitope Source Ending Position	Renamed	Reference Ending Position	Refers to the positions as listed in the reference
Epitope Conformational Sequence	Renamed	Reference Region	Refers to the positions as listed in the reference
Epitope Source Antigen	Renamed	Epitope Source Molecule	
Epitope Author Identified Mimotopes (Yes/No flag)	Renamed	Epitope Related Object	New drop-down list with the following choices: "The epitope is an analog of" and "The epitope is a mimotope of"
Epitope Chemical Type	Renamed	Object Subtype	of the epitope object
Epitope Conformational Type	Renamed	Object Subtype	of the epitope object
Epitope Linear Sequence	Renamed	Epitope Description	of the epitope object
Epitope Modifications	Enhanced	Epitope Description	Abbreviations now provided
Epitope Source Epitope Swiss-Prot Positions	Renamed	Epitope Source Molecule	The positions are concatenated with the source molecule name
	New field	Epitope Discontinuous Residues	Discontinuous residues found in the protein source of the epitope may differ from reference cited positions and were not previously captured
Source Species	Renamed	Epitope Organism Name	of the epitope object
Species Strain	Renamed	Epitope Organism Name	of the epitope object
	New field	Epitope Evidence Code	Field displays how certain the curator was of the source of the epitope structure. Field choices include: Representative Selection, Author Provided Identifier, Exact Match to Reference Information, and Internal Identifier-No External Match Available.
	New field	Epitope Related Object Sub-Type	Allows for description of the object to which the epitope is an analog or mimic
	New field	Epitope Related Object Description	Allows for description of the object to which the epitope is an analog or mimic
	New field	Epitope Related Object Source Molecule	Allows for description of the object to which the epitope is an analog or mimic
	New field	Epitope Related Object Organism Name	Allows for description of the object to which the epitope is an analog or mimic

2.4.2 Immunization procedures

The IEDB describes T cell and B cell assays beginning with the initial exposures of the host (or host effectors) to an immunogen that ultimately results in recognition of the assay antigen. The host, the immunogen, and the circumstances regarding how the host came to be exposed to the immunogen are captured. Enhanced detail and further clarification regarding the immunization procedure has been added. Most importantly, the IEDB is able to capture up to two *in vivo* processes. This is relevant in cases where, for example, a prime boost vaccination with two different immunogens is performed. Below are the enhancements to the *in vivo* immunization fields.

Table 2.2 IEDB 2.0 enhancements to the *in vivo* immunization fields

1.0 Field Name	Change	2.0 Field Name	Note
Immunized Species	Renamed	Organism Name	These two fields are now captured in one field
Immunized Species Strain/Ethnicity	Renamed	Organism Name	These two fields are now captured in one field
Immunization Category	Renamed	In Vivo Process Type	Describes the process (if any) that occurred in vivo
Immunogen Name	Renamed	Immunogen Reference Name	Clarifies that the name is the one used by the authors
Immunogen Type	Renamed	Immunogen Epitope Relation	Clarifies that the field describes how the immunogen relates to the epitope
Number of Immunizations	Renamed	Dose Schedule	
Immunogen Source Name	Renamed	Immunogen Source Molecule	
Immunogen Source Species	Renamed	Immunogen Organism Name	These two fields are now captured in one field
Immunogen Source Species Strain	Renamed	Immunogen Organism Name	These two fields are now captured in one field
Immunogen Chemical Type	Renamed	Immunogen subtype	
Immunogen Sequence	Renamed	Description (where applicable)	The description field displays a different set of data depending on what the object type of the immunogen is.
Immunogen Derivative Type	Renamed	Description (where applicable)	
Immunogen SMILES Structure	Renamed	Captured as part of the object fields.	
	New field	Immunogen Evidence Code	Describes how certain the object being utilized in the assay as immunogen is known
	New field	Immunogen Modifications	Can now describe any modifications made to a peptide or protein immunogen
	New field	Immunogen Modified Residues	Can now describe any modifications made to a peptide or protein immunogen
Carrier Chemical Type	Renamed	Immunogen Containing Object Subtype	
Immunogen Carrier Sequence	Renamed	Immunogen Containing Object Description (where applicable)	Description field displays a different formula depending on the object type. Field is devised to concatenate and show what the object is, encodes, expresses, or is composed of.
Immunogen Carrier Source Species	Renamed	Immunogen Containing Object Description (where applicable)	
Immunogen Carrier Species Strain	Renamed	Immunogen Containing Object Description (where applicable)	
Immunogen Carrier GenBank ID	Renamed	Immunogen Containing Object Description (where applicable)	
Immunogen Swiss-Prot ID	Renamed	Immunogen Containing Object Description (where applicable)	
Immunogen Carrier SMILES Structure	Renamed	Immunogen Containing Object Description (where applicable)	

In addition to changes to the immunization related field names, new terms were created to describe the processes by which the host came to be exposed to the immunogen. All previously curated IEDB 1.0 immunization categories were mapped to the new *in vivo* process types as shown below.

Table 2.3 Mappings from IEDB 1.0 data fields to IEDB 2.0 data fields for *in vivo* process types

1.0 Immunization Category	Change	2.0 Process Type	Note
Administration	Mapped as applicable	Administration in vivo	
		Administration in vitro	
Administration in vivo	Mapped as applicable	Administration in vivo to cause disease	
		Administration in vivo to prevent or reduce disease	
		Administration in vivo	
Administration in vivo plus restimulation in vitro	Mapped into two separate procedures	Administration in vivo	
		Administration in vitro	
Administration in vivo plus treatment in vivo	Mapped into two separate procedures	Administration in vivo	
		Administration in vivo to prevent or reduce disease	
Natural Exposure/Occurrence	Mapped into those with disease	Occurrence of infectious disease	Curation of both disease state and stage were verified.
		Occurrence of allergy	
		Occurrence of disease	
	Or mapped into those without disease	Exposure with existing immune reactivity without evidence for disease	Exposures are hierarchical
		Documented exposure without evidence for disease	
		Environmental exposure to endemic/ubiquitous agent without evidence for disease	
	Exposure without evidence for disease		
Autoimmune (No Administered Immunization)	Renamed	Occurrence of autoimmune disease	
Cancer (No Administered Immunization)	Renamed	Occurrence of cancer	
Phage Display (No Immunization)	Mapped to valid selection		
No immunization	Retained	No immunization	
Unknown	Retained	Unknown	

Additionally, the field immunogen type was reevaluated in order to better describe the relationship of the object playing the role of immunogen in each assay to the epitope structure the assay is describing. The new field of immunogen epitope relation provides a more thorough description of this relationship, enabling more insight into cross-reactivity and homologous structures. All previously curated data was mapped into these new field options as applicable.

Table 2.4 Mappings from IEDB 1.0 data fields to IEDB 2.0 data fields for immunogen type

1.0 Immunogen Type	Change	2.0 Immunogen Epitope Relation	Note
Epitope	Retained	Epitope	
Source Antigen	Renamed	Source Molecule	
Source Species	Renamed	Source Organism	Clarified to include exactly the same species and strain as the epitope source
Other	Mapped appropriately	Taxonomic Parent	
		Taxonomic Sibling	
		Taxonomic Child	
		Structurally Related	
		Other	

T cell assays may also involve an immunization step performed *in vitro*. In order to better describe this process, new fields were added to the database.

Table 2.5 New and renamed fields describing immunization in IEDB 2.0

1.0 Field Name	Change	2.0 Field Name	Note
Immunization Category	Renamed	In Vitro Process Type	Describes the process (if any) that occurred in vitro
	New field	Immunogen Reference Name	Clarifies that the name is the one used by the authors
	New field	Immunogen Epitope Relation	Clarifies that the field describes how the immunogen relates to the epitope
	New field	Immunogen Source Molecule	
	New field	Immunogen Organism Name	
	New field	Immunogen subtype	
	New field	Immunogen Description	The description field displays a different set of data depending on what the object type of the immunogen is.
	New field	Immunogen Modifications	Can now describe any modifications made to a peptide or protein immunogen
	New field	Immunogen Modified Residues	Can now describe any modifications made to a peptide or protein immunogen
	New field	Immunogen Containing Object Subtype	
	New field	Immunogen Containing Object Description	Description field displays a different formula depending on the object type. Field is devised to concatenate and show what the object is, encodes, expresses, or is composed of.
	New field	Immunogen Evidence Code	Describes how certain the object being utilized in the assay as immunogen is known

2.4.3 Adoptive transfer

In order to facilitate curation of experiments utilizing adoptive transfer of immune function, an entirely new section was added to the database. These additional fields allow for description of the recipient organism, the immune material being transferred, *in vivo* procedures in the recipient (such as a subsequent infection), and comments to further clarify the transfer. These fields include a duplication of the above immunization fields with additional fields specific to either the transfer of B cell recognition (antibodies) or T cell recognition (effector cells).

Table 2.6 New data fields added in IEDB 2.0 to describe adoptive transfer

Assay Type	2.0 Field Name
T Cell	Transferred Effector Cell Tissue Type
T Cell	Transferred Effector Cell Type
T Cell	Transferred Effector Cell Culture Conditions
T Cell	Transferred TCR Molecule Name
T Cell	Transferred TCR Molecule Chain 1 Type
T Cell	Transferred TCR Molecule Chain 2 Type
T Cell	Transferred TCR Molecule
B Cell	Transferred Antibody Molecule Source Material
B Cell	Transferred Antibody Molecule Immunoglobulin Domain
B Cell	Transferred Antibody Molecule Purification Status
B Cell	Transferred Antibody Molecule Name
B Cell	Transferred Antibody Heavy Chain Type
B Cell	Transferred Antibody Light Chain Type
B Cell	Transferred Antibody Molecule

2.4.4 Changes relating to the fields describing the various types of assays used to characterize epitopes

All assay types share a set of fields used to describe the type of experiment that was performed, the antigen tested, and the outcome. The fields used to describe the assay antigen were enhanced in the same manner as the immunogen fields. Additionally, new fields were added to better describe the level of the response being captured through a calculated response frequency field and new qualitative value selections.

Table 2.7 Additions and changes made in IEDB 2.0 data fields related to assays

1.0 Field Name	Change	2.0 Field Name	Note
	New field	Location of Data	Displays the figure, table or text where the assay information was described in the curated manuscript
Qualitative Measurement	Enhanced	Qualitative Measurement	Now includes Positive, Positive-High, Positive-Intermediate, Positive-Low, Negative
	New field	Response Frequency (%)	Displays the percentage of subjects tested that responded in the assay
Antigen Name	Renamed	Antigen Reference Name	Clarifies that the name is the one used by the authors
Antigen Type	Renamed	Antigen Epitope Relation	Clarifies that the field describes how the antigen relates to the epitope
Antigen Source Name	Renamed	Antigen Source Molecule	
Antigen Source Species	Renamed	Antigen Organism Name	These two fields are now captured in one field
Antigen Source Species Strain	Renamed	Antigen Organism Name	These two fields are now captured in one field
Antigen Chemical Type	Renamed	Antigen subtype	
Antigen Sequence	Renamed	Description (where applicable)	The description field displays a different set of data depending on what the object type of the antigen is
Antigen Derivative Type	Renamed	Description (where applicable)	
Antigen SMILES Structure	Renamed	Captured as part of the object fields.	
	New field	Antigen Evidence Code	Describes how certain the object being utilized in the assay as antigen is known
	New field	Antigen Modifications	Can now describe any modifications made to a peptide or protein antigen
	New field	Antigen Modified Residues	Can now describe any modifications made to a peptide or protein antigen
Carrier Chemical Type	Renamed	Antigen Containing Object Subtype	
Antigen Carrier Sequence	Renamed	Antigen Containing Object Description (where applicable)	Description field displays a different formula depending on the object type. Field is devised to concatenate and show what the object is, encodes, expresses, or is composed of.
Antigen Carrier Source Species	Renamed	Antigen Containing Object Description (where applicable)	
Antigen Carrier Species Strain	Renamed	Antigen Containing Object Description (where applicable)	
Antigen Carrier GenBank ID	Renamed	Antigen Containing Object Description (where applicable)	
Antigen Swiss-Prot ID	Renamed	Antigen Containing Object Description (where applicable)	
Antigen Carrier SMILES Structure	Renamed	Antigen Containing Object Description (where applicable)	

2.4.5 T cell

Further changes were made specific to individual assay types. The fields of both B cell assays and T cell assays were reevaluated, resulting in the renaming and revision of several fields. MHC Elution assays underwent the greatest changes with many new fields added and almost all field names edited to make more immunological sense.

T cell fields capturing the T cell receptor (TCR) were mapped into a multi-chain TCR object. This allows for the exact description of each chain, when provided. Additionally, the fields utilized for the effector material were clarified and the nomenclature used for cell types was revised to include all of the most commonly used cell lines.

Table 2.8 Changes made in IEDB 2.0 to data fields describing T cell assays

1.0 Field Name	Change	2.0 Field Name	Note
Effector Cell Tissue Type	Enhanced	Effector Cell Tissue Type	List of tissues was improved to include relevant sources and alphabetized
Effector Cell Type	Enhanced	Effector Cell Type	List of tissues was improved to include common cell lines/clones and was alphabetized
Origin	Renamed and revised	Effector Cell Culture Conditions	Now includes more specific cell conditions commonly used in the laboratory
TCR Source Species	Renamed	Assayed TCR Molecule Organism	Captured as part of the TCR object
Species Strain/Ethnicity	Renamed	Assayed TCR Molecule Organism	Captured as part of the TCR object
TCR Chain #1 Type:	Renamed	Assayed TCR Molecule Chain 1 Type	
TCR Chain #1 GenBank ID:	Renamed	Assayed TCR Source Molecule	Captured as part of the TCR object
TCR Chain #1 Swiss-Prot ID:	Renamed	Assayed TCR Source Molecule	Captured as part of the TCR object
TCR Chain #2 Type:	Renamed	Assayed TCR Molecule Chain 2 Type	
TCR Chain #2 GenBank ID:	Renamed	Assayed TCR Source Molecule	Captured as part of the TCR object
TCR Chain #2 Swiss-Prot ID:	Renamed	Assayed TCR Source Molecule	Captured as part of the TCR object

2.4.6 B cell

The fields used to describe the assayed antibody were also revised. As with the TCR, the antibody itself was mapped into an antibody object, also a multi-chain molecule.

Table 2.9 Changes made in IEDB 2.0 to data fields describing antibody assays

1.0 Field Name	Change	2.0 Field Name	Note
Antibody Type	Renamed and revised	Assayed Antibody Purification Status	The list now includes monoclonal, polyclonal, and polyclonal-mono-specific
Materials Assayed	Renamed and revised	Assayed Antibody Source Material	The list of materials was revised to include the most commonly encountered sources and was alphabetized
Source Species:	Renamed	Assayed Antibody Organism	Captured as part of the assayed antibody object
Species Strain/Ethnicity:	Renamed	Assayed Antibody Organism	Captured as part of the assayed antibody object
Heavy Chain Class	Renamed	Assayed Antibody Heavy Chain Type	Two fields were combined into one
Heavy Chain Class/Subclass	Renamed	Assayed Antibody Heavy Chain Type	Two fields were combined into one
Light Chain Type	Renamed	Assayed Antibody Light Chain Type	Two fields were combined into one
Light Chain Type/Subtype	Renamed	Assayed Antibody Light Chain Type	Two fields were combined into one
Heavy Chain GenBank ID:	Renamed	Assayed Antibody Molecule	Captured as part of the assayed antibody object
Heavy Chain Swiss-Prot ID:	Renamed	Assayed Antibody Molecule	Captured as part of the assayed antibody object
Heavy Chain PDB Chain:	Renamed	Assayed Antibody Molecule	Captured as part of the assayed antibody object
Light Chain GenBank ID:	Renamed	Assayed Antibody Molecule	Captured as part of the assayed antibody object
Light Chain Swiss-Prot ID:	Renamed	Assayed Antibody Molecule	Captured as part of the assayed antibody object

2.4.7 MHC ligand elution

The fields of MHC ligand elution assays were extensively expanded. Before IEDB 2.0, only the molecule or organism that was processed, the MHC allele involved, and the antigen processing cells were captured. As the procedures involved in these assays were depicted by the ontology, it was made clear that both *in vivo* and *in vitro* processes could be involved in how the entity that was processed came to be exposed to the processing cells. Therefore, fields to capture a host organism, the disease state of this organism, and *in vivo* and *in vitro* processes were added. The field names in elution assays vary from those of T cell or B cell assays because antigen processing and elution do not involve an effector response, as in the case of T cell or antibody recognition.

Table 2.10 Additions and changes made in IEDB 2.0 data fields describing MHC ligand elution assays

1.0 Field Name	Change	2.0 Field Name	Note
	New field	Location of Assay Data in Reference	Displays the figure, table or text where the assay information was described in the curated manuscript
	New field	In Vivo Process Type	
Antigen Presenting Cells Source Species	Renamed	Host Organism	
Antigen Presenting Cells Species Strain/Ethnicity	Renamed	Host Organism	
Antigen Presenting Cells Sex	Renamed	Host Sex	
Antigen Presenting Cells Age	Renamed	Host Age	
Antigen Presenting Cells MHC Types Present	Renamed	Host MHC Types Present	
Antigen Presenting Cells Disease State	Renamed	Disease State	
Antigen Presenting Cells Disease Stage	Renamed	Disease Stage	
	New field	Adjuvants	
	New field	Route	
	New field	Dose Schedule	
Antigen Name	Renamed	In Vivo Processed Antigen Reference Name	Clarifies that the name is the one used by the authors
Antigen Type	Renamed and	In Vivo Processed Antigen Epitope Relation	Clarifies that the field describes how the antigen relates to the epitope
Antigen Source Name	Renamed	In Vivo Processed Antigen Source Molecule	
Antigen Source Species	Renamed	In Vivo Processed Antigen Organism Name	These two fields are now captured in one field
Antigen Source Species Strain	Renamed	In Vivo Processed Antigen Organism Name	These two fields are now captured in one field
Antigen Chemical Type	Renamed	In Vivo Processed Antigen subtype	
Antigen Sequence	Renamed	Description (where applicable)	The description field displays a different set of data depending on what the object type of the processed antigen is
Antigen Derivative Type	Renamed	Description (where applicable)	
	New field	In Vivo Processed Antigen Evidence Code	Describes how certain the object being processed in the assay is known
	New field	In Vivo Processed Antigen Modifications	Can now describe any modifications made to a peptide or protein antigen
	New field	In Vivo Processed Antigen Modified Residues	Can now describe any modifications made to a peptide or protein antigen
Carrier Chemical Type	Renamed	In Vivo Processed Antigen Containing Object Subtype	
Antigen Carrier Sequence	Renamed	In Vivo Processed Antigen Containing Object Description (where applicable)	Description field displays a different formula depending on the object type. Field is devised to concatenate and show what the object is, encodes, expresses, or is composed of.
Antigen Carrier Source Species	Renamed	In Vivo Processed Antigen Containing Object Description (where applicable)	
Antigen Carrier Species Strain	Renamed	In Vivo Processed Antigen Containing Object Description (where applicable)	
Antigen Carrier GenBank ID	Renamed	In Vivo Processed Antigen Containing Object Description (where applicable)	
Antigen Swiss-Prot ID	Renamed	In Vivo Processed Antigen Containing Object Description (where applicable)	
	New field	In Vitro Administration Type	
	New field	In Vitro Processed Antigen Reference Name	Clarifies that the name is the one used by the authors
	New field	In Vitro Processed Antigen Epitope Relation	Clarifies that the field describes how the antigen relates to the epitope
	New field	In Vitro Processed Antigen Source Molecule	
	New field	In Vitro Processed Antigen Organism Name	
	New field	In Vitro Processed Antigen subtype	
	New field	Description (where applicable)	The description field displays a different set of data depending on what the object type of the processed antigen is
	New field	In Vivo Processed Antigen Evidence Code	Describes how certain the object being processed in the assay is known
	New field	In Vivo Processed Antigen Modifications	
	New field	In Vivo Processed Antigen Modified Residues	
	New field	In Vivo Processed Antigen Containing Object Description (where applicable)	Description field displays a different formula depending on the object type. Field is devised to concatenate and show what the object is, encodes, expresses, or is composed of.
	New field	MHC Ligand Reference Name	Describes what was eluted; the epitope
	New field	MHC Ligand Subtype	Describes what was eluted; the epitope
	New field	MHC Ligand Source Molecule	Describes what was eluted; the epitope
	New field	MHC Ligand Organism	Describes what was eluted; the epitope

3 Website Features

The IEDB 2.0 website functionality can be divided into five categories– Browse, Query, Tools, Support, and More IEDB, which largely correspond to the pull-down menus at the top of the home page. The subsections that follow describe the website features within these categories.

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

3.1 Home Page

The IEDB Home Page 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 3.1, the page is divided into three columns that contain a basic search capability, introductory information, Summary Metrics of the data, available Resources, user Support, and project-related News. As users browse the IEDB system, they can return to the home page anytime by clicking *Home* on the far left of the main menu bar.

Summary Metrics are displayed in the center column of the screen. These numbers are intended to be a gauge of the volume of data available in the system. The Summary Metrics provide the number of epitopes (peptidic and non-peptidic), assays (T cell, B cell, MHC ligand elution, and MHC binding), epitope source organisms, epitope source antigens, host organisms, restricting MHC alleles, and references.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Home | Browse | Search | Tools | Support | More IEDB

Search

Epitope Structure

Structure Type:


Linear Sequence:

Epitope Source

Source Organism:

Source Antigen:

Immune Recognition Context

B Cell Response 

T Cell Response

MHC Binding

MHC Ligand Elution

Host Organism:

MHC Restriction:

MHC Class:

Welcome!

This is a **beta version** of our new web site, we welcome your **feedback**. Data and functionality may not be consistent with the production quality IEDB website.

The IEDB contains data related to antibody and T cell epitopes for humans, non-human primates, rodents, and other animal species. Curation of data relating to NIAID Category A, B, and C priority pathogens, NIAID Emerging and Re-emerging infectious diseases, Malaria, Hepatitis B, Clostridium tetani, Leishmania, Candida albicans, and herpesviruses is current through June 2008.

Curation of epitopes related to allergies and other infectious diseases is in progress. Curation of autoimmune epitopes will start in 2009. [More ...](#)

Summary Metric	Count
Peptidic Epitopes	38883
Non-Peptidic Epitopes	282
T Cell Assays	88758
B Cell Assays	58046
MHC Ligand Elution Assays	744
MHC Binding Assays	83637
Epitope Source Organisms	1661
Restricting MHC Alleles	423
References	5800
See all Metrics	

Resources

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

- T Cell Epitope Prediction
- B Cell Epitope Prediction
- Epitope Analysis Tools
- Database Export

Support

Need Help? Use the following links to get support or find useful information:

- Solutions Center
- Provide Feedback
- Help Request
- Data Field Descriptions

News

- 10/02/2008 September 2008 Newsletter
- 04/16/2008 April 2008 Newsletter
- 01/15/2008 January 2008 Newsletter
- 01/01/2008 Annual IEDB Compendium
- 07/30/2007 2007 Annual Workshop Summary

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

Sponsored By:
National Institute of Allergy and Infectious Diseases (NIAID)
National Institutes of Health (NIH)
Department of Health and Human Services (HHS)

Site Last Updated: January 02, 2009

Figure 3.1 IEDB 2.0 Home Page

3.2 Browse

The IEDB allows users to browse for records in two different ways – by MHC allele and by source species. The previously available Browse by 3D Structure will be re-implemented later in 2009.

3.2.1 Browse Records by MHC Allele

All users can find records associated with a specific MHC allele by browsing records by allele. To browse records by allele, the user selects *Browse by MHC Allele* under the *Browse* heading on the main menu. The interface for the Browse by MHC Allele is a tree structure that makes it easy for users to find and investigate information on specific MHC alleles. As Figure 3.2 shows, the tree structure expands (and collapses) so users can drill down on species, MHC type, and allele to find the number of records in the IEDB for their MHC allele of interest. This number serves as a link that will display the records associated with the selected allele.

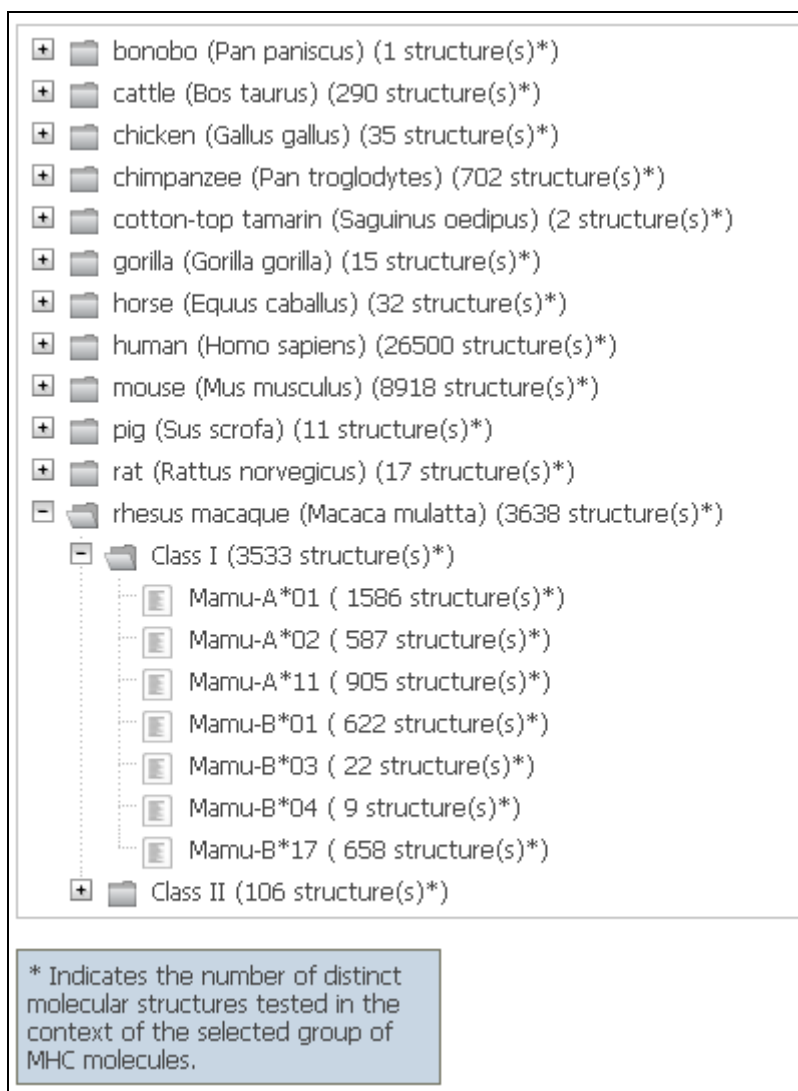


Figure 3.2 Browse by MHC allele interface

3.2.2 Browse Records by Source Organism

Users can find records associated with a specific epitope source species by browsing records by source organism. To do this, the user accesses the *Browse by Source Organism* page via the Browse pull-down menu. The interface for the Browse by Source Organism is a tree structure that expands (and collapses) so users can drill down on species as Figure 3.3 shows. Each entry in the tree indicates the number of distinct molecular structures tested from the selected group of source organisms. This number serves as a link that will display the records associated with the selected source organism. The user can also search for names. For example, a search for “human”, as shown in Figure 3.4, generates a table of responses for the term and corresponding synonyms. If the user clicks on [Details], Source Organism Information is displayed. The page for the first result, *Homo sapiens*, is displayed in Figure 3.5, and includes the NCBI taxonomy identifier numbers and information on relevant literature and submission references, epitope structure, source antigens, and assays. If the user clicks on [Highlight] the tree expands and highlights the location. In the case of “*Homo sapiens*”, the tree expands to over 20 levels.

Clicking on the number structures displays the same Source Organism Information as seen in Figure 3.5.

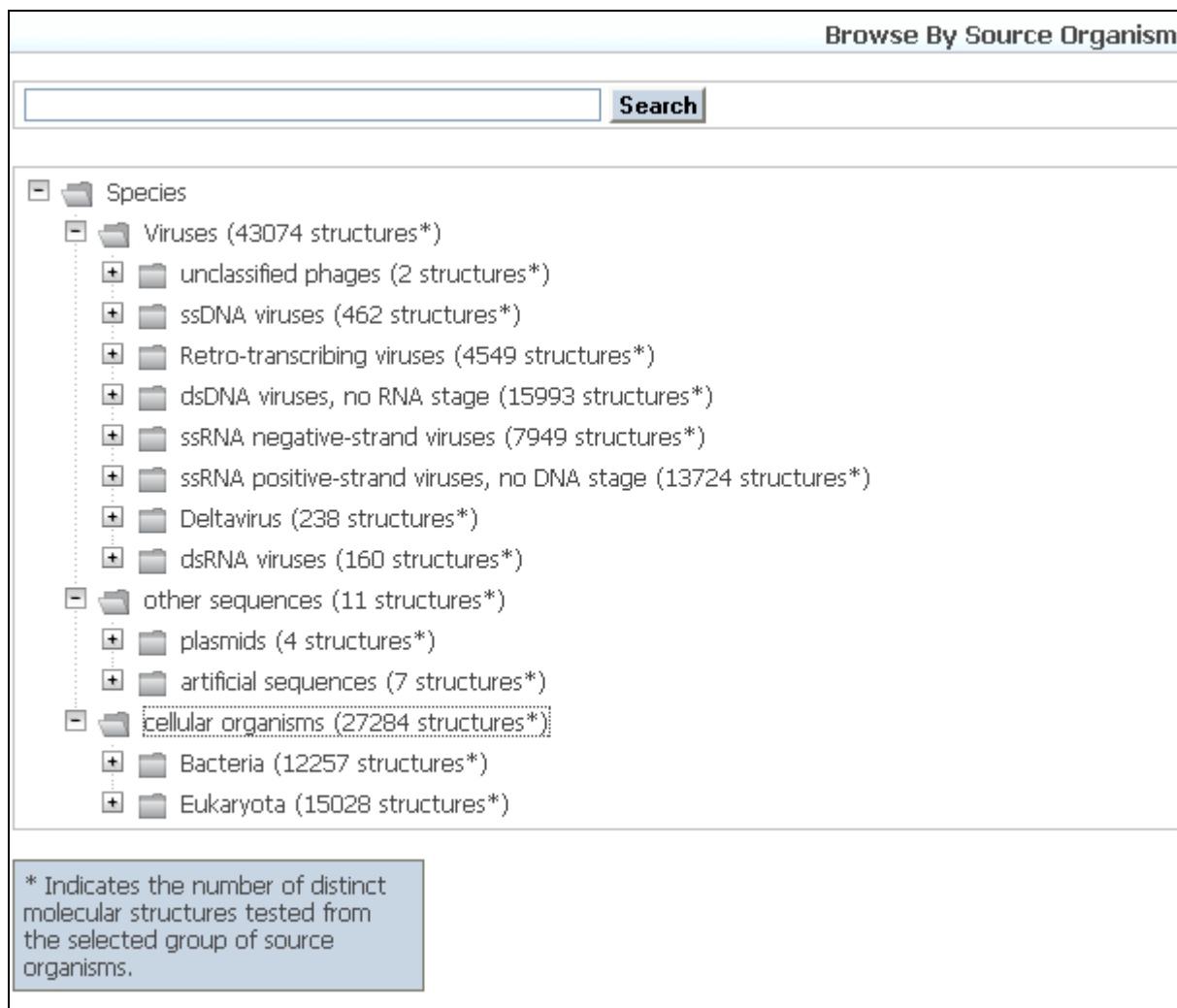


Figure 3.3 Browse by Source Organism interface

human

Search Results

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

<< previous **1** 2 3 4 5 6 7 8 9 ... 68 69 next >>

Organism Name	Matched Value
Homo sapiens [Details] [Highlight]	Genbank common name: human
Human respiratory syncytial virus [Details] [Highlight]	Synonym: human RSV
Human rotavirus 2 [Details] [Highlight]	Scientific name: Human rotavirus 2
Human rotavirus 4 [Details] [Highlight]	Scientific name: Human rotavirus 4
Human rotavirus A [Details] [Highlight]	Scientific name: Human rotavirus A

341 item(s) found, displaying 1 to 5

<< previous **1** 2 3 4 5 6 7 8 9 ... 68 69 next >>

Species
 Viruses (44692 structure(s)*)

Figure 3.4 Using the search feature on the Browse by Source Organism page

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE Keyword Search

Home Browse Search Tools Support More IEDB

Source Organism Information

Source Organism

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

Reference (373)
Structure (2337)
Source Antigen (563)
MHC Binding (5130)
B Cell Assay (1038)
T Cell Assay (852)
MHC Ligand Elution (282)

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

« previous **1** 2 3 4 5 6 7 8 9 ... 14 15 next »

Export all results: Excel

Reference ID ↑	Author	Title	Abstract	Publication Summary
279	Gayatri B Chavali; Anastassios C Papageorgiou; Karen A Olson; James W Fett; Guo fu Hu; Robert Shapiro; K Ravi Acharya	The crystal structure of human angiogenin in complex with an antitumor neutralizing antibody.	The murine monoclonal antibody 26-2F neutralizes the angiogenic and ribonucleolytic activities of hu...	Structure (Camb), 2003
309	Kelly L Arnett; Stephen C Harrison; Don C Wiley	Crystal structure of a human CD3-epsilon/delta dimer in complex with a UCHT1 single-chain antibody fragment.	The alpha/beta T cell receptor complex transmits signals from MHC/peptide antigens through a set of ...	Proc Natl Acad Sci U S A, 2004
310	Lars Kjer-Nielsen; Michelle A Dunstone; Lyudmila Kostenko; Lauren K Ely; Travis Beddoe; Nicole A Mifsud; Anthony W Purcell; Andrew G Brooks; James McCluskey; Jamie Rossjohn	Crystal structure of the human T cell receptor CD3 epsilon gamma heterodimer complexed to the therapeutic mAb OKT3.	The CD3 epsilon gamma heterodimer is essential for expression and function of the T cell receptor. T...	Proc Natl Acad Sci U S A, 2004
321	S Sogabe; F Stuart; C Henke; A Bridges; G Williams; A Birch; F K Winkler; J A Robinson	Neutralizing epitopes on the extracellular interferon gamma receptor (IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis and X-ray crystal structure of the A6 fab-IFNgammaR1-108 complex.	The extracellular interferon gamma receptor alpha-chain comprises two immunoglobulin-like domains, e...	J Mol Biol, 1997

Figure 3.5 Source Organism Information page

3.3 Query

In addition to the Browse functions, there are several other ways users can find information in the IEDB. A keyword search is available on the menu bar on each page. A family of detailed query-by-example searches can be accessed on the Query pull-down menu and consist of “B Cell Query”, “T Cell Query”, “MHC Binding Query”, “Ligand Elution Query”, and “Epitope Query”. This group of queries will be referred to as Detailed Queries in this document. A simplified search that is especially designed for the needs of most immunologists appears on the home page. This document will refer to this particular query as the Simple Search. All of these methods return results in a common format, as described in Section 3.3.4. These methods are elaborated in the subsections below.

3.3.1 Perform a Keyword Search

The keyword search allows users to locate records in the database using a keyword, identifier, or sequence. Wild card characters '*' and '?' can be used in the search field. The '*' character will match zero or more characters and the '?' character will match exactly one character. Additionally, the operators 'AND', 'OR', and 'NOT' can be utilized. A logical 'OR' is the default option. These three logical operators must be uppercase in order to be identified as operators instead of search terms. In all other cases, the keyword search is case insensitive, so "ABC" is the same as "abc". Regular expressions cannot be used in the search field.

To perform a search, users enter criteria such as a keyword, identifier, or sequence into the text box in the upper right corner of each page next to the “Search” button (Figure 3.1). They then click the Search button and view the Search Result Summary, which is described in Section 3.3.4.

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

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

3.3.2 Perform a Home Page Search

The search feature available on the left-hand portion of the home page (Figure 3.6) was designed to simplify the search process for many commonly asked queries by immunologists. It allows greater control in the search than available in the keyword search and is less involved than the Detailed Queries. Users can specify the structure type (e.g. peptide from protein or carbohydrate fragment) or a linear peptide sequence, including wildcard characters (wildcards are automatically placed at both ends of the sequence). The epitope source can be prescribed for the source organism and source antigen by using the organism finder (Section 3.3.5.5) and molecule finder (Section 3.3.5.4), respectively. The user can decide whether to include B cell responses, T cell responses, MHC binding, and/or MHC ligand elution 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 3.3.5.1). The fields using finders will allow multiple selections as search criteria. In these cases the selections are treated as a set. Records will be considered a match if they include at least one of the selected values in the set. The search is executed by selecting the Search button and query results can be viewed on the Search Result Summary page, which is described in Section 3.3.4.

Search

Epitope Structure

Structure Type:

Linear Sequence:

Epitope Source

Source Organism:

Source Antigen:


Immune Recognition Context

B Cell Response

T Cell Response

MHC Binding

MHC Ligand Elution



Host Organism:

MHC Restriction:

MHC Class:

Figure 3.6 Home Page Simple Search

3.3.3 Detailed Query

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

The fully expanded input screen for the Epitope Query is shown in Figure 3.7. The user can search on several reference criteria, such as author name, article title, the IEDB Reference ID, keywords in the reference abstract, year, author affiliation, and reference type. References are either published literature articles that have been curated by the IEDB curation staff or data submitted directly by researchers. Users can also specify search criteria for the epitope, such as epitope type (e.g. peptide from protein, carbohydrate), source molecule and organism, and various reference details. Further explanation of the search terms can be found in the Curation Manual. This query type returns T cell, B cell, MHC binding, and MHC ligand elution data.

Epitope Search

Reference

Author

Title

Reference Details

Reference ID

Abstract

Affiliations

Date (Year)

Reference Type Journal Article Submission Any

Epitope

Type

Source Molecule

Source Organism

Epitope Reference Details

Epitope Structure Defines

Evidence Code for Epitope Source Antigen

Epitope Name

Reference Start Position

Reference End Position

Reference Region

Comments

Location of Data in Reference

Epitope Related Object

Related Object

Type

Source Molecule

Source Organism

Figure 3.7 Epitope Search input screen

There are four other Detailed Queries that can be used to select search criteria for references, epitopes, and assays. These four are B Cell Search, T Cell Search, MHC Binding Search, and MHC Ligand Elution Search. As an example, the B Cell Search input screen is shown in Figure 3.8. As is the case for all four search input screens, the Reference and Epitope criteria fields are listed first, followed by the fields specific for each assay type.

Figure 3.8 B Cell Search input screen

The B cell response assay category captures B cell-mediated immunity information and describes antibody responses related to the epitope/antigen. In a B cell response, B lymphocytes (a type of

white blood cell) produce proteins called antibodies that bind to antigens. Antibodies are present on the surface on B lymphocytes and are also secreted. Once an antibody binds an antigen, the bound antigen molecule can be engulfed by phagocytes and broken into fragments.

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 Binding assay category captures details relating to the in vitro interaction of the epitope with specific MHC molecules along with available Epitope-MHC complex structure details. In other words, assays in this category assess the epitope's binding capacity to the MHC molecule.

The MHC Ligand Elution assay category captures data related to epitopes that are naturally processed and presented on the surface of an antigen presenting cell. The MHC Ligand Elution category differs from the MHC Binding category 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.

3.3.4 Search Results Summary

The Search Results Summary page displays the results of all the different queries. An example is displayed in Figure 3.9, which was generated with a keyword search for “*aae*”. The Search Results Summary allows the user to quickly assess the results of their search and drill down the level of detail that is of interest.

The number peptidic and non-peptidic epitopes are displayed in a table at the top of the form. Because the IEDB captures both positive and negative assay responses, some “epitopes” lack a positive binding value and therefore are not actually epitopes; the number of these molecular structures is indicated in the Negative column of the table. The user can click on the number in the Positive and All columns to view all the results for that category, as seen in Figure 3.10. The columns displayed include the number of corresponding epitope, source antigen, and source species.

The second table on the page summarizes the positive and negative assay responses for the four general assay types. The user can drill down on any of these values to see the corresponding epitopes. The detail page for the positive T Cell Responses of this search is displayed in Figure 3.11.

The third table lists the number of epitope source organisms, host organisms, restricting MHC alleles, and references resulting from the input search criteria. As before, the user can drill down on the values in the table to find more detail related to each category, as seen in Figure 3.12, Figure 3.13, Figure 3.14, and Figure 3.15.

Search Result Summary			
Epitopes	Positive*	Negative**	All
Peptidic	328	276	604
Non-Peptidic	0	0	0
Assays	Positive	Negative	All
T Cell Response	124	210	334
B Cell Response	391	457	848
MHC Ligand Elution	1	0	1
MHC Binding	115	201	316
Summary			
Epitope Source Organism		121	
Host Organism		52	
Restricting MHC Allele		85	
References		209	
<p>* At least one positive measurement. ** Only negative measurements.</p>			

Figure 3.9 Sample of Search Result Summary

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE Keyword Search

Home Browse Search Tools Support More IEDB

Epitope

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

« previous **1** 2 3 4 5 6 7 8 9 ... 13 14 next »

Export all results: Excel

Epitope ID ↑	Structure	Source Antigen	Source Organism
14	AAAAAVAAEAY		
32	AAAETGVGVKSIAP	Toxin coregulated pilin precursor	Vibrio cholerae O1
100	AAEAACFK	Parvalbumin beta	Gadus callarias
101	AAECPFLPKPKVA	nucleoprotein	Andes virus CHI-7913
103	AAEESKLPIINPLSNLLRH	Genome polyprotein	Hepatitis C virus
105	AAEFTINKPK	Major outer membrane porin, serovar L1 precursor (MOMP)	Chlamydia trachomatis Serovar L1
106	AAEGATPEAKYD	Pollen allergen Lol p VA precursor	Lolium perenne
107	AAEGGGQKQENT	mucin TcMUCI	Trypanosoma cruzi
111	AAELLAKQRAEAE	IgA-specific serine endopeptidase	Neisseria meningitidis
115	AAEPAAAAAY		
116	AAEPAALAY		
117	AAEQAAAARRRIVDHLAHAG	hypothetical protein Mb2555	Mycobacterium bovis AF2122/97
118	AAEQLWVTVYYGVPVWKEAT	envelope glycoprotein	Human immunodeficiency virus 1
120	AAERPRGVFNRQLVLGENLD	18 kDa antigen	Mycobacterium leprae
121	AAESERFVRQGTGNDEAGAA	exotoxin type A	Pseudomonas aeruginosa
122	AAESQIRDVDFAAESANYSKANILAQSGSY	flagellin	Campylobacter jejuni subsp. jejuni NCTC 11168
125	AAEWVLAYMLFTKFF	Replicase polyprotein 1ab	SARS coronavirus Tor2
126	AAEYAAAAAAKAAAA		
128	AAEYKAAAAAAKAAAA		
129	AAEYWNSQKEVLER	HLA class II histocompatibility antigen, DQ	Homo sapiens
682	ADIGSVQNVQVSTINNITVTVQVNVKAAESQ	flagellin	Campylobacter jejuni subsp. jejuni NCTC 11168
707	ADLGFENSAAAAETGVGVKSIASIA	Toxin coregulated pilin precursor	Vibrio cholerae
843	AEATKVAEAEKQKA	flagellar repetitive antigen protein	Trypanosoma cruzi
848	AEDAAEISVPAEIL	Polyprotein	Hepatitis C virus subtype 1a
877	AEEBKPIEAETATTEVPV	Major latex allergen Hev b 5	Hevea brasiliensis

328 item(s) found, displaying 1 to 25

« previous **1** 2 3 4 5 6 7 8 9 ... 13 14 next »

Export all results: Excel

Figure 3.10 Screen generated by drilling down on the positive epitope hyperlink in the Search Result Summary

T Cell Response Assays								
T Cell ID	Reference	Epitope	Host	Immunization	Antigen Epitope Relation	Antigen	MHC Restriction	Assay Description
234	C. T. Fonseca; Mem Inst Oswaldo Cruz 2004	NSELIRRAKAAESLASD Paramyosin (355-371) Schistosoma mansoni	Homo sapiens	Infectious disease via exposure to Schistosoma mansoni (Source Organism)	Epitope	NSELIRRAKAAESLASD Paramyosin (355-371) Schistosoma mansoni	HLA-DR	Proliferation assay (3H-Thymidine) Cell proliferation Positive
5206	Jean-Paul Vernot; Immunol Cell Biol 2005	SKYSNTFNINAYNMVIRRSRM	Aotus nancymaae	Administration in vivo with SKYSNTFNINAYNMVIRRSRM (Epitope) followed by restimulation in vitro	Epitope	SKYSNTFNINAYNMVIRRSRM		Proliferation assay (3H-Thymidine) Cell proliferation Positive
5209	Jean-Paul Vernot; Immunol Cell Biol 2005	SKYSNTFNINAYNMVIRRSRM	Aotus nancymaae	Administration in vivo with SKYSNTFNINAYNMVIRRSRM (Epitope) followed by restimulation in vitro	Epitope	SKYSNTFNINAYNMVIRRSRM		Proliferation assay (3H-Thymidine) Cell proliferation Positive
5213	Jean-Paul Vernot; Immunol Cell Biol 2005	SKYSNTFNINAYNMVIRRSRM	Aotus nancymaae	Administration in vivo with SKYSNTFNINAYNMVIRRSRM (Structurally Related) followed by restimulation in vitro	Epitope	SKYSNTFNINAYNMVIRRSRM		Proliferation assay (3H-Thymidine) Cell proliferation Positive
5214	Jean-Paul Vernot; Immunol Cell Biol 2005	SKYSNTFNINAYNMAIRRSRM	Aotus nancymaae	Administration in vivo with SKYSNTFNINAYNMVIRRSRM (Structurally Related) followed by restimulation in vitro	Epitope	SKYSNTFNINAYNMAIRRSRM		Proliferation assay (3H-Thymidine) Cell proliferation Positive
5363	Samia Ragheb; J Neuroimmunol 2005	MKSDEESSNAAEEWKYVAMVIDHILL Acetylcholine receptor subunit alpha precursor (410-435) Torpedo marmorata	Homo sapiens		Epitope	MKSDEESSNAAEEWKYVAMVIDHILL Acetylcholine receptor subunit alpha precursor (410-435) Torpedo marmorata		Proliferation assay (3H-Thymidine) Cell proliferation Positive
5364	Samia Ragheb; J Neuroimmunol 2005	MKSDEESSNAAEEWKYVAMVIDHILL Acetylcholine receptor subunit alpha precursor (410-435) Torpedo marmorata	Homo sapiens		Epitope	MKSDEESSNAAEEWKYVAMVIDHILL Acetylcholine receptor subunit alpha precursor (410-435) Torpedo marmorata		Proliferation assay (3H-Thymidine) Cell proliferation Positive
5365	Samia Ragheb; J Neuroimmunol 2005	MKSDQESNNAEEWKYVAMVMDHILL Acetylcholine receptor subunit alpha precursor (406-431) Bos taurus	Homo sapiens		Epitope	MKSDQESNNAEEWKYVAMVMDHILL Acetylcholine receptor subunit alpha precursor (406-431) Bos taurus		Proliferation assay (3H-Thymidine) Cell proliferation Positive

Figure 3.11 Screen generated by drilling down on the positive T cell assay hyperlink in the Search Result Summary

Source Organism

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

<< previous **1** 2 3 4 5 next >>

Export all results: Excel

Source Organism ↑
Acanthamoeba castellanii
Andes virus CHI-7913
Bacillus licheniformis
Batillus cornutus
Bluetongue virus (serotype 10 / American isolate)
Bluetongue virus 17
Borrelia burgdorferi
Bos taurus
Campylobacter jejuni subsp. jejuni NCTC 11168
Canine oral papillomavirus
Cercopithecine herpesvirus 8
Chlamydia trachomatis Serovar B
Chlamydia trachomatis Serovar L1
Clostridium botulinum
Clostridium botulinum A
Clostridium botulinum A str. Hall
Coxsackievirus B3 (strain Nancy)
Coxsackievirus B4 (strain E2)
Coxsackievirus B4 (strain JVB / Benschoten / New York/51)
Dengue virus type 2
Dengue virus type 2 Thailand/16681/84
Dengue virus type 3
Dengue virus type 4
Enterobacteria phage T4
Enterovirus

121 item(s) found, displaying 1 to 25

<< previous **1** 2 3 4 5 next >>

Export all results: Excel

Figure 3.12 Screen generated by drilling down on the Epitope Source Organism link in the Search Result Summary

Host Organism

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

« previous **1** 2 3 next »

Export all results:  Excel

Host Organism ↑
Aotus nancymae
Bos taurus
Canis familiaris
Canis familiaris beagle
Equus caballus
Gallus gallus
Gallus gallus Leghorn
Homo sapiens
Homo sapiens Argentinian
Homo sapiens Brazilian
Homo sapiens Caucasian
Homo sapiens Chilean
Homo sapiens Gabonese
Homo sapiens Ivorian
Homo sapiens Nepalese
Homo sapiens Pakistani
Homo sapiens Senegalese
Homo sapiens Sudanese
Macaca cyclopis
Macaca mulatta
Mus
Mus musculus
Mus musculus B10.A-H2a H2-T18a/SgSnJ

52 item(s) found, displaying 1 to 25

« previous **1** 2 3 next »

Export all results:  Excel

Figure 3.13 Screen generated by drilling down on the Host Organism link in the Search Result Summary

Restricting MHC Allele								
85 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)								
« previous 1 2 3 4 next »								
Export all results: <input checked="" type="checkbox"/> Excel								
MHC Allele ↑	Class	Organism	Synonyms	Restriction Level	Haplotype	Locus	Serotype	Molecule
H-2-b class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-b			
H-2-b class II	II	mouse (Mus musculus)		HAPLOTYPE	H-2-b			
H-2-d class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-d			
H-2-d class II	II	mouse (Mus musculus)		HAPLOTYPE	H-2-d			
H-2-Db	I	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-b	D		Db
H-2-Dd	I	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-d	D		Dd
H-2-IAb	II	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-b	IA		IAb
H-2-IAd	II	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-d	IA		IAd
H-2-k class II	II	mouse (Mus musculus)		HAPLOTYPE	H-2-k			
H-2-Kb	I	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-b	K		Kb
H-2-Kd	I	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-d	K		Kd
HLA-A*0101	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A1	A*0101
HLA-A*0201	I	human (Homo sapiens)	HLA-A2.1	COMPLETE MOLECULE		A	A2	A*0201
HLA-A*0202	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A2	A*0202
HLA-A*0203	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A203	A*0203
HLA-A*0206	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A2	A*0206
HLA-A*0301	I	human (Homo sapiens)	HLA-A3.1	COMPLETE MOLECULE		A	A3	A*0301
HLA-A*1101	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A11	A*1101
HLA-A*2301	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A23	A*2301
HLA-A*2402	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A24	A*2402
HLA-A*2403	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A2403	A*2403
HLA-A*2407	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A24	A*2407
HLA-A*2601	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A26	A*2601
HLA-A*2902	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A29	A*2902
HLA-A*3001	I	human (Homo sapiens)		COMPLETE MOLECULE		A	A30	A*3001
85 item(s) found, displaying 1 to 25								
« previous 1 2 3 4 next »								
Export all results: <input checked="" type="checkbox"/> Excel								

Figure 3.14 Screen generated by drilling down on the Restricting MHC Allele link in the Search Result Summary

Reference List

Sort By: Order By:

209 item(s) found, displaying 1 to 25

[J. Thomas August, Ernesto Marques, Jerome Salmon and Keun-Ok Jung.](#)
Systematic identification of HLA DRB1*0401-restricted peptide sequences of the complete West Nile Virus (NY99-flamingo382-99) proteome by IFN-g ELISpot assay of T-cell response from peptide-immunized transgenic mice. 2008

[Tien-Tien Cheng, Ming F Tam, Hong Chou, Hsiao-Yun Tai, Horng-Der Shen.](#)
Lys89, Lys90, and Phe91 are critical core amino acid residues of the Pen ch 18 major fungal allergen recognized by human IgE antibodies. Biochemical and biophysical research communications (Biochem Biophys Res Commun). 2008; 375(1090-2104):671-4
PMID: 18760997

[Taiki Aoshi, Toshi Nagata, Mina Suzuki, Masato Uchijima, Dai Hashimoto, Alreza Rafiei, Takafumi Suda, Kingo Chida, Yukio Koide.](#)
Identification of an HLA-A*0201-restricted T-cell epitope on the MPT51 protein, a major secreted protein derived from Mycobacterium tuberculosis, by MPT51 overlapping peptide screening. Infection and immunity (Infect Immun). 2008; 76(1098-5522):1565-71
PMID: 18212086

[Karuna P Karunakaran, Jose Rey-Ladino, Nikolay Stoyanov, Kyra Berg, Cakia Shen, Xiaozhou Jiang, Brent R Gabel, Hong Yu, Leonard J Foster, Robert C Brunham.](#)
Immunoproteomic discovery of novel T cell antigens from the obligate intracellular pathogen Chlamydia. Journal of immunology (Baltimore, Md. : 1950) (J Immunol). 2008; 180(0022-1767):2459-65
PMID: 18250455

[Ursula Fernando, Debabrata Biswas, Brenda Allan, Sam Attah-Poku, Philip Willson, Alfonso Valdivieso-Garcia, Andrew A Potter.](#)
Serological assessment of synthetic peptides of Campylobacter jejuni NCTC11168 FlaA protein using antibodies against multiple serotypes. Medical microbiology and immunology (Med Microbiol Immunol). 2008; 197(0300-8584):45-53
PMID: 17704944

[Stefanie L Slezak, Maria Bettinotti, Silvia Selleri, Sharon Adams, Francesco M Marincola, David F Stroncek.](#)
CMV pp65 and IE-1 T cell epitopes recognized by healthy subjects. Journal of translational medicine (J Transl Med). 2007; 5(1479-5876):17
PMID: 17391521

[Satoko Matsueda, Akira Yamada, Yukari Takao, Mayumi Tamura, Nobukazu Komatsu, Shigeru Yutani, Tatsuya Ide, Michio Sata, Kyogo Itoh.](#)
A new epitope peptide derived from hepatitis C virus 1b possessing the capacity to induce cytotoxic T-lymphocytes in HCV1b-infected patients with HLA-A11, -A31, and -A33. Cancer immunology, immunotherapy : CII (Cancer Immunol Immunother). 2007; 56(0340-7004):1359-66
PMID: 17265020

[Tim J Bull, Sarah C Gilbert, Saranya Sridhar, Richard Linedale, Nicola Dierkes, Karim Sidi-Boumedine, John Hermon-Taylor.](#)
A Novel Multi-Antigen Virally Vectors Vaccine against Mycobacterium avium Subspecies paratuberculosis. PLoS ONE (PLoS ONE). 2007; 2(1932-6203):e1229
PMID: 18043737

Figure 3.15 Screen generated by drilling down on the reference hyperlink in the Search Result Summary

When users click on the number of references on the Search Results Summary screen, the system will display the Reference List. This list will display all the references that matched the user's search criteria. Enough information is listed to identify each reference uniquely, including authors, article title, year, PubMed ID, and journal name. To view all the information related to a given reference, click the highlighted author line. The list can be sorted by date, author, PubMed ID, and title in ascending or descending order. Clicking on the PubMed identifier will open the PubMed citation in a new window.

3.3.4.1 Download Query Results

All users can download the results of any Query in a comma separated value (CSV) format that can be read by a text editor or a spreadsheet application, such as Microsoft Excel. To download the results of a query, users must first perform the query for which they wish to download the results. The columns that are downloaded are the columns displayed in the Results Table when the user selects the link designated by "Export all results".

3.3.4.2 Accessing the EpitopeViewer

The EpitopeViewer is an application for three dimensional viewing of receptor-antigen interactions that can be accessed from the Assay List screens. The EpitopeViewer can be used with all assays that have receptor-antigen interaction data available. It is not available for

epitopes and assays, and when it is available, a link is provided in the leftmost ID column, as illustrated in Figure 3.16.

B Cell Response Assays							
B Cell ID	Reference	Epitope	Host	Immunization	Antigen Epitope Relation	Antigen	Assay Description
5 Epitope Viewer	J Lescar; J Biol Chem 1995	H15, G16, Y20, R21, W63, R73, L75, N77, N93, K96, ... Lysozyme C Numida meleagris		The immunization procedure is unknown	Source Antigen	Lysozyme C Lysozyme C Numida meleagris	X-Ray Crystallography Characterization of Ab binding Positive
14 Epitope Viewer	S E Mylvaganam; J Mol Biol 1998	F37, G38, K61, E62, E63, A97, K100, K101, N104, E1... Cytochrome c Equus caballus	Mus musculus	The immunization procedure is unknown	Source Antigen	Cytochrome c Cytochrome c Equus caballus	X-Ray Crystallography Characterization of Ab binding Positive
31 Epitope Viewer	H Kondo; J Biol Chem 1999	H33, G34, N37, Y38, R39, W81, R91, L93, T107, N111... Lysozyme C precursor Gallus gallus		The immunization procedure is unknown	Source Antigen	Lysozyme C precursor Lysozyme C precursor Gallus gallus	X-Ray Crystallography Characterization of Ab binding Positive
32 Epitope Viewer	Gayatri B Chavali; Structure (Camb) 2003	G58, L59, S61, P62, C63, K64, D65, G109, G110, S11... Angiogenin precursor Homo sapiens	Mus musculus BALB/c	Administration in vivo with Angiogenin precursor (Source Antigen)	Source Antigen	Angiogenin precursor Angiogenin precursor Homo sapiens	X-Ray Crystallography Characterization of Ab binding Positive
33 Epitope Viewer	W Ding; J Mol Biol 2000	S206, S207, A208, A209, T210, K211, K212, T213, A2... Outer surface protein A precursor Borrelia burgdorferi		The immunization procedure is unknown	Source Antigen	Outer surface protein A precursor Outer surface protein A precursor Borrelia burgdorferi	X-Ray Crystallography Characterization of Ab binding Positive
82 Epitope Viewer	Peng Zou; Int Immunopharmacol 2005	EVETPIRN Matrix protein 2 (6-13) Influenza A virus (A/Puerto Rico/8/34(H1N1))	Mus musculus BALB/c	Administration in vivo with EVETPIRN (Epitope) to prevent or reduce disease	Source Organism	Influenza A virus (A/Puerto Rico/8/34(H1N1)) Influenza A virus (A/Puerto Rico/8/34(H1N1))	Survival After Challenge Antibody Binding leading to Biological Activity Positive

Figure 3.16 B Cell Response screen with Epitope Viewer links in the leftmost column

3.3.5 Finders Overview

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

3.3.5.1 Allele Finder

The MHC Allele Finder facilitates the selection of one or more MHC alleles. Initially the Allele Finder lists all alleles ordered by allele name. The Allele Finder allows the user to find alleles by organism, class {I, II, non-classical}, and allele in the Find box (Figure 3.17). After the user supplies their search criteria and clicks the Search button, the system will filter the list of MHC alleles using the organism, class, and allele provided. The allele finder uses wild card characters by default on both ends of criteria entered into the allele field. The system then returns any alleles that contain the value in the name field and match the class selected.

Figure 3.17 Find form on the Allele Finder

3.3.5.2 Assay Finder

The Assay Finder is used to facilitate the selection of one or more assay types and lists all assay types in the selected assay category. The Assay Finder allows the user to find assay by assay type name, assay group, and/or units in the Find box (Figure 3.18). After the user supplies their search criteria and clicks the Search button, the system filters the list of assay types using the selections provided in the Find box.

Figure 3.18 Search form on the Assay Type Finder

3.3.5.3 Disease Finder

The disease finder is used to facilitate the selection of a disease state and input the selection into a Disease State field. It includes all diseases from The International Statistical Classification of Diseases and Related Health Problems, tenth revision (ICD-10) and displays diseases with their corresponding ICD-10 codes in a hierarchical tree. The first level of the tree displays similar groups of diseases, and each additional level of the tree further breaks down the groups of diseases. Variations of each disease are not included. Searching capabilities are provided so users can quickly select a disease state.

The Disease Finder will allow the user to find diseases using the disease name or ICD-10 code (Figure 3.19). When the user performs a search, the system will display the first match and then allow the user to move forward and backward through the matching records using Next and Previous buttons (Figure 3.20). When the user provides a name, any disease name that contains the character string provided will be considered a match.

Figure 3.19 Search form on the Disease Finder

The selections in the disease finder are displayed in a tree (Figure 3.20). To expand a node of the tree, the user clicks the plus sign next to the name. To collapse a node, a user clicks the corresponding minus sign. The ICD-10 code is displayed next to each selection in square brackets. For example the ICD-10 code for Bartonellosis in the Figure 3.20 is A44.

Figure 3.20 Disease List

3.3.5.4 Molecule Finder

The Molecule Finder is used to facilitate the selection of source antigens, immunogens, and epitopes. Records in the Source Finder come from GenBank, UniProt and IEDB curators. Among the finders, the Source Finder has the most comprehensive and flexible search form, and even includes the Organism Finder. Due to the large volume of possible selections, the Molecule Finder initially won't display any selections. Users need to perform a search to narrow the list down. After the user enters search criteria (Figure 3.21) and clicks the Search button, the system will list the matching sources from which the user may select, as seen in Figure 3.22. The user can then select their desired sources from the list by click on *Select* in the far left column.

Find:

Molecule Accession: Database:

Chemical Type:

Sequence:

Molecule Name:

Source Organism:

Figure 3.21 Find form on the Molecule Finder

1,844 items found, displaying 1 to 25.
Pages [First/Prev] [1](#), [2](#), [3](#), [4](#), [5](#), [6](#), [7](#), [8](#) [Next/Last]

Options	Molecule Accession	Database	Molecule Names	Organism Name	Chemical Type	Structure	Position
Select	A0PJ22	Swiss-Prot	RNA-dependent RNA polymerase	Amapari virus	Protein		1371-1373
Select	A0PSF8	Swiss-Prot	NADH dehydrogenase Ndh; ndh, MUL_3025	Mycobacterium ulcerans Agy99	Protein		356-358
Select	A0QI56	Swiss-Prot	Peptidase, M24 family protein; MAV_3412	Mycobacterium avium 104	Protein		64-66
Select	A1KNE0	Swiss-Prot	PPE family protein; PPE52, BCG_3167c	Mycobacterium bovis BCG str. Pasteur 1173P2	Protein		135-137
Select	A1KP34	Swiss-Prot	PPE family protein; PPE54, BCG_3413c	Mycobacterium bovis BCG str. Pasteur 1173P2	Protein		35-37
Select	A1KP43	Swiss-Prot	PPE Family protein [first part]; PPE56a, BCG_3422c	Mycobacterium bovis BCG str. Pasteur 1173P2	Protein		82-84
Select	A1QN60	Swiss-Prot	Putative uncharacterized protein; Conserved membrane protein, TBEF_00283, TBEF_10291	Mycobacterium tuberculosis F11	Protein		119-121

Figure 3.22 Molecule Finder source list

3.3.5.5 Organism Finder

The organism finder is used to facilitate the selection of a species or virus from the NCBI Taxonomy Database. Common selections are displayed initially to speed the selection of the usual suspects, as seen in Figure 3.23. To view the entire NCBI taxonomy data set click *NCBI Taxonomy Tree* in the accordion slider. The Common Selection bar will move down to reveal the taxonomy tree. An Allergen tree has also been provided. The Allergen tree consists of species from the NCBI taxonomy, but is organized to help allergists locate common allergen selections more easily. To use the Allergen tree click the Allergen Tree heading in the accordion slider.

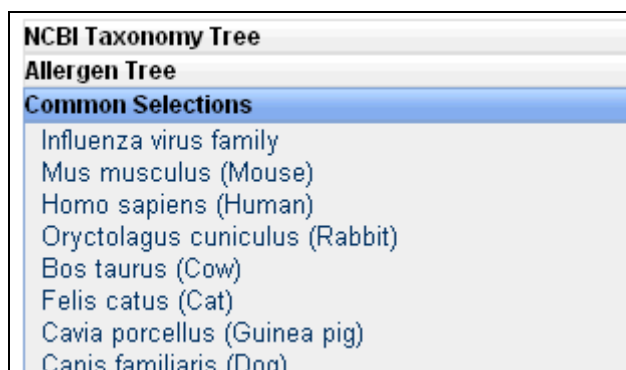


Figure 3.23 Common selections in Organism finder

The Organism finder will allow the user to find species using their name or taxonomy identifier (assigned by NCBI). When the user performs a search, the system will display the first match then allow the user to move forward and backward through the matching records using Next and Previous buttons as in Figure 3.24. When the user provides a name, any species name or synonym that contains the name provided will be considered a match. Search results will always appear in the NCBI Taxonomy tree, not the Allergen Tree or Common Selections.

The selections in the organism finder are displayed in a tree (Figure 3.24). The taxonomy identifier is displayed next to each node of the tree in square brackets. For example, the taxonomy identifier for the selection in the example below is 301536. To see the synonyms for a selection, users can place their computer mouse over the scientific name.

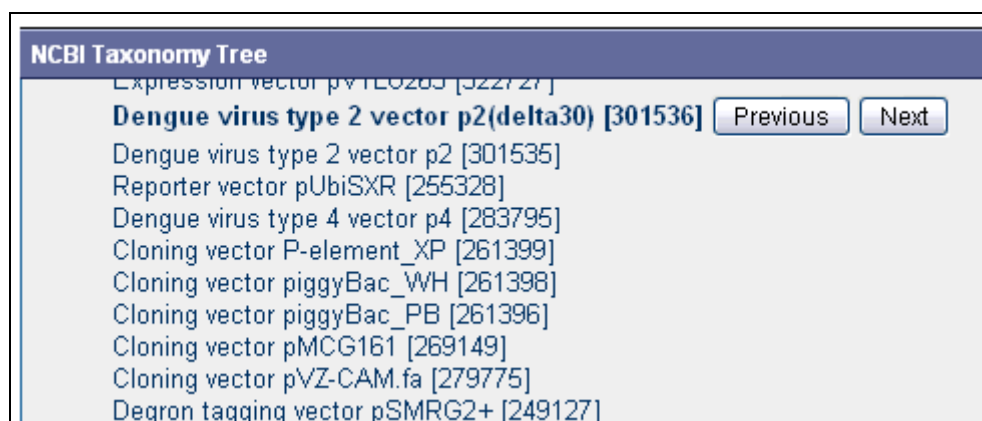


Figure 3.24 NCBI Taxonomy Tree

3.4 Tools

The Tools pull-down menu access the IEDB Analysis Resource and has three items – T Cell Epitope Prediction, B Cell Epitope Prediction, and Analysis Tools. The purpose of the Analysis Resource of the IEDB is to provide computational tools that enhance the value of the IEDB database to the user. Providing access to tools in one centralized location helps make users aware of available solutions to their problems. All of the information contained within the

Analysis Resource, including analysis tools and algorithms developed by the IEDB staff, are freely available to the scientific community.

The tools provided in the analysis resource fall into two categories – predictive tools and analysis tools. Predictive 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 predictive 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 predictive tool. As the ANN method is trained on different data sets, different corresponding predictive 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 predictive tools as the database grows.

Predictive 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 predictive and analytical tool in more detail.

3.4.1 T Cell Epitope Prediction

3.4.1.1 T Cell Epitopes - MHC binding prediction

The Analysis Resource provides tools for predicting peptide binding to MHC class I and II molecules. For class I binding predictions, users can select predictions performed with tools derived from three different methods – artificial neural network, average relative binding, and stabilized matrix. For class II binding predictions, users can select the ARB method, the SMM_align method, a method devised by Sturniolo et al. and used in TEPITOPE, and consensus method derived from the three aforementioned methods. Tutorials and example data are available for both the class I and II tools.

3.4.1.1.1 *Peptide Binding to MHC Class I Molecules*

Users can select from three different methods for predicting class I epitopes – ANN, ARB, and SMM, which are described further below.

Artificial Neural Network

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

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

Average Relative Binding (ARB)

Average relative binding (ARB) matrix binding prediction method is based on the assumption that each residue along the peptide molecule independently contributes to binding affinity. When a residue R occurs at position i in the peptide, it is assumed to contribute a constant amount of R_i to the free energy of binding of the peptide. The effect of each of the 20 possible amino acids at each possible position along the peptide sequence, therefore, can be estimated by a matrix of coefficients. The overall binding propensity of each peptide sequence, an algorithm “score”, is calculated by multiplying the R_i coefficients. Predicted IC_{50} values, which provide quantitative K_D (IC_{50}) predictions, are then calculated by mathematical transformations of the algorithm scores (Bui et al., Immunogenetics 2005).

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.

3.4.1.1.1 MHC Class I Binding Prediction Resource

In addition to prediction tools, the Analysis Resource makes data sets and method evaluations available to users. The IEDB MHC Class I Binding Prediction Resource (<http://mhcbindingpredictions.immuneepitope.org>) contains training data, test data, and other resources for tool developers interested in predictions of peptide binding to MHC class I molecules. The user can follow links to a manuscript describing the resource in detail (Peters et al., PLoS Comput. Biol. 2006), a dataset of experimental affinities of peptide to MHC molecules, and a description of the framework used for the evaluation of prediction methods. A link to this site appears at the bottom of the T Cell Tools tab in the Analysis Resource.

As described in the manuscript, predictions were obtained from public web-servers for all relevant peptide-MHC affinities in the dataset. The correlation between predicted and measured affinities was evaluated using scatter plots, linear regression, and ROC analyses. The evaluation of these external tools can be accessed on the site by name of the method or the MHC allele. As

carefully noted in the manuscript, this is not a fair evaluation of the value of each method, primarily because the data available to each method are highly divergent.

A similar evaluation of the prediction performance of three prediction methods available in the IEDB Analysis Resource (ANN, ARB, and SMM) was carried out using cross-validation on the dataset. In contrast to the comparison of external predictions, this is a fair evaluation of prediction performance of the three methods, since these three internal methods all used the same training data and testing data, while the external methods used a variety of training and testing data sets. Again, the evaluations of these three internal methods can be accessed by name of the method or the MHC allele.

3.4.1.1.2 Peptide Binding to MHC Class II Molecules

Users can select from four different methods for predicting class II epitopes – ARB, and SMM-align, Sturniolo, and Consensus. The Consensus method has been selected as the default method. An evaluation conducted by the IEDB team has indicated that this method generally performs better than the others. The other three 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).

Consensus

The consensus method was developed by the IEDB team by exploiting features of the other three aforementioned methods. A paper describing the method was published by Wang et al. (PLoS Comput Biol, 2008)

3.4.1.2 T Cell Epitopes – MHC I Processing Prediction

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

For the prediction of antigen processing through the MHC class I antigen presentation pathway, we incorporated predictions of proteasomal cleavage and TAP transport similar to the MHCPathway website described in (Tenzer et al, CMLS, 2005). The predictions are based on in vitro experiments characterizing the sequence specificity of proteasomal cleavage and TAP

transport. The goal of the prediction is to identify MHC-I ligands (peptides that are naturally processed from their source proteins and presented by MHC class I molecules).

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

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

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).

3.4.2 B Cell Epitope Prediction

3.4.2.1 Prediction of linear epitopes from protein sequence

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

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

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

3.4.2.2 DiscoTope - Prediction of epitopes from protein structure

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. The method is described in Haste Andersen et al. (Protein Sci., 2006).

3.4.2.3 ElliPro - Epitope prediction based upon structural protrusion

ElliPro predicts linear and discontinuous antibody epitopes based on a protein antigen's 3D structure. ElliPro accepts either a protein structure (preferred) or a protein sequence as an input. If a protein sequence is used, ElliPro will predict its 3D structure by homology modeling. Its use 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).

3.4.3 Epitope Analysis Tools

3.4.3.1 Population coverage

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

An important consideration in the process of epitope selection is that the patient population coverage afforded by a given set is not simply corresponding to the sum of the coverage of its individual components. Thus, to calculate the coverage afforded by a given mixture of epitopes, a more comprehensive approach and a suitable algorithm has been developed for this specific purpose (Bui et al. BMC Bioinformatics 2006). This method calculates the fraction of individuals predicted to respond to a given epitope set on the basis of HLA genotypic frequencies, assuming non-linkage disequilibrium between HLA loci, and on the basis of MHC binding and/or T cell restriction data. The algorithm is briefly explained here. First, genotypic frequencies of various MHC are tabulated. Each time a peptide binds to a given MHC, a "hit" is recorded for that MHC. The process is repeated for all peptides. Then the hits for MHC are tallied. Next, the frequency of each possible diploid MHC combination (phenotype) is calculated. For n MHC types, this corresponds to an $n \times n$ 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.

We have derived HLA allele genotypic frequencies from the dbMHC database (<http://www.ncbi.nlm.nih.gov/mhc/>) and stored them in a database on the IEDB tool server. At present, dbMHC provides allele frequencies for 78 populations and 11 different geographical areas. It is envisioned that the compiled data will be updated regularly as further HLA frequency data become available. Furthermore, customized frequency data can be utilized in the calculation, should studies of specific and particular patient populations be of interest to a given user. Multiple population coverages can be simultaneously calculated and an average population coverage is generated. Since MHC class I and II restricted epitopes elicit immune responses from two different T cell populations (CTL and Th cells, respectively), the program provides three different coverage calculation modes – (1) class I separate, (2) class II separate, and (3) class I and class II combined.

3.4.3.2 Epitope conservancy

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

3.4.3.3 Epitope Cluster Analysis

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

3.4.3.4 Homology Mapping Tool and EpitopeViewer

This Homology Mapping Tool maps linear epitopes to 3D structures of proteins (Beaver, et al., Immunome Res 2007). This is done by comparing the epitope source protein sequence with that of proteins with known 3D structures in the PDB. The tool generates an alignment between the query sequence of the epitope source sequence and a homologous sequence from the PDB, and allows to visualize 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.

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

The EpitopeViewer provides the following functionality:

- Link to the PDB web-page displaying a particular structure.
- Visualization of the 3D structure of epitope/antigen in complex with immune receptor(s) as curated within the IEDB and available in the PDB.
- Visualization of the 3D structure of epitope and antigen mapped to a PDB structure using the Homology Mapping tool.
- Visualization of sequences of epitope/antigen and immune receptor(s).
- 3D-visualization of intermolecular (epitope-paratope, epitope-antibody CDR, epitope-MHC, pMHC-TCR, pMHC-TCR CDR), inter-atom and inter-residue interactions curated within the IEDB and/or calculated on the fly from the PDB file with essential details (contact type, atoms, distance) provided;
- 2D-plot of inter-residue interactions between epitope and immune receptor.
- Generation of publication-quality pictures of structures, sequences, and plots of contacting residues.

3.5 Support Overview

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

3.5.1 Solutions Center

The IEDB Solutions Center is the primary resource for information on using the website's features. The user can submit help requests, check on the status of requests, browse and search the knowledge base and forums, and link to help documentation, such as the Curation Manual. In order to submit and subsequently track a help request via the Solutions Center, users must follow a simple registration procedure in order to provide an email address, name, and password.

3.5.2 Provide Feedback

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

3.5.3 Help Request

Users can submit help requests in three ways. At the bottom of most pages is a "Help request" link. Selecting this will initiate an email to help@iedb.org. The email help request can also be initiated by selecting "Help Request" from the Support pull-down menu. The user can describe their request and send the email. The third method utilizes the IEDB Solutions Center. The top menu bar on the IEDB Solutions Center web page has a "SUBMIT A REQUEST TO THE HELP DESK" link. Selecting this link brings the user to a "Submit a request" web page. The user must fill in their email address, the subject line, and a description of the help request. All help requests are forwarded to the same help desk.

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

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

3.5.4 Data Field Descriptions

The Data Field Descriptions item in the Support pull-down menu gives the user access to the Curation Manual. Using the Find function of their web browser, users can search for the data field name of interest in order to gain a fuller understanding of the field definition and the possible values.

3.6 More IEDB

The "More IEDB" pull-down menu contains links that do not logically fit into the other menu headings. Its component links are described below.

3.6.1 Acknowledgements

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

3.6.2 Citing the IEDB

Data and tools within the IEDB are presented as a public resource. Users are requested to consider citing the IEDB when they present information obtained from the IEDB or use tools contained in the Analysis Resource. It is expected that the authors of an entry as well as the IEDB are properly cited whenever their work is referred to:

1. The IEDB website should be cited using the URL: www.iedb.org
2. The journal reference for the IEDB should be cited as:

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.

3.6.3 Database Export

The contents of the Immune Epitope Database are exported weekly to files in XML format. The database export page (Figure 3.25) 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 version 2.0 export also contains ZIP archives of XML files that provide users with the full record for the various identifiers that are referenced in the full database export, such as the IEDB source organism accession identifier list, the MHC allele name list, and the organism list. The supporting XML files only contain full records when the record is not otherwise available from the original source.

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

In addition, an archive of the data as they appeared in IEDB 1.0 is available. The archive file, IEDB_2008_4_1_3_28.zip, contains an XML for each reference. The corresponding XSD files are also available for download.

Database Export			
Version 2.0			
XML Database Export		IEDB Schema	
Complete Database Export	30MB	Curation.xsd (Primary IEDB schema) (v. 2.0)	42kB
		CurationSimpleTypes.xsd (v. 2.0)	383kB
		IedbPDBViewerSchema.xsd (v. 1.0)	7kB
IedbAccessionList.zip	25kB	IedbAccessionList.xsd (v. 2.0)	909B
MhcAlleleNameList.zip	15kB	MhcAlleleNameList.xsd (v. 2.0)	2kB
OrganismList.zip	6MB	OrganismList.xsd (v. 2.0)	751B
AssayTypeList.zip	4kB	AssayTypeList.xsd (v. 2.0)	771B
Version 1.0			
XML Database Export		IEDB Schema	
Complete Database Export	20MB	IEDBSchema.xsd (v. 1.0)	53kB
		IedbSimpleTypes.xsd (v. 1.0)	453kB

Figure 3.25 IEDB Database Export web page

3.6.4 Documents

A variety of IEDB reference materials is available for download by all users. The Documents page lists the files available for download by category. The files available for download include an Introduction to IEDB and Analysis Resource, IEDB Annual Workshop Executive Summaries, the Annual Compendia, and quarterly newsletters. Additional reference materials will be added for download over time.

3.6.5 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 Links under the Resources heading on the main menu. The hyperlinks on the links page are grouped by category:

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

3.6.6 Patent List

As part of the IEDB curation effort, the Derwent World Patent Index has been searched for potentially relevant patent items. These are presented in a table on the Patent List web page that lists the publication number, patent title, inventors, assignee name, patent abstract, date filed, and date published. The enhanced abstracts of all of the 795 listed patent items have been reviewed, but the actual patents have not been read or curated. This information is presented for those users who wish to explore these patent items further.

The list mostly includes patents related to Category A-C priority pathogens, emerging and re-emerging infectious diseases, Malaria, Hepatitis B, Clostridium tetani, Leishmania, and Candida albicans, as well as other diseases. Users can search the table by using the "find" feature of their browser.

3.6.7 Terms of Use

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

3.6.8 Publications

A list of publications relevant to the IEDB can be found on the Publications page. They have been grouped into four categories – General IEDB, Analysis Resource, Curation, and Epitope Meta-analyses.

4 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 five 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. A search in PubMed using "immune epitope database" or "IEDB" did not add any new citations to the list compiled from Google Scholar and ISI. Citations for 2007 are included this year because a substantial number of references not listed in last year's compendium were discovered in the course of generating the 2008 citation list.

4.1 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 2008, nine articles were published, while twelve were published in 2007, three in 2006, four in 2005, and one in 2004. In all, the team has written 29 scientific articles about the IEDB.

4.1.1 2008

1. 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
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13. 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
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4.1.3 2006

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In 2008, 112 references cited at least one of the 29 papers written by the IEDB team over the past five years. This list was compiled by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the 29 papers. This total may increase over time since these databases may not include references published late in 2008.

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4.3 Publications Citing the IEDB in 2007

In 2007, 69 references cited at least one of the 21 papers written by the IEDB team in the first four years of the contract. This list compiled in last year's Annual Compendium used citation searches in PubMed and Google Scholar, which resulted in 27 citations total. In compiling the list of 2008 citations for this compendium, it was observed that Google Scholar and the ISI Web of Knowledge yielded 21 citations for the primary IEDB citation (PLoS Biology 2005) reference alone. It was therefore decided to recompile the 2007 list of citations using the same methodology as was used for the 2008 citations. The net result was the addition of 42 references. The discrepancy may be due to the addition of another citation resource and the possible inclusion in the databases of 2007 references added in the course of the year.

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