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Immune Epitope Database and Analysis Program

2009 Annual IEDB Compendium (Rev. 1)

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

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

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Introduction

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

This fifth Annual Compendium of the Immune Epitope Database and Analysis Resource consists of three sections. The first section contains a list of the antibody and T cell epitope information in the database as of 14 January 2009. The second section describes the features of the IEDB 2.3 website. The third section lists the scientific publications in 2009 and 2008 for which the IEDB played a contributory role.

Since the publication of last year's 2008 Annual Compendium, the quantity of data available in the IEDB has increased significantly with the addition of almost 3000 fully curated references. By the end of the year, curation of peptidic epitope data relating to all infectious diseases, including NIAID Category A, B, and C priority pathogens, NIAID Emerging and Re-emerging infectious diseases, allergens, diabetes, and rheumatoid arthritis was current through September 2009. Curation of peptidic epitopes related to multiple sclerosis was over 50% complete. Curation of non-peptidic allergen epitopes was also completed.

1 Antibody and T Cell Epitopes

Many new references and many new pathogens were added to the IEDB in 2009, 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 2008 and 2009. Of the 1402 species/strains listed, 347 were added in 2009. It should be noted that the source organism is the species/strain from which the epitopes originate, and may not be from an infecting organism or vaccine target. The curation of MHC binding peptides, cross-reactive epitopes, and autoimmune epitopes has resulted in the appearance of human (Homo sapiens) and mouse (Mus musculus) epitopes on the list.

In the table below, the leftmost column labeled "New 2009" indicates with an "X" if epitopes for the species/strain was added to the IEDB in 2009. 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-08", "T-08", "B-09", and "T-09" indicate the cumulative number of distinct B cell and T cell epitopes in the database at the end of 2008 and 2009, respectively. The two rightmost columns display the differences in the B and T cell epitope counts from 2008 to 2009. The changes in B and T cell epitope counts are shown in red. In 2009, the number of B cell epitopes increased by 6624, from 13,974 to 20,598, and the number of T cell epitopes increased by 16,972, from 27,166 to 44,138.

Table 1-1 Summary of B and T cell epitopes contained in the IEDB

NEW 2009	ORGANISM ID	SPECIES STRAIN	B-08	T-08	B-09	T-09	∆ B	∆ T
	222523	Bacillus cereus ATCC 10987		1		1		
	226900	Bacillus cereus ATCC 14579		1		1		
X	405532	Bacillus cereus B4264				1		1
	269801	Bacillus cereus G9241		3		3		
X	405531	Bacillus cereus G9842				1		1
X	451708	Bacillus cereus H3081.97				11		11
X	451707	Bacillus cereus NVH0597-99				7		7
X	405917	Bacillus cereus W				1		1
X	441769	Bacillus coahuilensis m4-4				1		1
	315749	Bacillus cytotoxicus NVH 391-98		2		2		
	1467	Bacillus lentus		1		1		
	1402	Bacillus licheniformis		9		9		
	1404	Bacillus megaterium		1		1		
X	1423	Bacillus subtilis			2	1	2	1
	1428	Bacillus thuringiensis	2		5		3	
	339854	Bacillus thuringiensis serovar israelensis ATCC 35646		2		2		
X	29339	Bacillus thuringiensis serovar kurstaki			3		3	
	1435	Bacillus thuringiensis serovar san diego		2		2		
	412694	Bacillus thuringiensis str. Al Hakam		2		2		
	315730	Bacillus weihenstephanensis KBAB4		3		3		
	2	Bacteria	2		2			
X	12040	Barley yellow dwarf virus-PAV			1		1	
	37962	Bayou virus	1		1			
	12260	Bean pod mottle virus	2		2			
	31715	Bean-pod mottle virus (strain Kentucky G7)	9	1	9	1		
	31721	Beet necrotic yellow vein virus	8		10		2	
	12161	Beet yellows virus	5		5			
	3645	Bertholletia excelsa	7	24	7	24		
	3505	Betula pendula	15	182	36	182	21	
	10629	BK polyomavirus		12		45		33
	65743	Blackcurrant reversion virus	2		2			
	6973	Blattella germanica		15	5	15	5	
	40697	Blomia tropicalis	5		18		13	
	40051	Bluetongue virus	6		7		1	
	10904	Bluetongue virus (serotype 1 / isolate Australia)	7		7			
X	10900	Bluetongue virus (serotype 10 / American isolate)			3		3	
	33717	Bluetongue virus (serotype 13 / isolate USA)	1		2		1	
	33718	Bluetongue virus (serotype 17 / isolate USA)	4		4			
X	35327	Bluetongue virus 1			3		3	
	10906	Bluetongue virus 10	3		3			
X	35329	Bluetongue virus 11			6		6	
X	35330	Bluetongue virus 13			1		1	
X	10903	Bluetongue virus 17			4		4	
X	94967	Bluetongue virus 4			2		2	
X	388634	Bombyx mandarina nuclear polyhedrosis virus				1		1

NEW 2009	ORGAN-ISM ID	SPECIES STRAIN	B-08	T-08	B-09	T-09	∆ B	∆ T
	271108	Bombyx mori NPV	2		2			
	360910	Bordetella avium 197N		1		1		
	518	Bordetella bronchiseptica		1		1		
	520	Bordetella pertussis	75	15	221	44	146	29
X	257313	Bordetella pertussis Tohama I			1	11	1	11
	12455	Borna disease virus	8	4	8	4		
	29518	Borrelia afzelii		1		1		
	390236	Borrelia afzelii PKo	2		2			
	139	Borrelia burgdorferi	39	34	39	38		4
X	498740	Borrelia burgdorferi 64b				2		2
	224326	Borrelia burgdorferi B31	66		66	10		10
	10001091	Borrelia burgdorferi BEP4	1		1			
	10000675	Borrelia burgdorferi CA12		6		6		
	64895	Borrelia burgdorferi group	3		3			
	521007	Borrelia burgdorferi N40	4		4	3		3
	445985	Borrelia burgdorferi ZS7	2	45	2	45		
	412419	Borrelia duttonii Ly	7		7			
	29519	Borrelia garinii	2		2	29		29
	10000530	Borrelia garinii IP90	3		3			
	9913	Bos taurus	222	111	847	236	625	125
	8722	Bothrops asper	1		1			
	11128	Bovine coronavirus	7		7			
	12064	Bovine enterovirus	13		13			
	12065	Bovine enterovirus strain VG-5-27	6		6			
	10000472	Bovine ephemeral fever virus BB7721	2		2			
	10320	Bovine herpesvirus 1	4	1	4	35		34
	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			
	11901	Bovine leukemia virus	25	12	33	28	8	16
	10562	Bovine papillomavirus - 4	3	3	10	3	7	
	10559	Bovine papillomavirus type 1	1		1			
	11215	Bovine parainfluenza virus 3		1		1		
	11246	Bovine respiratory syncytial virus	2	1	2	1		
X	31611	Bovine respiratory syncytial virus (strain 391-2)			3		3	
	11249	Bovine respiratory syncytial virus (strain RB94)	3		3			
X	82823	Bovine respiratory syncytial virus strain lelystad			1		1	
	82824	Bovine respiratory syncytial virus strain snook		75		75		
	10927	Bovine rotavirus	7		7	1		1
X	36439	Bovine rotavirus strain NCDV/G6			1		1	
	10933	Bovine rotavirus strain RF	12		12	7		7
X	10934	Bovine rotavirus strain UK/G6				1		1
	11099	Bovine viral diarrhea virus 1	1	11	1	11		
	11100	Bovine viral diarrhea virus 1-NADL	3	3	3	3		
	54315	Bovine viral diarrhea virus 2	1		1			

NEW 2009	ORGAN-ISM ID	SPECIES STRAIN	B-08	T-08	B-09	T-09	∆ B	∆ T
	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	29	3	29		
	35802	Brucella abortus bv. 1	1		1			
	29459	Brucella melitensis	3	32	3	32		
	359391	Brucella melitensis biovar Abortus 2308		30		30		
	224914	Brucella melitensis bv. 1 str. 16M	4		4	2		2
	236	Brucella ovis	2		2			
X	444178	Brucella ovis ATCC 25840				1		1
	29461	Brucella suis		7		7		
X	204722	Brucella suis 1330				26		26
X	470137	Brucella suis ATCC 23445				1		1
X	6279	Brugia malayi				1		1
	89462	Bubalus bubalis		1		1		
	32605	Buffalopox virus		2		2		
	8616	Bungarus multicinctus	5		20	3	15	3
	339670	Burkholderia ambifaria AMMD		3		3		
	350702	Burkholderia cenocepacia PC184		1		1		
	292	Burkholderia cepacia		1		1		
	13373	Burkholderia mallei		44		45		1
	243160	Burkholderia mallei ATCC 23344		1		36		35
	412022	Burkholderia mallei NCTC 10229		1		1		
	28450	Burkholderia pseudomallei		1		1		
	320372	Burkholderia pseudomallei 1710b		3		3		
	320373	Burkholderia pseudomallei 668		1		1		
	269483	Burkholderia sp. 383		2		2		
	271848	Burkholderia thailandensis E264		2		2		
	6239	Caenorhabditis elegans		4		11		7
	35305	California encephalitis virus		1		1		
	28873	Camelpox virus		2		2		
	203172	Camelpox virus CMS		26		26		
	203174	Camelpox virus CP1		1		1		
	203173	Camelpox virus M-96		132		132		
	306254	Campylobacter coli RM2228		1		1		
	32019	Campylobacter fetus subsp. fetus	3		3			
	197	Campylobacter jejuni		14	1	16	1	2
	195099	Campylobacter jejuni RM1221		11		13		2
X	407148	Campylobacter jejuni subsp. jejuni 81116				13		13
X	354242	Campylobacter jejuni subsp. jejuni 81-176				1		1
	360112	Campylobacter jejuni subsp. jejuni HB93-13		1		2		1
	192222	Campylobacter jejuni subsp. jejuni NCTC 11168	10		10			
X	44088	Canarypox virus				2		2
	5476	Candida albicans	83	55	83	55		
	10000335	Candida albicans A-9 (serotype B)	1		1			
	10000337	Candida albicans KIT 1113	1		1			
	10000338	Candida albicans LGH1095 (serotype B)	1		1			

NEW 2009	ORGAN-ISM ID	SPECIES STRAIN	B-08	T-08	B-09	T-09	∆ B	∆ T
	5480	Candida parapsilosis	1		1			
	234267	Candidatus Solibacter usitatus Ellin6076		1		1		
	292348	Canine calicivirus (strain 48)	2		2			
	11232	Canine distemper virus		1		1		
	11233	Canine distemper virus strain Onderstepoort	6		6	19		19
	35258	Canine oral papillomavirus		25		25		
	10788	Canine parvovirus	8		21	20	13	20
X	246878	Canine parvovirus 2			3		3	
X	10790	Canine parvovirus strain CPV-D CORNELL 320			1		1	
	9615	Canis lupus familiaris		60		61		1
	11660	Caprine arthritis encephalitis virus	10	1	12	1	2	
	11662	Caprine arthritis encephalitis virus G63	6		6			
X	11661	Caprine arthritis encephalitis virus strain Cork			9		9	
	7957	Carassius auratus	3		3			
	64289	Carey Island virus		2		2		
X	10141	Cavia porcellus			15	63	15	63
	6878	Centruroides noxius	6		7		1	
	13415	Chamaecyparis obtusa		28	1	62	1	34
	12618	Chicken anemia virus	3		3			
X	37124	Chikungunya virus				3		3
	310542	Chimpanzee adenovirus	2		2			
	7154	Chironomus thummi	2	3	2	3		
	7155	Chironomus thummi thummi	8	27	58	27	50	
	810	Chlamydia	9		9			
	243161	Chlamydia muridarum Nigg		14		14		
	813	Chlamydia trachomatis	31	43	77	43	46	
	315277	Chlamydia trachomatis A/HAR-13	6	1	6	1		
	10000858	Chlamydia trachomatis B/Jali-20/OT	2		2			
	10000762	Chlamydia trachomatis B/Tw-5/OT	5		5			
	272561	Chlamydia trachomatis D/UW-3/CX		1		1		
X	10001141	Chlamydia trachomatis Serovar A			22	8	22	8
	10000804	Chlamydia trachomatis Serovar B	3		42	5	39	5
	10000763	Chlamydia trachomatis Serovar C	2		16	1	14	1
X	10001085	Chlamydia trachomatis Serovar D			1		1	
X	10001121	Chlamydia trachomatis Serovar Da			1		1	
	10000764	Chlamydia trachomatis Serovar E	2	1	18	1	16	
X	10000845	Chlamydia trachomatis Serovar F			3		3	
	10000765	Chlamydia trachomatis Serovar H	1		7		6	
	10000766	Chlamydia trachomatis Serovar I	1		10		9	
X	10001008	Chlamydia trachomatis Serovar J			6		6	
	10000767	Chlamydia trachomatis serovar K	9		14		5	
	10000853	Chlamydia trachomatis Serovar L1	17	1	21	3	4	2
	10000768	Chlamydia trachomatis Serovar L2	4	5	15	7	11	2
	10000769	Chlamydia trachomatis Serovar L3	1		1			
	204428	Chlamydiae	1		1			
	83555	Chlamydophila abortus	3		3			
	10000559	Chlamydophila abortus B-577	11		11			

NEW 2009	ORGAN-ISM ID	SPECIES STRAIN	B-08	T-08	B-09	T-09	∆ B	∆ T
	83558	Chlamydophila pneumoniae		18	52	19	52	1
	115713	Chlamydophila pneumoniae CWL029		48		49		1
	10000852	Chlamydophila pneumoniae Kajaani 6		7		7		
X	182082	Chlamydophila pneumoniae TW-183			7		7	
	83554	Chlamydophila psittaci	72		72			
	9534	Chlorocebus aethiops		1		3		2
	12162	Citrus tristeza virus	1		1			
	11096	Classical swine fever virus	3	1	3	1		
	358769	Classical swine fever virus - Alfort/187	2		2			
X	358805	Classical swine fever virus - Alfort/Tuebingen			5		5	
	11098	Classical swine fever virus - Brescia	4		4			
	10001025	Classical swine fever virus Glentorf		26		26		
	10000451	Classical swine fever virus Shimen	16		16			
	36911	Clavispora lusitaniae	2		2			
	214432	Cloning vector pscFvCA-E8VHd		1		1		
	1491	Clostridium botulinum	121	57	121	57		
	36826	Clostridium botulinum A	44		44			
	10000293	Clostridium botulinum A 1	1		1			
	10000294	Clostridium botulinum A 2	2		2			
	10000302	Clostridium botulinum A Kyoto-F	1		1			
	441771	Clostridium botulinum A str. Hall	42		43		1	
	10000301	Clostridium botulinum A str. Hall hyper	3		3			
X	36827	Clostridium botulinum B			28		28	
	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		3	3	1	3
	10000299	Clostridium botulinum E Beluga	2		2			
	36831	Clostridium botulinum F	2		2			
	10000304	Clostridium botulinum F NCTC 10281	1		1			
X	445335	Clostridium botulinum NCTC 2916				2		2
	445338	Clostridium botulinum str. Iwanei E	6		6			
	1496	Clostridium difficile	15		15			
	10000307	Clostridium difficile BART'S W1	1		1			
X	29362	Clostridium papyrosolvens			1		1	
	1502	Clostridium perfringens	7		10		3	
	107819	Clostridium perfringens D	1		1			
	195102	Clostridium perfringens str. 13		1		1		
	1513	Clostridium tetani	75	224	76	227	1	3
X	212717	Clostridium tetani E88				16		16
	5501	Coccidioides immitis		1		1		
	199306	Coccidioides posadasii		2		2		
X	5503	Cochliobolus lunatus			10	10	10	10

NEW 2009	ORGAN-ISM ID	SPECIES STRAIN	B-08	T-08	B-09	T-09	∆ B	∆ T
	9014	Colinus virginianus		2		2		
	8932	Columba livia		8		8		
X	6491	Conus geographus			30		30	
X	6492	Conus magus			2		2	
X	6493	Conus striatus			11		11	
	32614	Convict Creek 107 virus		3	1	3	1	
	13451	Corylus avellana	2	27	27	27	25	
	1717	Corynebacterium diphtheriae	2	11	10	50	8	39
	152794	Corynebacterium efficiens		5		5		
	1718	Corynebacterium glutamicum		21		21		
	306537	Corynebacterium jeikeium K411		1		1		
X	10703	Corynephage beta			2		2	
	186541	Cote d'Ivoire ebolavirus		1		1		
	128999	Cote d'Ivoire ebolavirus - Cote d'Ivoire (Tai Forest, 1994)		3		3		
X	10623	Cottontail rabbit papillomavirus			3	5	3	5
	12264	Cowpea mosaic virus		1		1		
	10243	Cowpox virus		16		19		3
	265872	Cowpox virus (Brighton Red)		1		1		
	10000571	Cowpox virus (Brighton Red) White-pock		1		1		
	777	Coxiella burnetii		31		32		1
X	360117	Coxiella burnetii RSA 334				14		14
X	227377	Coxiella burnetii RSA 493				1		1
	103903	Coxsackievirus B3 (strain Nancy)	13	30	13	30		
	103905	Coxsackievirus B4 (strain E2)	5	41	5	41		
	103906	Coxsackievirus B4 (strain JVB / Benschoten / New York/51)		76		76		
X	10029	Cricetulus griseus			1		1	
X	11593	Crimean-Congo hemorrhagic fever virus				1		1
X	368445	Crocodilepox virus				1		1
	8732	Crotalus durissus terrificus	2		4		2	
X	10001132	Cryptococcus neoformans var. neoformans Serotype A			1		1	
	3369	Cryptomeria japonica	25	170	25	181		11
	237895	Cryptosporidium hominis		3		3		
	5807	Cryptosporidium parvum		21		23		2
	353152	Cryptosporidium parvum Iowa II		1		27		26
	220837	Cryptosporidium sp. MNJ-1		1		1		
X	12305	Cucumber mosaic virus			1		1	
	3656	Cucumis melo	12		12			
	208899	Cupixi virus		1		1		
	301964	CY1014 virus		1		1		
	46457	Cycloclasticus oligotrophus		1		1		
	28909	Cynodon dactylon	1	23	3	23	2	
	10358	Cytomegalovirus		32		32		
	7955	Danio rerio		3		3		
	4039	Daucus carota		1		1		
X	305674	Deerpox virus W-848-83				1		1

NEW 2009	ORGAN-ISM ID	SPECIES STRAIN	B-08	T-08	B-09	T-09	∆ B	∆ T
	243164	Dehalococcoides ethenogenes 195		1		1		
	12637	Dengue virus		25	1	25	1	
	11053	Dengue virus 1	3	41	3	46		5
	11059	Dengue virus 1 Nauru/West Pac/1974	1		1			
	33741	Dengue virus 1 Singapore/S275/1990		30		30		
	11060	Dengue virus 2	49	80	79	92	30	12
	31635	Dengue virus 2 16681-PDK53		2		2		
	11064	Dengue virus 2 Jamaica/1409/1983	262	11	262	11		
X	11062	Dengue virus 2 Malaysia M2			1		1	
	11066	Dengue virus 2 Puerto Rico/PR159-S1/1969	30		30			
	31634	Dengue virus 2 Thailand/16681/84	9	50	9	55		5
	11065	Dengue virus 2 Thailand/NGS-C/1944	10	10	14	10	4	
	11069	Dengue virus 3		53	2	58	2	5
X	408870	Dengue virus 3 Philippines/H87/1956			4		4	
	11070	Dengue virus 4	5	37	5	41		4
	408871	Dengue virus 4 Dominica/814669/1981	1	5	1	5		
	408688	Dengue virus 4 Thailand/0348/1991		1		1		
	10000965	Dengue virus type 1 FGA/89	1		1			
	10000440	Dengue virus type 1 Hawaii		9		9		
	10000442	Dengue virus type 3 CH53489		6		6		
	6954	Dermatophagoides farinae	11	36	12	36	1	
	6956	Dermatophagoides pteronyssinus	44	97	54	104	10	7
X	11319	Dhori virus (strain Indian/1313/61)			1		1	
	12506	Dobrava-Belgrade virus		13		13		
X	7441	Dolichovespula maculata			11	20	11	20
	7227	Drosophila melanogaster	2	1	2	2		1
	12639	Duck hepatitis B virus	189	20	189	20		
	10000466	Duvenhage virus 6		2		2		
	11022	Eastern equine encephalitis virus (STRAIN VA33[TEN BROECK])		1		1		
	10000439	Eastern equine encephalitis virus SV	8		8			
	205488	Ebola virus sp.		1		1		
	6210	Echinococcus granulosus	19		37		18	
	99586	Echis ocellatus	5		5			
	31705	Echovirus 11 (strain Gregory)		1		1		
	12643	Ectromelia virus		2		2		
X	944	Ehrlichia canis			7		7	
X	945	Ehrlichia chaffeensis			9		9	
X	35795	Ehrlichia muris				1		1
	779	Ehrlichia ruminantium	3		3			
X	5801	Eimeria acervulina			1		1	
	5802	Eimeria tenella	4		6		2	
	35321	El Moro Canyon virus		2		2		
	6035	Encephalitozoon cuniculi		5		5		
X	284813	Encephalitozoon cuniculi GB-M1				5		5
	12104	Encephalomyocarditis virus		1		1		
	5759	Entamoeba histolytica	27	5	29	8	2	3

NEW 2009	ORGAN-ISM ID	SPECIES STRAIN	B-08	T-08	B-09	T-09	∆ B	∆ T
	294381	Entamoeba histolytica HM-1:IMSS		22		46		24
	10000352	Entamoeba histolytica YS-27	1		1			
	12340	Enterobacteria phage 933J	1		2		1	
	10730	Enterobacteria phage 933W	1		1			
	10863	Enterobacteria phage f1		1		1		
X	10864	Enterobacteria phage fd			7		7	
	10710	Enterobacteria phage lambda		4		4		
	10754	Enterobacteria phage P22	5		5			
X	10658	Enterobacteria phage PRD1			2		2	
	10665	Enterobacteria phage T4	5	20	10	20	5	
X	10760	Enterobacteria phage T7			1		1	
	12022	Enterobacterio phage MS2	1		1			
X	1351	Enterococcus faecalis			1		1	
X	1352	Enterococcus faecium			6		6	
	12059	Enterovirus		9		9		
	150846	Enterovirus 5865/sin/000009	2		2			
	82830	Epstein-barr virus strain ag876	1	1	1	1		
	10326	Equid herpesvirus 1	5		5			
	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	33	78	91	109	58	31
	11670	Equine infectious anemia virus (CLONE 1369)		1		1		
	11671	Equine infectious anemia virus (STRAIN WSU5)		16		16		
	10000499	Equine infectious anemia virus PV		2		2		
	10000835	Equine rhinitis A virus 393/76	4		4			
	9796	Equus caballus	1	43	2	43	1	
X	9798	Equus przewalskii				1		1
	562	Escherichia coli	113	38	176	46	63	8
X	10001145	Escherichia coli 1471			2		2	
	10000727	Escherichia coli 180/C3	1		1			
	362663	Escherichia coli 536		2		2		
X	525281	Escherichia coli 83972				2		2
	37762	Escherichia coli B	1	1	1	1		
	10000728	Escherichia coli B B/r CM6		1		1		
	316401	Escherichia coli ETEC H10407	62	31	62	31		
X	585034	Escherichia coli IAI1			3		3	
	83333	Escherichia coli K-12	3	7	4	7	1	
	168807	Escherichia coli O127:H6	1		1			
	83334	Escherichia coli O157:H7	2	103	2	103		
X	155864	Escherichia coli O157:H7 EDL933				1		1

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X	478005	Escherichia coli O157:H7 str. EC4486				1		1
X	478006	Escherichia coli O157:H7 str. EC4501				2		2
X	478008	Escherichia coli O157:H7 str. EC869				13		13
	10000733	Escherichia coli O5:K4:H4	1		1			
	217992	Escherichia coli O6		7		7		
	10000734	Escherichia coli O65:K-:H-	1		1			
	364106	Escherichia coli UTI89		2		2		
	2759	Eukaryota	1		1			
	6958	Euroglyphus maynei		10		10		
	420521	Expression vector pNIC-NHT-CF	1		1			
	3617	Fagopyrum esculentum	28		39		11	
	6690	Farfantepenaeus aztecus	43		43			
	46835	Fasciola gigantica	2		2			
	6192	Fasciola hepatica	24	11	24	11		
	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		
	11674	Feline immunodeficiency virus (isolate Petaluma)	2	3	2	3		
X	45409	Feline immunodeficiency virus (isolate wo)			3		3	
X	36372	Feline immunodeficiency virus (strain UK8)				1		1
	33734	Feline infectious peritonitis virus (strain 79-1146)	4		4			
X	11769	Feline leukemia virus strain A/Glasgow-1			6		6	
X	10001130	Feline leukemia virus subtype A			2		2	
X	10786	Feline panleukopenia virus				4		4
	9685	Felis catus	18	26	18	48		22
	4606	Festuca arundinacea	1		1			
	156586	Flavobacteria bacterium BBFL7		1		1		
	12110	Foot-and-mouth disease virus	8	2	22	2	14	
	10000991	Foot-and-mouth disease virus - type A (strain A22 Iraq)	5		5			
	10000989	Foot-and-mouth disease virus - type A (strain A22)	8	6	8	6		
	110195	Foot-and-mouth disease virus - type Asia 1	2	2	2	2		
	10000995	Foot-and-mouth disease virus - type Asia 1 Pakistan	1		1			
	12116	Foot-and-mouth disease virus - type C	3		6	25	3	25
	12118	Foot-and-mouth disease virus - type O	3	2	16	3	13	1
	10000801	Foot-and-mouth disease virus - type O (O/SKR/2002)	1		1			
	10001118	Foot-and-mouth disease virus - type O (strain HKN/14/82)	2		2			
	10000856	Foot-and-mouth disease virus - type O isolate O/UKG/35/2001		13		13		
	10000992	Foot-and-mouth disease virus - type SAT 1 (Strain Bot 1/68)	1		1			
	10000993	Foot-and-mouth disease virus - type SAT 2 (Strain Ken 3/57)	1		1			
	10001000	Foot-and-mouth disease virus - type SAT 2 (strain Rho 1/48)	4		4			
	10000994	Foot-and-mouth disease virus - type SAT 3 (Strain Bec 1/65)	1		1			

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	12112	Foot-and-mouth disease virus (strain A10-61)	8		8			
	12114	Foot-and-mouth disease virus (strain A12)	17		21		4	
	12115	Foot-and-mouth disease virus (strain A24 Cruzeiro)	1		14	3	13	3
	12113	Foot-and-mouth disease virus (strain A5)	3		3			
X	12120	Foot-and-mouth disease virus (strain C1-Santa Pau)			1		1	
	12117	Foot-and-mouth disease virus (strain C3 Indaial)	1		2		1	
	73482	Foot-and-mouth disease virus (strain O1)	16	1	18	1	2	
	10000820	Foot-and-mouth disease virus (strain O1) (O/Taiwan/1/97)	1		1			
	10000964	Foot-and-mouth disease virus (strain O1) (O1 Brugge)	2		2			
	10000516	Foot-and-mouth disease virus (strain O1) (O1 Campos)	6	5	18	18	12	13
	10000513	Foot-and-mouth disease virus (strain O1) (O1 Kaufbeuren)	37	8	37	8		
	10000514	Foot-and-mouth disease virus (strain O1) (O1BFS 1860)	8		8			
	10000515	Foot-and-mouth disease virus (strain O1) (O1BFS)	3		4		1	
	10000556	Foot-and-mouth disease virus (strain O1) Kaufbeuren	26	11	42	11	16	
	161727	Foot-and-mouth disease virus A10/Holland	11	14	11	14		
	12121	Foot-and-mouth disease virus C1	1		1			
	10000840	Foot-and-mouth disease virus C1 Brescia It/64	2		2			
	10000836	Foot-and-mouth disease virus C1 CS8	22	24	22	24		
	46290	Foot-and-mouth disease virus C3	3	1	3	1		
	10001039	Foot-and-mouth disease virus C3 (strain Resendne-Br/55)	1		1			
	244367	Foot-and-mouth disease virus C-S8c1	9	1	12	17	3	16
	13067	Forficula		2		2		
	31621	Four Corners hantavirus	2	1	2	1		
	10261	Fowlpox virus		1		3		2
	10263	Fowlpox virus (isolate HP-438[Munich])		1		1		
	263	Francisella tularensis		4		5		1
	376619	Francisella tularensis subsp. holarctica LVS		67		68		1
	393011	Francisella tularensis subsp. holarctica OSU18		2		2		
	119856	Francisella tularensis subsp. tularensis		4		5		1
X	430557	Francisella tularensis subsp. tularensis FSC033				26		26
	393115	Francisella tularensis subsp. tularensis FSC198		3		3		
	177416	Francisella tularensis subsp. tularensis SCHU S4		89		90		1
X	418136	Francisella tularensis subsp. tularensis WY96-3418				1		1
	11795	Friend murine leukemia virus		4	6	21	6	17
	11797	Friend murine leukemia virus (ISOLATE FB29)		1		1		
	8053	Gadus callarias	10		10			
	9031	Gallus gallus	66	104	193	132	127	28
	11824	Gardner-Arnstein feline leukemia oncovirus B	1		13		12	
	54290	GB virus C	9		14		5	
X	471223	Geobacillus sp. WCH70				2		2
	1422	Geobacillus stearothermophilus	1		1			
	5741	Giardia intestinalis		8		8		
	184922	Giardia lamblia ATCC 50803		157		194		37

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	3847	Glycine max	68	1	71	1	3	
	9595	Gorilla gorilla gorilla		4		4		
	55951	Grapevine leafroll-associated virus 3	1		1			
	35288	Grapevine virus A	19		19			
	45219	Guanarito virus		11		835		824
	114727	H1N1 subtype	1		1			
X	10001225	H1N1 subtype Influenza A/Oklahoma/7485/01				6		6
	10001315	H1N1 swine influenza virus (A/swine/Korea/S10/2004(H1N1))		3		3		
	10001316	H1N1 swine influenza virus (A/swine/Korea/S175/2004(H1N1))		1		1		
X	119210	H3N2 subtype			1	2	1	2
	10001157	H3N2 subtype Influenza A virus (A/Hong Kong(H3N2))		15		15		
	102793	H5N1 subtype		16	2	16	2	
	10001317	H9N2 subtype Influenza A virus (A/swine/Korea/S81/2004(H9N2))		1		1		
	10001318	H9N2 subtype Influenza A virus (A/swine/Korea/S83/2004(H9N2))		2		2		
	730	Haemophilus ducreyi		1		1		
	727	Haemophilus influenzae	10	52	17	54	7	2
	10001055	Haemophilus influenzae 6U	1		2		1	
X	521005	Haemophilus influenzae 7P49H1				1		1
	281310	Haemophilus influenzae 86-028NP	1		1			
X	10001056	Haemophilus influenzae ATCC 9795			2		2	
	10001053	Haemophilus influenzae MinnA	8		9		1	
	10000833	Haemophilus influenzae NTHi 1128	6		6			
	10001042	Haemophilus influenzae NTHi 1479	11	4	12	4	1	
	10000807	Haemophilus influenzae NTHi UC19	2	2	2	2		
	374928	Haemophilus influenzae PittAA		1		1		
X	374932	Haemophilus influenzae PittHH			1		1	
X	375432	Haemophilus influenzae R3021				1		1
	10000860	Haemophilus influenzae Serotype B	3		14	9	11	9
X	10001155	Haemophilus influenzae strain 1479			2		2	
X	10001149	Haemophilus influenzae Subtype 1H			23		23	
	10000861	Haemophilus influenzae Variant d1	18		18			
X	10690	Haemophilus phage HP1				1		1
	205914	Haemophilus somnus 129PT		1		1		
	6454	Haliotis rufescens	1		1			
X	10626	Hamster polyomavirus			11		11	
	11599	Hantaan virus	2	40	2	41		1
	11602	Hantaan virus 76-118	11	8	11	8		
X	370830	Hantaan virus Q32				4		4
X	458678	Hantaanvirus CGRn93P8				2		2
	74942	Hantavirus CRF355		1		1		
	42358	Hantavirus Monongahela-3		5		5		
	37741	Hantavirus sp.		2		2		
	13557	Hapalemur griseus		1		1		
	4232	Helianthus annuus	18		18			

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	32025	Helicobacter hepaticus		1		1		
	235279	Helicobacter hepaticus ATCC 51449	2		2			
	210	Helicobacter pylori	26	4	27	4	1	
	85962	Helicobacter pylori 26695	13		13	1		1
	10000718	Helicobacter pylori J223	2		2			
X	570508	Helicobacter pylori P12				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	9	23	9	1	
	10407	Hepatitis B virus	186	445	210	456	24	11
	12513	Hepatitis B virus 2		1		1		
	31512	Hepatitis B virus adr/mutant		1		1		
	10409	Hepatitis B virus adr4	1	11	1	11		
	10410	Hepatitis B virus adw/991	2	2	2	2		
	10412	Hepatitis B virus adw/Indonesia/PIDW420		2		2		
	10415	Hepatitis B virus adw/Okinawa/PODW282		4		4		
	45410	Hepatitis B virus adw4/Brazil/isolate w4b		6		6		
	10411	Hepatitis B virus alpha1		15		15		
X	489469	Hepatitis B virus ayw/China/Tibet127/2002			1		1	
	391647	Hepatitis B virus ayw2	6		6			
	391646	Hepatitis B virus ayw3	1		1			
	391650	Hepatitis B virus ayw4	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			
	10414	Hepatitis B virus LSH/chimpanzee		2		2		
	10001156	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		
	10408	Hepatitis B virus subtype adw2	70	59	71	59	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	31	164	57	165	26	1
	11103	Hepatitis C virus	605	703	649	847	44	144
	11104	Hepatitis C virus (isolate 1)	35	215	37	215	2	
	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		

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	63746	Hepatitis C virus (isolate H77)	31	149	32	174	1	25
	356410	Hepatitis C virus (isolate HC-G9)	2	1	2	1		
	11110	Hepatitis C virus (isolate HCT18)	1		1			
	356416	Hepatitis C virus (isolate HCV-K3a/650)		14		14		
	31644	Hepatitis C virus (isolate HCV-KF)	1	1	1	1		
	356386	Hepatitis C virus (isolate India)		1		1		
	11116	Hepatitis C virus (isolate Japanese)	6	26	6	26		
	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	43		15
	40271	Hepatitis C virus genotype 2	41		41	5		5
	356114	Hepatitis C virus genotype 3	114	3	114	10		7
	33745	Hepatitis C virus genotype 4		1		2		1
X	33746	Hepatitis C virus genotype 5				1		1
X	42182	Hepatitis C virus genotype 6				6		6
	421877	Hepatitis C virus isolate HC-J1	2	26	3	26	1	
	11113	Hepatitis C virus isolate HC-J6	2	2	3	2	1	
	11115	Hepatitis C virus isolate HC-J8	2	1	2	1		
	356411	Hepatitis C virus JFH-1	2	1	2	1		
	31646	Hepatitis C virus subtype 1a	142	236	143	312	1	76
	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	146	525	157	2	11
	10000456	Hepatitis C virus subtype 1b AD78	71		71			
	10000968	Hepatitis C virus subtype 1b isolate BE-11	3		3			
X	10000460	Hepatitis C virus subtype 1b JK1			13		13	
	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	5	3	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	45	2	48	7	3	5
	10000522	Hepatitis delta virus (isolate TW2667)		5		5		
	12461	Hepatitis E virus	131	27	131	27		
	31767	Hepatitis E virus (strain Burma)	160		160			
	31768	Hepatitis E virus (strain Mexico)	31		31			
	10000519	Hepatitis E virus China Xinjiang	1		1			
	10000520	Hepatitis E virus SAR-55	1	6	1	6		
	39113	Hepatitis GB virus B		4		4		
	28300	Heron hepatitis B virus		1		1		
	10299	Herpes simplex virus (type 1 / strain 17)	44	22	44	30		8

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	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		6		1	
	10292	Herpesviridae	5	1	5	4		3
X	49011	Hesperocyparis arizonica			1		1	
	3981	Hevea brasiliensis	43	42	164	43	121	1
	11685	HIV-1 M:B_ARV2/SF2		43		43		
	11706	HIV-1 M:B_HXB2R		12		12		
	11696	HIV-1 M:B_MN		21	1	21	1	
	11583	HoJo virus		1		1		
	29679	Holcus lanatus	14		14			
	9606	Homo sapiens	355	1455	1349	2771	994	1316
	343462	Human adenovirus 11p	7		7			
	28282	Human adenovirus 12		1	9	1	9	
X	28276	Human adenovirus 15			1		1	
	10515	Human adenovirus 2	22	5	28	5	6	
	45659	Human adenovirus 3		1	15	1	15	
	28284	Human adenovirus 40		1	2	1	2	
	28285	Human adenovirus 5	17	21	22	117	5	96
X	31545	Human adenovirus 8			1		1	
X	10001392	Human adenovirus B strain Harbin04B			5		5	
	129951	Human adenovirus C		1		2		1
X	130309	Human adenovirus F			1		1	
	11137	Human coronavirus 229E		2		2		
X	31631	Human coronavirus OC43				1		1
	12067	Human coxsackievirus A9	7		7			
	12071	Human coxsackievirus B1	4		12		8	
	12072	Human coxsackievirus B3	7	9	7	11		2
X	10001213	Human coxsackievirus B3 (strain RK)			1		1	
	12073	Human coxsackievirus B4	4	2	5	49	1	47
	11827	Human endogenous retrovirus	1	1	1	1		
	39054	Human enterovirus 71	2		2			
	138950	Human enterovirus C	5	3	6	3	1	
	208726	Human hepatitis A virus	4		4			
	12098	Human hepatitis A virus Hu/Australia/HM175/1976	86	2	86	62		60
	10298	Human herpesvirus 1	130	66	134	68	4	2
	10000394	Human herpesvirus 1 103/65	1		1			
	10000396	Human herpesvirus 1 McIntyre		1		1		
	10000398	Human herpesvirus 1 NS	1		1			
	10306	Human herpesvirus 1 strain KOS	17	4	17	4		
	10310	Human herpesvirus 2	87	38	88	109	1	71
	10312	Human herpesvirus 2 strain 186		1		1		
	10313	Human herpesvirus 2 strain 333		4		4		
	10315	Human herpesvirus 2 strain HG52		14		33		19
	10335	Human herpesvirus 3	4	62	4	78		16

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	10000406	Human herpesvirus 3 H-551	26	15	26	15		
	10338	Human herpesvirus 3 strain Dumas		28		28		
	10376	Human herpesvirus 4	65	285	80	320	15	35
	10377	Human herpesvirus 4 (strain B95-8)	37	175	62	234	25	59
	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	3	11	2	3
	12509	Human herpesvirus 4 type 2	1	1	1	1		
	10000427	Human herpesvirus 4 type A		5		5		
	10359	Human herpesvirus 5	75	324	76	338	1	14
	10360	Human herpesvirus 5 strain AD169	27	244	27	302		58
	10363	Human herpesvirus 5 strain Towne	4	21	4	23		2
	10368	Human herpesvirus 6	2	1	2	1		
	10369	Human herpesvirus 6 (strain GS)	2		2			
	10370	Human herpesvirus 6 (strain Uganda-1102)	1	2	1	2		
X	36351	Human herpesvirus 6 strain Z29			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	127		2
	12721	Human immunodeficiency virus	1	11	1	15		4
	11676	Human immunodeficiency virus 1	4	111	7	190	3	79
	10000500	Human immunodeficiency virus 1 IIIB		2		2		
	11709	Human immunodeficiency virus 2		5		6		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		6		1
	11689	Human immunodeficiency virus type 1 (ELI ISOLATE)		4		4		
	362651	Human immunodeficiency virus type 1 (isolate YU2)		21		21		
	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		
	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)	1	19	1	19		
	11691	Human immunodeficiency virus type 1 (SF162 ISOLATE)		1		1		

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	11690	Human immunodeficiency virus type 1 (SF33 ISOLATE)		2		2		
	11703	Human immunodeficiency virus type 1 (STRAIN UGANDAN / ISOLATE U455)		14		14		
	31678	Human immunodeficiency virus type 1 (WMJ1 isolate)		15		15		
	11705	Human immunodeficiency virus type 1 (WMJ2 ISOLATE)		1		1		
	11683	Human immunodeficiency virus type 1 (Z2/CDC-Z34 ISOLATE)		1		1		
	11678	Human immunodeficiency virus type 1 BH10		16		16		
	11714	Human immunodeficiency virus type 2 (ISOLATE BEN)		7		7		
	11715	Human immunodeficiency virus type 2 (ISOLATE CAM2)		1		1		
	11713	Human immunodeficiency virus type 2 (ISOLATE D194)		1		1		
	11716	Human immunodeficiency virus type 2 (ISOLATE D205,7)		1		1		
	11717	Human immunodeficiency virus type 2 (ISOLATE GHANA-1)		5		5		
	73484	Human immunodeficiency virus type 2 (isolate KR)		2		2		
	11718	Human immunodeficiency virus type 2 (ISOLATE SBLISY)		2		2		
	162145	Human metapneumovirus		22	7	22	7	
	10566	Human papillomavirus		3	4	3	4	
	334203	Human papillomavirus - 1		1		41		40
X	337042	Human papillomavirus - 18			9	4	9	4
X	337043	Human papillomavirus - 2				6		6
	10580	Human papillomavirus type 11		5	4	32	4	27
X	10573	Human papillomavirus type 13			1		1	
	333760	Human papillomavirus type 16	4	56	232	305	228	249
	333761	Human papillomavirus type 18		10	18	75	18	65
X	10583	Human papillomavirus type 1a			7	7	7	7
X	333751	Human papillomavirus type 2				2		2
X	333762	Human papillomavirus type 26				1		1
	37112	Human papillomavirus type 29		1		1		
X	10614	Human papillomavirus type 3				3		3
	10585	Human papillomavirus type 31		5	2	6	2	1
X	333763	Human papillomavirus type 32			1		1	
	10586	Human papillomavirus type 33		3	5	8	5	5
X	10587	Human papillomavirus type 35				1		1
X	10588	Human papillomavirus type 39				1		1
X	10617	Human papillomavirus type 4				4		4
X	10615	Human papillomavirus type 40			1		1	
	10592	Human papillomavirus type 44		1		1		
	10593	Human papillomavirus type 45		2		5		3
X	10595	Human papillomavirus type 51				1		1
	10618	Human papillomavirus type 52		4		4		
	333765	Human papillomavirus type 53		1		1		
	10596	Human papillomavirus type 56		3		3		

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	10598	Human papillomavirus type 58		3		4		1
	37115	Human papillomavirus type 59		1		1		
X	31552	Human papillomavirus type 6			9	3	9	3
	45240	Human papillomavirus type 68		1		1		
	10600	Human papillomavirus type 6b		3	11	24	11	21
X	10620	Human papillomavirus type 7			1	1	1	1
X	51033	Human papillomavirus type 73				1		1
	36412	Human parainfluenza 1 virus (strains A1426 / 86-315 / 62M-753)		1		1		
	11217	Human parainfluenza 3 virus (strain NIH 47885)	5		8		3	
X	11212	Human parainfluenza virus 2			10		10	
X	11214	Human parainfluenza virus 2 (strain Toshiba)			3		3	
X	11216	Human parainfluenza virus 3			2		2	
	12063	Human parechovirus 1	5		5			
	10798	Human parvovirus B19	90	44	90	44		
	10000438	Human parvovirus B19 genotype 1	1		1			
	12080	Human poliovirus 1	2	1	4	1	2	
	12081	Human poliovirus 1 Mahoney	38	9	49	20	11	11
	12082	Human poliovirus 1 strain Sabin	7		7			
	10001028	Human poliovirus 2 (strain MEF-1)	1		1			
	10001040	Human poliovirus 2 (strain Sabin)	2		2	7		7
	12086	Human poliovirus 3	3	2	3	2		
	10001086	Human poliovirus 3 (strain Sabin)	3		36	1	33	1
	11250	Human respiratory syncytial virus	11	16	11	31		15
	11255	Human respiratory syncytial virus (strain RSB6190)	6		6			
	11256	Human respiratory syncytial virus (strain RSB6256)	10		10			
	11252	Human respiratory syncytial virus (strain RSB642)	1		1			
	11251	Human respiratory syncytial virus (subgroup B / strain 18537)	2	1	2	1		
	208893	Human respiratory syncytial virus A	1	2	1	3		1
	10000960	Human respiratory syncytial virus A Mon/3/88	6		6			
	11260	Human respiratory syncytial virus A strain Long	65	7	120	7	55	
	11259	Human respiratory syncytial virus A2	46	90	48	107	2	17
	410078	Human respiratory syncytial virus S2	1		1			
	12131	Human rhinovirus 14	9		12		3	
X	12134	Human rhinovirus 1A				19		19
	12130	Human rhinovirus 2	11		11			
	10000987	Human rhinovirus 2 Vienna	5		5			
X	147711	Human rhinovirus A			1		1	
	10950	Human rotavirus (SEROTYPE 2 / STRAIN DS1)	1		1			
X	31569	Human rotavirus (serotype 2 / strain RV-5)			1		1	
	10941	Human rotavirus A	1	2	13	2	12	
	10960	Human rotavirus G4 strain St. Thomas 3		1	6	1	6	
X	374507	Human rotavirus G9 isolate F45			7		7	
X	10001215	Human rotavirus G9 WI61			1		1	
X	408599	Human rotavirus G9P[8]			1		1	
X	10952	Human rotavirus strain KU			9		9	
X	10957	Human rotavirus strain P			1		1	

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X	10958	Human rotavirus strain RRV			1		1	
	10962	Human rotavirus strain WA	8	4	10	7	2	3
	11927	Human T-cell lymphotrophic virus type 1 (Caribbean isolate)		4		5		1
	10001004	Human T-cell lymphotrophic virus type 1 (Caribbean isolate) (Strain HS35)	1		1			
	11928	Human T-cell lymphotrophic virus type 1 (isolate MT-2)	1		1			
	11926	Human T-cell lymphotrophic virus type 1 (strain ATK)	25	3	30	118	5	115
X	39015	Human T-cell lymphotropic virus type 1 (african isolate)				2		2
	11908	Human T-lymphotropic virus 1	128	94	214	162	86	68
	11909	Human T-lymphotropic virus 2	63	1	63	2		1
	77644	IncQ plasmid pIE1120		1		1		
	11120	Infectious bronchitis virus	1		5		4	
	10000825	Infectious bronchitis virus Avian strain D207	11		11			
	10995	Infectious bursal disease virus	11		11			
X	10997	Infectious bursal disease virus 002-73/AUS			1		1	
	11290	Infectious hematopoietic necrosis virus	8		8			
	11320	Influenza A virus	16	167	29	245	13	78
	387139	Influenza A virus (A/Aichi/2/1968(H3N2))	4	10	5	10	1	
X	553345	Influenza A virus (A/Aichi/72/2007(H3N2))			1		1	
	385576	Influenza A virus (A/Alaska/6/1977(H3N2))		1		1		
	383602	Influenza A virus (A/Anas acuta/Primorje/695/1976(H2N3))		10		10		
	384498	Influenza A virus (A/Ann Arbor/6/1960(H2N2))		180	1	180	1	
	62446	Influenza A virus (A/Argentina/3779/94(H3N2))		1		1		
	385630	Influenza A virus (A/Bangkok/1/1979(H3N2))	1	4	1	4		
	384500	Influenza A virus (A/Beijing/11/1956(H1N1))		22		22		
	380950	Influenza A virus (A/Beijing/32/1992(H3N2))		54		54		
	282811	Influenza A virus (A/Bilthoven/4791/81(H3N2))		3		3		
X	88776	Influenza A virus (A/Brevig Mission/1/1918(H1N1))			1		1	
	385587	Influenza A virus (A/budgerigar/Hokkaido/1/1977(H4N6))		4		4		
X	352963	Influenza A virus (A/California/7/2004(H3N2))				1		1
	387191	Influenza A virus (A/camel/Mongolia/1982(H1N1))		8		8		
	205946	Influenza A virus (A/Chicken/Beijing/1/95(H9N2))		1		1		
	404137	Influenza A virus (A/chicken/Beijing/nl/2002(H9N2))		1		1		
	36418	Influenza A virus (A/chicken/Brescia/1902(H7N7))		1		1		
	342137	Influenza A virus (A/chicken/CA/375TR/2002(H6N2))		1		1		
	11384	Influenza A virus (A/chicken/FPV/Weybridge(H7N7))		1		1		
X	197579	Influenza A virus (A/Chicken/Guangdong/11/97(H9N2))				1		1
X	435359	Influenza A virus (A/chicken/Hebei/706/2005(H5N1))				1		1
	357205	Influenza A virus (A/chicken/Hong Kong/3123.1/2002(H5N1))		1		1		
	97348	Influenza A virus (A/Chicken/Hong Kong/G23/97(H9N2))		1		1		
	404150	Influenza A virus (A/chicken/Hubei/wk/1997(H5N1))		2		2		
	404155	Influenza A virus (A/chicken/Hunan/fg/2004(H5N1))		2		2		

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X	447133	Influenza A virus (A/chicken/Japan/1925(H7N7))			1		1	
	404163	Influenza A virus (A/chicken/Jilin/hg/2002(H5N1))		1		1		
	342221	Influenza A virus (A/chicken/Korea/S4/2003(H9N2))		1		1		
	298713	Influenza A virus (A/chicken/Korea/SNU0091/00(H9N2))		1		1		
	298716	Influenza A virus (A/chicken/Korea/SNU1035C/00(H9N2))		1		1		
	270490	Influenza A virus (A/chicken/Nakorn-Patom/Thailand/CU-K3/2004(H5N1))		1		1		
	215862	Influenza A virus (A/Chicken/Nanchang/2-220/2001(H3N6))		1		1		
	385617	Influenza A virus (A/chicken/Pennsylvania/1370/1983(H5N2))	1		1			
	392810	Influenza A virus (A/chicken/Rostock/8/1934(H7N1))	2	4	2	4		
	197585	Influenza A virus (A/chicken/Shandong/6/96(H9N2))	1		1			
	264510	Influenza A virus (A/chicken/Thailand/LV1NF/2004(H5N1))		1		1		
	393548	Influenza A virus (A/chicken/Tula/Russia/Oct-5/2005(H5N1))		1		1		
	299730	Influenza A virus (A/chicken/Viet Nam/AG-010/2004(H5N1))		1		1		
	299387	Influenza A virus (A/chicken/Viet Nam/DT-171/2004(H5N1))		1		1		
	380836	Influenza A virus (A/chicken/Vietnam/5/2003(H5N1))		1		1		
	380985	Influenza A virus (A/Chile/1/1983(H1N1))		1		1		
	62541	Influenza A virus (A/Christchurch/2/1988(H3N2))		1		1		
	284168	Influenza A virus (A/Ck/HK/2133.1/2003(H5N1))		1		1		
	354235	Influenza A virus (A/Ck/HK/CSW161/2003(H9N2))		1		1		
	284195	Influenza A virus (A/Ck/YN/115/2004(H5N1))		1		1		
	107493	Influenza A virus (A/Cordoba/3278/96(H3N2))		1		1		
X	291592	Influenza A virus (A/crow/Kyoto/53/2004(H5N1))			1		1	
	385583	Influenza A virus (A/Denver/1957(H1N1))		1		1		
	383550	Influenza A virus (A/duck/England/1/1956(H11N6))		1		1		
	274829	Influenza A virus (A/duck/Fujian/17/2001(H5N1))		1		1		
	365078	Influenza A virus (A/duck/Guangxi/1586/2004(H5N1))		1		1		
	395841	Influenza A virus (A/duck/Hokkaido/1130/01(H1N1))		1		1		
X	249372	Influenza A virus (A/duck/Hokkaido/13/00(H9N2))			2		2	
	387207	Influenza A virus (A/duck/Hokkaido/8/1980(H3N8))		6		6		
X	176672	Influenza A virus (A/Duck/Hong Kong/ww461/2000(H5N1))				1		1
	384946	Influenza A virus (A/duck/Hungary/1/1970(H6N2))		1		1		
	370813	Influenza A virus (A/duck/IT/701/2005(H10N7))		1		1		
	311169	Influenza A virus (A/duck/Korea/S10/03(H3N2))		1		1		
	441962	Influenza A virus (A/duck/Mongolia/47/2001(H7N1))		3		3		
	353253	Influenza A virus (A/duck/Novosibirsk/56/2005(H5N1))		2		2		
	210656	Influenza A virus (A/Duck/Shantou/1881/00(H9N2))		1		1		
	210659	Influenza A virus (A/Duck/Shantou/2088/01(H9N2))		1		1		
	210663	Influenza A virus (A/Duck/Shantou/2134/00(H9N2))		1		1		
	210655	Influenza A virus (A/Duck/Shantou/2144/00(H9N2))		1		1		
	385580	Influenza A virus (A/duck/Ukraine/1/1963(H3N8))	3		3			

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	380842	Influenza A virus (A/duck/Vietnam/15/2003(H5N1))		1		1		
	11375	Influenza A virus (A/Dunedin/4/73(H3N2))	2		2			
	279797	Influenza A virus (A/egret/Hong Kong/757.3/2002(H5N1))		3		3		
	192549	Influenza A virus (A/Egypt/96/2002(H1N2))		1		1		
	380210	Influenza A virus (A/England/333/1980(H1N1))	1	1	1	1		
	198059	Influenza A virus (A/England/627/01(H1N2))		2		2		
X	573797	Influenza A virus (A/England/654/2007(H1N1))				1		1
	387147	Influenza A virus (A/England/878/1969(H3N2))	1	2	1	2		
	137578	Influenza A virus (A/England/939/69 x A/PR/8/34)		2		2		
	336794	Influenza A virus (A/equine/Massachussetts/213/2003(H3N8))		1		1		
	387223	Influenza A virus (A/equine/Miami/1963(H3N8))	5		5			
	336800	Influenza A virus (A/equine/New York/1/1999(H3N8))		3		3		
	207401	Influenza A virus (A/finch/Canada/NS1301/2001(H3N8))		2		2		
X	367120	Influenza A virus (A/Fort Monmouth/1/1947(H1N1))			1		1	
	380282	Influenza A virus (A/Fort Monmouth/1/1947-mouse adapted(H1N1))		6		6		
	260806	Influenza A virus (A/fowl/Dutch/27(H7N7))	1		1			
	107558	Influenza A virus (A/France/75/97(H3N2))		1		1		
X	165512	Influenza A virus (A/goose/Guangdong/3/1997(H5N1))			3		3	
	182781	Influenza A virus (A/Goose/Hong Kong/385.3/2000(H5N1))		1		1		
	380330	Influenza A virus (A/goose/Hong Kong/8/1976(H1N1))		2		2		
X	384499	Influenza A virus (A/gull/Maryland/704/1977(H13N6))				1		1
	31661	Influenza A virus (A/Harbin/1/88(H1N2))		4		4		
X	462695	Influenza A virus (A/Hiroshima/52/2005(H3))			2		2	
	506350	Influenza A virus (A/Hong Kong/1/1968(H3N2))		2		2		
	130760	Influenza A virus (A/Hong Kong/1073/99(H9N2))	1		1			
	164326	Influenza A virus (A/Hong Kong/1131/1998(H1N1))		1		1		
	130763	Influenza A virus (A/Hong Kong/156/97(H5N1))		2	1	2	1	
	317652	Influenza A virus (A/Hong Kong/2/68(H3N2))		2		3		1
	432070	Influenza A virus (A/Hong Kong/213/2003(H5N1))		4		4		
	88104	Influenza A virus (A/Hong Kong/483/1997(H5N1))	1		1			
	132612	Influenza A virus (A/Hong Kong/485/97(H5N1))		1		1		
	155222	Influenza A virus (A/Hong Kong/488/97(H5N1))		1		1		
	155225	Influenza A virus (A/Hong Kong/507/97(H5N1))		5		5		
	155226	Influenza A virus (A/Hong Kong/514/97(H5N1))		2		2		
	155227	Influenza A virus (A/Hong Kong/516/97(H5N1))		2		2		
	304883	Influenza A virus (A/human/Belfast/53582/2004(H3N?))		2		2		
X	400788	Influenza A virus (A/Indonesia/5/2005(H5N1))			1	1	1	1
X	400828	Influenza A virus (A/Indonesia/CDC669/2006(H5N1))			1		1	
X	400830	Influenza A virus (A/Indonesia/CDC699/2006(H5N1))			2		2	
	402194	Influenza A virus (A/Istanbul/CTF/10/2004(H3N2))		1		1		

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	387161	Influenza A virus (A/Japan/305/1957(H2N2))	2	26	2	27		1
	307819	Influenza A virus (A/Jiangsu/38/2004(H3N2))		1		1		
	203126	Influenza A virus (A/Kamata/14/91(H3N2))	1		1			
	384495	Influenza A virus (A/Kiev/59/1979(H1N1))		1		1		
	327310	Influenza A virus (A/Kinmen/645/04(H3N2))		1		1		
	488241	Influenza A virus (A/Korea/426/1968(H2N2))		1		1		
	436004	Influenza A virus (A/kunke/1/71(H3N2))		1		1		
	393557	Influenza A virus (A/Leningrad/1954/1(H1N1))		2		2		
	393697	Influenza A virus (A/Liaoning/25/2000(H1N1))		1		1		
	62559	Influenza A virus (A/Los Angeles/1987(H3N2))	5		5			
	95888	Influenza A virus (A/mallard duck/PA/10218/84(H5N2))	5		8		3	
	282124	Influenza A virus (A/mallard/Alberta/127/00(H3N8))		1		1		
	352520	Influenza A virus (A/mallard/Alberta/35/1976(H1N1))		2		2		
	185794	Influenza A virus (A/mallard/NZ/1/97(H5N2))		1		1		
	383586	Influenza A virus (A/Memphis/1/1971(H3N2))	19	11	19	11		
	79695	Influenza A virus (A/Memphis/1/71H-A/Bellamy/42N)		1		1		
	385640	Influenza A virus (A/Memphis/102/1972(H3N2))		7		7		
	228928	Influenza A virus (A/Memphis/31/98(H3N2))	6		6			
	383571	Influenza A virus (A/Memphis/6/1986(H3N2))	2		2			
	480019	Influenza A virus (A/Moscow/10/1999(H3N2))		2		2		
	334590	Influenza A virus (A/Moscow/343/2003(H3N2))		1		1		
	389259	Influenza A virus (A/Nagasaki/N03/2005(H3N2))		1		1		
	62488	Influenza A virus (A/Nanchang/58/1993(H3N2))		1		1		
	132884	Influenza A virus (A/Netherlands/458/98 (H3N2))		1		1		
	132841	Influenza A virus (A/Netherlands/785e/90 (H3N2))		1		1		
	381512	Influenza A virus (A/New Caledonia/20/1999(H1N1))		4	2	51	2	47
	311695	Influenza A virus (A/New York/124/2001(H3N2))		1		1		
X	335358	Influenza A virus (A/New York/232/2004(H3N2))				102		102
	335313	Influenza A virus (A/New York/364/2004(H3N2))		1		1		
X	335337	Influenza A virus (A/New York/388/2005(H3N2))				14		14
	62564	Influenza A virus (A/New_York/15/94(H3N2))		1		1		
	62496	Influenza A virus (A/New_York/17/94(H3N2))		1		1		
	384505	Influenza A virus (A/nt/60/1968(H3N2))		61		61		
	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		
X	428486	Influenza A virus (A/Oklahoma/309/06(H3N2))				3		3
	223935	Influenza A virus (A/Okuda/57(H2N2))	1	9	1	9		
	381513	Influenza A virus (A/Panama/2007/1999(H3N2))	10	1	10	8		7
	382825	Influenza A virus (A/Philippines/2/1982(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))	18	327	21	355	3	28
	183764	Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))	7	86	7	86		
	216877	Influenza A virus (A/quail/Hong Kong/FY298/00(H9N2))		4		4		

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	197589	Influenza A virus (A/Quail/Shanghai/8/96(H9N2))		1		1		
X	417758	Influenza A virus (A/quail/Shantou/1475/2004(H9N2))			1		1	
	382828	Influenza A virus (A/RI/5-/1957(H2N2))		1		1		
	221012	Influenza A virus (A/Rio/6/69(H3N2))		1		1		
X	142948	Influenza A virus (A/ruddy turnstone/Delaware/67/1998(H12N4))				1		1
	192720	Influenza A virus (A/Saudi Arabia/2581/2001(H1N2))		1		1		
	192535	Influenza A virus (A/Saudi Arabia/7971/2000(H1N1))		1		1		
	384493	Influenza A virus (A/seal/Mass/1/1980(H7N7))	1	1	1	1		
	62512	Influenza A virus (A/Shangdong/5/94(H3N2))		1		1		
	380948	Influenza A virus (A/Shangdong/9/1993(H3N2))	12		13		1	
	383567	Influenza A virus (A/Shanghai/16/1989(H3N2))		1		1		
	342207	Influenza A virus (A/shorebird/Delaware/141/2002(H9N9))		1		1		
	342210	Influenza A virus (A/shorebird/Delaware/275/2001(H9N7))		1		1		
	342211	Influenza A virus (A/shorebird/Delaware/277/2000(H9N7))		1		1		
	62575	Influenza A virus (A/Sichuan/2/1987(H3N2))		3		3		
	382781	Influenza A virus (A/Singapore/1/1957(H2N2))	1		1			
X	59375	Influenza A virus (A/South Carolina/1/1918(H1N1))			2		2	
	177131	Influenza A virus (A/SW/KS/13481-T/00(H1N2))		1		1		
	177128	Influenza A virus (A/SW/MN/12883/00(H1N2))		2		2		
	177188	Influenza A virus (A/SW/MN/3227/00(H1N2))		1		1		
	382842	Influenza A virus (A/swine/29/1937(H1N1))		2		2		
	336207	Influenza A virus (A/swine/Bakum/1832/00(H1N2))		3		3		
	336205	Influenza A virus (A/swine/Bakum/5/95(H1N1))		2		2		
	256045	Influenza A virus (A/swine/Chiai/77-10/2001(H3N1))		1		1		
	169169	Influenza A virus (A/swine/Cotes d'Armor/1482/1999(H1N1))		1		1		
	158306	Influenza A virus (A/swine/Cotes d'Armor/800/00(H1N2))		1		1		
X	145306	Influenza A virus (A/swine/Hong Kong/10/98(H9N2))			5		5	
	11498	Influenza A virus (A/swine/Hong Kong/126/82(H3N2))		1		1		
	173473	Influenza A virus (A/swine/Hong Kong/2106/98(H9N2))		2		2		
	380332	Influenza A virus (A/swine/Hong Kong/273/1994(H1N1))		1		1		
	173477	Influenza A virus (A/swine/Hong Kong/3297/98(H9N2))		3		3		
	253682	Influenza A virus (A/swine/Hong Kong/5190/99(H3N2))		3		3		
	384484	Influenza A virus (A/swine/Hong Kong/81/1978(H3N2))		8		8		
	145307	Influenza A virus (A/swine/Hong Kong/9/98(H9N2))	2		2			
	253691	Influenza A virus (A/swine/Hong Kong/9840/01(H3N2))		1		1		
	306061	Influenza A virus (A/swine/IDT/Bakum1832/2000(H1N2))		1		1		
	384487	Influenza A virus (A/Swine/Indiana/1726/1988(H1N1))		1		1		

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	170342	Influenza A virus (A/swine/Italy/1654-1/99(H1N2))		1		1		
	383561	Influenza A virus (A/swine/Italy/1850/1977(H3N2))		1		1		
	147095	Influenza A virus (A/Swine/Italy/25823/94(H3N2))		2		2		
	383566	Influenza A virus (A/swine/Italy/425/1976(H1N1))		1		1		
	383564	Influenza A virus (A/swine/Italy/547/1985(H1N1))		3		3		
	383558	Influenza A virus (A/swine/Italy/809/1989(H3N2))		1		1		
	300748	Influenza A virus (A/swine/Korea/S190/2004(H9N2))		3		3		
	426738	Influenza A virus (A/swine/Miyagi/5/2003(H1N2))		2		2		
	186460	Influenza A virus (A/swine/New Jersey/11/1976(H1N1))	1		1			
	385644	Influenza A virus (A/swine/Ukkel/1/1984(H3N2))		1		1		
	82372	Influenza A virus (A/Sydney/05/97-like(H3N2))		1		1		
X	371082	Influenza A virus (A/Taiwan/2/2006(H1N1))				8		8
	395842	Influenza A virus (A/tern/Australia/1/04(H2N5))		1		1		
	405050	Influenza A virus (A/tern/Australia/1402/2004(H2N5))		1		1		
	384509	Influenza A virus (A/tern/Australia/G70C/1975(H11N9))	10		10			
	444318	Influenza A virus (A/Texas/1/1977(H3N2))	2	12	2	13		1
X	427773	Influenza A virus (A/Thailand/SP83/2004(H5N1))			1		1	
	270484	Influenza A virus (A/tiger/Thailand/CU-LV/2004(H5N1))		2		2		
	322564	Influenza A virus (A/tiger/Thailand/CU-T4/04(H5N1))		6		6		
	322566	Influenza A virus (A/tiger/Thailand/CU-T6/04(H5N1))		1		1		
	342396	Influenza A virus (A/turkey/Canada-Ontario/NS-01839-1/05(H3))		1		1		
	402489	Influenza A virus (A/turkey/Minnesota/1200/1980(H7N3))		1		1		
	342197	Influenza A virus (A/turkey/MN/511/78(H9N2))		2		2		
	342145	Influenza A virus (A/turkey/MN/735/79(H6N2))		2		2		
	165420	Influenza A virus (A/Turkey/MO/24093/99(H1N2))		5		5		
	533026	Influenza A virus (A/turkey/Ohio/313053/2004(H3N2))		1		1		
	293054	Influenza A virus (A/turkey/Ontario/6213/66(H5N?))	1		1			
	380301	Influenza A virus (A/turkey/Ontario/7732/1966(H5N9))	5	6	5	6		
X	385599	Influenza A virus (A/udorn/1972(H3N2))				1		1
	381517	Influenza A virus (A/Udorn/307/1972(H3N2))		4		4		
	62596	Influenza A virus (A/USSR/26/1985(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))		4	1	4	1	
	284218	Influenza A virus (A/Viet Nam/1203/2004(H5N1))		50	43	50	43	
	299390	Influenza A virus (A/Viet Nam/HN/2004(H5N1))		6		6		
X	357208	Influenza A virus (A/Vietnam/CL26/2004(H5N1))				72		72
	382832	Influenza A virus (A/VM113-V1(H1N1))	1		1			
X	191090	Influenza A virus (A/Weiss/1943(H1N1))				1		1
	11484	Influenza A virus (A/whale/Maine/1/84(H13N9))	3		3			
	344598	Influenza A virus (A/whooper swan/Mongolia/6/05(H5N1))		1		1		
	381518	Influenza A virus (A/Wilson-Smith/1933(H1N1))		108		108		

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X	461772	Influenza A virus (A/Wisconsin/43/2006(H3N2))			1		1	
	380978	Influenza A virus (A/Wisconsin/4755/1994(H1N1))		6		6		
	382835	Influenza A virus (A/WSN/1933(H1N1))	4	2	4	2		
	63106	Influenza A virus (A/Wuhan/359/95(H3N2))	5		5			
	480024	Influenza A virus (A/Wyoming/03/2003(H3N2))		1		5		4
	132504	Influenza A virus (A/X-31(H3N2))	74	151	77	151	3	
	380905	Influenza A virus (A/X-47(H3N2))	3	2	3	2		
	327311	Influenza A virus (A/Yilan/515/03(H3N2))		1		1		
	11408	Influenza A virus (STRAIN A/EQUINE/NEW MARKET/76)		1		1		
	41857	Influenza A virus H3N2	1	6	1	15		9
	10000865	Influenza A virus H3N2 (A/Kiev/301/94)	3		3			
	10000550	Influenza A virus H3N2 (A/Netherlands/9/03 (H3N2))		1		1		
	10000474	Influenza A virus H3N2 (A/Resvir-9 (H3N2))		10		10		
X	415166	Influenza A virus(A/swine/Henan/2/2004(H9N2))				1		1
X	415167	Influenza A virus(A/swine/Henan/3/2004(H9N2))				2		2
X	415169	Influenza A virus(A/swine/Henan/5/2004(H9N2))				1		1
X	415172	Influenza A virus(A/swine/Henan/8/2004(H9N2))				2		2
X	415176	Influenza A virus(A/swine/Shandong/fNY/2003(H9N2))				3		3
X	415177	Influenza A virus(A/swine/Shandong/fZC/2003(H9N2))				7		7
	11520	Influenza B virus	2	6	2	6		
	11521	Influenza B virus (B/Ann Arbor/1/1986)		3		3		
X	107404	Influenza B virus (B/Beijing/184/93)				1		1
X	107406	Influenza B virus (B/Chiba/447/98)				1		1
	206203	Influenza B virus (B/Hong Kong/330/2001)		7		16		9
X	224964	Influenza B virus (B/Johannesburg/5/99)			1		1	
	184816	Influenza B virus (B/Kadoma/122/99)	2		2			
	256080	Influenza B virus (B/Kobe/1/2003)	1		1			
X	504664	Influenza B virus (B/Kobe/113/2005)			1		1	
X	504666	Influenza B virus (B/Kobe/115/2005-T1)			1		1	
X	503386	Influenza B virus (B/Kobe/3/2004)			1		1	
X	504662	Influenza B virus (B/Kobe/39/2005)			1		1	
X	504660	Influenza B virus (B/Kobe/67/2005)			1		1	
X	171425	Influenza B virus (B/Kobe/87/2001)			1		1	
	107412	Influenza B virus (B/Lee/40)	5	3	5	3		
	11541	Influenza B virus (B/Oregon/5/80)	16		16			
	150127	Influenza B virus (B/Osaka/983/97-V3)	1		1			
X	335812	Influenza B virus (B/Shanghai/361/2002)			1		1	
	107418	Influenza B virus (B/Victoria/2/87)	2		2			
	11531	Influenza B virus (STRAIN B/HONG KONG/8/73)		1		1		
	11532	Influenza B virus (STRAIN B/HT/84)		1		1		
X	11552	Influenza C virus				1		1
	11553	Influenza C virus (C/Ann Arbor/1/50)	9		9			
	197911	Influenzavirus A		6		6		
	9725	Inia geoffrensis		1		1		
	42097	Isla Vista virus	1	2	1	2		

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	261204	Itapua hantavirus		10		10		
	11072	Japanese encephalitis virus	18	13	19	13	1	
	10000444	Japanese encephalitis virus CH2195LA	1		1			
	10000445	Japanese encephalitis virus JaOH0566	1		1			
	11075	Japanese encephalitis virus strain JAOARS982	4	4	4	4		
	11076	Japanese encephalitis virus strain Nakayama	2	2	2	2		
	11073	Japanese encephalitis virus strain SA-14	1	1	1	1		
X	10001335	Japanese encephalitis virus Vellore P20778			1		1	
	10632	JC polyomavirus		2	1	5	1	3
	51240	Juglans regia	5		27		22	
	11619	Junin virus		46	3	867	3	821
	13101	Juniperus ashei	12		13		1	
X	453927	Juniperus formosana			1		1	
	430511	Juquitiba virus		2		2		
	573	Klebsiella pneumoniae	15	2	16	2	1	
	11077	Kunjin virus		1		1		
	11078	Kunjin virus (STRAIN MRM61C)		2		2		
	11577	La Crosse virus		1	2	1	2	
	11578	La Crosse virus (isolate L74)		1		1		
	8753	Lachesis muta muta	21		21			
X	300015	Lactate dehydrogenase elevating virus C			1		1	
X	300016	Lactate dehydrogenase elevating virus Plagemann			1		1	
	11048	Lactate dehydrogenase-elevating virus	13		14		1	
	61172	Laguna Negra virus		9		9		
	11269	Lake Victoria marburgvirus		3		18		15
	33727	Lake Victoria marburgvirus - Musoke	4	81	4	81		
	33728	Lake Victoria marburgvirus - Popp	1	14	1	14		
X	378809	Lake Victoria marburgvirus - Ravn				32		32
X	11085	Langat virus				1		1
	11620	Lassa virus	4	70	4	626		556
	11621	Lassa virus GA391		10		43		33
	11622	Lassa virus Josiah		72		372		300
X	6925	Latrodectus tredecimguttatus				1		1
	69245	Lechiguanas virus		1		1		
	5667	Leishmania aethiopica	16		16			
	5659	Leishmania amazonensis		2		2		
	5660	Leishmania braziliensis	6		6			
	44271	Leishmania chagasi	2		2			
	5661	Leishmania donovani	9	38	9	38		
	99875	Leishmania donovani donovani	1		1			
	10000341	Leishmania donovani donovani 1S2D	1		1			
	5671	Leishmania infantum	93	1	93	1		
	10000345	Leishmania infantum LEM 75	14		14			
	5664	Leishmania major	12	113	12	117		4
X	347515	Leishmania major strain Friedlin				14		14
	5665	Leishmania mexicana	1		1			
	5679	Leishmania panamensis	3	6	3	6		

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	5682	Leishmania pifanoi		20		20		
	11049	Lelystad virus	20		20			
	36936	Lepidoglyphus destructor	5	10	5	10		
	267671	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	11		11			
	189518	Leptospira interrogans serovar Lai str. 56601	1		1			
	10000814	Leptospira interrogans serovar Lai str. HY-1	1		1			
	10000847	Leptospira sp. Akiyami A AUT10	1		1			
	1642	Listeria innocua	2	3	2	3		
	1639	Listeria monocytogenes	18	73	18	75		2
	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	45		3
X	393124	Listeria monocytogenes FSL N3-165				2		2
	267409	Listeria monocytogenes str. 1/2a F6854		1		2		1
	265669	Listeria monocytogenes str. 4b F2365		3		3		
	267410	Listeria monocytogenes str. 4b H7858		3		19		16
X	55601	Listonella anguillarum			1		1	
X	6299	Litomosoides carinii			3		3	
	217686	Little cherry virus 1		1		1		
	4522	Lolium perenne	24	78	36	78	12	
	36386	Louping ill virus (strain 31)	1		1			
	11623	Lymphocytic choriomeningitis virus	1	51	2	339	1	288
	11624	Lymphocytic choriomeningitis virus (strain Armstrong)		66		1145		1079
	10000496	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 3)		1		1		
	10000487	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 4)	1		1			
	10000497	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 5)	1		1			
	10000488	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 53b)		45		45		
	11625	Lymphocytic choriomeningitis virus (strain Pasteur)		2		5		3
X	11626	Lymphocytic choriomeningitis virus (strain Traub)				3		3
	11627	Lymphocytic choriomeningitis virus (strain WE)		11		70		59
	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		3	1	3	1	
	9544	Macaca mulatta		1		1		
	10373	Macaca mulatta cytomegalovirus		35		44		9
	10325	Macacine herpesvirus 1	1		1			
	47929	Macacine herpesvirus 3		67		68		1
	45455	Macacine herpesvirus 4		18		18		
	11628	Machupo virus		7		778		771

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X	76777	Malassezia sympodialis			1		1	
	3750	Malus x domestica	25	1	27	1	2	
	40674	Mammalia	2	1	3	1	1	
	7130	Manduca sexta		3		3		
X	29780	Mangifera indica			1		1	
	45201	Mannheimia haemolytica serotype 1	13		82		69	
	221988	Mannheimia succiniciproducens MBEL55E		2		2		
X	186537	Marburgvirus				2		2
	270374	Marinobacter sp. ELB17		1		1		
	11234	Measles virus	50	30	54	36	4	6
	10000462	Measles virus CAM/RB		1		1		
	11235	Measles virus strain Edmonston	164	131	167	203	3	72
	70146	Measles virus strain Edmonston-B		13		13		
	11236	Measles virus strain Halle		4		34		30
	132487	Measles virus strain Schwarz	1	1	1	1		
	12107	Mengo virus	1		5	13	4	13
	10036	Mesocricetus auratus	28		31		3	
X	243232	Methanocaldococcus jannaschii DSM 2661				1		1
X	187420	Methanothermobacter thermautotrophicus str. Delta H				1		1
X	10793	Mink enteritis virus strain Abashiri			1		1	
	467144	Modified Vaccinia Ankara virus		51		54		3
	11801	Moloney murine leukemia virus		2		5		3
	10244	Monkeypox virus	5		5			
	264732	Moorella thermoacetica ATCC 39073		1		1		
	300180	Mopeia Lassa reassortant 29		1		1		
	11629	Mopeia virus		2		12		10
	480	Moraxella catarrhalis	7		9		2	
	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		41		41		
	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	1	31	1	19
	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)		26		30		4
X	10001396	Murine cytomegalovirus (strain Smith) MW97.01				5		5
	35275	Murine endogenous retrovirus		11		11		
	11138	Murine hepatitis virus		5	3	14	3	9
	12760	Murine hepatitis virus strain 4		1		6		5
	11142	Murine hepatitis virus strain A59	26	2	26	3		1
	11144	Murine hepatitis virus strain JHM	4	11	8	14	4	3

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	11786	Murine leukemia virus		2		7		5
X	10001207	Murine leukemia virus LP-BM5				1		1
	223997	Murine norovirus 1	1		1			
	10634	Murine polyomavirus		14	1	25	1	11
	10636	Murine polyomavirus strain A2		1		1		
	28327	Murine rotavirus		3		3		
	70865	Murine rotavirus EDIM		27		27		
	11812	Murine sarcoma virus 3611	4		4			
	44561	Murine type C retrovirus		1		1		
	11079	Murray Valley encephalitis virus	12	4	12	6		2
	301478	Murray valley encephalitis virus (strain MVE-1-51)	10	10	11	10	1	
	10090	Mus musculus	125	526	244	908	119	382
	10000000	Mus musculus BALB/c		2		2		
	10092	Mus musculus domesticus		12		12		
X	10095	Mus sp.				1		1
	4641	Musa acuminata		1	50	1	50	
X	214697	Musa acuminata AAA Group			1		1	
	1763	Mycobacterium	4	7	4	10		3
	1764	Mycobacterium avium	7	11	7	12		1
	243243	Mycobacterium avium 104		10		10		
	10000313	Mycobacterium avium serovar 1	1		1			
	10000314	Mycobacterium avium serovar 2	1		1			
	10000316	Mycobacterium avium serovar 25	1		1			
	10000317	Mycobacterium avium serovar 26	1		1			
	10000318	Mycobacterium avium serovar 4	2		2			
	10000319	Mycobacterium avium serovar 8		1		1		
	10000320	Mycobacterium avium serovar 9	1		1			
	1770	Mycobacterium avium subsp. paratuberculosis		3		3		
	10000328	Mycobacterium avium subsp. paratuberculosis Strain Ben		1		1		
	1765	Mycobacterium bovis	41	106	44	118	3	12
	233413	Mycobacterium bovis AF2122/97		49		49		
	10000322	Mycobacterium bovis AN5	9	28	9	28		
	33892	Mycobacterium bovis BCG	9	136	11	136	2	
	410289	Mycobacterium bovis BCG str. Pasteur 1173P2	1	15	1	15		
	10000323	Mycobacterium bovis T/91/1378		6		6		
	1766	Mycobacterium fortuitum		1		1		
	144549	Mycobacterium fortuitum subsp. fortuitum		1		1		
	10000331	Mycobacterium gastri W471	1		1			
	1767	Mycobacterium intracellulare	1	1	1	1		
	1768	Mycobacterium kansasii	9	7	9	8		1
	557599	Mycobacterium kansasii ATCC 12478	1		1			
	10000325	Mycobacterium kansasii Subspecies IV		3		3		
	10000326	Mycobacterium kansasii Subspecies V		2		2		
	1769	Mycobacterium leprae	120	299	120	356		57
	272631	Mycobacterium leprae TN		5		6		1
	43304	Mycobacterium peregrinum	2		2			

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	1783	Mycobacterium scrofulaceum	4		4			
	1772	Mycobacterium smegmatis		3		3		
	1785	Mycobacterium sp.		2		2		
	164757	Mycobacterium sp. JLS		1		1		
	189918	Mycobacterium sp. KMS		1		1		
	1773	Mycobacterium tuberculosis	206	920	448	993	242	73
	10000329	Mycobacterium tuberculosis 103	1		1			
	348776	Mycobacterium tuberculosis C		11		13		2
	83331	Mycobacterium tuberculosis CDC1551		16		16		
	10000330	Mycobacterium tuberculosis Erdman	15	17	15	19		2
	336982	Mycobacterium tuberculosis F11		6		9		3
	419947	Mycobacterium tuberculosis H37Ra		6		10		4
	83332	Mycobacterium tuberculosis H37Rv	20	320	23	377	3	57
	395095	Mycobacterium tuberculosis str. Haarlem		9		82		73
X	182785	Mycobacterium tuberculosis subsp. tuberculosis				1		1
X	1809	Mycobacterium ulcerans				7		7
	362242	Mycobacterium ulcerans Agy99		1		1		
	347257	Mycoplasma agalactiae PG2	3		3			
	28903	Mycoplasma bovis	21		21			
	10001075	Mycoplasma gallisepticum strain S6	1		1			
	2097	Mycoplasma genitalium		1		1		
X	243273	Mycoplasma genitalium G37			7		7	
X	2099	Mycoplasma hyopneumoniae			1		1	
X	28227	Mycoplasma penetrans			34		34	
	2104	Mycoplasma pneumoniae	9	2	9	2		
	10000332	Mycoplasma pneumoniae FH	1		1			
	272634	Mycoplasma pneumoniae M129	9		9			
	13618	Myrmecia pilosula	2		2			
X	8656	Naja atra			7		7	
	35670	Naja naja	2		3		1	
	8654	Naja nigricollis	2		3	2	1	2
X	8657	Naja oxiana			4		4	
	8658	Naja pallida	1	1	1	1		
	367400	Neembucu hantavirus		3		3		
	485	Neisseria gonorrhoeae	17	10	19	10	2	
	528354	Neisseria gonorrhoeae MS11	4		8		4	
X	10001077	Neisseria gonorrhoeae SU89			1		1	
X	10001078	Neisseria gonorrhoeae SU96			3		3	
	487	Neisseria meningitidis	13	18	39	18	26	
	272831	Neisseria meningitidis FAM18	1		1			
	122586	Neisseria meningitidis MC58	1		12		11	
X	65699	Neisseria meningitidis serogroup A			1		1	
	10001051	Neisseria meningitidis serogroup A Strain 8659	1		1			
	491	Neisseria meningitidis serogroup B	1		36	1	35	1
	10000843	Neisseria meningitidis serogroup B H44/76	10		72	22	62	22
	10001003	Neisseria meningitidis serogroup B CU385	2		2			
	10001050	Neisseria meningitidis serogroup B Strain 7967	1		1			

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	10000979	Neisseria meningitidis serogroup B Strain 8047	1		4		3	
	10000972	Neisseria meningitidis serogroup B Strain B16.B6	1		1			
X	10001162	Neisseria meningitidis serogroup B Strain M1239			2		2	
	10001049	Neisseria meningitidis serogroup B Strain S3446	1		1			
	10001044	Neisseria meningitidis serogroup C MC51	1		1			
	29176	Neospora caninum	2	2	2	2		
	452646	Neovison vison		1		1		
	5141	Neurospora crassa	4		4			
	11176	Newcastle disease virus	9		11		2	
	11177	Newcastle disease virus (STRAIN AUSTRALIA-VICTORIA/32)	3		4		1	
	11178	Newcastle disease virus (STRAIN BEAUDETTE C/45)	12		12			
X	10001138	Newcastle disease virus (strain Eaves)			1		1	
X	10001032	Newcastle disease virus (strain La Sota)			1		1	
X	10001140	Newcastle disease virus (strain WA2116)			1		1	
X	351071	Newcastle disease virus AF2240			1		1	
	11180	Newcastle disease virus strain D26/76	4		4			
X	11186	Newcastle disease virus strain Queensland/66			4		4	
	4097	Nicotiana tabacum	1		2		1	
	121791	Nipah virus	4		5		1	
	314278	Nitrococcus mobilis Nb-231		1		1		
	122928	Norovirus genogroup 1	1		1			
X	10001116	Norovirus genogroup 1 isolates 96-908			4		4	
	122929	Norovirus genogroup 2	2		2			
	10000829	Norovirus genogroup 2 Mexico type strain 36	3		3			
	10000560	Norovirus genogroup 3 Bo/Jena/1980/DE	1		1			
X	489821	Norovirus genogroup GII.4			1		1	
X	150080	Norovirus isolates			1		1	
X	8663	Notechis scutatus			2		2	
	8996	Numida meleagris	1		1			
	4146	Olea europaea	1	14	65	14	64	
	42764	Oliveros virus		1		1		
	6282	Onchocerca volvulus	3	5	3	38		33
	69247	Oran virus		2		2		
	9733	Orcinus orca		1		1		
	784	Orientia tsutsugamushi	86		86			
	10000761	Orientia tsutsugamushi Karp	1		1			
	357244	Orientia tsutsugamushi str. Boryong	2		2	1		1
	9986	Oryctolagus cuniculus		1	1	6	1	5
	39947	Oryza sativa Japonica Group		1	5	1	5	
	28869	Ovine respiratory syncytial virus	1		1			
	9940	Ovis aries	68	1	74	2	6	1
X	8667	Oxyuranus scutellatus scutellatus			3		3	
	9598	Pan troglodytes	4	13	6	13	2	
	188763	Panine herpesvirus 2		2		2		
	3469	Papaver somniferum	1		1			
	61183	Papio sp.	1		1			

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	121759	Paracoccidioides brasiliensis	4	14	4	14		
	10000566	Paracoccidioides brasiliensis B339		8		8		
X	502780	Paracoccidioides brasiliensis Pb18			1		1	
	266	Paracoccus denitrificans	1		1			
	11207	Parainfluenza virus 5		1		1		
	45222	Parana virus		1		1		
	33127	Parietaria judaica	4	1	61	1	57	
	13187	Parietaria officinalis	2		2			
	747	Pasteurella multocida		10		10		
	10000759	Pasteurella multocida X-73	2		2			
	1254	Pediococcus acidilactici	1		1			
	133894	Penaeus	2		2			
	5076	Penicillium chrysogenum	45		45			
	69248	Pergamino virus		1		1		
	6978	Periplaneta americana	7		9		2	
	31604	Peste-des-petits-ruminants virus	9	1	9	1		
	10001020	Peste-des-petits-ruminants virus (strain Nigeria 75/1)		1		1		
	3885	Phaseolus vulgaris		1		1		
	15957	Phleum pratense	46	54	49	72	3	18
	9742	Phocoena phocoena		1		1		
	72539	Physalis mottle virus	2		2			
	9755	Physeter catodon	1	25	1	27		2
	11630	Pichinde virus		4		7		3
X	3352	Pinus taeda			4		4	
X	2439	Plasmid ColB2			1		1	
X	2465	Plasmid F			1		1	
	141833	Plasmid pIPO2T		2		2		
	28399	Plasmid R100		1		1		
	5820	Plasmodium	5	8	5	8		
	5821	Plasmodium berghei	11	44	14	44	3	
	10000356	Plasmodium berghei NK65	2	2	2	2		
	5823	Plasmodium berghei str. ANKA	5		6		1	
	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	509	666	564	691	55	25
	10000358	Plasmodium falciparum 366		1		1		
	36329	Plasmodium falciparum 3D7	118	197	120	197	2	
	57266	Plasmodium falciparum 7G8	40	50	40	50		
	10000363	Plasmodium falciparum Brazil-608	1	1	1	1		
	5835	Plasmodium falciparum CAMP/Malaysia	36	3	36	3		
	5836	Plasmodium falciparum CDC/Honduras	1		1			
	10000364	Plasmodium falciparum Clone PNG3		1		1		
	5837	Plasmodium falciparum FC27/Papua New Guinea	40	45	40	45		
	10000366	Plasmodium falciparum FCB-2	1		1			
	5838	Plasmodium falciparum FCR-3/Gambia	7		8		1	

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	10000371	Plasmodium falciparum Indochina I/CDC	32		32			
	5848	Plasmodium falciparum isolate WELLCOME	23	26	26	53	3	27
	10000373	Plasmodium falciparum ItG2G1		1		1		
	5839	Plasmodium falciparum K1	15	19	15	19		
	5840	Plasmodium falciparum LE5		2		2		
	5841	Plasmodium falciparum Mad20/Papua New Guinea	8	20	8	47		27
	5843	Plasmodium falciparum NF54	13	28	14	33	1	5
	5842	Plasmodium falciparum NF7/Ghana	3		5		2	
	57270	Plasmodium falciparum Palo Alto/Uganda	14		14			
	5834	Plasmodium falciparum RO-33	8	1	8	1		
	10000375	Plasmodium falciparum RO71	1	1	1	1		
	5846	Plasmodium falciparum T4/Thailand	25		25			
	10000816	Plasmodium falciparum T9/96	1	1	1	1		
	10000376	Plasmodium falciparum UF-5	2		2			
	5857	Plasmodium fragile		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	57	143	1	4
	31273	Plasmodium vivax (strain Belem)	6	34	6	34		
	10000378	Plasmodium vivax NK		2		2		
	126793	Plasmodium vivax Sal-1	3	1	3	1		
	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	25	22	26	1	1
	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		
	12211	Plum pox virus	1		1			
	12213	Plum pox virus (isolate NAT)		1		1		
	10001100	Plum pox virus (strain W)	6		6			
	4754	Pneumocystis carinii	2		2			
	263815	Pneumocystis murina	3		3			
	270473	Pneumonia virus of mice J3666		6		6		
	11245	Pneumovirus	4		4			
	4545	Poa pratensis	21	17	34	18	13	1
	12088	Poliovirus type 3 (strains P3/LEON/37 AND P3/LEON 12A[1]B)	4		4	15		15
	80956	Pomacentrus moluccensis		1		1		
	9600	Pongo pygmaeus		2		2		
	46221	Porcine circovirus		49		49		

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	133704	Porcine circovirus 1	5		5			
	85708	Porcine circovirus 2	5		13		8	
X	10001239	Porcine circovirus strain ISU31			7		7	
	194958	Porcine endogenous retrovirus A	2		2			
	28295	Porcine epidemic diarrhea virus	1		1			
	229032	Porcine epidemic diarrhea virus (strain CV777)	4		4			
X	10796	Porcine parvovirus			37		37	
	28344	Porcine reproductive and respiratory syndrome virus	22		62	3	40	3
	10000969	Porcine respiratory and reproductive syndrome virus 111/92	9		9			
	10000529	Porcine respiratory and reproductive syndrome virus CH-1a	6		6			
	10000859	Porcine respiratory and reproductive syndrome virus JA142	1		1			
	10000864	Porcine respiratory and reproductive syndrome virus MD-001	1		1			
	10000888	Porcine respiratory and reproductive syndrome virus Olot/91	3		3			
	10919	Porcine rotavirus (STRAIN YM)	1	1	2	1	1	
	101350	Porcine rotavirus strain A253	2		2			
X	10917	Porcine rotavirus strain Gottfried			2		2	
	53179	Porcine rubulavirus	3		3			
	11150	Porcine transmissible gastroenteritis coronavirus strain FS772/70	1		2		1	
	11151	Porcine transmissible gastroenteritis coronavirus strain Purdue	14		14			
	837	Porphyromonas gingivalis	14	11	72	18	58	7
	10001079	Porphyromonas gingivalis 381	1		71	55	70	55
	10001081	Porphyromonas gingivalis HG66	2		2			
X	10001223	Porphyromonas gingivalis OMZ 409			23		23	
X	242619	Porphyromonas gingivalis W83			1		1	
X	37128	Potato mop-top virus			8		8	
	12216	Potato virus Y	1		1			
X	10001152	Potato virus Y strain D			6		6	
	11603	Prospect Hill virus	1	2	1	2		
	584	Proteus mirabilis	1		1			
	10001006	Proteus mirabilis CFT322	1		1			
	88086	Protobothrops elegans	7		7			
	300559	PRRSV VR2332	17		18		1	
	36596	Prunus armeniaca	4		4			
	42229	Prunus avium	3	1	3	1		
	3758	Prunus domestica	4		4			
	3760	Prunus persica	15		15	43		43
X	8671	Pseudechis porphyriacus			3		3	
	287	Pseudomonas aeruginosa	51	47	57	47	6	
	10001057	Pseudomonas aeruginosa CD4	1		1			
	10000723	Pseudomonas aeruginosa Immunotype 4	4		4			
	10001058	Pseudomonas aeruginosa K122-4	1		1			
	10000817	Pseudomonas aeruginosa KB7	2		2			
	10000818	Pseudomonas aeruginosa P1	1		1			

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	10000725	Pseudomonas aeruginosa PAK	7	3	7	3		
	10000815	Pseudomonas aeruginosa PAO	2	2	2	2		
X	208964	Pseudomonas aeruginosa PAO1			1		1	
	208963	Pseudomonas aeruginosa UCBPP-PA14		16		16		
	294	Pseudomonas fluorescens		4		4		
X	10879	Pseudomonas phage phi6			7		7	
	303	Pseudomonas putida	1	7	1	7		
	351746	Pseudomonas putida F1		2		2		
	76869	Pseudomonas putida GB-1		1		1		
	306	Pseudomonas sp.		1		1		
	74138	Pseudomonas sp. DJ-12		1		1		
	71238	Pseudomonas sp. G-179		1		1		
	159091	Pseudomonas sp. KIE171		1		1		
	237609	Pseudomonas sp. KL28		1		1		
	150396	Pseudomonas sp. MT-1		1		1		
	264730	Pseudomonas syringae pv. phaseolicola 1448A		1		1		
	29442	Pseudomonas tolaasii		1		1		
	11604	Puumala virus	30	13	30	13		
	10000485	Puumala virus (STRAIN HALLNAS B1) Vranica/Hallnas	4		4			
	39002	Puumala virus (strain sotkamo/v-2969/81)	196		196			
X	10001238	Puumala virus (strain Umea/hu)			1		1	
	10000483	Puumala virus CG18-20	5		5			
	10000484	Puumala virus Kazan	25	7	25	7		
X	272844	Pyrococcus abyssi GE5				1		1
	10000507	Rabbit hemorrhagic disease virus Olot/89	1		1			
X	122291	Rabbit oral papillomavirus			2		2	
	11292	Rabies virus	5	10	6	13	1	3
	11293	Rabies virus AVO1		4		4		
	10000467	Rabies virus CVS	14		14			
	11294	Rabies virus CVS-11	1		1			
	11295	Rabies virus ERA	9	21	9	23		2
	10000470	Rabies virus Flury LEP		1		1		
	11296	Rabies virus HEP-FLURY	7	1	7	1		
	11298	Rabies virus Nishigahara RCEH	1		1			
	37132	Rabies virus Ontario fox	3		3			
	10000471	Rabies virus RC-HL	4		4			
	103929	Rabies virus strain Pasteur vaccin	1	1	1	1		
X	10114	Rattus			5	7	5	7
	10116	Rattus norvegicus	6	21	57	223	51	202
	1646	Renibacterium salmoninarum	12		12			
	12814	Respiratory syncytial virus	3	3	3	6		3
	186539	Reston ebolavirus		3		3		
	129003	Reston ebolavirus - Reston	2	27	2	27		
	103930	Rhesus cytomegalovirus strain 68-1		5		5		
	10969	Rhesus rotavirus	6		8	1	2	1
	60189	Rhipicephalus decoloratus	4		4			

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	43767	Rhodococcus equi	15		15			
	1833	Rhodococcus erythropolis		1		1		
	160061	Ricinus		1		1		
	3988	Ricinus communis	7	3	7	3		
	35788	Rickettsia africae		1		1		
	787	Rickettsia australis		1		1		
X	391896	Rickettsia bellii OSU 85-389				3		3
	336407	Rickettsia bellii RML369-C		3		4		1
	788	Rickettsia canadensis		1		1		
	781	Rickettsia conorii		13		13		
	272944	Rickettsia conorii str. Malish 7		5		5		
	42862	Rickettsia felis		1		1		
X	315456	Rickettsia felis URRWXCal2				1		1
	35791	Rickettsia massiliae		1		1		
	782	Rickettsia prowazekii		19		20		1
X	272947	Rickettsia prowazekii str. Madrid E				2		2
	783	Rickettsia rickettsii		1		1		
X	452659	Rickettsia rickettsii str. Iowa				1		1
	35793	Rickettsia sibirica		4		4		
	272951	Rickettsia sibirica 246		3		8		5
	785	Rickettsia typhi		2		3		1
X	257363	Rickettsia typhi str. Wilmington				1		1
	11588	Rift Valley fever virus	4		4	2		2
	11589	Rift valley fever virus (STRAIN ZH-548 M12)		2		2		
	10000482	Rift Valley fever virus ZH501	2		2			
	11241	Rinderpest virus	1	2	1	2		
	11243	Rinderpest virus (strain L)	6		6			
	36409	Rinderpest virus (strain RBOK)	33	5	33	5		
	10000465	Rinderpest virus LATC	3		3			
	46920	Rio Mamore virus	1	1	1	1		
	37207	Rio Segundo virus	1		1			
	1	root	2	1	2	1		
	314262	Roseobacter sp. MED193		1		1		
X	11029	Ross River virus				1		1
	11032	Ross river virus (STRAIN T48)	3		3			
	10912	Rotavirus		1		1		
X	10930	Rotavirus A bovine/B223/G10			2		2	
	72132	Rotavirus G1		1	1	1	1	
X	10001216	Rotavirus G3 strain RV-3			1		1	
	11886	Rous sarcoma virus		4	4	4	4	
	11041	Rubella virus	46	58	77	92	31	34
	11043	Rubella virus (strain M33)		10	3	11	3	1
	11045	Rubella virus (strain THERIEN)	1	29	20	35	19	6
	11044	Rubella virus (vaccine strain RA27/3)		4	2	6	2	2
X	159479	Saaremaa virus				3		3
	45709	Sabia virus		14		874		860
	64284	Saboya virus		1		1		

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	4932	Saccharomyces cerevisiae	2	3	15	5	13	2
X	545124	Saccharomyces cerevisiae AWRI1631				2		2
	285006	Saccharomyces cerevisiae RM11-1a		1		2		1
	10381	Saimiriine herpesvirus 2		1		3		2
	28901	Salmonella enterica		49		51		2
	59203	Salmonella enterica subsp. arizonae		1		1		
X	41514	Salmonella enterica subsp. arizonae serovar 62:z4,z23:--				1		1
	119912	Salmonella enterica subsp. enterica serovar Choleraesuis		1		1		
X	321314	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67				2		2
	98360	Salmonella enterica subsp. enterica serovar Dublin		1		2		1
X	149539	Salmonella enterica subsp. enterica serovar Enteritidis				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			
	54388	Salmonella enterica subsp. enterica serovar Paratyphi A		1		1		
X	295319	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150				3		3
	605	Salmonella enterica subsp. enterica serovar Pullorum		1		1		
	90370	Salmonella enterica subsp. enterica serovar Typhi	9	21	9	22		1
X	220341	Salmonella enterica subsp. enterica serovar Typhi str. CT18				2		2
X	209261	Salmonella enterica subsp. enterica serovar Typhi str. Ty2				1		1
	90371	Salmonella enterica subsp. enterica serovar Typhimurium	9	54	9	64		10
	99287	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2		1		23		22
X	48409	Salmonella enterica subsp. enterica serovar Virchow				1		1
	599	Salmonella sp.	1		1			
	72590	Salmonella sp. 'group B'	2		2			
	10000739	Salmonella typhi 620Ty	1		1			
	10000740	Salmonella typhi Ty21a		6		6		
	10000738	Salmonella typhimurium PL5 (O9,12)	1		1			
	10000743	Salmonella typhimurium SL3261		4		4		
	10000746	Salmonella typhimurium TV119	1		1			
	8015	Salmonidae	1		1			
	358400	Sangassou virus		2		6		4
X	11607	Sapporo rat virus			1	4	1	4
	82659	Sapporo virus-Manchester		1		1		
X	7386	Sarcophaga peregrina				1		1
	227859	SARS coronavirus	140	198	141	226	1	28
	228407	SARS coronavirus BJ01	25	28	25	28		
	228415	SARS coronavirus CUHK-W1	17		17			
	229992	SARS coronavirus Frankfurt 1	6		6			

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	227984	SARS coronavirus Tor2	171	1957	171	1965		8
	228330	SARS coronavirus Urbani	22	34	22	42		8
X	6184	Schistosoma bovis			2		2	
	6182	Schistosoma japonicum	36	12	36	12		
	6183	Schistosoma mansoni	26	22	41	44	15	22
	10000385	Schistosoma mansoni Puerto Rico	17	6	17	7		1
	4550	Secale cereale	51		51			
	11033	Semliki forest virus	25		35	5	10	5
	11191	Sendai virus		5	1	7	1	2
	11194	Sendai virus (strain Enders)	7	11	7	11		
	11196	Sendai virus (strain Harris)	2		2			
	302272	Sendai virus (strain Ohita)	1		1			
	11198	Sendai virus (Z)		1		1		
	11608	Seoul virus		1		1		
	12557	Seoul virus 80-39		1		1		
	11610	Seoul virus SR11	1		1			
	44026	Sepik virus		1		1		
X	8570	Serpentes			4		4	
	615	Serratia marcescens		1		1		
	399741	Serratia proteamaculans 568		1		1		
	4182	Sesamum indicum	11		11			
	621	Shigella boydii		1		1		
	300268	Shigella boydii Sb227		2		2		
	622	Shigella dysenteriae	5	2	5	2		
	10000748	Shigella dysenteriae serotype 1	2		2			
	10000749	Shigella dysenteriae serotype 1 114Sd	3		3			
	623	Shigella flexneri	75	10	75	10		
	41434	Shigella flexneri 1b	1		1			
	42897	Shigella flexneri 2a	26		26			
	10000750	Shigella flexneri 2b	1		1			
	424717	Shigella flexneri 3a	2		2			
	10000751	Shigella flexneri 4b	1		1			
X	373384	Shigella flexneri 5 str. 8401				2		2
	424718	Shigella flexneri 5a	2		2			
	10000752	Shigella flexneri 5b	1		1			
	10000754	Shigella flexneri X	1		1			
	424720	Shigella flexneri Y	3		3			
	624	Shigella sonnei		1		1		
	300269	Shigella sonnei Ss046		3		3		
	92652	Shrimp white spot syndrome virus	3		3			
	11723	Simian immunodeficiency virus		152		154		2
	11711	Simian immunodeficiency virus - mac		1		1		
	10000501	Simian immunodeficiency virus - mac - mac 239		279		279		
	10000502	Simian immunodeficiency virus - mac - mac 32H		7		7		
	10000503	Simian immunodeficiency virus - mac - mac BK28		3		3		
	10000504	Simian immunodeficiency virus - mac - mac F965		1		1		
	31682	Simian immunodeficiency virus - mac1A11		8		8		

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	10000506	Simian immunodeficiency virus - sm - sm PT573		1		1		
	31683	Simian immunodeficiency virus - stm		3		3		
	11737	Simian immunodeficiency virus (F236/SMH4 ISOLATE) (SOOTY MANGABEY)		7		7		
	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		
	11942	Simian retrovirus 1	1		1			
	10923	Simian rotavirus A/SA11	1		8	4	7	4
	37137	Simian rotavirus A/SA11-both	17		20	2	3	2
	10633	Simian virus 40	5	19	13	40	8	21
	31608	Simian virus 5 (isolate canine/CPI+)	1		1			
	57667	Simian-Human immunodeficiency virus		1		1		
	37705	Sin Nombre virus	1	4	1	4		
	10000544	Sin Nombre virus NM H10	4	8	4	8		
	3728	Sinapis alba	2		2			
	11034	Sindbis virus	1		9		8	
	366394	Sinorhizobium medicae WSM419		1		1		
X	382	Sinorhizobium meliloti				1		1
	254355	Small ruminant lentivirus	1		1			
X	10001307	Small ruminant lentivirus strain It-561			1		1	
X	10001308	Small ruminant lentivirus strain It-Pi1			1		1	
	11780	Snyder-Theilen feline sarcoma virus	1		1			
X	28375	Soil-borne wheat mosaic virus			1		1	
X	4081	Solanum lycopersicum			2		2	
X	11307	Sonchus yellow net virus				1		1
	11984	Southampton virus	1		1			
	2133	Spiroplasma citri		1		1		
X	371647	Squirrelpox virus				1		1
	11080	St. Louis encephalitis virus	2		2			
	11081	St. Louis encephalitis virus (strain MS1-7)	7		7			
X	1279	Staphylococcus			1		1	
	1280	Staphylococcus aureus	84	31	87	33	3	2
	93062	Staphylococcus aureus subsp. aureus COL	17	1	17	1		
	282458	Staphylococcus aureus subsp. aureus MRSA252	40		40			
X	1301	Streptococcus			2		2	
X	1311	Streptococcus agalactiae			1		1	
	1317	Streptococcus downei	2		2	1		1
	119602	Streptococcus dysgalactiae subsp. equisimilis	18		21		3	
	1336	Streptococcus equi	17		17			
	1309	Streptococcus mutans	22	6	137	87	115	81
	10000974	Streptococcus mutans GS-5		14		14		
	10000773	Streptococcus mutans MT 8148	1	9	39	11	38	2
	10000813	Streptococcus mutans SJ	1	1	1	1		
X	1303	Streptococcus oralis			12		12	

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	1313	Streptococcus pneumoniae	9	2	9	2		
	373153	Streptococcus pneumoniae D39		1		1		
	1314	Streptococcus pyogenes	71	72	84	79	13	7
	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	1		1
	10000780	Streptococcus pyogenes serotype M12 A374	1		1			
	10000787	Streptococcus pyogenes serotype M13	1		1			
	301451	Streptococcus pyogenes serotype M18	1		1			
	404330	Streptococcus pyogenes serotype M2	2		2			
	10000788	Streptococcus pyogenes serotype M22	1		1			
	10000789	Streptococcus pyogenes serotype M24	2	1	6	2	4	1
	301448	Streptococcus pyogenes serotype M3	1		1			
	10000542	Streptococcus pyogenes serotype M3 D58	2		2			
	10000790	Streptococcus pyogenes serotype M30	1		1			
	404331	Streptococcus pyogenes serotype M4	2		2			
	10000791	Streptococcus pyogenes serotype M41	1		1			
	301452	Streptococcus pyogenes serotype M49	1		1			
	301449	Streptococcus pyogenes serotype M5	52	51	53	53	1	2
	10000792	Streptococcus pyogenes serotype M52	1		1			
	10000793	Streptococcus pyogenes serotype M54	1		1			
	10000794	Streptococcus pyogenes serotype M55	1		1			
	10000795	Streptococcus pyogenes serotype M57	1		1			
	301450	Streptococcus pyogenes serotype M6	8	5	9	7	1	2
	10000824	Streptococcus pyogenes serotype M6 strain D471	4		4			
	10000796	Streptococcus pyogenes serotype M60	1		1			
	10000797	Streptococcus pyogenes serotype M75	1		1			
	10000798	Streptococcus pyogenes serotype M8	1		1			
	410069	Streptococcus pyogenes serotype M80	1		1			
	160491	Streptococcus pyogenes str. Manfredo	3	17	3	17		
	246202	Streptococcus sobrinus 6715	4	4	4	4		
	36470	Streptococcus sp. 'group A'	16		16			
	1307	Streptococcus suis	1		1			
	1349	Streptococcus uberis	5		5			
	80859	Streptomyces ribosidificus		1		1		
X	465541	Streptomyces sp. Mg1				1		1

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X	35297	Striped Jack nervous necrosis virus			1		1	
X	186540	Sudan ebolavirus				261		261
	128948	Sudan ebolavirus - Boniface (1976)		1		1		
	128949	Sudan ebolavirus - Maleo (1979)		30		30		
	386033	Sudan ebolavirus - Uganda (2000)		6		6		
	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	1	8	5	4	4
X	9825	Sus scrofa domestica				3		3
X	12075	Swine vesicular disease virus			1		1	
	12076	Swine vesicular disease virus (STRAIN H/3 '76)	5		5			
	12077	Swine vesicular disease virus (STRAIN UKG/27/72)	2		3		1	
	10000809	Swine vesicular disease virus ITL/1/66	1		1			
	10000842	Swine vesicular disease virus NET/1/92	1		1			
	10001002	Swine vesicular disease virus SPA/1/93	16		16			
X	10276	Swinepox virus				1		1
X	32049	Synechococcus sp. PCC 7002				1		1
X	1148	Synechocystis sp. PCC 6803				1		1
	32630	synthetic construct		3		3		
	11631	Tacaribe virus		4		105		101
	31616	Tacaribe virus (strain V7)		1		1		
	6202	Taenia		1		1		
	6207	Taenia crassiceps	4		7	1	3	1
	10000802	Taenia crassiceps Strain ORF	3	3	3	3		
	6206	Taenia saginata	5		5			
	6204	Taenia solium	8	3	8	3		
X	127999	Tanacetum parthenium				1		1
	425088	Tanganya virus		1		1		
	99883	Tetraodon nigroviridis		1		1		
	5874	Theileria annulata	1		1			
	5875	Theileria parva	28		28			
	333668	Theileria parva strain Muguga		15	14	15	14	
	10000848	Theileria sergenti Type B1		1		1		
	10000849	Theileria sergenti Type B2		2		2		
	10000850	Theileria sergenti Type C		5		5		
	10000851	Theileria sergenti Type I		1		1		
	12124	Theiler's encephalomyelitis virus		13		15		2
	12125	Theiler's encephalomyelitis virus (STRAIN BEAN 8386)	16	23	16	52		29
	12126	Theiler's encephalomyelitis virus (STRAIN DA)	3	2	3	2		
	10000855	Theiler's murine encephalomyelitis virus (strain BeAn 8386) (variant M2)		1		1		
	204711	Theilovirus		1		5		4
X	6437	Themiste zostericola			1		1	
	10479	Thermoproteus tenax virus 1	1		1			
	271	Thermus aquaticus	1		1			
X	13286	Theromyzon tessulatum			1		1	

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	11084	Tick-borne encephalitis virus	13	1	14	1	1	
	11087	Tick-borne encephalitis virus (STRAIN SOFJIN)	6		6			
	10000449	Tick-borne encephalitis virus (WESTERN SUBTYPE) - Neudoerfl	2		2			
	6887	Tityus serrulatus	85		92		7	
	223337	Tobacco leaf curl Zimbabwe virus		1		1		
	12242	Tobacco mosaic virus	9		28	9	19	9
	12246	Tobacco mosaic virus (strain Dahlemense)	2		2			
X	10001210	Tobacco mosaic virus (strain Ni568)			1		1	
X	10001209	Tobacco mosaic virus (strain PM5)			1		1	
X	12243	Tobacco mosaic virus (vulgare)			1		1	
X	12146	Tomato bushy stunt virus (STRAIN BS-3)			3		3	
	83192	Topografov virus	1		1			
	7787	Torpedo californica	8		18		10	
	7788	Torpedo marmorata		3		3		
	5811	Toxoplasma gondii	12	23	12	29		6
	10000353	Toxoplasma gondii 76K	5	5	5	5		
	10000354	Toxoplasma gondii BK	1	1	1	1		
	383379	Toxoplasma gondii RH	5	5	5	11		6
	11149	Transmissible gastroenteritis virus	6		9		3	
X	10001154	Transmissible gastroenteritis virus MAD88				1		1
	158	Treponema denticola		1		1		
	160	Treponema pallidum	5	1	5	1		
	10001021	Treponema pallidum subsp. pallidum (strain Chicago)	18		18			
	243276	Treponema pallidum subsp. pallidum str. Nichols	204	9	204	9		
	6334	Trichinella spiralis		1		1		
	5722	Trichomonas vaginalis	2		2			
	5551	Trichophyton rubrum	2	27	2	27		
	3677	Trichosanthes kirilowii	1		1			
X	5554	Trichosporon cutaneum			1		1	
	88087	Trimeresurus flavoviridis	3		3			
	4565	Triticum aestivum	134	191	273	239	139	48
	279889	Triticum aestivum var. arduini		4		4		
	4567	Triticum turgidum subsp. durum		1		1		
	5691	Trypanosoma brucei	4		4	6		6
X	31286	Trypanosoma brucei rhodesiense				9		9
	5693	Trypanosoma cruzi	110	293	110	321		28
	10000347	Trypanosoma cruzi Dm28c	1		1			
	353153	Trypanosoma cruzi strain CL Brener	2		2			
	37133	Tula virus	1		1	3		3
	63673	Turbo cornutus	2		2			
	10001158	unclassified Poxviridae Mule deer poxvirus		1		1		
	11309	unidentified influenza virus		12		13		1
	38018	unidentified phage		1		1		
	10245	Vaccinia virus		133		298		165
	332193	Vaccinia Virus Acambis 3000 MVA		2		2		
	126794	Vaccinia virus Ankara		5		17		12

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	10001027	Vaccinia virus Connaught	1		1			
	10249	Vaccinia virus Copenhagen		157	31	472	31	315
	10251	Vaccinia virus IHD-J	1		1			
	10248	Vaccinia virus LC16M8		4		4		
X	31531	Vaccinia virus L-IPV				2		2
	10000388	Vaccinia virus NYCBH - Dryvax		29		29		
	10253	Vaccinia virus Tian Tan		2		3		1
	10254	Vaccinia virus WR	25	3160	25	5306		2146
	12870	Variola major virus		11		11		
	10000390	Variola major virus India-1967		1		1		
	10255	Variola virus		3		176		173
	36382	Venezuelan equine encephalitis virus (strain 3880)		1		1		
	11037	Venezuelan equine encephalitis virus (strain TC-83)	21		21			
	11038	Venezuelan equine encephalitis virus (strain Trinidad donkey)	14		15		1	
	7742	Vertebrata	13	1	13	1		
	11277	Vesicular stomatitis Indiana virus		1	6	7	6	6
	11278	Vesicular stomatitis Indiana virus strain Glasgow		1		1		
X	11279	Vesicular stomatitis Indiana virus strain Mudd-Summers			1		1	
	11285	Vesicular stomatitis Indiana virus strain San Juan		1		1		
X	11280	Vesicular stomatitis New Jersey virus				1		1
	11276	Vesicular stomatitis virus		5		6		1
	7444	Vespa basalis	1		1			
X	7453	Vespula maculifrons			1		1	
	7454	Vespula vulgaris		36		36		
	314288	Vibrio alginolyticus 12G01		3		3		
	666	Vibrio cholerae	33	79	33	81		2
	44104	Vibrio cholerae 569B	30		37		7	
	127906	Vibrio cholerae O1	10		10			
	686	Vibrio cholerae O1 biovar El Tor	3		3	1		1
	10000567	Vibrio cholerae O1 serotype Inaba	4		4			
	10000568	Vibrio cholerae O1 serotype Ogawa	4		4			
X	345073	Vibrio cholerae O395				3		3
X	345075	Vibrio cholerae V51				1		1
X	345076	Vibrio cholerae V52				24		24
	670	Vibrio parahaemolyticus		57		57		
X	419109	Vibrio parahaemolyticus AQ3810				23		23
	223926	Vibrio parahaemolyticus RIMD 2210633	2		2	8		8
	672	Vibrio vulnificus		64	1	64	1	
X	216895	Vibrio vulnificus CMCP6				35		35
	196600	Vibrio vulnificus YJ016		16		24		8
X	8704	Vipera ammodytes			1		1	
	11288	Viral hemorrhagic septicemia virus (STRAIN 07-71)	1		11	1	10	1
	3972	Viscum album	17		17			
X	11743	Visna lentivirus (strain 1514 / clone LV1-1KS1)			3		3	
	11742	Visna lentivirus (strain 1514)	1		1			
	11741	Visna/Maedi virus	5		5	7		7

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	12750	Visna/maedi virus EV1	1		1			
X	36374	Visna/maedi virus EV1 KV1772			2		2	
X	29760	Vitis vinifera			1		1	
	74537	Vladivostok virus	1		1			
X	148360	Watermelon mosaic virus 2 (isolate USA)			2		2	
	43141	Watermelon silver mottle virus	3		3			
	11082	West Nile virus	15	183	16	332	1	149
	10000447	West Nile virus 3000.0259	2		2			
	10000971	West Nile virus NY-99	7	6	7	19		13
X	449278	West Nile virus SPU116/89				1		1
	10001047	West Nile virus strain 2741	31		32		1	
	307044	West Nile virus strain 385-99	4	12	4	12		
X	406269	West Nile virus strain PTRoxo				12		12
	46919	Whitewater Arroyo virus		2		344		342
	4963	Williopsis saturnus var. mrakii	1		1	1		1
	66077	Wolbachia sp. wMel		1		1		
	35269	Woodchuck hepatitis virus	5	2	5	2		
	10430	Woodchuck hepatitis virus 1	3		3			
	341946	Woodchuck hepatitis virus 2	4		4			
	10433	Woodchuck hepatitis virus 8		24		24		
	280	Xanthobacter autotrophicus		1		1		
	8364	Xenopus (Silurana) tropicalis		1		1		
	8355	Xenopus laevis		2		2		
	11089	Yellow fever virus		90		219		129
	11090	Yellow fever virus 17D		120		121		1
	617102	Yellow fever virus 17D/Tiantan	4		4			
	31641	Yellow fever virus 1899/81		12		12		
	407141	Yellow fever virus isolate Ethiopia/Couma/1961		1		1		
	407134	Yellow fever virus strain Ghana/Asibi/1927		5		5		
	630	Yersinia enterocolitica	3	17	3	17		
	393305	Yersinia enterocolitica subsp. enterocolitica 8081		1		12		11
	632	Yersinia pestis	14	125	14	125		
	10000757	Yersinia pestis 195/P	5		5			
	360102	Yersinia pestis Antiqua		7		8		1
X	412420	Yersinia pestis CA88-4125				21		21
	214092	Yersinia pestis CO92		4		4		
X	187410	Yersinia pestis KIM 10				2		2
	10000756	Yersinia pestis KIM 5	21		21			
	377628	Yersinia pestis Nepal516		7		7		
X	386656	Yersinia pestis Pestoides F				1		1
	633	Yersinia pseudotuberculosis		1		1		
	186538	Zaire ebolavirus		50		778		728
	129000	Zaire ebolavirus - Eckron (Zaire, 1976)		12		12		
	128947	Zaire ebolavirus - Gabon (1994-1997)		18		18		
	128952	Zaire ebolavirus - Mayinga (Zaire, 1976)	13	14	13	14		
	128951	Zaire ebolavirus - Zaire (1995)		1		1		
X	4577	Zea mays			2		2	

NEW 2009	ORGAN-ISM ID	SPECIES STRAIN	B-08	T-08	B-09	T-09	∆ B	∆ T
	34245	Zinnia violacea		1		1		
	157914	Ziziphus mauritiana	4		4			

2 Website Features

IEDB 2.3 was released on 19 January 2010. The narrative presented in this section describes this most recent version of the website, even though it was deployed after the time frame for this compendium. This is being done to make this document as relevant and up to date as possible.

A number of new features were introduced in 2009, as summarized below:

- Browse by 3D structure
- Identifier Search
- Exact, substring, and sequence homology (BLAST) search added to the home page Simple Search
- Peptide MHC allele binding motif diagrams and their corresponding amino acid binding charts
- Search parameters listed at the top of the query results page, along with the ability to revise the search
- Comma Separated Value (CSV) exports of query results in compact and full formats
- Links to the Analysis Resource and relevant Bioinformatics Resource Centers
- Expansion of MHC class I and II prediction tools to include three new methods for class I and two new methods for class II
- Database export of the entire contents of the IEDB in two SQL formats

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

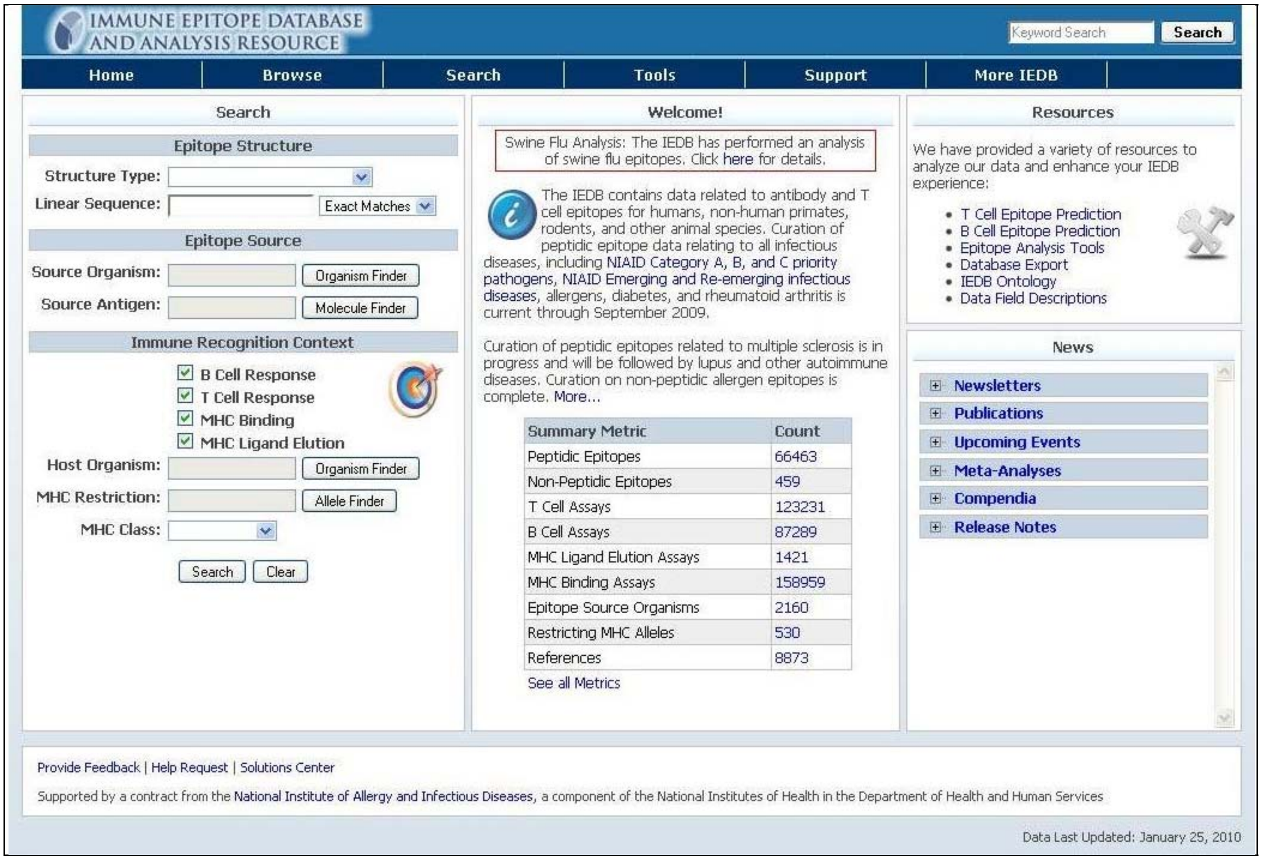
The reader will find it helpful to keep in mind how data are stored in the IEDB. Each item contained in the IEDB consists of a reference (article or submission) containing information about one or more epitopes and associated binding or response information. The same epitope can exist in multiple references.

2.1 Home Page

The IEDB Home Page is the default screen displayed when users enter the IEDB system. Besides providing a general description of the IEDB project, the home page displays system level status and notification of scheduled updates or maintenance. As one can see in Figure 2.1, the page is divided into three columns that contain a basic search capability, introductory information, Summary Metrics of the data, available Resources, and project-related News. As users browse the IEDB system, they can return to the home page anytime by clicking *Home* on the far left of the main menu bar.

Summary Metrics are displayed in the center column of the screen. These numbers are intended to be a gauge of the volume of data available in the system. The Summary Metrics provide the number of epitopes (peptidic and non-peptidic), assays (T cell, B cell, MHC ligand elution, and MHC binding), epitope source organisms, restricting MHC alleles, and references. Clicking on the "See all Metrics" brings up a Summary Metrics page that shows the positive, negative, and total (all) count for epitopes and assays, and the counts for epitope source organism, host organism, restricting MHC allele, and references. Further detail is revealed when the user clicks on the counts.

The Support panel was eliminated and the News panel was expanded and modified to show six categories – Newsletters, Publications, Upcoming Events, Meta-analyses, Annual Compendia, and Release Notes. Each category can be expanded to show its linkable content.



Swine Flu Analysis: The IEDB has performed an analysis of swine flu epitopes. Click here for details.

The IEDB contains data related to antibody and T cell epitopes for humans, non-human primates, rodents, and other animal species. Curation of peptidic epitope data relating to all infectious diseases, including NIAID Category A, B, and C priority pathogens, NIAID Emerging and Re-emerging infectious diseases, allergens, diabetes, and rheumatoid arthritis is current through September 2009.

Curation of peptidic epitopes related to multiple sclerosis is in progress and will be followed by lupus and other autoimmune diseases. Curation on non-peptidic allergen epitopes is complete. More...

Summary Metric	Count
Peptidic Epitopes	66463
Non-Peptidic Epitopes	459
T Cell Assays	123231
B Cell Assays	87289
MHC Ligand Elution Assays	1421
MHC Binding Assays	158959
Epitope Source Organisms	2160
Restricting MHC Alleles	530
References	8873

See all Metrics

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

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

Provide Feedback | Help Request | Solutions Center

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

Data Last Updated: January 25, 2010

Figure 2.1 IEDB 2.3 Home Page

2.2 Browse

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

2.2.1 Browse Records by MHC Allele

All users can find records associated with a specific MHC allele by browsing records by allele. To browse records by allele, the user selects *Browse by MHC Allele* under the *Browse* heading on the main menu. The interface for the Browse by MHC Allele is a tree structure that makes it easy for users to find and investigate information on specific MHC alleles. As Figure 2.2 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.

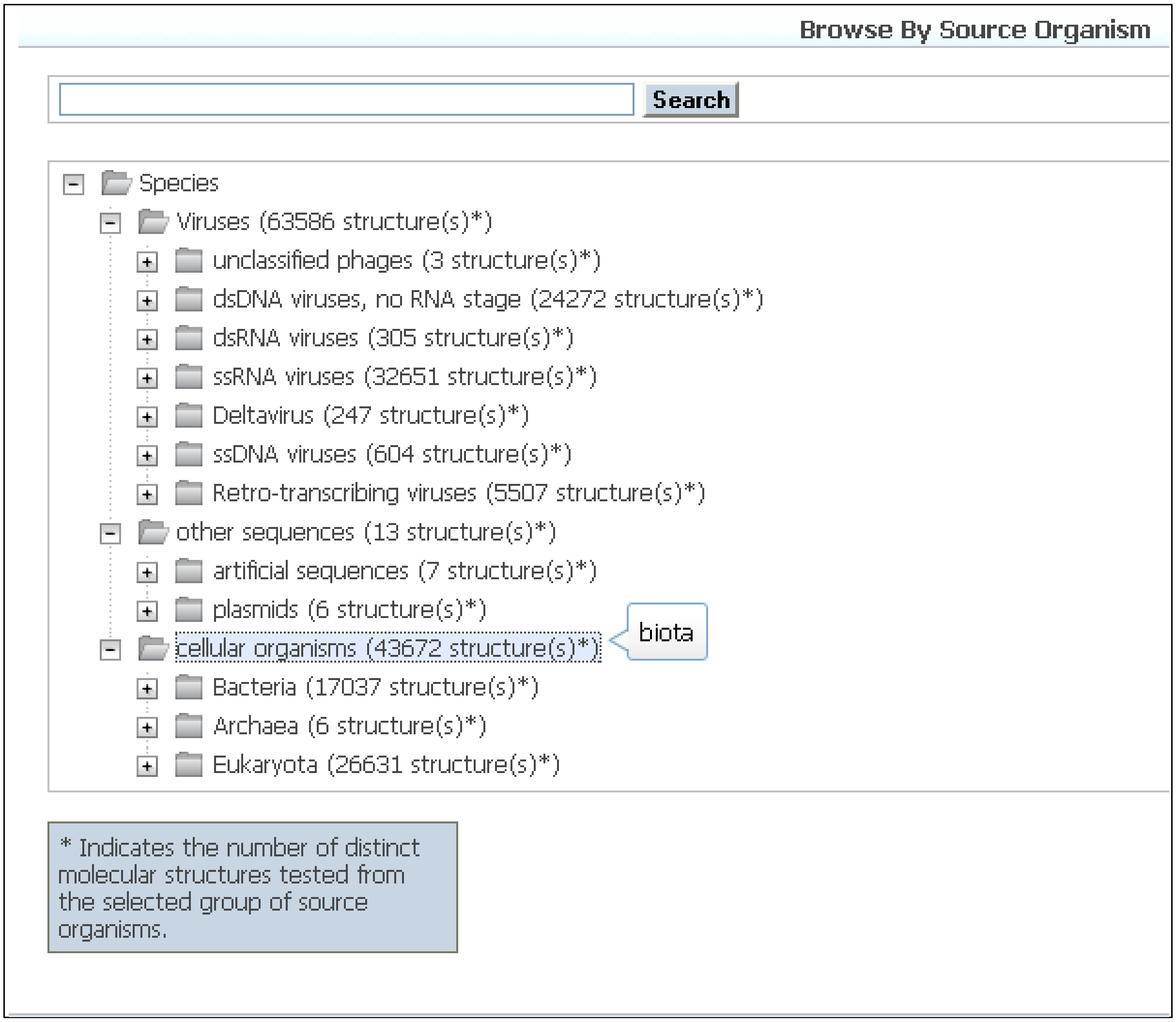
- bonobo (Pan paniscus) (1 structure(s)*)
- cattle (Bos taurus) (354 structure(s)*)
- chicken (Gallus gallus) (37 structure(s)*)
- chimpanzee (Pan troglodytes) (705 structure(s)*)
- cotton-top tamarin (Saguinus oedipus) (2 structure(s)*)
- dog (Canis lupus familiaris) (27 structure(s)*)
- gorilla (Gorilla gorilla) (15 structure(s)*)
- horse (Equus caballus) (75 structure(s)*)
- human (Homo sapiens) (41459 structure(s)*)
- mouse (Mus musculus) (15493 structure(s)*)
- pig (Sus scrofa) (25 structure(s)*)
- rat (Rattus norvegicus) (114 structure(s)*)
- rhesus macaque (Macaca mulatta) (4721 structure(s)*)
  - Class I (4614 structure(s)*)
    - Mamu-A*01 (1972 structure(s)*)
    - Mamu-A*02 (595 structure(s)*)
    - Mamu-A*08 (1 structure(s)*)
    - Mamu-A*11 (913 structure(s)*)
    - Mamu-B*01 (630 structure(s)*)
    - Mamu-B*03 (32 structure(s)*)
    - Mamu-B*04 (9 structure(s)*)
    - Mamu-B*08 (10 structure(s)*)
    - Mamu-B*17 (1360 structure(s)*)
  - Class II (108 structure(s)*)
- sheep (Ovis aries) (8 structure(s)*)

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

Figure 2.2 Browse by MHC Allele interface

2.2.2 Browse Records by Source Organism

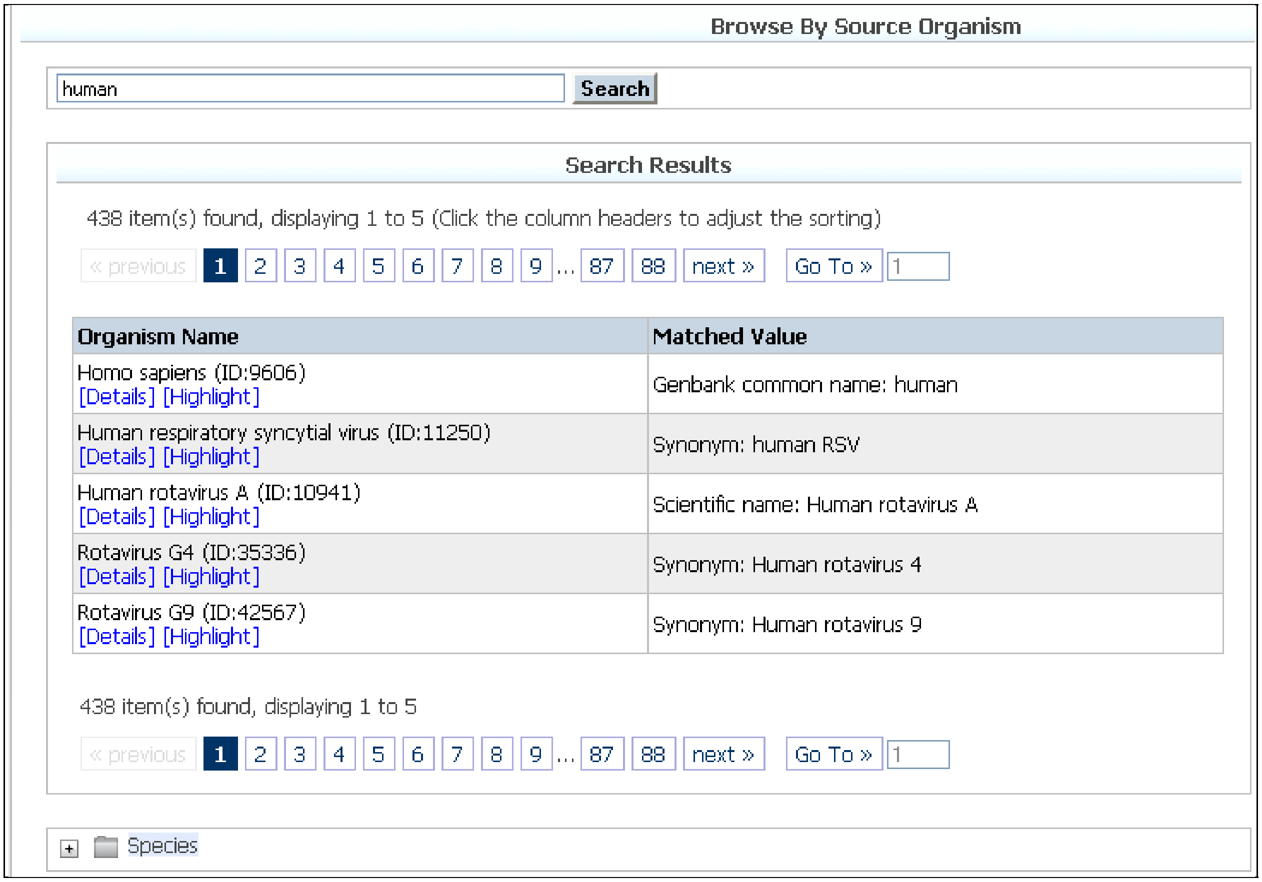
Users can find records associated with a specific epitope source species by browsing records by source organism. To do this, the user accesses the *Browse by Source Organism* page via the Browse pull-down menu. The interface for the Browse by Source Organism is a tree structure that expands (and collapses) so users can drill down on species as Figure 2.3 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. As one mouses over an entry, a descriptive balloon appears. As seen in the figure, “biota” appears to describe “cellular organisms”. The user can also search for names. For example, a search for “human”, as shown in Figure 2.4, 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 2.5, and includes the NCBI taxonomy identifier numbers and information on epitope structure, relevant literature and submission references, source antigens, and assays. If the user clicks on [Highlight] the tree expands and highlights the location. In the case of “Homo sapiens”, the tree expands to over 20 levels. Clicking on the number structures displays the same Source Organism Information as seen in Figure 2.5.



- Species
  - Viruses (63586 structure(s)*)
    - unclassified phages (3 structure(s)*)
    - dsDNA viruses, no RNA stage (24272 structure(s)*)
    - dsRNA viruses (305 structure(s)*)
    - ssRNA viruses (32651 structure(s)*)
    - Deltavirus (247 structure(s)*)
    - ssDNA viruses (604 structure(s)*)
    - Retro-transcribing viruses (5507 structure(s)*)
  - other sequences (13 structure(s)*)
    - artificial sequences (7 structure(s)*)
    - plasmids (6 structure(s)*)
  - cellular organisms (43672 structure(s)*)
    - Bacteria (17037 structure(s)*)
    - Archaea (6 structure(s)*)
    - Eukaryota (26631 structure(s)*)

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

Figure 2.3 Browse by Source Organism interface

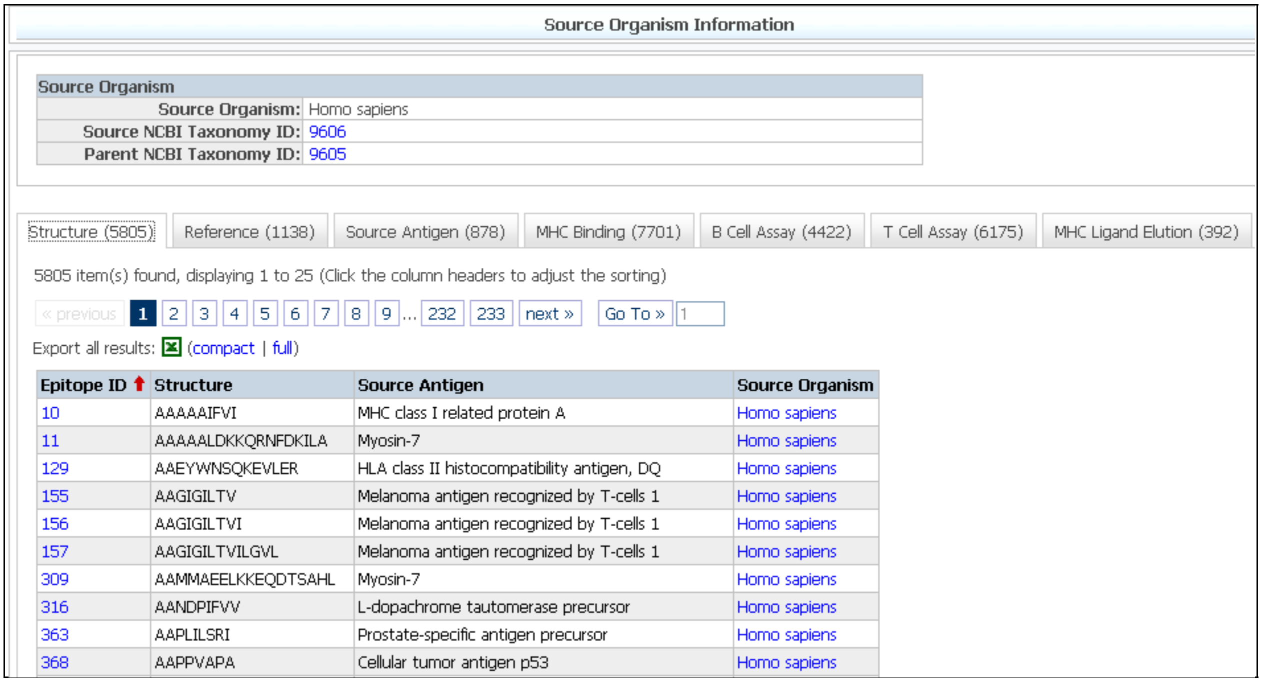


438 item(s) found, displaying 1 to 5 (Click the column headers to adjust the sorting)

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

438 item(s) found, displaying 1 to 5

Figure 2.4 Using the search feature on the Browse by Source Organism page



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

5805 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

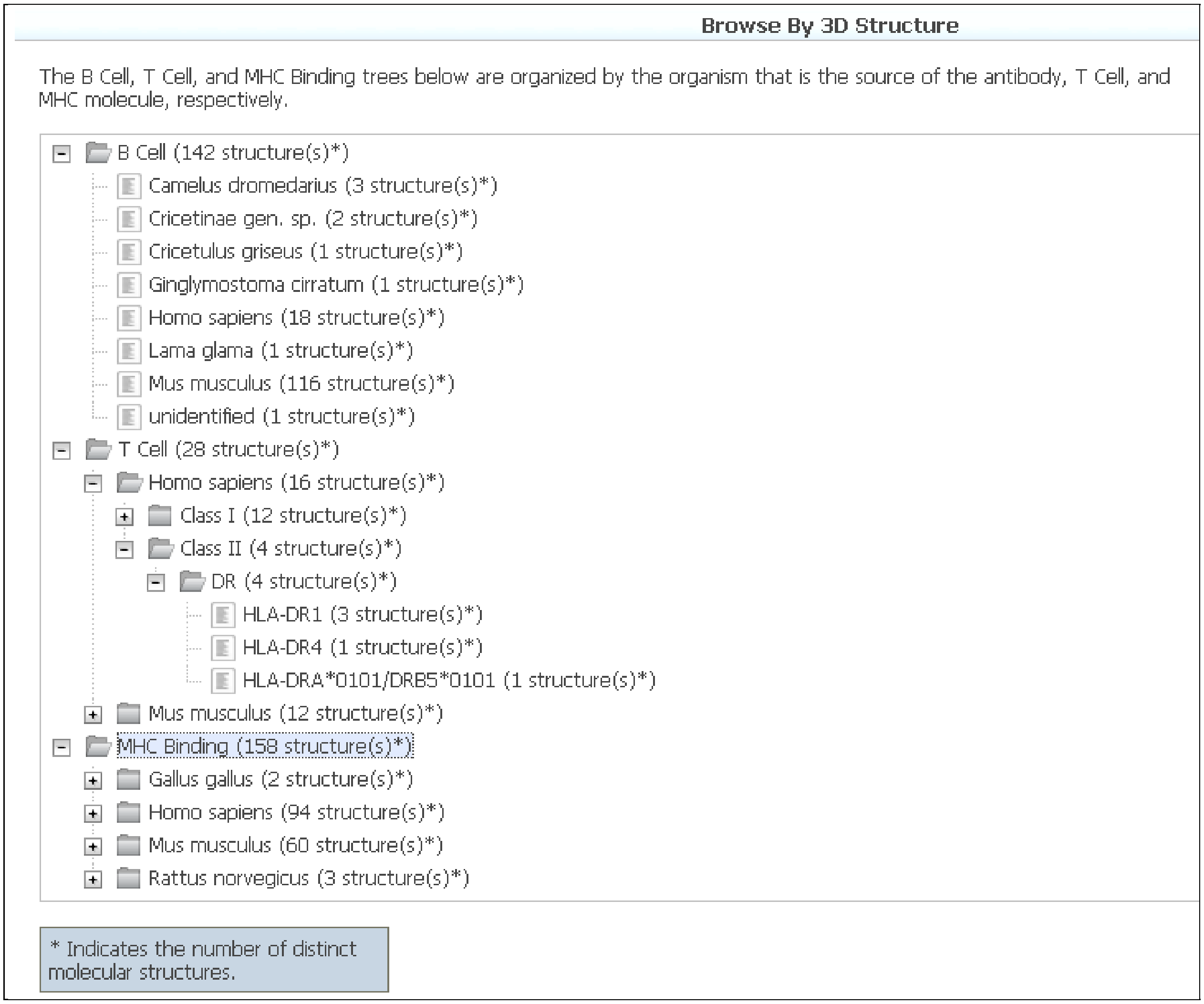
Export all results: (compact | full)

Epitope ID	Structure	Source Antigen	Source Organism
10	AAAAAIFVI	MHC class I related protein A	Homo sapiens
11	AAAAALDKKQRNFDKILA	Myosin-7	Homo sapiens
129	AAEYWNSQKEVLER	HLA class II histocompatibility antigen, DQ	Homo sapiens
155	AAGIGILTV	Melanoma antigen recognized by T-cells 1	Homo sapiens
156	AAGIGILTVI	Melanoma antigen recognized by T-cells 1	Homo sapiens
157	AAGIGILTVILGVL	Melanoma antigen recognized by T-cells 1	Homo sapiens
309	AAMMAEELKKEQDTSAHL	Myosin-7	Homo sapiens
316	AANDPIFVV	L-dopachrome tautomerase precursor	Homo sapiens
363	AAPLILSRI	Prostate-specific antigen precursor	Homo sapiens
368	AAPPVAPA	Cellular tumor antigen p53	Homo sapiens

Figure 2.5 Source Organism Information page

2.2.3 Browse by 3D Structure

All users can find records associated with a curated 3D structure by using *Browse by 3D Structure* found under the *Browse* heading on the main menu. The interface for the Browse by 3D Structure is a tree structure that makes it easy for users to find and investigate information on B cell, T cell, and MHC binding structures. As seen in Figure 2.6, the tree structure expands (and collapses) so users can drill down on species, MHC type, and/or allele to find the number of records in the IEDB for their structure of interest. This entry serves as a link that will display the records associated with the selected structure.



Browse By 3D Structure

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

- ⊟ B Cell (142 structure(s)*)
  - Camelus dromedarius (3 structure(s)*)
  - Cricetinae gen. sp. (2 structure(s)*)
  - Cricetulus griseus (1 structure(s)*)
  - Ginglymostoma cirratum (1 structure(s)*)
  - Homo sapiens (18 structure(s)*)
  - Lama glama (1 structure(s)*)
  - Mus musculus (116 structure(s)*)
  - unidentified (1 structure(s)*)
- ⊟ T Cell (28 structure(s)*)
  - ⊟ Homo sapiens (16 structure(s)*)
    - ⊞ Class I (12 structure(s)*)
    - ⊟ Class II (4 structure(s)*)
      - ⊟ DR (4 structure(s)*)
        - HLA-DR1 (3 structure(s)*)
        - HLA-DR4 (1 structure(s)*)
        - HLA-DRA*0101/DRB5*0101 (1 structure(s)*)
  - ⊞ Mus musculus (12 structure(s)*)
- ⊟ MHC Binding (158 structure(s)*)
  - ⊞ Gallus gallus (2 structure(s)*)
  - ⊞ Homo sapiens (94 structure(s)*)
  - ⊞ Mus musculus (60 structure(s)*)
  - ⊞ Rattus norvegicus (3 structure(s)*)

* Indicates the number of distinct molecular structures.

Figure 2.6 Browse by 3D Structure interface

2.3 Query

In addition to the Browse functions, there are several other ways users can find information in the IEDB. A keyword search is available on the menu bar on each page. A family of detailed query-by-example searches can be accessed on the Search pull-down menu and consist of "B Cell Search", "T Cell Search", "MHC Binding Search", "Ligand Elution Search", "Epitope Search", and "Identifier Search". The Identifier Search is a new feature introduced in 2009. This group of queries will be referred to as Detailed Searches in this document. A simplified search that is especially designed for the needs of most immunologists appears on the home page. This document will refer to this particular query as the Simple Search. All of these methods return results in a common format, as described in Section 2.3.4. These methods are elaborated in the subsections below.

2.3.1 Perform a Keyword Search

The keyword search allows users to locate records in the database using a keyword, identifier, or sequence. Wild card characters '*' and '?' can be used in the search field. The '*' character will match zero or more characters and the '?' character will match exactly one character. Additionally, the operators 'AND', 'OR', and 'NOT' can be utilized. A logical 'OR' is the default option. These three logical operators 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 2.1). They then click the Search button and view the Search Result Summary, which is described in Section 2.3.4.

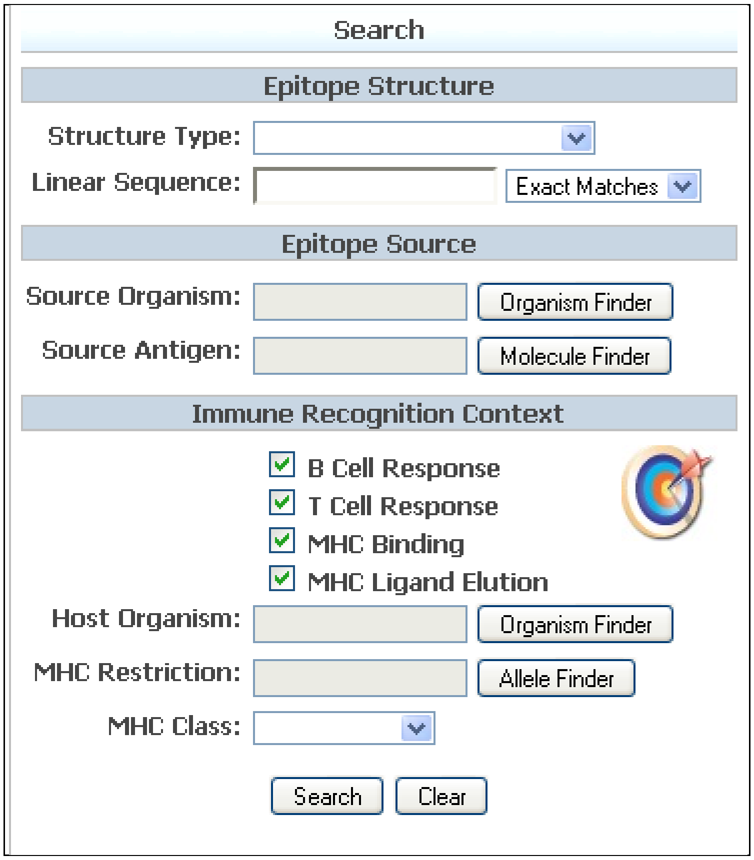
In addition to using the search function from the menu bar, users can submit searches via a properly constructed URL. The example below will perform a search using the URL for records that contain 'dengue'. This would return the equivalent of typing 'dengue' in the search option on the menu bar and clicking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

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

2.3.2 Perform a Home Page Search

The search feature available on the left-hand portion of the home page (Figure 2.7) was originally 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. The ability to specify peptide sequences and the types of searching was greatly enhanced in 2009. In addition to the option of specifying the structure type (e.g. peptide from protein or carbohydrate fragment), the user can prescribe a linear peptide sequence and the type of search to be performed on it. Entering the sequence has also been improved. When specifying a linear sequence, a window appears in which the user must enter the sequence and press "Apply". The user can prescribe the type of search desired - an exact match to the entered sequence, a substring search where epitopes are found that contain the sequence within its overall structure, or a homologous peptides at sequence at identity levels of 70%, 80%, or 90% as determined by BLAST.

The epitope source can be prescribed for the source organism and source antigen by using the organism finder (Section 2.3.5.5) and molecule finder (Section 2.3.5.4), respectively. The user can decide whether to include B cell responses, T cell responses, 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 2.3.5.1). The fields using finders will allow multiple selections as search criteria. In these cases the selections are treated as a set. Records will be considered a match if they include at least one of the selected values in the set. The search is executed by selecting the Search button and query results can be viewed on the Search Result Summary page, which is described in Section 2.3.4.



Linear Sequence: Exact Matches

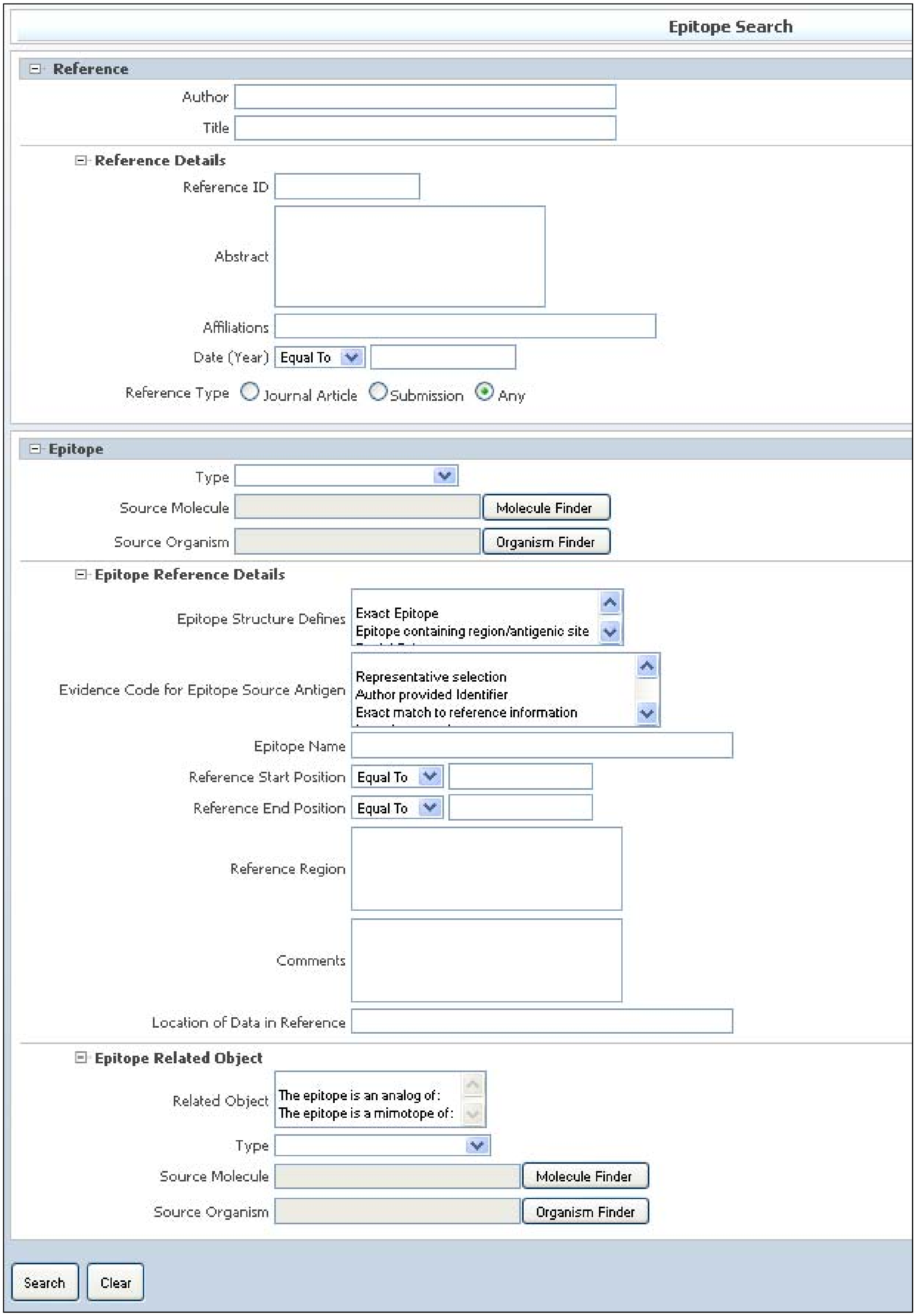
☑ B Cell Response
☑ T Cell Response
☑ MHC Binding
☑ MHC Ligand Elution

Figure 2.7 Home page Simple Search

2.3.3 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 Search is shown in Figure 2.8. 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.



Date (Year) Equal To

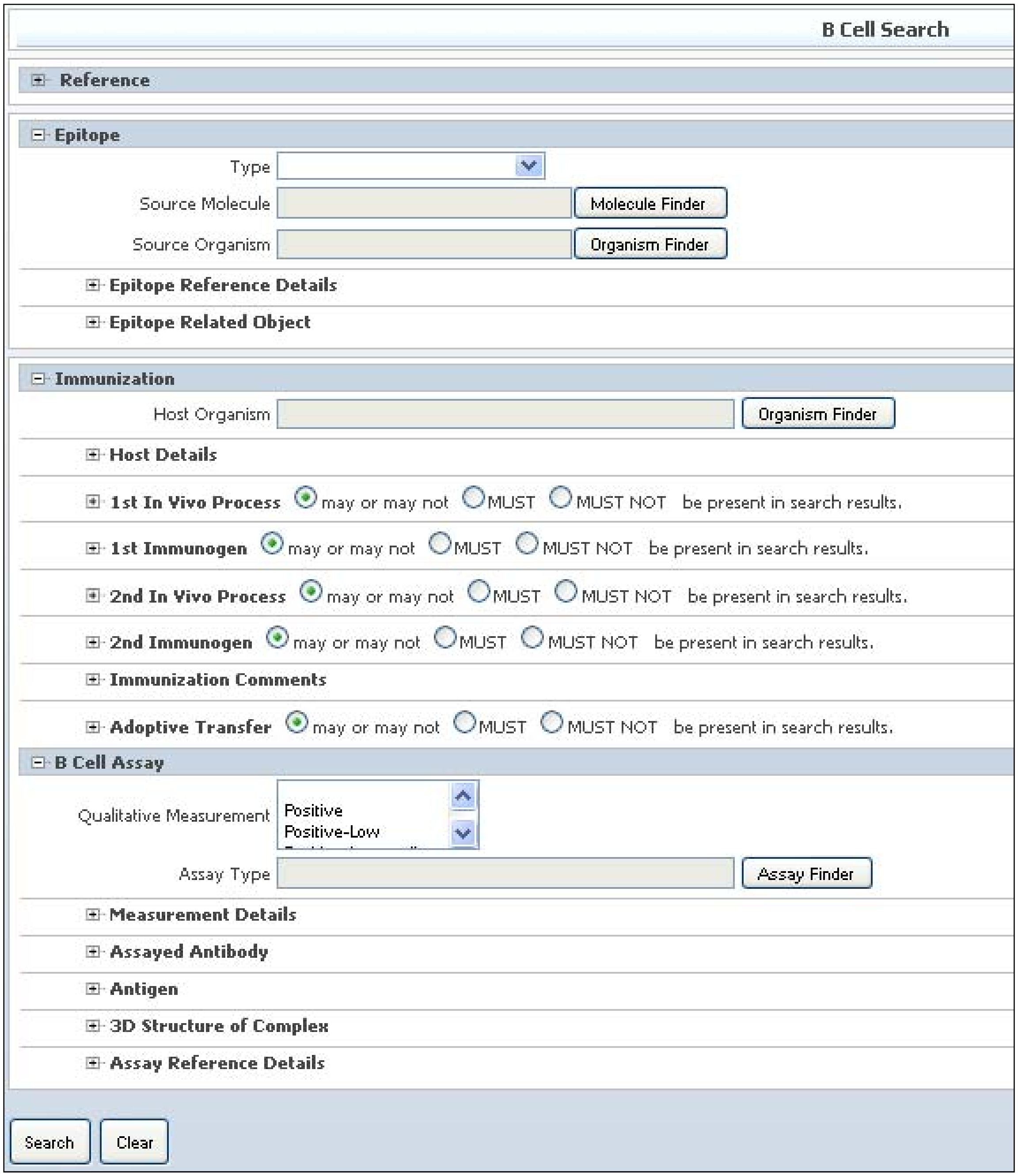
Reference Type ○ Journal Article ○ Submission ● Any

Reference Start Position Equal To

Reference End Position Equal To

Figure 2.8 Epitope Search input screen

There are five other Detailed Queries that can be used to select search criteria for references, epitopes, and assays. These five are B Cell Search, T Cell Search, MHC Binding Search, MHC Ligand Elution Search, and the recently added Identifier Search. As an example, the B Cell Search input screen is shown in Figure 2.9. As is the case for all four assay search input screens, the Reference and Epitope criteria fields are listed first, followed by the fields specific for each assay type.



⊞ 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.

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

Figure 2.9 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.

The Identifier Search input screen is shown in Figure 2.10. If user know the epitope, reference, submission, or assay identifier they are seeking, they can enter that information into one of the four IEDB Identifiers fields. Users can also look for information based on the PubMed ID of a reference or the PDB ID of a structure by using the External Identifiers fields.

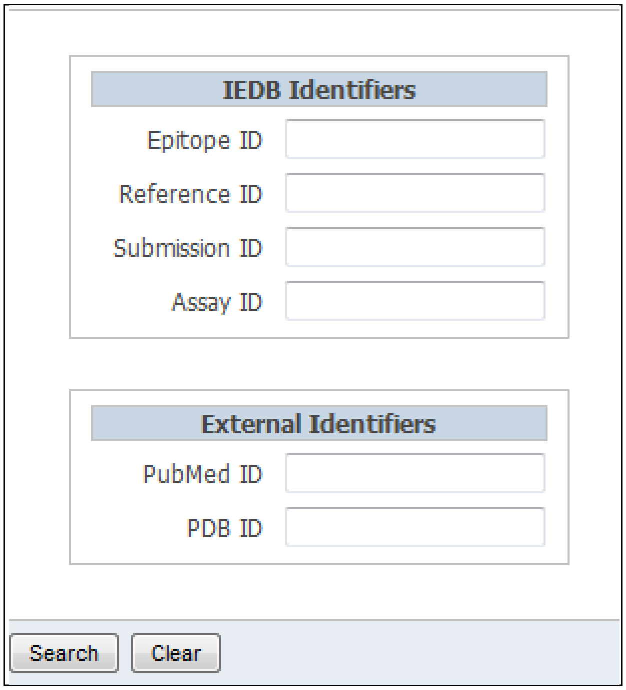


Figure 2.10 Identifier Search input screen

2.3.4 Search Results Summary

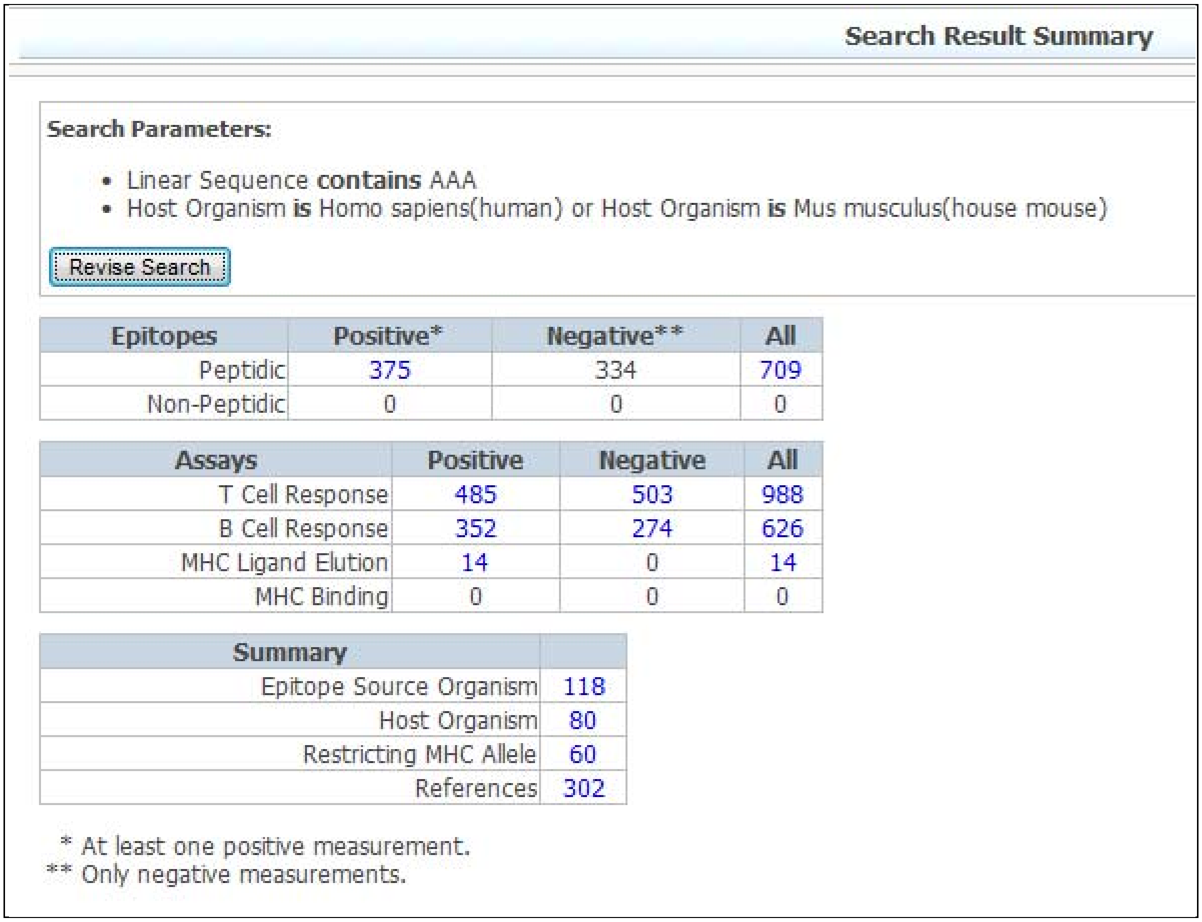
The Search Results Summary page displays the results of all the different queries. An example is displayed in Figure 2.11, which was generated with the Home page Simple Search for the linear sequence substring "AAA" for human and mouse host organisms. The Search Results Summary allows the user to quickly assess the results of their search and drill down the level of detail that is of interest. As a convenience, the display of Search Parameters was added to the Search Result Summary page, along with the ability to revise the search criteria. Clicking on the "Revise Search" button will take the user back to the original search form, either the home page for the Simple Search or to the appropriate Detailed Search form.

The number peptidic and non-peptidic epitopes are displayed in the topmost table on the Result Summary. Because the IEDB captures both positive and negative assay responses, some "epitopes" lack a positive binding value and therefore are not actually epitopes; the number of these molecular structures is indicated in the Negative column of the table. The user can click on the number in the Positive and All columns to view all the results for that category, as seen in Figure 2.12 for the positive peptidic epitopes. The columns displayed include the number of corresponding epitope, source antigen, and source species.

Figure 2.12 also demonstrates another new feature added in 2009. Comma separated values (CSV) file exports are available on-demand from all list pages and list tabs throughout the site, except for the patent list, which is only provided in PDF format. The CSV file exports are available in two formats, a compact format that only contains the data presented in the list the user is viewing, and a full record format that contains all of the data associated with the records in the list the user is viewing. The full record format was introduced in 2009. The CSV format can be easily manipulated using a spreadsheet program, such as Microsoft Excel, or edited with a word processing program, such as Microsoft Word or Notepad.

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 2.13.

The third table lists the number of epitope source organisms, host organisms, restricting MHC alleles, and references resulting from the input search criteria. As before, the user can drill down on the values in the table to find more detail related to each category, as seen in Figure 2.14, Figure 2.15, Figure 2.16, and Figure 2.17.



Search Result Summary

Search Parameters:

- Linear Sequence **contains** AAA
- Host Organism **is** Homo sapiens(human) or Host Organism **is** Mus musculus(house mouse)

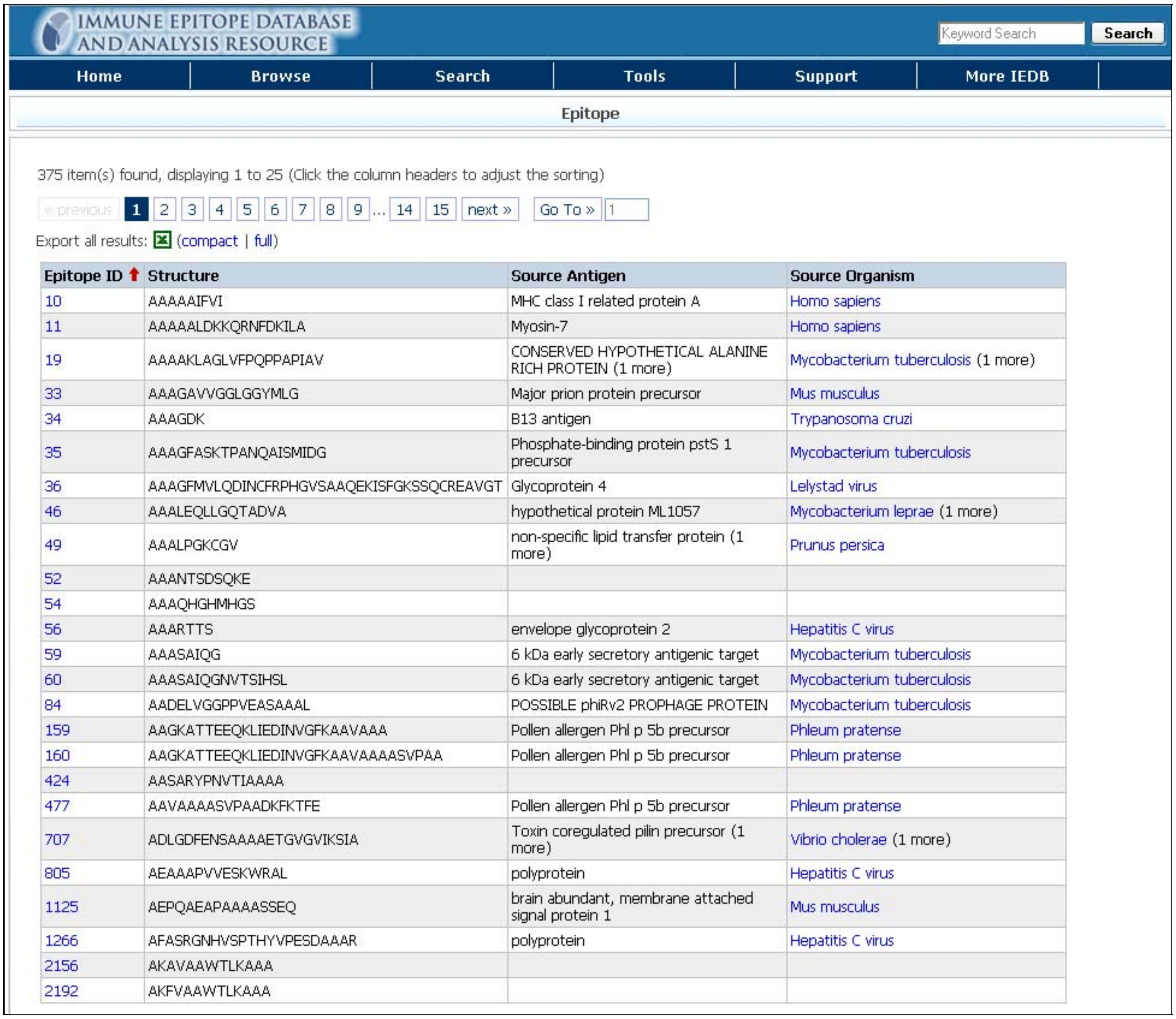
Epitopes	Positive*	Negative**	All
Peptidic	375	334	709
Non-Peptidic	0	0	0

Assays	Positive	Negative	All
T Cell Response	485	503	988
B Cell Response	352	274	626
MHC Ligand Elution	14	0	14
MHC Binding	0	0	0

Summary	
Epitope Source Organism	118
Host Organism	80
Restricting MHC Allele	60
References	302

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

Figure 2.11 Sample of Search Result Summary

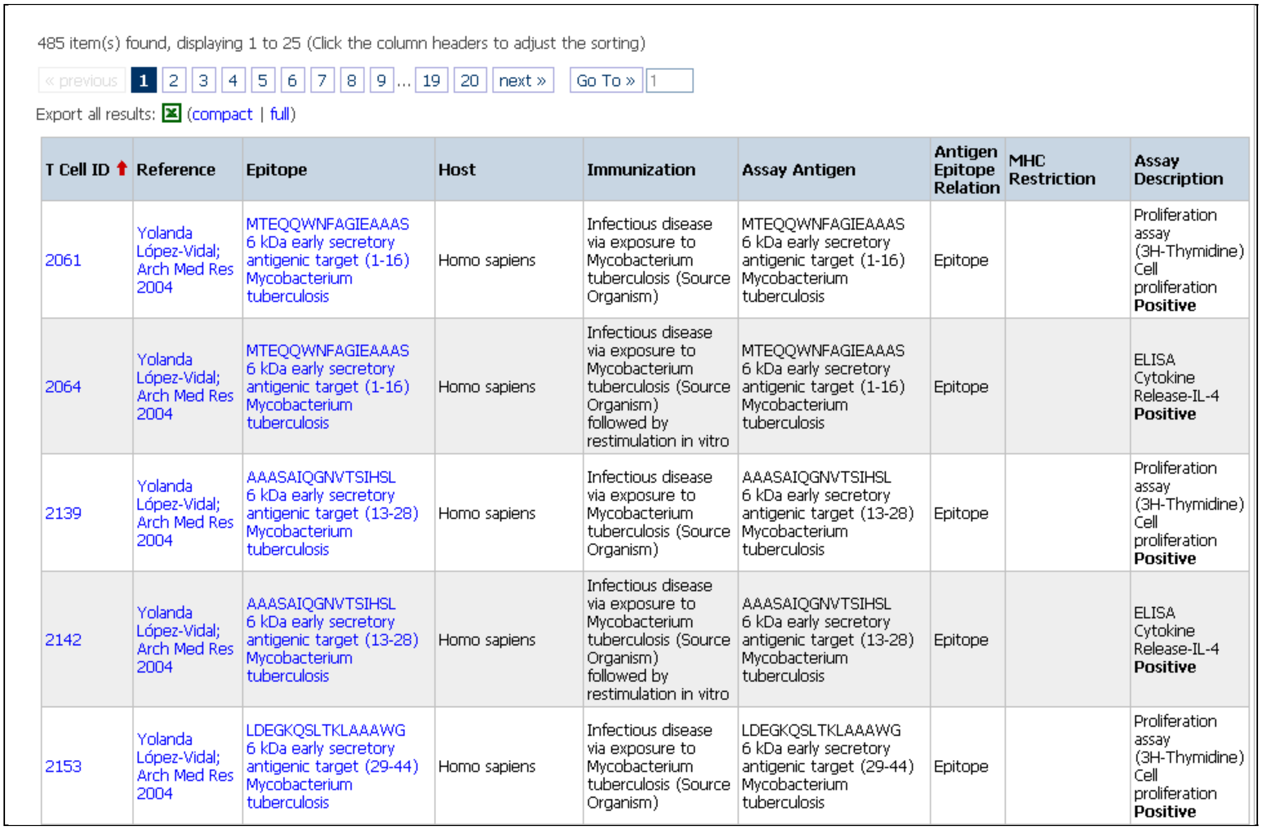


375 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

Export all results: (compact | full)

Epitope ID ↑	Structure	Source Antigen	Source Organism
10	AAAAAIFVI	MHC class I related protein A	Homo sapiens
11	AAAAALDKKQRNFDKILA	Myosin-7	Homo sapiens
19	AAAAKLAGLVFPQPPAPIAV	CONSERVED HYPOTHETICAL ALANINE RICH PROTEIN (1 more)	Mycobacterium tuberculosis (1 more)
33	AAAGAVVGGLGGYMLG	Major prion protein precursor	Mus musculus
34	AAAGDK	B13 antigen	Trypanosoma cruzi
35	AAAGFASKTPANQAISMIDG	Phosphate-binding protein pstS 1 precursor	Mycobacterium tuberculosis
36	AAAGFMVLQDINCFRPHGVSAAQEKISFGKSSQCREAVGT	Glycoprotein 4	Lelystad virus
46	AAALEQLLGQTADVA	hypothetical protein ML1057	Mycobacterium leprae (1 more)
49	AAALPGKCGV	non-specific lipid transfer protein (1 more)	Prunus persica
52	AAANTSDSQKE		
54	AAAQHGHMHGS		
56	AAARTTS	envelope glycoprotein 2	Hepatitis C virus
59	AAASAIQG	6 kDa early secretory antigenic target	Mycobacterium tuberculosis
60	AAASAIQGNVTSIHSL	6 kDa early secretory antigenic target	Mycobacterium tuberculosis
84	AADELVGGPPVEASAAAL	POSSIBLE phiRv2 PROPHAGE PROTEIN	Mycobacterium tuberculosis
159	AAGKATTEEQKLIEDINVGFKAAVAAA	Pollen allergen Phl p 5b precursor	Phleum pratense
160	AAGKATTEEQKLIEDINVGFKAAVAAAASVPAA	Pollen allergen Phl p 5b precursor	Phleum pratense
424	AASARYPNVTIAAAA		
477	AAVAAAASVPAADKFKTFE	Pollen allergen Phl p 5b precursor	Phleum pratense
707	ADLGDFENSAAAAETGVGVIKSIA	Toxin coregulated pilin precursor (1 more)	Vibrio cholerae (1 more)
805	AEAAAPVVESKWRAL	polyprotein	Hepatitis C virus
1125	AEPQAEAPAAAASSEQ	brain abundant, membrane attached signal protein 1	Mus musculus
1266	AFASRGNHVSPTHYVPESDAAAR	polyprotein	Hepatitis C virus
2156	AKAVAAWTLKAAA		
2192	AKFVAAWTLKAAA		

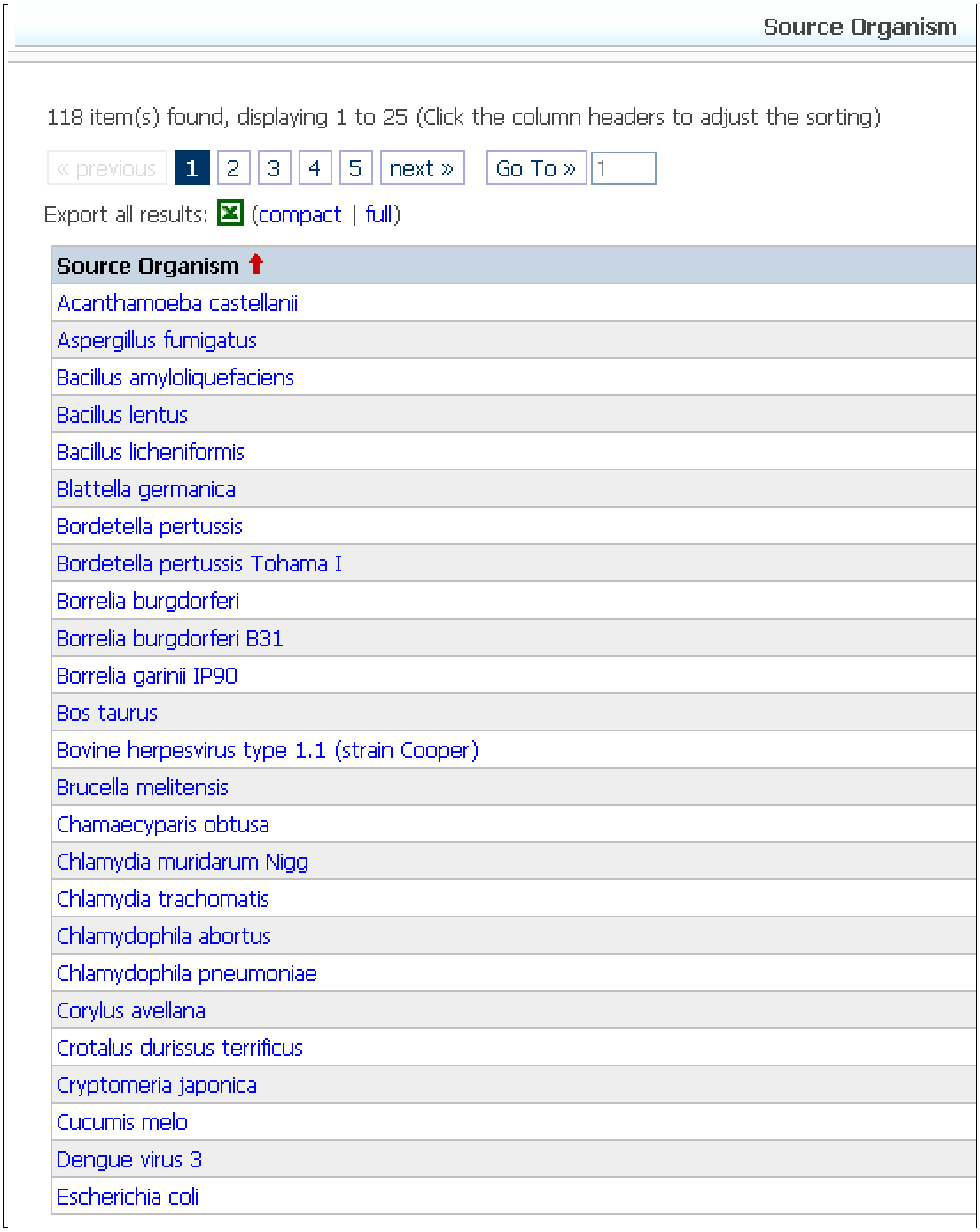
Figure 2.12 Screen generated by drilling down on the positive epitope hyperlink in the Search Result Summary


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

Export all results: (compact | full)

T Cell ID	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	MHC Restriction	Assay Description
2061	Yolanda López-Vidal; Arch Med Res 2004	MTEQQWNFAGIEAAAS 6 kDa early secretory antigenic target (1-16) Mycobacterium tuberculosis	Homo sapiens	Infectious disease via exposure to Mycobacterium tuberculosis (Source Organism)	MTEQQWNFAGIEAAAS 6 kDa early secretory antigenic target (1-16) Mycobacterium tuberculosis	Epitope		Proliferation assay (3H-Thymidine) Cell proliferation **Positive**
2064	Yolanda López-Vidal; Arch Med Res 2004	MTEQQWNFAGIEAAAS 6 kDa early secretory antigenic target (1-16) Mycobacterium tuberculosis	Homo sapiens	Infectious disease via exposure to Mycobacterium tuberculosis (Source Organism) followed by restimulation in vitro	MTEQQWNFAGIEAAAS 6 kDa early secretory antigenic target (1-16) Mycobacterium tuberculosis	Epitope		ELISA Cytokine Release-IL-4 **Positive**
2139	Yolanda López-Vidal; Arch Med Res 2004	AAASAIQGNVTSIHSL 6 kDa early secretory antigenic target (13-28) Mycobacterium tuberculosis	Homo sapiens	Infectious disease via exposure to Mycobacterium tuberculosis (Source Organism)	AAASAIQGNVTSIHSL 6 kDa early secretory antigenic target (13-28) Mycobacterium tuberculosis	Epitope		Proliferation assay (3H-Thymidine) Cell proliferation **Positive**
2142	Yolanda López-Vidal; Arch Med Res 2004	AAASAIQGNVTSIHSL 6 kDa early secretory antigenic target (13-28) Mycobacterium tuberculosis	Homo sapiens	Infectious disease via exposure to Mycobacterium tuberculosis (Source Organism) followed by restimulation in vitro	AAASAIQGNVTSIHSL 6 kDa early secretory antigenic target (13-28) Mycobacterium tuberculosis	Epitope		ELISA Cytokine Release-IL-4 **Positive**
2153	Yolanda López-Vidal; Arch Med Res 2004	LDEGKQSLTKLAAAWG 6 kDa early secretory antigenic target (29-44) Mycobacterium tuberculosis	Homo sapiens	Infectious disease via exposure to Mycobacterium tuberculosis (Source Organism)	LDEGKQSLTKLAAAWG 6 kDa early secretory antigenic target (29-44) Mycobacterium tuberculosis	Epitope		Proliferation assay (3H-Thymidine) Cell proliferation **Positive**

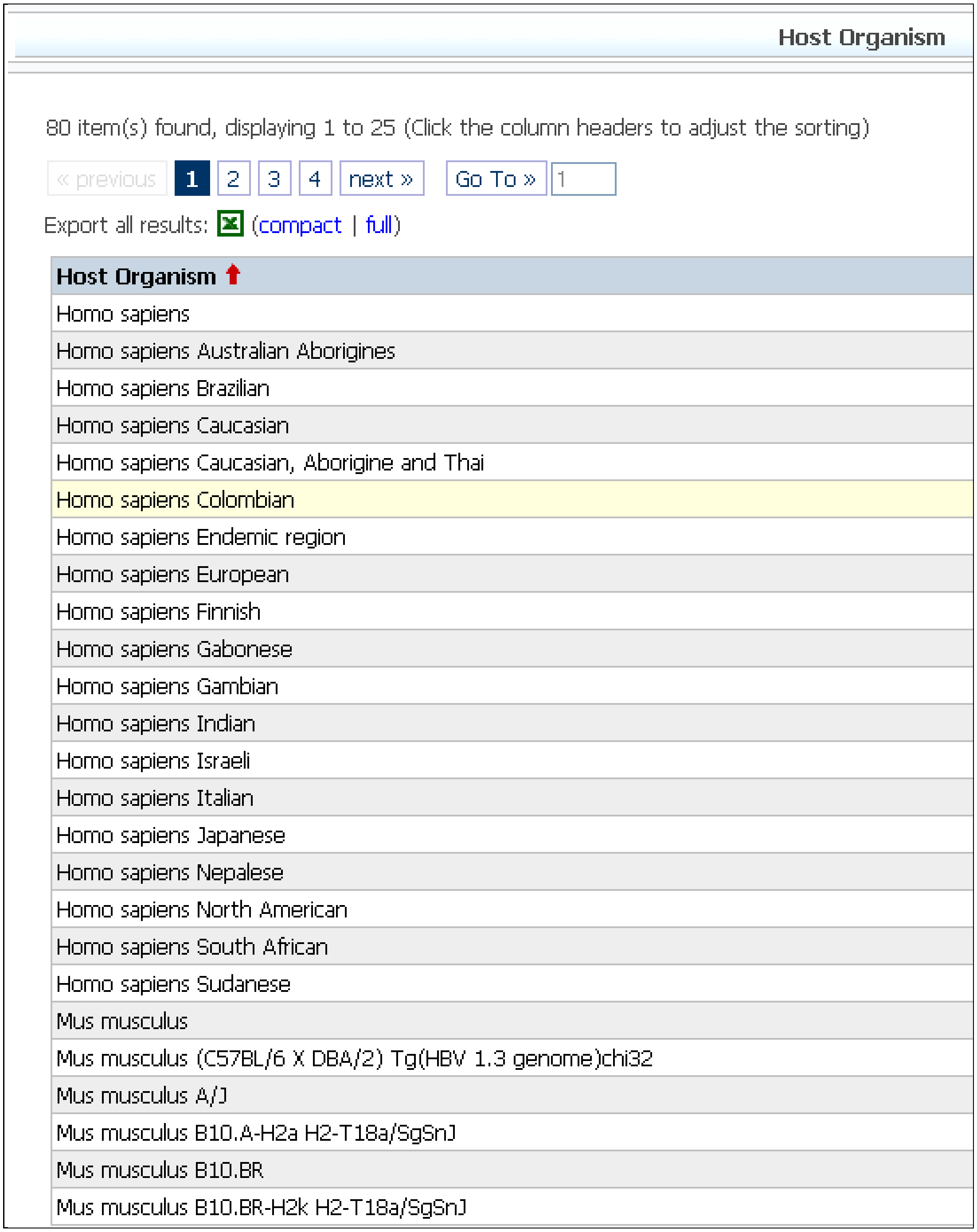
Figure 2.13 Screen generated by drilling down on the positive T cell assay hyperlink in the Search Result Summary



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

Source Organism
Acanthamoeba castellanii
Aspergillus fumigatus
Bacillus amyloliquefaciens
Bacillus lentus
Bacillus licheniformis
Blattella germanica
Bordetella pertussis
Bordetella pertussis Tohama I
Borrelia burgdorferi
Borrelia burgdorferi B31
Borrelia garinii IP90
Bos taurus
Bovine herpesvirus type 1.1 (strain Cooper)
Brucella melitensis
Chamaecyparis obtusa
Chlamydia muridarum Nigg
Chlamydia trachomatis
Chlamydophila abortus
Chlamydophila pneumoniae
Corylus avellana
Crotalus durissus terrificus
Cryptomeria japonica
Cucumis melo
Dengue virus 3
Escherichia coli

Figure 2.14 Screen generated by drilling down on the Epitope Source Organism link in the Search Result Summary

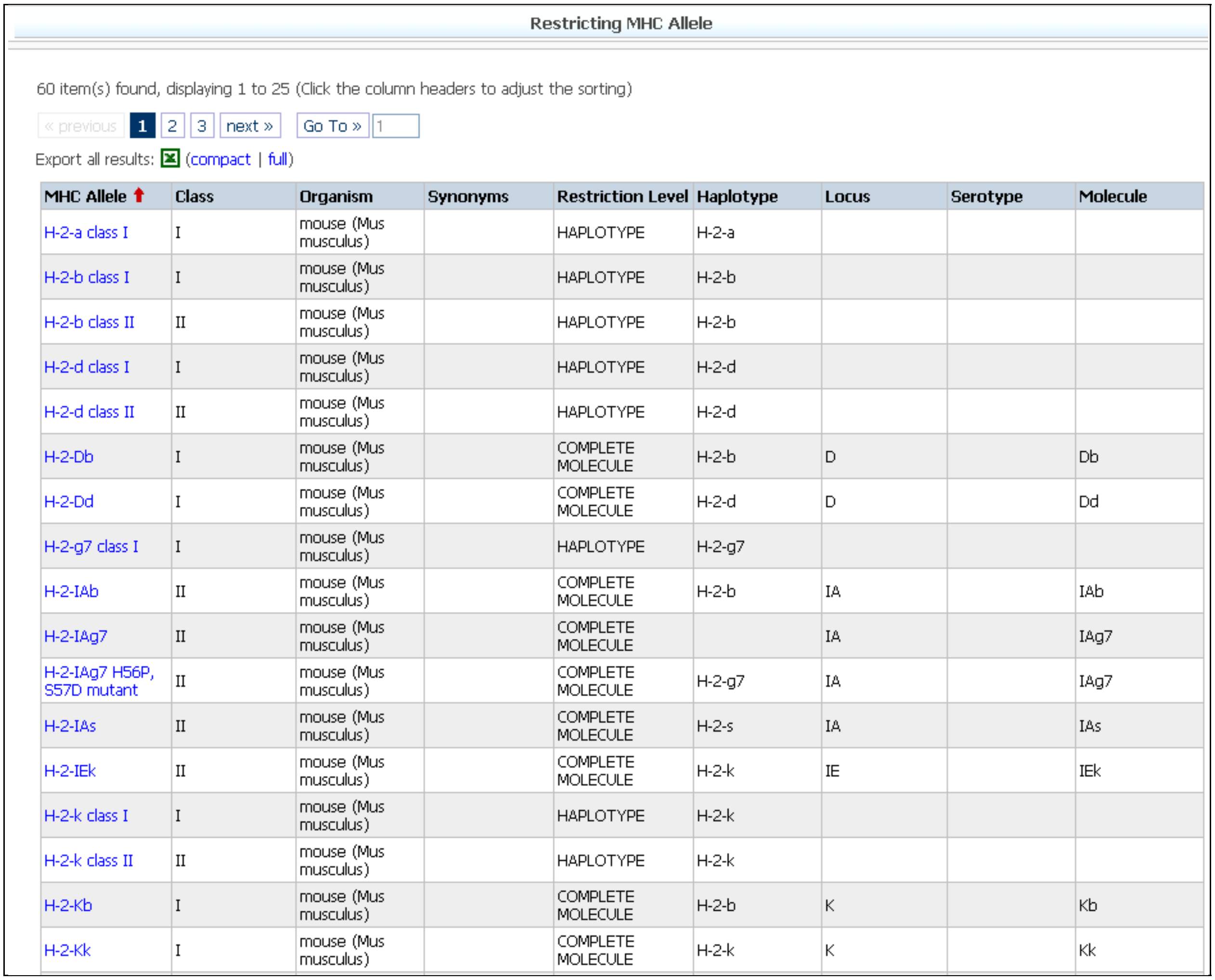


80 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

Export all results: (compact | full)

Host Organism
Homo sapiens
Homo sapiens Australian Aborigines
Homo sapiens Brazilian
Homo sapiens Caucasian
Homo sapiens Caucasian, Aborigine and Thai
Homo sapiens Colombian
Homo sapiens Endemic region
Homo sapiens European
Homo sapiens Finnish
Homo sapiens Gabonese
Homo sapiens Gambian
Homo sapiens Indian
Homo sapiens Israeli
Homo sapiens Italian
Homo sapiens Japanese
Homo sapiens Nepalese
Homo sapiens North American
Homo sapiens South African
Homo sapiens Sudanese
Mus musculus
Mus musculus (C57BL/6 X DBA/2) Tg(HBV 1.3 genome)chi32
Mus musculus A/J
Mus musculus B10.A-H2a H2-T18a/SgSnJ
Mus musculus B10.BR
Mus musculus B10.BR-H2k H2-T18a/SgSnJ

Figure 2.15 Screen generated by drilling down on the Host Organism link in the Search Result Summary



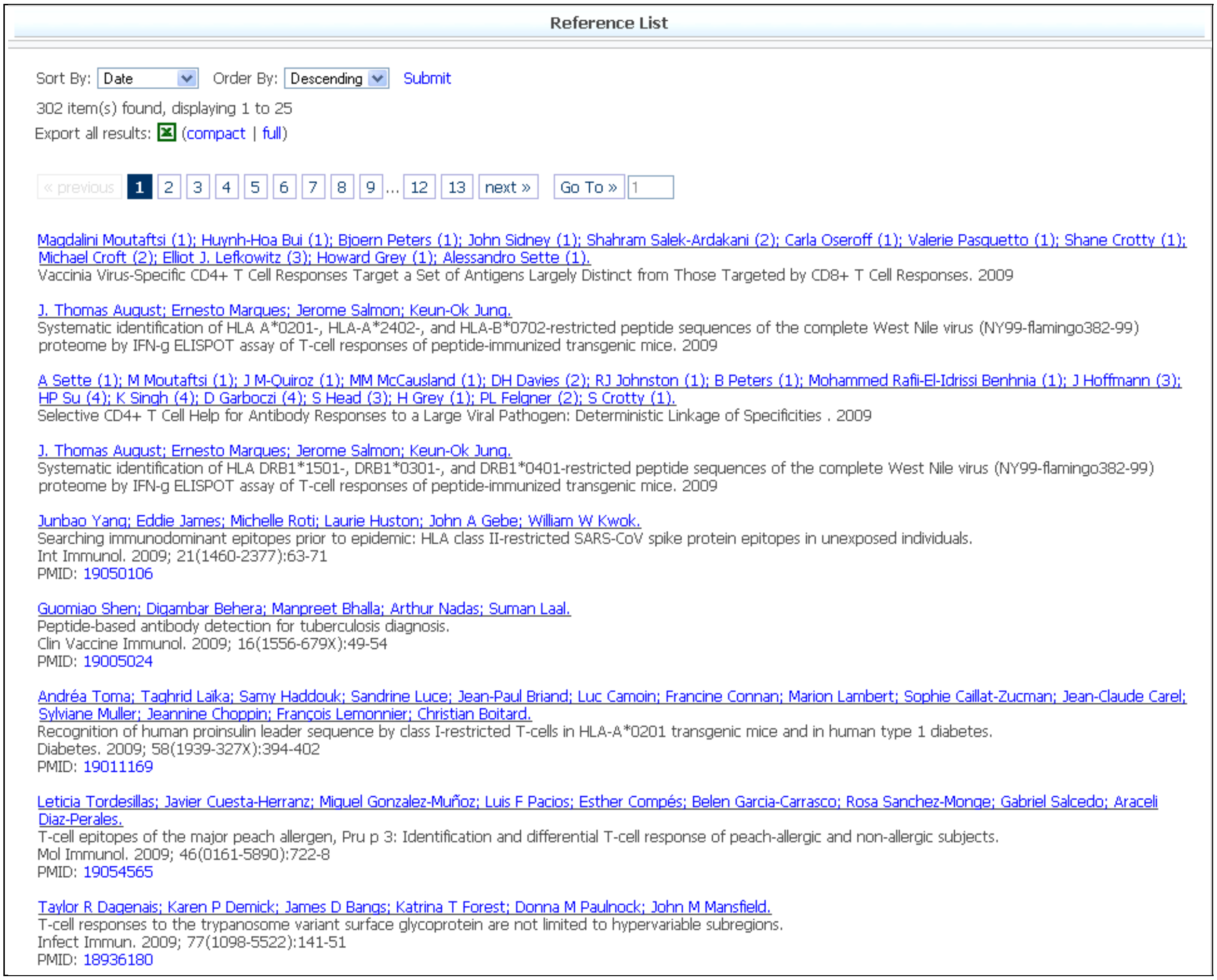
Restricting MHC Allele

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

Export all results: (compact | full)

MHC Allele ↑	Class	Organism	Synonyms	Restriction Level	Haplotype	Locus	Serotype	Molecule
H-2-a class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-a			
H-2-b class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-b			
H-2-b class II	II	mouse (Mus musculus)		HAPLOTYPE	H-2-b			
H-2-d class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-d			
H-2-d class II	II	mouse (Mus musculus)		HAPLOTYPE	H-2-d			
H-2-Db	I	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-b	D		Db
H-2-Dd	I	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-d	D		Dd
H-2-g7 class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-g7			
H-2-IAb	II	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-b	IA		IAb
H-2-IAg7	II	mouse (Mus musculus)		COMPLETE MOLECULE		IA		IAg7
H-2-IAg7 H56P, S57D mutant	II	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-g7	IA		IAg7
H-2-IAs	II	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-s	IA		IAs
H-2-IEk	II	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-k	IE		IEk
H-2-k class I	I	mouse (Mus musculus)		HAPLOTYPE	H-2-k			
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-Kk	I	mouse (Mus musculus)		COMPLETE MOLECULE	H-2-k	K		Kk

Figure 2.16 Screen generated by drilling down on the Restricting MHC Allele link in the Search Result Summary



Sort By: Date Order By: Descending

302 item(s) found, displaying 1 to 25

Export all results: (compact | full)

Magdalini Moutaftsi (1); Huynh-Hoa Bui (1); Bjoern Peters (1); John Sidney (1); Shahram Salek-Ardakani (2); Carla Oseroff (1); Valerie Pasquetto (1); Shane Crotty (1); Michael Croft (2); Elliot J. Lefkowitz (3); Howard Grey (1); Alessandro Sette (1).
Vaccinia Virus-Specific CD4+ T Cell Responses Target a Set of Antigens Largely Distinct from Those Targeted by CD8+ T Cell Responses. 2009

J. Thomas August; Ernesto Marques; Jerome Salmon; Keun-Ok Jung.
Systematic identification of HLA A*0201-, HLA-A*2402-, and HLA-B*0702-restricted peptide sequences of the complete West Nile virus (NY99-flamingo382-99) proteome by IFN-g ELISPOT assay of T-cell responses of peptide-immunized transgenic mice. 2009

A Sette (1); M Moutaftsi (1); J M-Quiroz (1); MM McCausland (1); DH Davies (2); RJ Johnston (1); B Peters (1); Mohammed Rafii-El-Idrissi Benhnia (1); J Hoffmann (3); HP Su (4); K Singh (4); D Garboczi (4); S Head (3); H Grey (1); PL Felgner (2); S Crotty (1).
Selective CD4+ T Cell Help for Antibody Responses to a Large Viral Pathogen: Deterministic Linkage of Specificities . 2009

J. Thomas August; Ernesto Marques; Jerome Salmon; Keun-Ok Jung.
Systematic identification of HLA DRB1*1501-, DRB1*0301-, and DRB1*0401-restricted peptide sequences of the complete West Nile virus (NY99-flamingo382-99) proteome by IFN-g ELISPOT assay of T-cell responses of peptide-immunized transgenic mice. 2009

Junbao Yang; Eddie James; Michelle Roti; Laurie Huston; John A Gebe; William W Kwok.
Searching immunodominant epitopes prior to epidemic: HLA class II-restricted SARS-CoV spike protein epitopes in unexposed individuals.
Int Immunol. 2009; 21(1460-2377):63-71
PMID: 19050106

Guomiao Shen; Digambar Behera; Manpreet Bhalla; Arthur Nadas; Suman Laal.
Peptide-based antibody detection for tuberculosis diagnosis.
Clin Vaccine Immunol. 2009; 16(1556-679X):49-54
PMID: 19005024

Andréa Toma; Taghrid Laika; Samy Haddouk; Sandrine Luce; Jean-Paul Briand; Luc Camoin; Francine Connan; Marion Lambert; Sophie Caillat-Zucman; Jean-Claude Carel; Sylviane Muller; Jeannine Choppin; François Lemonnier; Christian Boitard.
Recognition of human proinsulin leader sequence by class I-restricted T-cells in HLA-A*0201 transgenic mice and in human type 1 diabetes.
Diabetes. 2009; 58(1939-327X):394-402
PMID: 19011169

Leticia Tordesillas; Javier Cuesta-Herranz; Miguel Gonzalez-Muñoz; Luis F Pacios; Esther Compés; Belen Garcia-Carrasco; Rosa Sanchez-Monge; Gabriel Salcedo; Araceli Diaz-Perales.
T-cell epitopes of the major peach allergen, Pru p 3: Identification and differential T-cell response of peach-allergic and non-allergic subjects.
Mol Immunol. 2009; 46(0161-5890):722-8
PMID: 19054565

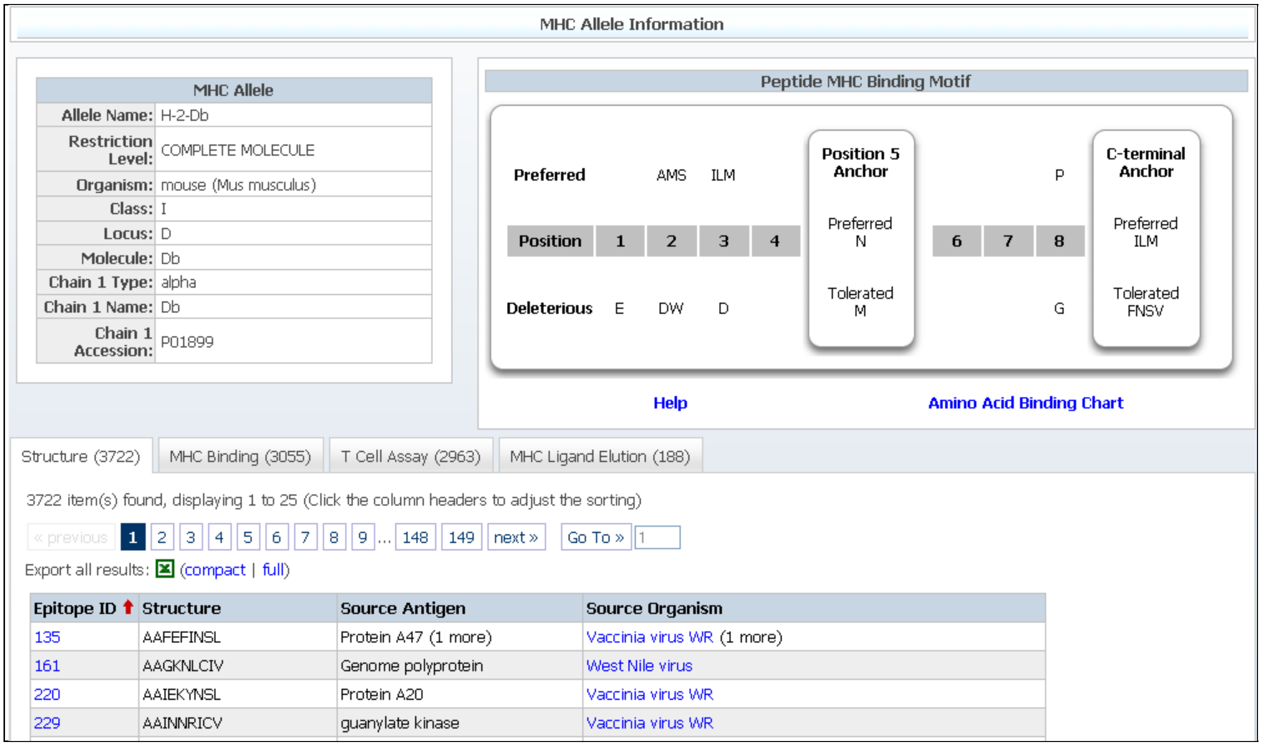
Taylor R Dagenais; Karen P Demick; James D Bangs; Katrina T Forest; Donna M Paulnock; John M Mansfield.
T-cell responses to the trypanosome variant surface glycoprotein are not limited to hypervariable subregions.
Infect Immun. 2009; 77(1098-5522):141-51
PMID: 18936180

Figure 2.17 Screen generated by drilling down on the reference hyperlink in the Search Result Summary

When users click on the number of references on the Search Results Summary screen, the system will display the Reference List, as seen in Figure 2.17. 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.

2.3.4.1 Peptide MHC Binding Motif Displays

One of the new features introduced in IEDB 2.3 is the display of peptide MHC binding motif diagrams and amino acid binding charts for a subset of MHC allele records. This information appears on the MHC Allele Information page. This page can be reached from the Restricting MHC Allele page shown in Figure 2.16. Clicking on H-2-Db in the left MHC Allele column in the sixth row, the user is brought to its MHC Allele Information page (Figure 2.18).



MHC Allele	
Allele Name:	H-2-Db
Restriction Level:	COMPLETE MOLECULE
Organism:	mouse (Mus musculus)
Class:	I
Locus:	D
Molecule:	Db
Chain 1 Type:	alpha
Chain 1 Name:	Db
Chain 1 Accession:	P01899

Position	1	2	3	4	**Position 5 Anchor**	6	7	8	**C-terminal Anchor**
Preferred		AMS	ILM		Preferred N			P	Preferred ILM
Deleterious	E	DW	D		Tolerated M			G	Tolerated FNSV

3722 item(s) found, displaying 1 to 25 (Click the column headers to adjust the sorting)

Epitope ID	Structure	Source Antigen	Source Organism
135	AAFEFINSL	Protein A47 (1 more)	Vaccinia virus WR (1 more)
161	AAGKNLCIV	Genome polyprotein	West Nile virus
220	AAIEKYNSL	Protein A20	Vaccinia virus WR
229	AAINNRICV	guanylate kinase	Vaccinia virus WR

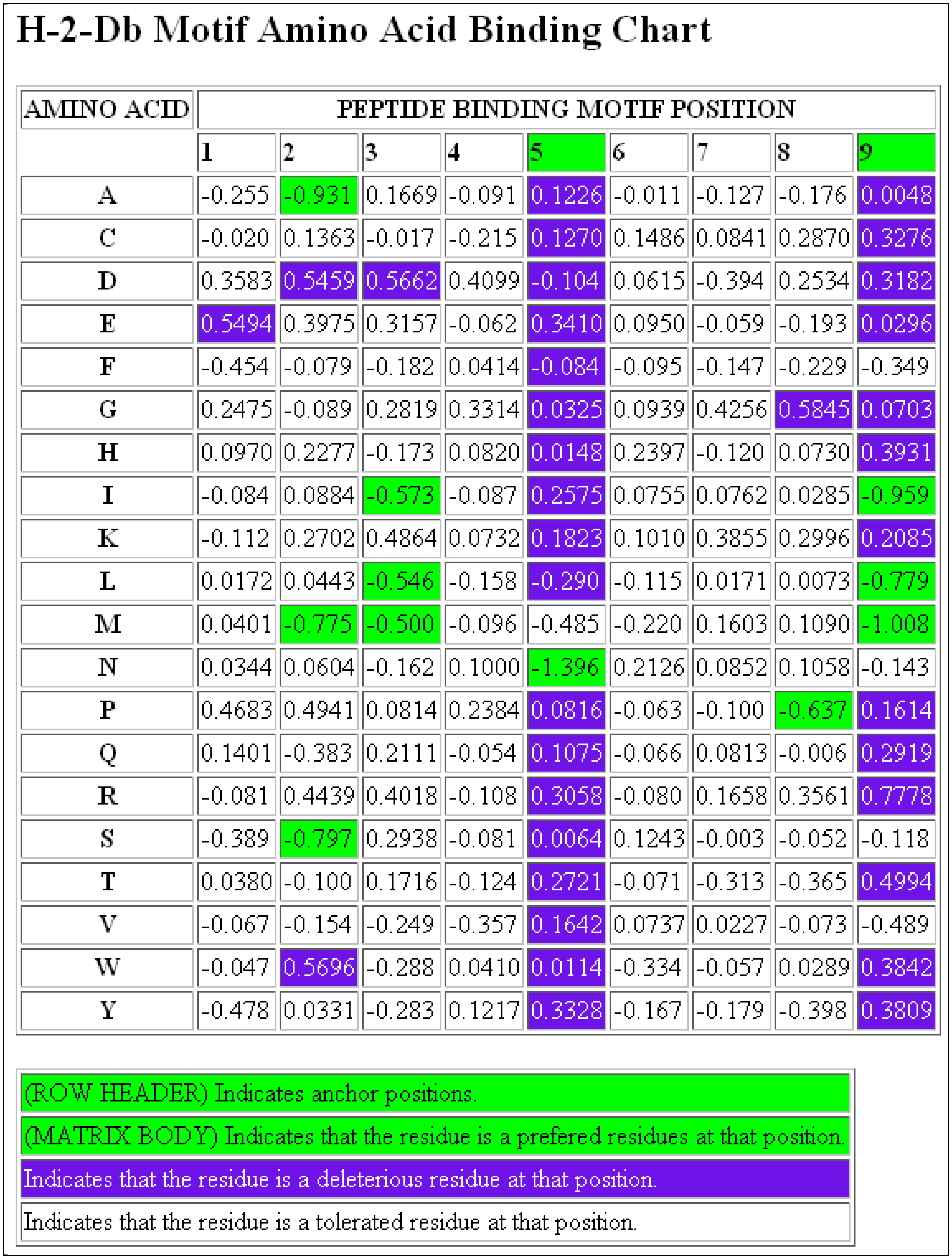
Figure 2.18 Sample MHC Allele Information page with Peptide MHC Binding Motif diagram for H-2_Db. Note the link to the corresponding Amino Acid Binding Chart on the bottom right of the diagram.

The Peptide MHC Binding Motid diagram summarizes the results of the amino acid binding for each position, which is shown in Figure 2.19. The amino acids are color-coded for each position, where green indicates the residue is preferred for binding, purple indicates it is deleterious for binding, and white indicates the residue is tolerated at that position. The motif diagram shows which residues are preferred and tolerated at the anchor positions, and which residues are preferred and deleterious at the non-anchor positions.

The residue preference is calculated from the SMM prediction matrix, which is described in Section 2.4.1.1. The following steps are taken in determining the residue preference at each position:

For anchor position:

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



H-2-Db Motif Amino Acid Binding Chart

AMINO ACID	PEPTIDE BINDING MOTIF POSITION								
	1	2	3	4	5	6	7	8	9
A	-0.255	-0.931	0.1669	-0.091	0.1226	-0.011	-0.127	-0.176	0.0048
C	-0.020	0.1363	-0.017	-0.215	0.1270	0.1486	0.0841	0.2870	0.3276
D	0.3583	0.5459	0.5662	0.4099	-0.104	0.0615	-0.394	0.2534	0.3182
E	0.5494	0.3975	0.3157	-0.062	0.3410	0.0950	-0.059	-0.193	0.0296
F	-0.454	-0.079	-0.182	0.0414	-0.084	-0.095	-0.147	-0.229	-0.349
G	0.2475	-0.089	0.2819	0.3314	0.0325	0.0939	0.4256	0.5845	0.0703
H	0.0970	0.2277	-0.173	0.0820	0.0148	0.2397	-0.120	0.0730	0.3931
I	-0.084	0.0884	-0.573	-0.087	0.2575	0.0755	0.0762	0.0285	-0.959
K	-0.112	0.2702	0.4864	0.0732	0.1823	0.1010	0.3855	0.2996	0.2085
L	0.0172	0.0443	-0.546	-0.158	-0.290	-0.115	0.0171	0.0073	-0.779
M	0.0401	-0.775	-0.500	-0.096	-0.485	-0.220	0.1603	0.1090	-1.008
N	0.0344	0.0604	-0.162	0.1000	-1.396	0.2126	0.0852	0.1058	-0.143
P	0.4683	0.4941	0.0814	0.2384	0.0816	-0.063	-0.100	-0.637	0.1614
Q	0.1401	-0.383	0.2111	-0.054	0.1075	-0.066	0.0813	-0.006	0.2919
R	-0.081	0.4439	0.4018	-0.108	0.3058	-0.080	0.1658	0.3561	0.7778
S	-0.389	-0.797	0.2938	-0.081	0.0064	0.1243	-0.003	-0.052	-0.118
T	0.0380	-0.100	0.1716	-0.124	0.2721	-0.071	-0.313	-0.365	0.4994
V	-0.067	-0.154	-0.249	-0.357	0.1642	0.0737	0.0227	-0.073	-0.489
W	-0.047	0.5696	-0.288	0.0410	0.0114	-0.334	-0.057	0.0289	0.3842
Y	-0.478	0.0331	-0.283	0.1217	0.3328	-0.167	-0.179	-0.398	0.3809

🟩 (ROW HEADER) Indicates anchor positions.

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

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

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

Figure 2.19 Amino acid binding matrix for MHC allele H-2-Db

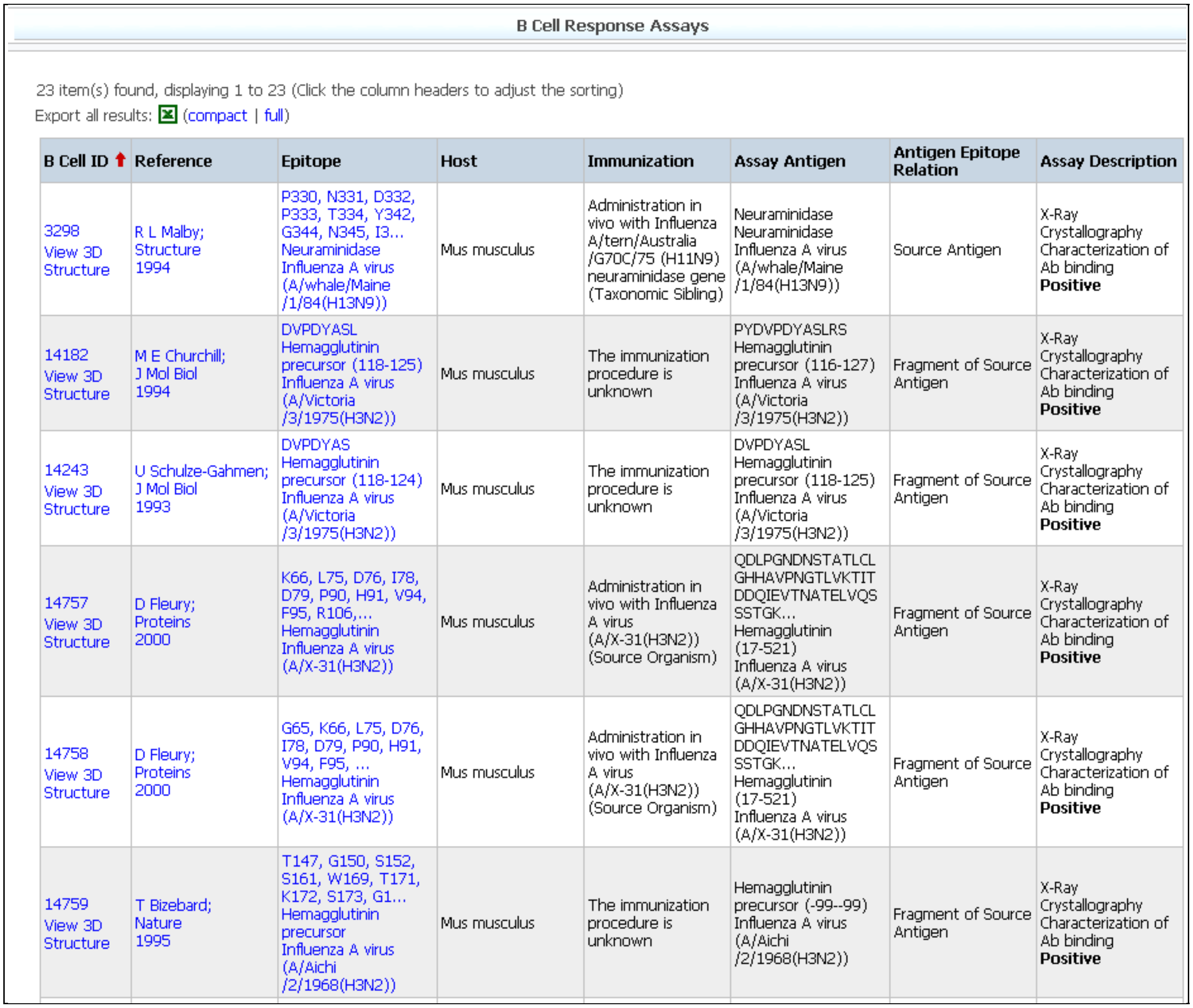
For non-anchor position:

1. determine the median value of this position from corresponding column of the SMM matrix

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

2.3.4.2 Accessing the EpitopeViewer

The EpitopeViewer is an application for three dimensional viewing of receptor-antigen interactions that can be accessed from the Assay List screens. The EpitopeViewer can be used with all assays that have receptor-antigen interaction data available. It is not available for epitopes and assays, and when it is available, a link is provided in the leftmost ID column, as illustrated by the "View 3D Structure" in Figure 2.20. The 23 B cell response assays shown are a result of using the B Cell Search for Epitope Source Organism = Influenza A and Assay Type = X-Ray Crystallography.



B Cell Response Assays

23 item(s) found, displaying 1 to 23 (Click the column headers to adjust the sorting)

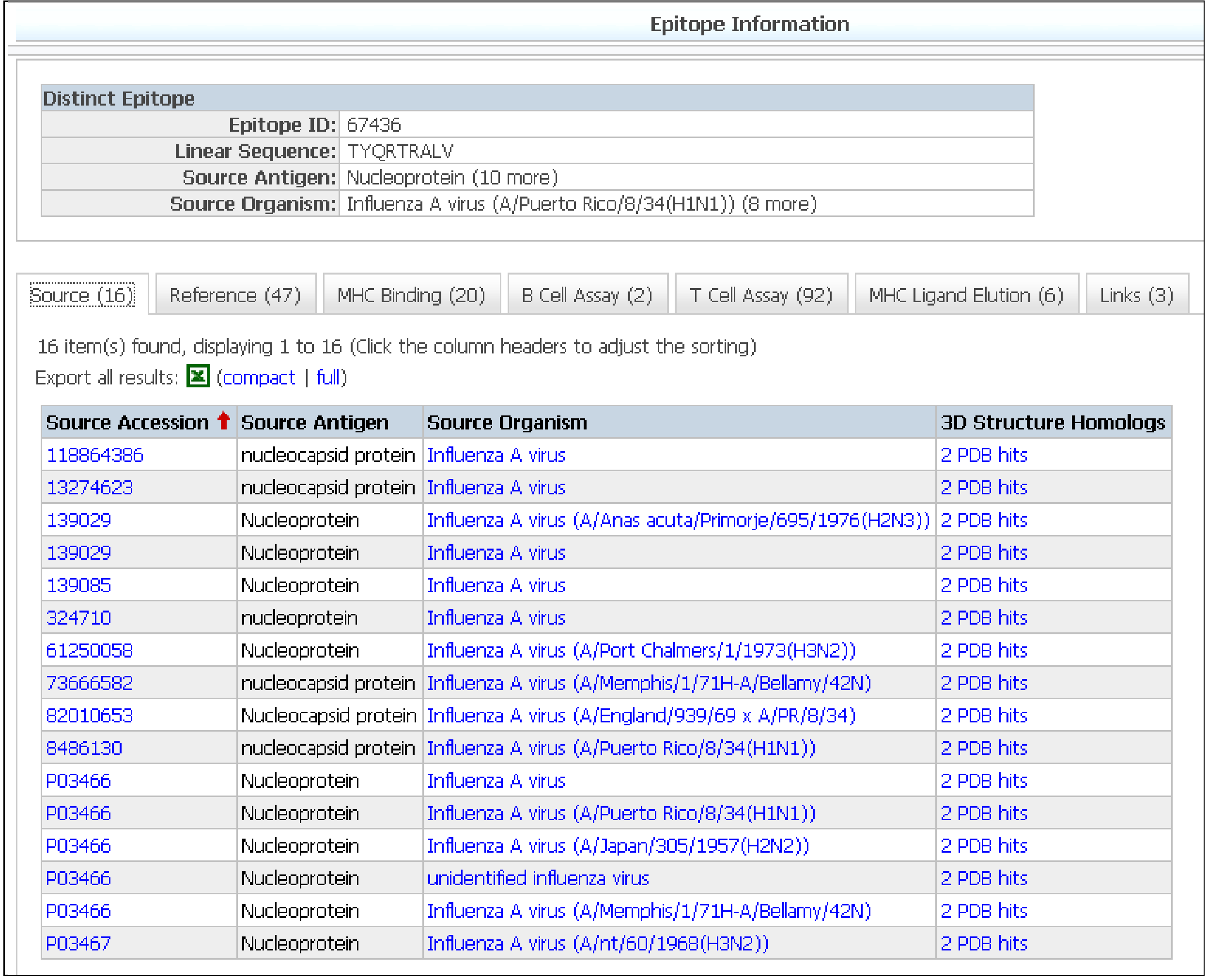
Export all results: ☒ (compact | full)

B Cell ID ↑	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	Assay Description
3298 View 3D Structure	R L Malby; Structure 1994	P330, N331, D332, P333, T334, Y342, G344, N345, I3... Neuraminidase Influenza A virus (A/whale/Maine /1/84(H13N9))	Mus musculus	Administration in vivo with Influenza A/tern/Australia /G70C/75 (H11N9) neuraminidase gene (Taxonomic Sibling)	Neuraminidase Neuraminidase Influenza A virus (A/whale/Maine /1/84(H13N9))	Source Antigen	X-Ray Crystallography Characterization of Ab binding **Positive**
14182 View 3D Structure	M E Churchill; J Mol Biol 1994	DVPDYASL Hemagglutinin precursor (118-125) Influenza A virus (A/Victoria /3/1975(H3N2))	Mus musculus	The immunization procedure is unknown	PYDVPDYASLRS Hemagglutinin precursor (116-127) Influenza A virus (A/Victoria /3/1975(H3N2))	Fragment of Source Antigen	X-Ray Crystallography Characterization of Ab binding **Positive**
14243 View 3D Structure	U Schulze-Gahmen; J Mol Biol 1993	DVPDYAS Hemagglutinin precursor (118-124) Influenza A virus (A/Victoria /3/1975(H3N2))	Mus musculus	The immunization procedure is unknown	DVPDYASL Hemagglutinin precursor (118-125) Influenza A virus (A/Victoria /3/1975(H3N2))	Fragment of Source Antigen	X-Ray Crystallography Characterization of Ab binding **Positive**
14757 View 3D Structure	D Fleury; Proteins 2000	K66, L75, D76, I78, D79, P90, H91, V94, F95, R106,... Hemagglutinin Influenza A virus (A/X-31(H3N2))	Mus musculus	Administration in vivo with Influenza A virus (A/X-31(H3N2)) (Source Organism)	QDLPGNDNSTATLCL GHHAVPNGTLVKTIT DDQIEVTNATELVQS SSTGK... Hemagglutinin (17-521) Influenza A virus (A/X-31(H3N2))	Fragment of Source Antigen	X-Ray Crystallography Characterization of Ab binding **Positive**
14758 View 3D Structure	D Fleury; Proteins 2000	G65, K66, L75, D76, I78, D79, P90, H91, V94, F95, ... Hemagglutinin Influenza A virus (A/X-31(H3N2))	Mus musculus	Administration in vivo with Influenza A virus (A/X-31(H3N2)) (Source Organism)	QDLPGNDNSTATLCL GHHAVPNGTLVKTIT DDQIEVTNATELVQS SSTGK... Hemagglutinin (17-521) Influenza A virus (A/X-31(H3N2))	Fragment of Source Antigen	X-Ray Crystallography Characterization of Ab binding **Positive**
14759 View 3D Structure	T Bizebard; Nature 1995	T147, G150, S152, S161, W169, T171, K172, S173, G1... Hemagglutinin precursor Influenza A virus (A/Aichi /2/1968(H3N2))	Mus musculus	The immunization procedure is unknown	Hemagglutinin precursor (-99--99) Influenza A virus (A/Aichi /2/1968(H3N2))	Fragment of Source Antigen	X-Ray Crystallography Characterization of Ab binding **Positive**

Figure 2.20 B Cell Response screen with Epitope Viewer links in the leftmost column

2.3.4.3 Result Tabs

As users drill down on hyperlinks to further explore the results of a query, they will find the information organized by tabs. As seen in Figure 2.21 for Epitope ID 67436, there are 16 source organisms listed from 47 references. There is also assay information for MHC binding, B cells, T cells, and MHC ligand elution. The Links tab contains links to relevant tools in the Analysis Resource. Links can also appear to two of the Bioinformatics Resource Centers (BRC), a feature introduced in 2009. These links will be expanded in the coming year after the BRCs complete their reorganization



Distinct Epitope	
Epitope ID:	67436
Linear Sequence:	TYQRTRALV
Source Antigen:	Nucleoprotein (10 more)
Source Organism:	Influenza A virus (A/Puerto Rico/8/34(H1N1)) (8 more)

16 item(s) found, displaying 1 to 16 (Click the column headers to adjust the sorting)

Export all results: (compact | full)

Source Accession ↑	Source Antigen	Source Organism	3D Structure Homologs
118864386	nucleocapsid protein	Influenza A virus	2 PDB hits
13274623	nucleocapsid protein	Influenza A virus	2 PDB hits
139029	Nucleoprotein	Influenza A virus (A/Anas acuta/Primorje/695/1976(H2N3))	2 PDB hits
139029	Nucleoprotein	Influenza A virus	2 PDB hits
139085	Nucleoprotein	Influenza A virus	2 PDB hits
324710	nucleoprotein	Influenza A virus	2 PDB hits
61250058	Nucleoprotein	Influenza A virus (A/Port Chalmers/1/1973(H3N2))	2 PDB hits
73666582	nucleocapsid protein	Influenza A virus (A/Memphis/1/71H-A/Bellamy/42N)	2 PDB hits
82010653	Nucleocapsid protein	Influenza A virus (A/England/939/69 x A/PR/8/34)	2 PDB hits
8486130	nucleocapsid protein	Influenza A virus (A/Puerto Rico/8/34(H1N1))	2 PDB hits
P03466	Nucleoprotein	Influenza A virus	2 PDB hits
P03466	Nucleoprotein	Influenza A virus (A/Puerto Rico/8/34(H1N1))	2 PDB hits
P03466	Nucleoprotein	Influenza A virus (A/Japan/305/1957(H2N2))	2 PDB hits
P03466	Nucleoprotein	unidentified influenza virus	2 PDB hits
P03466	Nucleoprotein	Influenza A virus (A/Memphis/1/71H-A/Bellamy/42N)	2 PDB hits
P03467	Nucleoprotein	Influenza A virus (A/nt/60/1968(H3N2))	2 PDB hits

Figure 2.21 Many results pages have information organized into tabs

2.3.5 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.

2.3.5.1 Allele Finder

The MHC Allele Finder facilitates the selection of one or more MHC alleles. Initially the Allele

Finder lists all alleles ordered by allele name. The Allele Finder allows the user to find alleles by organism, class {I, II, non-classical}, and allele in the Find box (Figure 2.22). After the user supplies their search criteria and clicks the Search button, the system will filter the list of MHC alleles using the organism, class, and allele provided. The allele finder uses wild card characters by default on both ends of criteria entered into the allele field. The system then returns any alleles that contain the value in the name field and match the class selected.

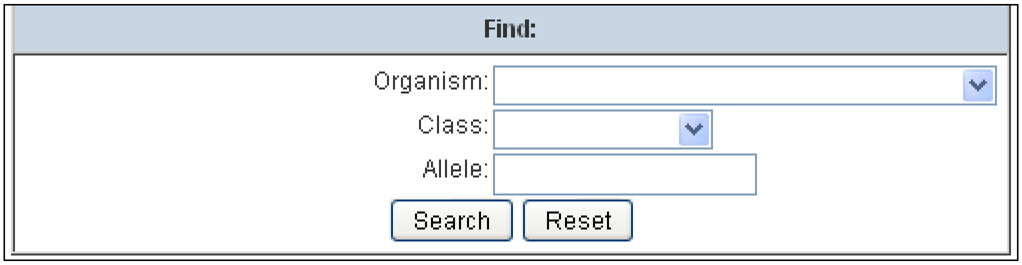


Figure 2.22 Find form on the Allele Finder

2.3.5.2 Assay Finder

The Assay Finder is used to facilitate the selection of one or more assay types and lists all assay types in the selected assay category. The Assay Finder allows the user to find assay by assay type name, assay group, and/or units in the Find box (Figure 2.23). 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.

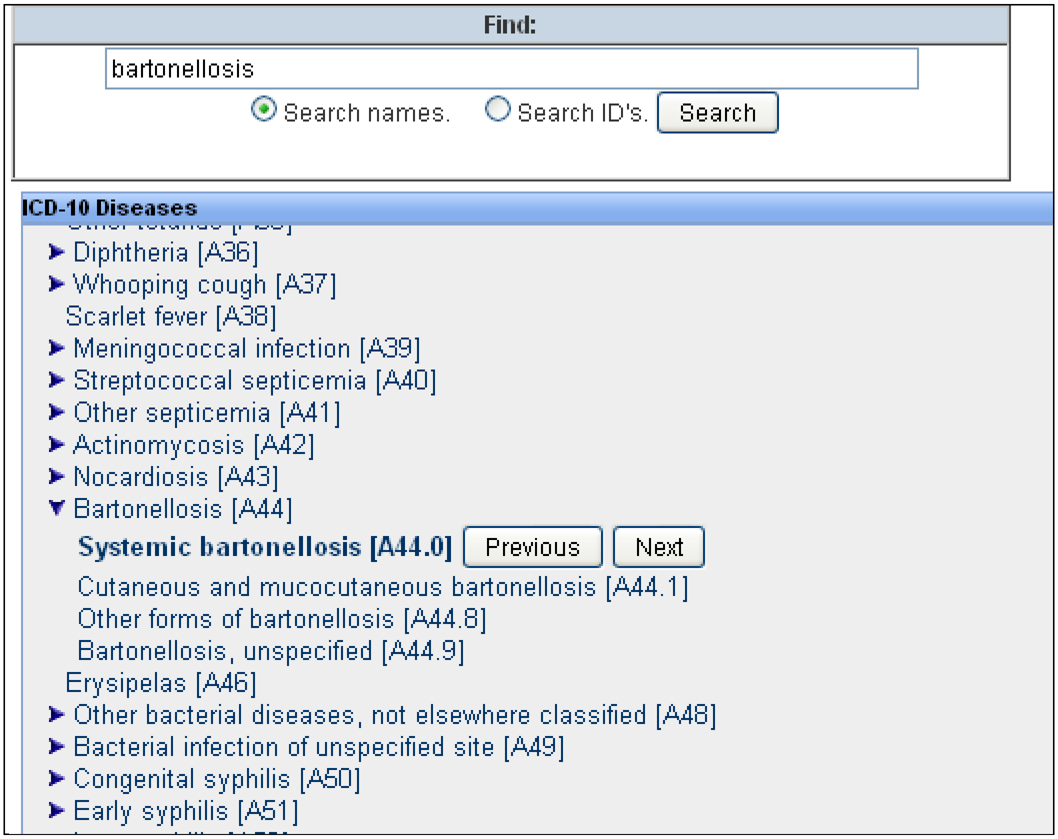
Figure 2.23 Search form on the Assay Type Finder

2.3.5.3 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 2.24). 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. When the user provides a name, any disease name that contains the character string provided will be considered a match.

The selections in the disease finder are displayed in a tree. 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 is A44 and the code for Systemic bartonellosis is A44.0.



bartonellosis

● Search names. ○ Search ID's.

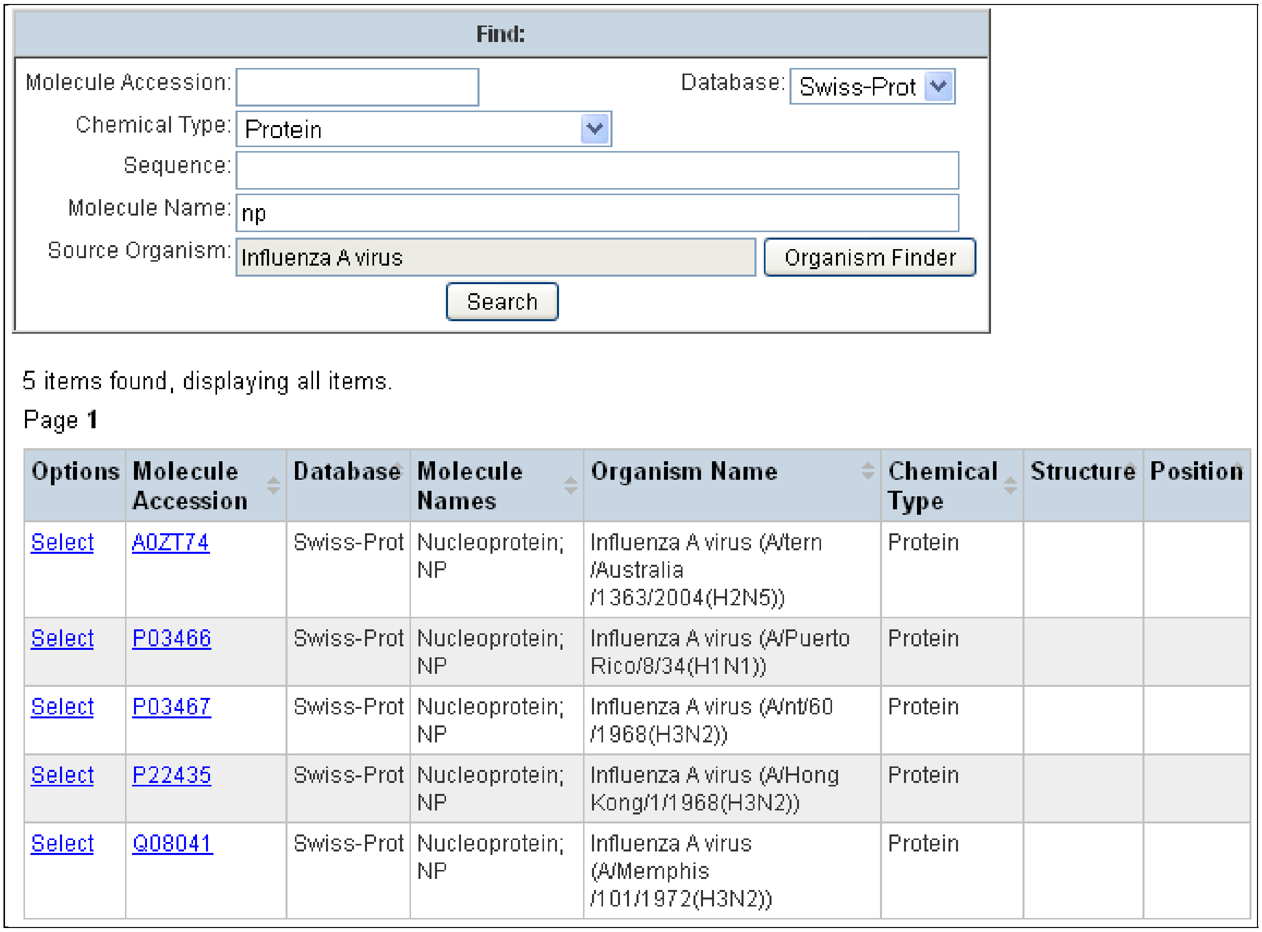
ICD-10 Diseases

- ▶ Diphtheria [A36]
- ▶ Whooping cough [A37]
- Scarlet fever [A38]
- ▶ Meningococcal infection [A39]
- ▶ Streptococcal septicemia [A40]
- ▶ Other septicemia [A41]
- ▶ Actinomycosis [A42]
- ▶ Nocardiosis [A43]
- ▼ Bartonellosis [A44]
  - **Systemic bartonellosis [A44.0]**
  - Cutaneous and mucocutaneous bartonellosis [A44.1]
  - Other forms of bartonellosis [A44.8]
  - Bartonellosis, unspecified [A44.9]
- Erysipelas [A46]
- ▶ Other bacterial diseases, not elsewhere classified [A48]
- ▶ Bacterial infection of unspecified site [A49]
- ▶ Congenital syphilis [A50]
- ▶ Early syphilis [A51]

Figure 2.24 Search form and disease list on the Disease Finder

2.3.5.4 Molecule Finder

The Molecule Finder is used to facilitate the selection of source antigens, immunogens, and epitopes. Records in the Source Finder come from GenPept, GenBank, ChEBI, Swiss-Prot, and IEDB curators. Among the finders, the Molecule 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. In the example shown in Figure 2.25, the user has entered search criteria for Influenza A Nucleoproteins that were curated from the Swiss-Prot database. The search on these criteria resulted in a list of five matching sources, and the user can select their desired sources from the list by click on *Select* in the far left column.



Molecule Accession:
Database: Swiss-Prot
Chemical Type: Protein
Sequence:
Molecule Name: np
Source Organism: Influenza A virus

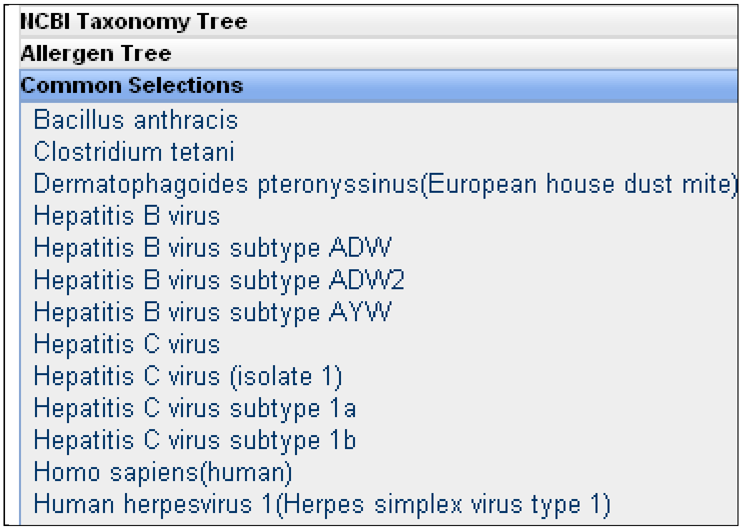
5 items found, displaying all items.
Page **1**

Options	Molecule Accession	Database	Molecule Names	Organism Name	Chemical Type	Structure	Position
Select	A0ZT74	Swiss-Prot	Nucleoprotein; NP	Influenza A virus (A/tern /Australia /1363/2004(H2N5))	Protein		
Select	P03466	Swiss-Prot	Nucleoprotein; NP	Influenza A virus (A/Puerto Rico/8/34(H1N1))	Protein		
Select	P03467	Swiss-Prot	Nucleoprotein; NP	Influenza A virus (A/nt/60 /1968(H3N2))	Protein		
Select	P22435	Swiss-Prot	Nucleoprotein; NP	Influenza A virus (A/Hong Kong/1/1968(H3N2))	Protein		
Select	Q08041	Swiss-Prot	Nucleoprotein; NP	Influenza A virus (A/Memphis /101/1972(H3N2))	Protein		

Figure 2.25 Molecule Finder Search form and resulting source list

2.3.5.5 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 2.26. 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.



Bacillus anthracis
Clostridium tetani
Dermatophagoides pteronyssinus(European house dust mite)
Hepatitis B virus
Hepatitis B virus subtype ADW
Hepatitis B virus subtype ADW2
Hepatitis B virus subtype AYW
Hepatitis C virus
Hepatitis C virus (isolate 1)
Hepatitis C virus subtype 1a
Hepatitis C virus subtype 1b
Homo sapiens(human)
Human herpesvirus 1(Herpes simplex virus type 1)

Figure 2.26 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 2.27. 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 2.27). The taxonomy identifier is displayed next to each node of the tree in square brackets. For example, the taxonomy identifier for the selection of Dengue Virus 2 in the example below is 11060. To see the synonyms for a selection, users can place their computer mouse over the scientific name.

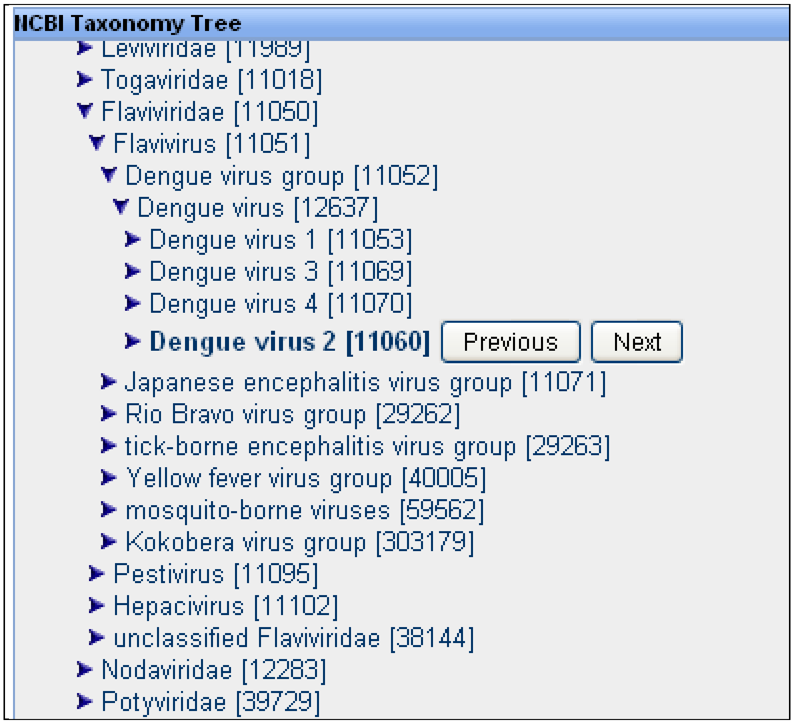


Figure 2.27 NCBI Taxonomy Tree

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

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

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

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

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

2.4.1 T Cell Epitope Prediction

2.4.1.1 T Cell Epitopes - MHC binding prediction

The Analysis Resource provides tools for predicting peptide binding to MHC class I and II molecules. For class I binding predictions, three new methods were introduced in 2009. Users can select predictions performed with tools derived from six different methods – artificial neural network (ANN), average relative binding (ARB), stabilized matrix method (SMM), SMM with a peptide:MHC binding energy covariance matrix (SMMPMBEC), Scoring matrices derived from combinatorial peptide libraries (Comblib_Sidney2008), and Consensus. The last three methods listed are new for the year. The first three methods were retrained with expanded data sets and released in August 2009. For class II binding predictions, one new method, the Combinatorial Library method, was added in 2009. Users can select the Combinatorial Library method, the ARB method, the SMM_align method, a method devised by Sturniolo et al. and used in TEPITOPE, and a consensus method derived from the ARB, SMM_align, and Sturniolo methods. Tutorials and example data are available for both the class I and II tools.

2.4.1.1.1 Peptide Binding to MHC Class I Molecules

Users can select from six different methods for predicting class I epitopes – ANN, ARB, SMM, SMMPMBEC, Comblib_Sidney2008, and Consensus, 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.

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

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

Scoring matrices derived from combinatorial peptide libraries (Comblib_Sidney2008)

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

Consensus

The Consensus predictor was motivated by an idea that predictions made by consulting "consensus" of individual predictions from multiple predictors may result in improved performance over that of any individual ones. For MHC-I, a work describing an early implementation can be found in Moutaftsi M et al. Nat Biotech 2006.

2.4.1.1.1.1 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.

2.4.1.1.2 Peptide Binding to MHC Class II Molecules

Users can select from five different methods for predicting class II epitopes – ARB, and SMM-align, Sturniolo, Combinatorial Library, and Consensus. The Combinatorial Library method was added in 2009. 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 five methods are described further below.

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

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

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

of 9 by 20 scoring matrices which could predict the binding of novel peptides to MHC molecules.

The methodology is the same as that used for the MHC class I combinatorial library tool as described in Sidney et al. Immunome Res. 2008. A paper specifically describing the class II tool will be published in 2010.

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

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

2.4.1.2 T Cell Epitopes – MHC I Processing Prediction

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

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

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

2.4.1.2.2 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).

2.4.2 B Cell Epitope Prediction

2.4.2.1 Prediction of linear epitopes from protein sequence

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

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

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

2.4.2.2 DiscoTope - Prediction of epitopes from protein structure

DiscoTope 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).

2.4.2.3 ElliPro - Epitope prediction based upon structural protrusion

ElliPro predicts linear and discontinuous antibody epitopes based on a protein antigen's 3D structure. ElliPro accepts either a protein structure (preferred) or a protein sequence as an input. If a protein sequence is used, ElliPro will predict its 3D structure by homology modeling. Its use if described in the Tutorial tab of the ElliPro section of the Analysis Resource. The method is described in Julia Ponomarenko et al. (BMC Bioinformatics, 2008).

2.4.3 Epitope Analysis Tools

2.4.3.1 Population coverage

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

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

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.

2.4.3.2 Epitope conservancy

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

2.4.3.3 Epitope Cluster Analysis

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

2.4.3.4 Homology Mapping Tool and EpitopeViewer

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

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

The EpitopeViewer provides the following functionality:

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

2.5 Support Overview

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

2.5.1 Solutions Center

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

2.5.2 Provide Feedback

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

2.5.3 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.

2.5.4 Data Field Descriptions

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

2.6 More IEDB

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

2.6.1 Acknowledgements

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

2.6.2 Citing the IEDB

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

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

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

   Vita R, Zarebski L, Greenbaum JA, Emami H, Hoof I, Salimi N, Damle R, Sette A, Peters B. The immune epitope database 2.0. Nucleic Acids Res. 2010 Jan; 38(Database issue):D854-62. Epub 2009 Nov 11.

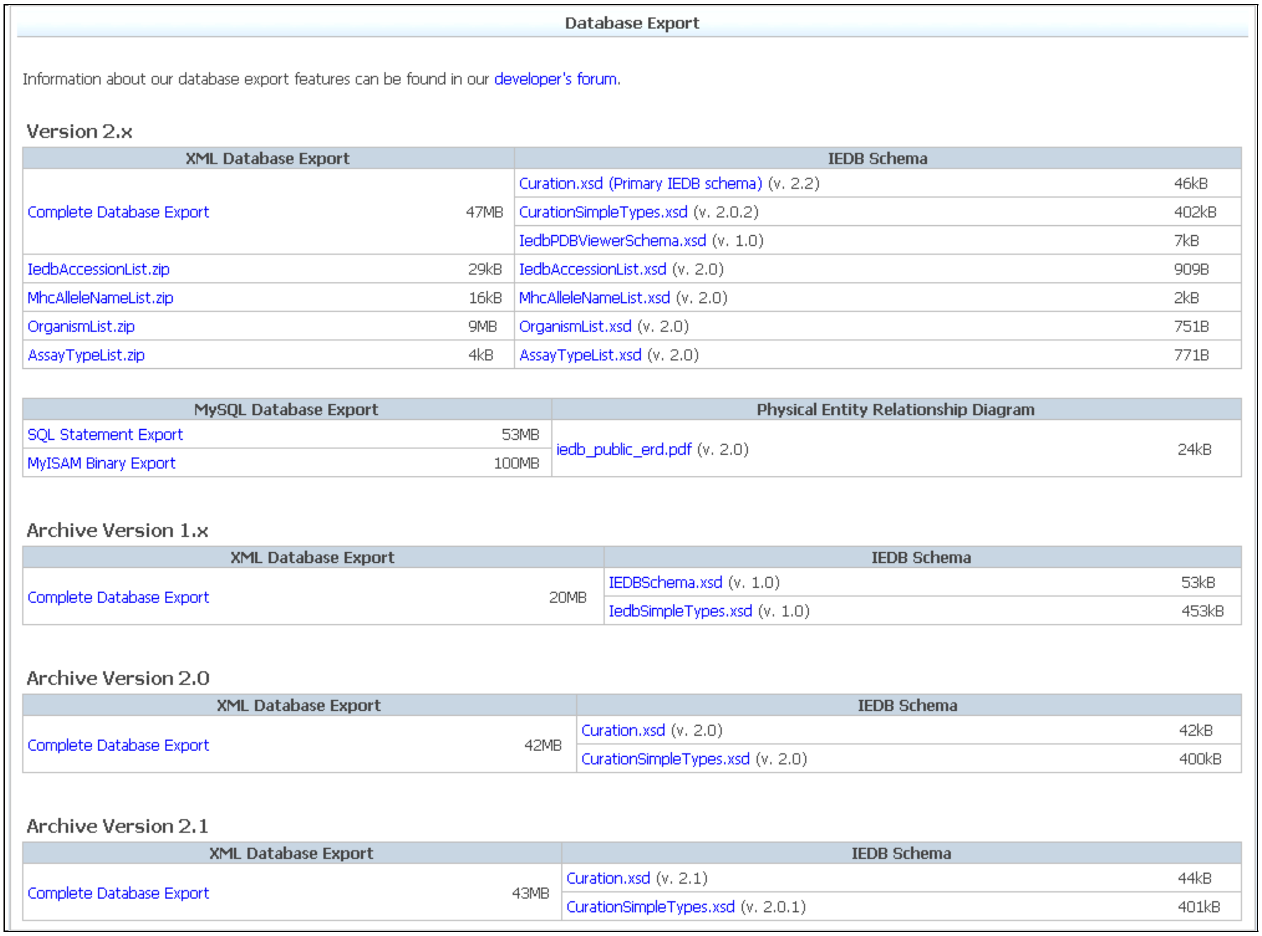
2.6.3 Database Export

The contents of the Immune Epitope Database are exported weekly to files in XML format. The database export page (Figure 2.28) 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.x 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.

One of the new features introduced in 2009 was the addition of two new database export formats. The contents of the IEDB are exported weekly as a MySQL Structure Query Language (SQL) database. The database export page contains the complete database export in two formats, a single SQL script (iedb_public.sql.gz), and a TAR archive of MyISAM binary tables (iedb_public.tar.gz). Both export formats are generated from a MySQL v5.0 database server. A physical entity relationship diagram (ERD) for the MySQL database is also available as a PDF file.

Archives of the data as they appeared in IEDB 1.0, 2.0, and 2.1 are available. The archive file, IEDB_2008_4_1_3_28.zip, IEDB_2009_10_30_3_32.zip, and IEDB_2009_12_7_3_32.zip, respectively, contain an XML for each reference. The corresponding XSD files are also available for download.



Database Export

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

Version 2.x

XML Database Export		IEDB Schema	
Complete Database Export	47MB	Curation.xsd (Primary IEDB schema) (v. 2.2)	46kB
		CurationSimpleTypes.xsd (v. 2.0.2)	402kB
		IedbPDBViewerSchema.xsd (v. 1.0)	7kB
IedbAccessionList.zip	29kB	IedbAccessionList.xsd (v. 2.0)	909B
MhcAlleleNameList.zip	16kB	MhcAlleleNameList.xsd (v. 2.0)	2kB
OrganismList.zip	9MB	OrganismList.xsd (v. 2.0)	751B
AssayTypeList.zip	4kB	AssayTypeList.xsd (v. 2.0)	771B

MySQL Database Export		Physical Entity Relationship Diagram	
SQL Statement Export	53MB	iedb_public_erd.pdf (v. 2.0)	24kB
MyISAM Binary Export	100MB		

Archive Version 1.x

XML Database Export		IEDB Schema	
Complete Database Export	20MB	IEDBSchema.xsd (v. 1.0)	53kB
		IedbSimpleTypes.xsd (v. 1.0)	453kB

Archive Version 2.0

XML Database Export		IEDB Schema	
Complete Database Export	42MB	Curation.xsd (v. 2.0)	42kB
		CurationSimpleTypes.xsd (v. 2.0)	400kB

Archive Version 2.1

XML Database Export		IEDB Schema	
Complete Database Export	43MB	Curation.xsd (v. 2.1)	44kB
		CurationSimpleTypes.xsd (v. 2.0.1)	401kB

Figure 2.28 IEDB Database Export web page

2.6.4 Documents

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

2.6.5 IEDB Ontology

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

2.6.6 Links to External Sources

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

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

2.6.7 Patent List

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

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

2.6.8 Publications

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

2.6.9 Terms of Use

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

3 Scientific Publications

This section lists the scientific publications for which the IEDB played a contributory role. The first section lists publications authored by the IEDB contractor team over the past six 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. Citations for 2008 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 2009 citation list.

3.1 Publications of the IEDB team by Year

Scientific articles written by the IEDB team members that are relevant to the IEDB are listed below by year of publication. In 2009, seven articles were published, while nine were published in 2008, twelve in 2007, three in 2006, four in 2005, and one in 2004. In all, the team has written 36 scientific articles about the IEDB in the last six years.

3.1.1 2009

1. Davies V, Vaughan K, Damle R, Peters B, Sette A. Classification of the universe of immune epitope literature: representation and knowledge gaps. PLoS One. 2009 Sep 14;4(9):e6948. PubMed PMID: 19774228;
2. Greenbaum JA, Kotturi MF, Kim Y, Oseroff C, Vaughan K, Salimi N, Vita R, Ponomarenko J, Scheuermann RH, Sette A, Peters B. Pre-existing immunity against swine-origin H1N1 influenza viruses in the general human population. Proc Natl Acad Sci U S A. 2009 Dec 1;106(48):20365-70. Epub 2009 Nov 16. PubMed PMID: 19918065; PubMed Central PMCID: PMC2777968.
3. Hoof I, Peters B, Sidney J, Pedersen LE, Sette A, Lund O, Buus S, Nielsen M, NetMHCpan, a method for MHC class I binding prediction beyond humans. Immunogenetics. 2009 Jan;61(1):1-13. PMID: 19002680
4. Kim Y, Sidney J, Pinilla C, Sette A, Peters B. Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior. BMC Bioinformatics. 2009 Nov 30;10:394. PubMed PMID: 19948066.
5. Vaughan K, Blythe M, Greenbaum J, Zhang Q, Peters B, Doolan DL, Sette A, Meta-analysis of immune epitope data for all Plasmodia: overview and applications for malarial immunobiology and vaccine-related issues. Parasite Immunol. 2009 Feb;31(2):78-97. [PMID: 19149776]
6. Vita R, Zarebski L, Greenbaum JA, Emami H, Hoof I, Salimi N, Damle R, Sette A, Peters B. The Immune Epitope Database 2.0. Nucleic Acids Res. 2009 Nov 11. [Epub ahead of print] PubMed PMID: 19906713.
7. Zhang H, Lund O, Nielsen M. The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: Application to MHC-peptide binding. Bioinformatics. 2009 Mar 17. PMID: 19297351

3.1.2 2008

8. 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

9. Nielsen, M., C. Lundegaard, T. Blicher, B. Peters, A. Sette, S. Justesen, S. Buus, O. Lund. (2008). "Quantitative Predictions of Peptide Binding to Any HLA-DR Molecule of Known Sequence: NetMHCIIpan." PLoS Computational Biology **4**(7). PMID: 18604266

10. Ponomarenko J, H. H. Bui, W. Li, N. Fusseder, P. E. Bourne, A. Sette, B. Peters. (2008). “ElliPro: a new structure-based tool for the prediction of antibody epitopes.” BMC Bioinformatics, 9(514). PMID: 19055730

11. Ponomarenko J. V., M. H. C. van Regenmortel (2008) “B-cell epitope prediction.” Structural Bioinformatics, Ed: Bourne PE, Gu J. Wiley-Liss; 2 edition.

12. Rapin N., I. Hoof, O. Lund, M. Nielsen. (2008). “MHC motif viewer.” Immunogenetics. 60(12): 759-65. PMID: 18766337

13. Vita R., B. Peters, A. Sette. (2008). “The Curation Guidelines of the Immune Epitope Database and Analysis Resource.” Cytometry A 73(11): 1066-1070. PMID: 18688821

14. Wang, P., J. Sidney, C. Dow, B. Mothe, A. Sette, B. Peters. (2008). "A Systematic Assessment of MHC Class II Peptide Binding Predictions and Evaluation of a Consensus Approach." PLoS Computational Biology **4**(4). PMID: 18389056

15. Zarebski L. M., K. Vaughan, J. Sidney, B. Peters, H. Grey, K. D. Janda, A. Casadevall, A. Sette. (2008). “Analysis of epitope information related to Bacillus anthracis and Clostridium botulinum.” Expert Rev Vaccines 7(1): 55-74. PMID: 18251694

16. Zhang, Q., P. Wang, et al. (2008). "Immune epitope database analysis resource (IEDB-AR)." Nucleic Acids Research **36**: W513-W518. PMID: 18515843

3.1.3 2007

17. Beaver JE, Bourne PE, Ponomarenko JV. EpitopeViewer: a Java application for the visualization and analysis of immune epitopes in the Immune Epitope Database and Analysis Resource (IEDB). Immunome Res. 2007 Feb 21;3:3. PMID: 17313688

18. Blythe MJ, Zhang Q, Vaughan K, de Castro R Jr, Salimi N, Bui HH, Lewinsohn DM, Ernst JD, Peters B, Sette A. An analysis of the epitope knowledge related to Mycobacteria. Immunome Res. 2007 Dec 14;3(1):10. PMID: 18081934

19. Bui HH, Peters B, Assarsson E, Mbawuike I, Sette A. Ab and T cell epitopes of influenza A virus, knowledge and opportunities. Proc Natl Acad Sci U S A. 2007 Jan 2;104(1):246-51. PMID: 17200302

20. 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

21. Ernst JD, Lewinsohn DM, Behar S, Blythe M, Schlesinger LS, Kornfeld H, Sette A. Meeting Report: NIH Workshop on the Tuberculosis Immune Epitope Database. Tuberculosis (Edinb). 2007 Dec 6. PMID: 18068490

22. Greenbaum JA, Andersen PH, Blythe M, Bui HH, Cachau RE, Crowe J, Davies M, Kolaskar AS, Lund O, Morrison S, Mumey B, Ofran Y, Pellequer JL, Pinilla C, Ponomarenko JV, Raghava GP, van Regenmortel MH, Roggen EL, Sette A, Schlessinger A, Sollner J, Zand M, Peters B. Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. J Mol Recognit. 2007 Mar-Apr;20(2):75-82. PMID: 17205610

23. Lundegaard C, Lund O, Kesmir C, Brunak S, Nielsen M. Modeling the adaptive immune system: predictions and simulations. Bioinformatics. 2007 Dec 15;23(24):3265-75. PMID: 18045832

24. Nielsen M, Lundegaard C, Blicher T, Lamberth K, Harndahl M, Justesen S, Røder G, Peters B, Sette A, Lund O, Buus S. NetMHCpan, a method for quantitative predictions of peptide binding to any HLA-A and -B locus protein of known sequence. PLoS ONE. 2007 Aug 29;2(8):e796. PMID: 17726526

25. Peters B, Sette A. Integrating epitope data into the emerging web of biomedical knowledge resources. Nat Rev Immunol. 2007 Jun;7(6):485-90. PMID: 17479127

26. Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. BMC Struct Biol. 2007 Oct 2;7(1):64. PMID: 17910770

27. Sette A, Peters B., Immune epitope mapping in the post-genomic era: lessons for vaccine development. Curr Opin Immunol. 2007 Feb;19(1):106-10. PMID: 17113275

28. Wang P, Morgan AA, Zhang Q, Sette A, Peters B. Automating document classification for the Immune Epitope Database. BMC Bioinformatics. 2007 Jul 26;8:269. PMID: 17655769

3.1.4 2006

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

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

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

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

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

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

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

3.1.6 2004

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

3.2 Publications Citing the IEDB in 2009

In 2009, 163 references cited at least one of the 36 papers written by the IEDB team over the past six years. This list was compiled by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the 36 papers. The list excludes self-citations by the 36 IEDB papers. This total may increase over time since these databases may not include references published late in 2009.

The papers have been categorized by the type of IEDB paper they cited – General IEDB, Analysis Resource (RA), Curation (C), or Meta-analysis (MA). When a paper cites an additional IEDB reference that is in a different category, the additional category is denoted with one of the three initials given above. For example, a paper that cites an analysis resource paper may also cite the primary IEDB PLoS Biology (2005) paper, and thus is listed under General IEDB and has an [AR] to indicate the Analysis Resource citation.

3.2.1 General IEDB

1. Akondy, R. S., Monson, N. D., Miller, J. D., Edupuganti, S., Teuwen, D., Wu, H., Quyyumi, F., Garg, S., Altman, J. D., and Del Rio, C. (2009). "The Yellow Fever Virus Vaccine Induces a Broad and Polyfunctional Human Memory CD8+ T Cell Response." The Journal of Immunology 183(12): 7919-7930.

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3. Ansari, H. R., Flower, D. R., and Raghava, G. P. S. (2009). "AntigenDB: an immunoinformatics database of pathogen antigens." Nucleic Acids Research 38(Database issue): D847-D853; doi: 10.1093/nar/gkp830.
4. Babon, J. A. B., Cruz, J., Orphin, L., Pazoles, P., Co, M. D. T., Ennis, F. A., and Terajima, M. (2009). "Genome-wide screening of human T-cell epitopes in influenza A virus reveals a broad spectrum of CD4+ T-cell responses to internal proteins, hemagglutinins, and neuraminidases." Human Immunology 70(9): 711-721. **[MA]**
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9. Chu, C. C., Ho, H. T., Lee, H. L., Chan, Y. S., Chang, F. J., Wang, C. L., and Lin, M. (2009). "Anti- ‘Mi(a)’ immunization is associated with HLA-DRB1* 0901." Transfusion 49(3): 472-478.
10. Clifford, M., Twigg, J., and Upton, C. (2009). "Evidence for a novel gene associated with human influenza A viruses." Virol J. 6:198; doi: 10.1186/1743-422X-6-198.
11. Cochrane, G. R. and Galperin, M. Y. (2009). "The 2010 Nucleic Acids Research Database Issue and online Database Collection: a community of data resources." Nucleic Acids Research 38(Database issue): D1-D4.
12. Davydov, Y. I. and Tonevitsky, A. G. (2009). "Prediction of linear B-cell epitopes." Molecular Biology 43(1): 150-158. **[AR]**
13. DeLuca, D. S., Beisswanger, E., Wermter, J., Horn, P. A., Hahn, U., and Blasczyk, R. (2009). "MaHCO: an ontology of the major histocompatibility complex for immunoinformatic applications and text mining." Bioinformatics 25(16): 2064-2070.
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3.3 Publications Citing the IEDB in 2008

Because previous experience has shown that the number of citations for the calendar year just completed increases after the publication of the Annual Compendium, the list of citations for 2008 was revisited. In last year's 2008 Annual Compendium, 115 references were identified using Google Scholar and the ISI Web of Knowledge databases that cited at least one of the 29 papers written by the IEDB team up to that point in time. By repeating this exercise one year later, 136 references, or 21 additional references, were found. The discrepancy in count is likely due to the amount of time needed for citations to be incorporated into the ISI and Google Scholar databases.

The new list of 2008 citations is listed below. The papers have been categorized by the type of IEDB paper they cited – General IEDB, Analysis Resource (RA), Curation (C), or Meta-analysis (MA). When a paper cites an additional IEDB reference that is in a different category, the additional category is denoted with one of the three initials given above. For example, a paper that cites an analysis resource paper may also cite the primary IEDB PLoS Biology (2005) paper, and thus is listed under General IEDB and has an [AR] to indicate the Analysis Resource citation. The citations include dissertations. The list excludes self-citations by papers written about the IEDB by IEDB team members.

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