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Immune Epitope Database and Analysis Resource Program

2019 Annual IEDB Compendium

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## Introduction

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

This Compendium of the Immune Epitope Database and Analysis Resource, and consists of three sections. The first section contains a list of the antibody and T cell epitope information in the database as of 17 January 2020. The second section describes the features of the IEDB 3.10 website and the Analysis Resource 2.20. The third section lists the scientific publications in 2019 for which the IEDB played a contributory role.

Since the publication of last year's 2018 Annual Compendium, the quantity of data available in the IEDB continues to increase significantly. As of January 2020, the IEDB contains data for over 945,000 epitopes, 54,000 antigens, 2,150,000 assays, and 34,000 receptors from more than 20,700 references. The focus of the IEDB remains on peptidic and non-peptidic epitope data relating to infectious diseases, allergens, autoimmune diseases, and transplant/alloantigens; with exceptions in respect to cancer and HIV.

## 1 Antibody and T Cell Epitopes

Many new references and many new species were added to the IEDB in 2019, 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 2018 and 2019. Of the 3,825 species/strains listed, 136 were added in 2019. It should be noted that the source organism is the species/strain from which the epitopes originate, and may not be from an infecting organism or vaccine target. The curation of MHC binding peptides, cross-reactive epitopes, and autoimmune epitopes has resulted in the appearance of human (*Homo sapiens*) and mouse (*Mus musculus*) epitopes on the list.

In the table below, the leftmost column labeled "New" indicates with an "X" if epitopes for the species/strain was added to the IEDB in 2019. A font color of red is used to highlight the information in the row. The Organism ID matches the NCBI taxonomy ID if it exists. Otherwise, it represents an IEDB-assigned identifier, which are eight-digit numbers starting with "1000". These are easily distinguishable from the NCBI identifiers which are six digits or less. The columns labeled "B-18", "T-18", "B-19", and "T-19" indicate the cumulative number of distinct B cell and T cell epitopes in the database at the end of 2018 and 2019, respectively. The two rightmost columns display the differences in the B and T cell epitope counts from 2018 to 2019. The changes in B and T cell epitope counts are shown in red. In 2019, the number of B cell epitopes increased by 5,301 from 50,617 to 55,918 and the number of T cell epitopes increased by 80,160 from 461,348 to 541,508.

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

ID	NEW 2019	ORGANISM ID	SPECIES / STRAIN	B 18	T 18	B 19	T 19	DELTA B	DELTA T
1		2	Bacteria	45		57		12	
2		106	<i>Runella slithyformis</i>		1		1		
3		108	<i>Spirosoma linguale</i>	1		1			
4		139	<i>Borrelia burgdorferi</i>	78	43	78	45		2
6		158	<i>Treponema denticola</i>		1		1		
7		160	<i>Treponema pallidum</i>	7	2	7	2		
8		173	<i>Leptospira interrogans</i>	6	4	6	4		
9		195	<i>Campylobacter coli</i>		2		2		
10		197	<i>Campylobacter jejuni</i>	108	29	115	30	7	1
11		210	<i>Helicobacter pylori</i>	47	56	49	56	2	
12		234	<i>Brucella</i>		28		28		
13		235	<i>Brucella abortus</i>	7	39	7	39		
14		236	<i>Brucella ovis</i>		3		3		
15		263	<i>Francisella tularensis</i>	4	14	4	14		
16		266	<i>Paracoccus denitrificans</i>	3		3			
17		271	<i>Thermus aquaticus</i>	1		1			
18		274	<i>Thermus thermophilus</i>	1	1	1	1		
19		280	<i>Xanthobacter autotrophicus</i>		1		1		
20		286	<i>Pseudomonas</i>	1		1	1		1
21		287	<i>Pseudomonas aeruginosa</i>	96	162	96	168		6
22		292	<i>Burkholderia cepacia</i>	3	2	3	2		
23		294	<i>Pseudomonas fluorescens</i>		4		4		
25		300	<i>Pseudomonas mendocina</i>		1		1		
26		303	<i>Pseudomonas putida</i>	1	8	1	8		
27		306	<i>Pseudomonas</i> sp.		1		1		
28		312	<i>Pseudomonas</i> sp. RS-16	1		1			
30		319	<i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i>	1		1			
31		354	<i>Azotobacter vinelandii</i>		2		2		
32		358	<i>Agrobacterium tumefaciens</i>	1	2	1	2		
33		382	<i>Sinorhizobium meliloti</i>		1		1		
34		384	<i>Rhizobium leguminosarum</i>		1		1		
35		446	<i>Legionella pneumophila</i>	1	1	1	1		
36		470	<i>Acinetobacter baumannii</i>	2	1	2	1		
37		471	<i>Acinetobacter calcoaceticus</i>		1		1		
38		480	<i>Moraxella catarrhalis</i>	10		10			
39		485	<i>Neisseria gonorrhoeae</i>	77	15	77	15		
40		487	<i>Neisseria meningitidis</i>	88	23	91	23	3	
41		491	<i>Neisseria meningitidis</i> serogroup B	46	1	46	1		
42		511	<i>Alcaligenes faecalis</i>	3	2	3	2		
43		520	<i>Bordetella pertussis</i>	338	218	338	218		

44		543	Enterobacteriaceae	4		4			
45		544	Citrobacter	1		1			
46		546	Citrobacter freundii	1		2		1	
47		548	Klebsiella aerogenes		1		1		
48		550	Enterobacter cloacae		9		9		
49		554	Pectobacterium carotovorum	2		2			
50	X	556	Dickeya chrysanthemi			1		1	
51		562	Escherichia coli	257	150	275	182	18	32
52		573	Klebsiella pneumoniae	29	9	29	9		
53		582	Morganella morganii	1		1			
54		583	Proteus	2		2			
55		584	Proteus mirabilis	7		7			
57		590	Salmonella	3		3			
58		596	Salmonella enterica subsp. enterica serovar Muenchen	1		1			
59		599	Salmonella sp.	1		1			
60		605	Salmonella enterica subsp. enterica serovar Pullorum		1		1		
61		611	Salmonella enterica subsp. enterica serovar Heidelberg	9		9			
62		615	Serratia marcescens	1	3	1	3		
63		621	Shigella boydii		2		2		
64		622	Shigella dysenteriae	6	2	6	2		
65		623	Shigella flexneri	77	11	77	11		
66		624	Shigella sonnei		1		1		
67		630	Yersinia enterocolitica	6	28	6	28		
68		632	Yersinia pestis	24	324	24	324		
69		633	Yersinia pseudotuberculosis		2		2		
71		644	Aeromonas hydrophila	9	3	9	3		
72		645	Aeromonas salmonicida	59		59			
73		659	Photobacterium phosphoreum		1		1		
74		666	Vibrio cholerae	38	91	38	91		
75		670	Vibrio parahaemolyticus		57		57		
76		671	Vibrio proteolyticus	1		1			
77		672	Vibrio vulnificus	1	66	1	66		
78		674	Vibrio mimicus	2		2			
79		686	Vibrio cholerae O1 biovar El Tor	3	1	3	1		
80		703	Plesiomonas shigelloides		2		2		
81		714	Aggregatibacter actinomycetemcomitans	1	4	1	4		
82		715	Actinobacillus pleuropneumoniae		2		2		
83		727	Haemophilus influenzae	30	68	31	68	1	
84		730	[Haemophilus] ducreyi	3	2	3	2		
85		738	Glaesserella parasuis	1		1			
86		747	Pasteurella multocida	1	10	1	10		
87		769	Anaplasma centrale		2		2		

88		770	Anaplasma marginale	25	14	25	14		
89		777	Coxiella burnetii	2	201	2	311		110
90		779	Ehrlichia ruminantium	3		3	23		23
91		781	Rickettsia conorii		13		13		
92		782	Rickettsia prowazekii		23		23		
93		783	Rickettsia rickettsii		1		1		
94		784	Orientia tsutsugamushi	87		87			
95		785	Rickettsia typhi		3		3		
96		787	Rickettsia australis		1		1		
97		788	Rickettsia canadensis		1		1		
98		813	Chlamydia trachomatis	178	69	208	69	30	
99		817	Bacteroides fragilis		3	27	3	27	
100		837	Porphyromonas gingivalis	91	21	108	22	17	1
101		920	Acidithiobacillus ferrooxidans		1		1		
102		944	Ehrlichia canis	7	1	7	1		
103		945	Ehrlichia chaffeensis	14	1	14	1		
105		948	Anaplasma phagocytophilum	33		45		12	
106		955	Wolbachia pipiensis	1		1			
107		1006	Marivirga tractuosa		1		1		
108		1018	Capnocytophaga ochracea		1		1		
109		1019	Capnocytophaga sputigena		1		1		
110		1022	Beggiatoa alba	1		1			
111		1063	Rhodobacter sphaeroides		1		1		
112		1076	Rhodopseudomonas palustris		2		2		
113		1224	Proteobacteria	3		3			
114		1245	Leuconostoc mesenteroides	1		1			
115		1254	Pediococcus acidilactici	1		1			
116		1260	Finegoldia magna		1		1		
117		1265	Ruminococcus flavefaciens		1		1		
118		1270	Micrococcus luteus	1		1			
119		1279	Staphylococcus	1		1			
120		1280	Staphylococcus aureus	134	46	135	47	1	1
122		1292	Staphylococcus warneri	1		1			
123		1299	Deinococcus radiodurans	3		3			
124		1301	Streptococcus	5		5			
125		1303	Streptococcus oralis	12		12			
127		1305	Streptococcus sanguinis		1		1		
128		1307	Streptococcus suis	1		1			
129		1309	Streptococcus mutans	146	89	146	89		
130		1310	Streptococcus sobrinus	1		1			
131		1311	Streptococcus agalactiae	18		18			
132		1313	Streptococcus pneumoniae	90	8	90	28		20
133		1314	Streptococcus pyogenes	377	115	377	125		10

134		1317	Streptococcus downei	2	1	2	1		
135		1319	Streptococcus sp. 'group B'	1		2		1	
137		1324	Streptococcus sp. G148	14	5	14	5		
138		1334	Streptococcus dysgalactiae	3	6	3	6		
139		1336	Streptococcus equi	22	14	22	14		
140		1349	Streptococcus uberis	8		8			
141		1351	Enterococcus faecalis	2		2			
142		1352	Enterococcus faecium	6		6			
143		1358	Lactococcus lactis		2		2		
144		1390	Bacillus amyloliquefaciens	18	3	18	3		
145		1392	Bacillus anthracis	399	209	402	209	3	
146		1396	Bacillus cereus	1	8	1	8		
147		1402	Bacillus licheniformis		10		10		
148		1404	Bacillus megaterium		1		1		
149		1405	Bacillus mycoides		1		1		
151		1408	Bacillus pumilus		1		1		
152		1422	Geobacillus stearothermophilus	2	1	2	1		
153		1423	Bacillus subtilis	2	4	2	4		
154		1428	Bacillus thuringiensis	7	7	7	7		
155		1435	Bacillus thuringiensis serovar san diego		2		2		
156		1467	Bacillus lentus		1		1		
157		1491	Clostridium botulinum	196	112	196	112		
158		1496	Clostridioides difficile	63	1	66	1	3	
159		1502	Clostridium perfringens	41	1	41	1		
160		1513	Clostridium tetani	79	272	79	275		3
161		1520	Clostridium beijerinckii	1		1			
162		1585	Lactobacillus delbrueckii subsp. bulgaricus	1		1			
163		1599	Lactobacillus sakei		1		1		
164		1604	Lactobacillus amylovorus		1		1		
165	X	1613	Lactobacillus fermentum			1		1	
167		1638	Listeria ivanovii	1	1	1	1		
168		1639	Listeria monocytogenes	22	99	22	100		1
169		1641	Listeria grayi		1		1		
170		1642	Listeria innocua	2	3	2	3		
171		1646	Renibacterium salmoninarum	12		12			
172		1661	Trueperella pyogenes	7		7			
173	X	1664	Arthrobacter glacialis				1		1
174		1681	Bifidobacterium bifidum		1		1		
175	X	1716	Corynebacterium				1		1
176		1717	Corynebacterium diphtheriae	15	52	15	52		
177		1718	Corynebacterium glutamicum		26		26		
178		1747	Cutibacterium acnes		2		2		

179		1752	<i>Propionibacterium freudenreichii</i> subsp. <i>shermanii</i>		1		1		
180		1763	<i>Mycobacterium</i>	29	20	29	21		1
181		1764	<i>Mycobacterium avium</i>	6	17	6	18		1
182		1765	<i>Mycobacterium tuberculosis</i> variant <i>bovis</i>	49	326	49	327		1
183		1766	<i>Mycolicibacterium fortuitum</i>		1		1		
184		1767	<i>Mycobacterium intracellulare</i>		1		1		
185		1768	<i>Mycobacterium kansasii</i>	9	13	9	13		
186		1769	<i>Mycobacterium leprae</i>	127	409	127	409		
187		1770	<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i>	105	15	105	15		
188		1771	<i>Mycolicibacterium phlei</i>		1		1		
189		1772	<i>Mycolicibacterium smegmatis</i>		28		28		
190		1773	<i>Mycobacterium tuberculosis</i>	642	2530	643	2577	1	47
191		1774	<i>Mycobacteroides chelonae</i>	1		1			
192		1778	<i>Mycobacterium gordoneae</i>	1		1			
193		1781	<i>Mycobacterium marinum</i>		1		1		
194		1783	<i>Mycobacterium scrofulaceum</i>	4		4			
195		1795	<i>Mycolicibacterium neoaurum</i>		1		1		
196		1804	<i>Mycolicibacterium gilvum</i>		1		1		
197		1809	<i>Mycobacterium ulcerans</i>		10		10		
199		1828	<i>Rhodococcus fascians</i>		2		2		
200		1830	<i>Rhodococcus ruber</i>		1		1		
201		1833	<i>Rhodococcus erythropolis</i>		2		2		
202		1836	<i>Saccharopolyspora erythraea</i>	1		2		1	
203		1895	<i>Streptomyces avidinii</i>	1		1			
204		1902	<i>Streptomyces coelicolor</i>		2		2		
205		1916	<i>Streptomyces lividans</i>	10		10			
206		1946	<i>Streptomyces kasugaensis</i>		1		1		
207		2039	<i>Tropheryma whipplei</i>	1		1			
208		2097	<i>Mycoplasma genitalium</i>		1		1		
209		2099	<i>Mycoplasma hyopneumoniae</i>	2		2			
210	X	2100	<i>Mycoplasma hyorhinis</i>			1		1	
211		2104	<i>Mycoplasma pneumoniae</i>	16	2	16	2		
213		2133	<i>Spiroplasma citri</i>		1		1		
214		2147	<i>Acholeplasma</i>	1		1			
215		2148	<i>Acholeplasma laidlawii</i>		2		2		
216		2190	<i>Methanocaldococcus jannaschii</i>		1		1		
217		2234	<i>Archaeoglobus fulgidus</i>	1	1	1	1		
218		2242	<i>Halobacterium salinarum</i>	1		1			
219		2287	<i>Saccharolobus solfataricus</i>	1		1			
220	X	2336	<i>Thermotoga maritima</i>			2		2	
221		2439	<i>Plasmid ColB2</i>	1		1			
222		2465	<i>Plasmid F</i>	1		1			

224	X	2736	<i>Verrucomicrobium spinosum</i>			1		1	
225		2759	Eukaryota	1		1			
226		2864	Dinophyceae	1		1			
227		2903	<i>Emiliania huxleyi</i>		1		1		
228		3039	<i>Euglena gracilis</i>	1		1			
229		3068	<i>Volvox carteri f. nagariensis</i>		1		1		
230		3318	Pinaceae	2		2			
231		3352	<i>Pinus taeda</i>	4		4			
232		3369	<i>Cryptomeria japonica</i>	45	300	45	300		
233		3469	<i>Papaver somniferum</i>	1		1			
234		3505	<i>Betula pendula</i>	85	335	85	337		2
235		3513	<i>Quercus alba</i>		5		5		
236		3517	<i>Alnus glutinosa</i>		17		17		
237		3562	<i>Spinacia oleracea</i>	4		4			
239		3617	<i>Fagopyrum esculentum</i>	40		40			
240		3645	<i>Bertholletia excelsa</i>	7	24	7	24		
241		3656	<i>Cucumis melo</i>	13		13			
242		3677	<i>Trichosanthes kirilowii</i>	4		4			
243		3702	<i>Arabidopsis thaliana</i>	3	10	6	10	3	
244		3704	<i>Armoracia rusticana</i>	5		5			
245		3707	<i>Brassica juncea</i>	9		9			
247		3711	<i>Brassica rapa</i>	1		1			
248		3726	<i>Raphanus sativus</i>	1		1			
249		3728	<i>Sinapis alba</i>	2		2			
250		3750	<i>Malus domestica</i>	27	48	27	48		
251		3755	<i>Prunus dulcis</i>	19		19			
252		3758	<i>Prunus domestica</i>	4		4			
253		3760	<i>Prunus persica</i>	18	51	18	51		
254		3816	<i>Abrus precatorius</i>	1		1			
255		3818	<i>Arachis hypogaea</i>	461	263	478	263	17	
256		3847	<i>Glycine max</i>	195	2	608	2	413	
257		3864	<i>Lens culinaris</i>	19		19			
258		3885	<i>Phaseolus vulgaris</i>	10	3	10	3		
260		3972	<i>Viscum album</i>	17		17			
261		3981	<i>Hevea brasiliensis</i>	212	43	212	43		
262		3988	<i>Ricinus communis</i>	61	6	81	6	20	
263		4012	<i>Rhus</i>		1		1		
264		4026	<i>Acer pseudoplatanus</i>	1		1			
265		4039	<i>Daucus carota</i>		46		46		
266		4045	<i>Apium graveolens</i>		14		14		
267		4081	<i>Solanum lycopersicum</i>	3		3			
268		4097	<i>Nicotiana tabacum</i>	5		5			
269		4100	<i>Nicotiana benthamiana</i>	5		5			

271		4146	Olea europaea	70	19	70	19		
272		4163	Digitalis	1		1			
273		4182	Sesamum indicum	11		11			
274		4212	Ambrosia artemisiifolia	4	215	4	215		
275		4214	Ambrosia trifida		10		10		
276		4215	Ambrosia artemisiifolia var. elatior	9	12	9	12		
277		4220	Artemisia vulgaris	1	70	1	70		
278		4232	Helianthus annuus	18		18			
279	X	4479	Poaceae			1		1	
280		4498	Avena sativa		16		16		
281		4509	Dactylis glomerata		12		12		
282		4513	Hordeum vulgare		26		26		
283		4522	Lolium perenne	44	123	44	123		
284		4530	Oryza sativa	2		2			
285		4545	Poa pratensis	34	35	34	35		
286		4550	Secale cereale	51	44	51	44		
287		4558	Sorghum bicolor		1		1		
288		4565	Triticum aestivum	649	583	650	586	1	3
289		4567	Triticum turgidum subsp. durum		1		1		
290		4568	Triticum monococcum		1		1		
292		4577	Zea mays	3	1	3	1		
293		4606	Festuca arundinacea	1		1			
294		4615	Ananas comosus	3		3			
295		4641	Musa acuminata	50	1	50	1		
296		4751	Fungi	2		4		2	
297		4754	Pneumocystis carinii	2	1	2	1		
298		4903	Cyberlindnera jadinii	12		12			
299		4932	Saccharomyces cerevisiae	29	14	29	14		
300		5039	Blastomyces dermatitidis		1		1		
301	X	5052	Aspergillus			4		4	
302	X	5059	Aspergillus flavus			6		6	
303	X	5060	Aspergillus giganteus				4		4
304		5061	Aspergillus niger		1		1		
305		5064	Aspergillus restrictus	1		1			
306		5067	Aspergillus parasiticus		1		1		
307		5076	Penicillium chrysogenum	45	19	45	19		
308		5077	Penicillium citrinum	13		13			
309		5141	Neurospora crassa	6	3	6	3		
310		5207	Cryptococcus neoformans	2	2	2	2		
311		5334	Schizophyllum commune	1	1	1	1		
312		5476	Candida albicans	108	80	111	80	3	
313		5480	Candida parapsilosis	1		1			
314		5501	Coccidioides immitis		1		1		

315		5503	Curvularia lunata	20	10	20	10		
316	X	5518	<i>Fusarium graminearum</i>			6		6	
317		5551	Trichophyton rubrum	2	27	2	27		
318		5554	Cutaneotrichosporon cutaneum	1		1			
319		5599	Alternaria alternata	5	36	6	36	1	
320		5658	Leishmania	4		4			
321		5659	<i>Leishmania amazonensis</i>		15		15		
322		5660	<i>Leishmania braziliensis</i>	6		6			
323		5661	<i>Leishmania donovani</i>	25	84	25	96		12
324		5664	<i>Leishmania major</i>	25	184	30	184	5	
325		5665	<i>Leishmania mexicana</i>	2	3	3	3	1	
326		5667	<i>Leishmania aethiopica</i>	16		16			
327		5671	<i>Leishmania infantum</i>	102	9	108	9	6	
328		5679	<i>Leishmania panamensis</i>	3	7	3	7		
329		5682	<i>Leishmania pifanoi</i>		20		20		
330		5691	<i>Trypanosoma brucei</i>	13	6	13	6		
331		5692	<i>Trypanosoma congolense</i>	1		1			
332		5693	<i>Trypanosoma cruzi</i>	161	454	164	454	3	
333		5702	<i>Trypanosoma brucei brucei</i>	5		5			
334		5722	<i>Trichomonas vaginalis</i>	75	1	75	1		
335		5741	<i>Giardia intestinalis</i>	1	13	1	13		
336		5755	<i>Acanthamoeba castellanii</i>	14	3	14	3		
337		5759	<i>Entamoeba histolytica</i>	30	14	30	14		
338		5801	<i>Eimeria acervulina</i>	1		1			
339		5802	<i>Eimeria tenella</i>	6		8		2	
340		5807	<i>Cryptosporidium parvum</i>	4	31	4	31		
341		5811	<i>Toxoplasma gondii</i>	83	103	85	103	2	
342		5820	<i>Plasmodium</i>	3	4	3	4		
343		5821	<i>Plasmodium berghei</i>	14	50	20	50	6	
344		5823	<i>Plasmodium berghei ANKA</i>	7	65	7	65		
345		5824	<i>Plasmodium brasilianum</i>	2		2			
346		5825	<i>Plasmodium chabaudi</i>	4	4	4	4		
347		5827	<i>Plasmodium cynomolgi</i>	2		2			
349		5833	<i>Plasmodium falciparum</i>	784	813	804	813	20	
350		5834	<i>Plasmodium falciparum RO-33</i>	8	1	8	1		
351		5835	<i>Plasmodium falciparum CAMP/Malaysia</i>	36	3	36	3		
352		5836	<i>Plasmodium falciparum CDC/Honduras</i>	18		18			
353		5837	<i>Plasmodium falciparum FC27/Papua New Guinea</i>	47	60	47	60		
354		5838	<i>Plasmodium falciparum FCR-3/Gambia</i>	94		94			
355		5839	<i>Plasmodium falciparum K1</i>	18	19	18	19		
356		5840	<i>Plasmodium falciparum LE5</i>		2		2		
357		5841	<i>Plasmodium falciparum Mad20/Papua New Guinea</i>	8	47	8	47		

358		5842	Plasmodium falciparum NF7/Ghana	4		4			
359		5843	Plasmodium falciparum NF54	20	31	20	31		
360		5846	Plasmodium falciparum T4/Thailand	25	1	25	1		
361		5848	Plasmodium falciparum isolate WELLCOME	25	51	25	51		
362		5850	Plasmodium knowlesi	2	17	2	17		
363		5851	Plasmodium knowlesi strain H	41	10	41	10		
364		5852	Plasmodium knowlesi strain Nuri		10		10		
365		5855	Plasmodium vivax	138	176	369	176	231	
366		5857	Plasmodium fragile		5		5		
367		5858	Plasmodium malariae	1		1			
368		5861	Plasmodium yoelii	17	39	17	39		
369		5865	Babesia bovis	3	8	5	8	2	
370		5866	Babesia bigemina		3		3		
371		5868	Babesia microti	5		5			
372		5872	Theileria equi	8		8			
373		5874	Theileria annulata	1		1			
374		5875	Theileria parva	28	20	28	20		
376		6035	Encephalitozoon cuniculi		5		5		
377		6100	Aequorea victoria	3	5	4	5	1	
378		6181	Schistosoma	3		3			
379		6182	Schistosoma japonicum	43	53	43	53		
380		6183	Schistosoma mansoni	99	52	102	52	3	
381		6184	Schistosoma bovis	2		2			
382		6192	Fasciola hepatica	298	28	300	28	2	
383		6203	Taenia ovis	8		8			
384		6204	Taenia solium	28	4	29	4	1	
385		6206	Taenia saginata	13		13			
386		6207	Taenia crassiceps	11	1	11	1		
387		6210	Echinococcus granulosus	41	2	41	2		
388		6211	Echinococcus multilocularis	6		6			
389		6238	Caenorhabditis briggsae	1		1			
390		6239	Caenorhabditis elegans	2	10	2	10		
392		6253	Ascaris suum	1	1	1	1		
393		6265	Toxocara canis	3		3			
394		6269	Anisakis simplex	38	28	38	28		
395		6279	Brugia malayi	10	5	10	5		
396		6280	Brugia pahangi	1		1			
397		6282	Onchocerca volvulus	3310	39	4394	39	1084	
398		6289	Haemonchus contortus	3		3			
399		6293	Wuchereria bancrofti	13	8	13	8		
400		6299	Litomosoides carinii	3		3			
401		6334	Trichinella spiralis	16	7	16	7		
402		6339	Heligmosomoides polygyrus	3		3			

403		6421	Hirudo medicinalis		3		3		
404		6454	Haliotis rufescens	1		1			
405		6491	Conus geographus	30		30			
406		6492	Conus magus	2		2			
407		6493	Conus striatus	11		11			
409		6536	Helix pomatia	1		1			
410		6594	Macrocallista nimbosa	1		1			
411		6661	Artemia franciscana	2		2			
412		6687	Penaeus monodon	10	23	10	23		
413		6689	Penaeus vannamei	140		140			
414		6690	Penaeus aztecus	51	31	51	31		
415		6728	Procambarus clarkii	3		3			
416		6761	Scylla serrata	13		13			
417		6850	Limulus polyphemus		1		1		
418		6853	Tachypleus tridentatus	1		1			
419		6858	Androctonus australis	9		9			
420		6860	Androctonus mauritanicus mauritanicus	1		1			
421		6878	Centruroides noxioides	10		10			
422		6887	Tityus serrulatus	92		92			
423		6925	Latrodectus tredecimguttatus		1		1		
424		6938	Ornithodoros moubata	20		20			
425		6941	Rhipicephalus microplus	1		1			
426		6945	Ixodes scapularis	11		11			
427		6953	Dermatophagooides		578		578		
428		6954	Dermatophagooides farinae	35	111	41	111	6	
429		6956	Dermatophagooides pteronyssinus	109	300	133	300	24	
430		6958	Euroglyphus maynei		10		10		
431		6973	Blattella germanica	23	501	23	501		
432		6978	Periplaneta americana	22	6	25	6	3	
433		7088	Lepidoptera		1		1		
434		7108	Spodoptera frugiperda		4		4		
435		7130	Manduca sexta		3		3		
436		7137	Galleria mellonella	2		2			
437		7154	Chironomus thummi	2	3	2	3		
438		7155	Chironomus thummi thummi	58	27	58	27		
439		7160	Aedes albopictus	7		7			
440		7165	Anopheles gambiae	8	2	8	2		
441		7227	Drosophila melanogaster	10	17	11	17	1	
442		7234	Drosophila persimilis	1		1			
443		7386	Sarcophaga peregrina		1		1		
444		7441	Dolichovespula maculata	11	20	11	20		
445		7444	Vespa basalis	1		1			
446		7453	Vespa maculifrons	1		1			

447		7454	Vespa vulgaris	2	95	2	95		
448		7460	Apis mellifera	15	106	15	108		2
449		7469	Apis mellifera ligustica		1		1		
450		7515	Ctenocephalides felis		2		2		
451		7719	Ciona intestinalis	2		2			
452		7726	Styela plicata	6		6			
453		7742	Vertebrata	4		4			
454		7777	Chondrichthyes	1		1			
455		7787	Tetronarce californica	149	75	151	75	2	
456		7788	Torpedo marmorata	3	3	3	3		
457		7955	Danio rerio	2	3	2	3		
458		7957	Carassius auratus	3	1	3	1		
459		7962	Cyprinus carpio	4	1	6	1	2	
460		8005	Electrophorus electricus	4		4			
461		8018	Oncorhynchus keta		6		6		
462		8022	Oncorhynchus mykiss	1		1			
463		8030	Salmo salar	31		35		4	
464		8049	Gadus morhua	43		44		1	
465		8053	Gadus morhua callarias	10		10			
466		8090	Oryzias latipes	2	1	2	1		
467		8255	Paralichthys olivaceus	1		1			
468	X	8342	Anura			1		1	
469		8355	Xenopus laevis	4	3	4	3		
470		8364	Xenopus tropicalis	2	2	2	2		
471		8554	Heloderma suspectum		1		1		
472		8613	Bungarus fasciatus	1		1			
473		8616	Bungarus multicinctus	17	3	17	3		
474		8620	Dendroaspis polylepis polylepis	22		22			
475		8654	Naja nigricollis	3	2	3	2		
477		8656	Naja atra	14		14			
478		8657	Naja oxiana	4		4			
479		8658	Naja pallida	1	1	1	1		
480		8663	Notechis scutatus	2		2			
481		8667	Oxyuranus scutellatus scutellatus	4		4			
482		8671	Pseudechis porphyriacus	3		3			
483		8704	Vipera ammodytes	1		1			
484		8722	Bothrops asper	1		28		27	
485	X	8724	Bothrops jararaca			5		5	
486		8725	Bothrops atrox	13		13			
487		8726	Bothrops jararacussu	13		13			
488		8732	Crotalus durissus terrificus	4		4			
489		8753	Lachesis muta muta	45		45			
490		8801	Struthio camelus	2		2			

491		8839	Anas platyrhynchos	2		2			
492		8845	Anser cygnoides	2		2			
493		8855	Cairina moschata	2	1	2	1		
494		8932	Columba livia		10		10		
495		8996	Numida meleagris	1		1			
496		9014	Colinus virginianus	1	3	1	3		
497		9031	Gallus gallus	338	346	340	371	2	25
498		9057	Phasianus colchicus colchicus	1		1			
500		9103	Meleagris gallopavo	6		6			
501		9258	Ornithorhynchus anatinus		1		1		
502		9322	Macropus sp.	1		1			
503		9337	Trichosurus vulpecula	45		45			
504		9397	Chiroptera	1		1			
506		9447	Lemur catta	1		1			
507		9479	Platyrrhini	1		1			
508		9483	Callithrix jacchus	1	4	1	4		
509		9488	Saguinus mystax	1		1			
510		9491	Saguinus imperator	1		1			
511		9502	Alouatta caraya	1		1			
512		9505	Aotus trivirgatus	1		1			
513		9509	Ateles geoffroyi		1		1		
514		9510	Ateles paniscus	1		1			
515		9511	Ateles sp.	1		1			
516		9515	Sapajus apella	1		1			
517		9519	Lagothrix lagotricha	1		1			
518		9521	Saimiri sciureus	1		1			
519		9534	Chlorocebus aethiops		5		5		
520		9538	Erythrocebus patas		1		1		
521		9541	Macaca fascicularis	3	3	3	3		
522		9544	Macaca mulatta	3	5	3	5		
523		9548	Macaca radiata	14	1	14	1		
524		9555	Papio anubis	1		1			
525		9556	Papio cynocephalus	1		1			
526		9580	Hylobates lar		1		1		
527		9593	Gorilla gorilla		2		2		
528		9595	Gorilla gorilla gorilla		6		6		
529		9597	Pan paniscus		1		1		
530		9598	Pan troglodytes	7	25	7	25		
531		9600	Pongo pygmaeus		2		2		
532		9601	Pongo abelii		2		2		
533		9606	Homo sapiens	9022	29825 4	9639	36877 2	617	70518
534		9615	Canis lupus familiaris	17	1575	19	1937	2	362
535		9627	Vulpes vulpes	1		1			

536		9666	Mustela lutreola	1		1			
537		9685	Felis catus	40	99	42	117	2	18
538		9721	Cetacea	1		1			
539		9755	Physeter catodon	1	34	1	34		
540		9796	Equus caballus	54	55	54	57		2
541		9798	Equus przewalskii		1		1		
542		9823	Sus scrofa	115	53	121	55	6	2
543		9825	Sus scrofa domesticus		5		5		
544		9844	Lama glama	1		1			
545		9860	Cervus elaphus	6		6			
546		9864	Cervus canadensis nelsoni	5		5			
547		9874	Odocoileus virginianus	2		2			
548		9913	Bos taurus	1320	843	1338	855	18	12
549		9925	Capra hircus	11		11			
550		9940	Ovis aries	95	17	95	17		
551		9978	Ochotona princeps		1		1		
552		9986	Oryctolagus cuniculus	66	10	67	10	1	
553		10029	Cricetus griseus	9		9			
554		10036	Mesocricetus auratus	58		58			
555	X	10042	Peromyscus maniculatus				1		1
556		10090	Mus musculus	699	20365	716	22929	17	2564
557		10092	Mus musculus domesticus		12		12		
558		10095	Mus sp.	1		1			
559		10114	Rattus	11		11			
560		10116	Rattus norvegicus	267	33167	279	33168	12	1
562		10118	Rattus sp.		1		1		
563		10141	Cavia porcellus	37	79	37	87		8
564		10243	Cowpox virus		25		26		1
565		10244	Monkeypox virus	5	2	5	2		
566		10245	Vaccinia virus	11	547	11	610		63
567		10247	Vaccinia virus WR 65-16		4		4		
568		10248	Vaccinia virus LC16M8		5		5		
569		10249	Vaccinia virus Copenhagen	31	846	31	846		
570		10251	Vaccinia virus IHD-J	1		1			
571		10253	Vaccinia virus Tian Tan		21		21		
572		10254	Vaccinia virus WR	31	6689	31	6822		133
573		10255	Variola virus		248		248		
574	X	10258	Orf virus			1		1	
575		10261	Fowlpox virus		7		7		
576		10263	Fowlpox virus isolate HP-438/Munich		1		1		
577		10273	Myxoma virus		4		4		
578		10276	Swinepox virus		2		2		
579		10292	Herpesviridae		1		1		

580		10298	Human alphaherpesvirus 1	181	181	181	585		404
581		10299	Human alphaherpesvirus 1 strain 17	44	46	44	46		
582		10301	Human alphaherpesvirus 1 strain Angelotti		4		4		
583		10303	Human alphaherpesvirus 1 strain HFEM	2		2			
584		10304	Human alphaherpesvirus 1 strain F	17	5	17	5		
585		10306	Human alphaherpesvirus 1 strain KOS	17	4	17	4		
586		10308	Human alphaherpesvirus 1 strain Patton	3		3			
587		10309	Human alphaherpesvirus 1 strain SC16	5	2	5	2		
588		10310	Human alphaherpesvirus 2	295	226	295	229		3
589		10312	Human herpesvirus 2 strain 186	1	1	1	1		
590		10313	Human herpesvirus 2 strain 333	2	5	2	5		
591		10315	Human herpesvirus 2 strain HG52		31		32		1
592		10317	Cercopithecine alphaherpesvirus 2		1		1		
593		10320	Bovine alphaherpesvirus 1	5	40	6	40		1
594		10323	Bovine herpesvirus type 1.1 (strain Cooper)	9	17	9	17		
595		10324	Bovine herpesvirus type 1.1 (strain P8-2)	1		1			
596		10325	Macacine alphaherpesvirus 1	1		366			365
597		10326	Equid alphaherpesvirus 1	7	218	7	218		
598		10331	Equid alphaherpesvirus 4	6		6			
599		10335	Human alphaherpesvirus 3	10	127	10	132		5
600		10338	Human herpesvirus 3 strain Dumas		29		29		
601		10345	Suid alphaherpesvirus 1	7	2	13	3	6	1
602		10349	Suid herpesvirus 1 (strain NIA-3)	4		4			
603		10359	Human betaherpesvirus 5	119	613	123	626	4	13
604		10360	Human herpesvirus 5 strain AD169	233	432	233	456		24
605		10363	Human herpesvirus 5 strain Towne	94	26	94	26		
606		10366	Murid betaherpesvirus 1	2	64	2	64		
607		10367	Murine cytomegalovirus (strain Smith)		32		32		
609		10369	Human herpesvirus 6 (strain GS)	2		2			
610		10370	Human herpesvirus 6 (strain Uganda-1102)	2	4	2	4		
611		10372	Human betaherpesvirus 7	2	4	2	4		
612		10373	Macaca mulatta cytomegalovirus		76		76		
613		10376	Human gammaherpesvirus 4	2324	632	2362	659	38	27
614		10377	Human herpesvirus 4 strain B95-8	181	355	187	355	6	
615		10378	Human herpesvirus 4 strain RAJI	1		1			
616		10381	Saimiriine gammaherpesvirus 2		3		3		
617		10390	Gallid alphaherpesvirus 2		1		1		
618		10407	Hepatitis B virus	267	645	277	712	10	67
619		10408	Hepatitis B virus subtype adw2	82	61	82	61		
620		10409	Hepatitis B virus adr4		13		13		
621		10410	Hepatitis B virus adw/991	2	2	2	2		

622		10411	Hepatitis B virus alpha1		24		24		
623		10412	Hepatitis B virus adw/Indonesia/PIDW420		3		3		
624		10414	Hepatitis B virus LSH/chimpanzee		2		2		
625		10415	Hepatitis B virus adw/Okinawa/PODW282		5		5		
626		10418	Hepatitis B virus subtype ayw	57	185	57	185		
627		10419	Hepatitis B virus subtype adyw	4	45	4	45		
628		10430	Woodchuck hepatitis virus 1	3		3			
629		10433	Woodchuck hepatitis virus 8		34		34		
630		10479	Thermoproteus tenax virus 1	1		1			
631		10497	African swine fever virus	5		5	26		26
632		10498	African swine fever virus BA71V	46		55		9	
633		10515	Human adenovirus 2	28	16	28	16		
634		10519	Human adenovirus 7	4		4			
635		10521	Human adenovirus 14	4		4			
636		10524	Human adenovirus 41	1		1			
637		10529	Human adenovirus 31		7		7		
638		10530	Murine adenovirus 1	1	2	1	2		
639		10533	Human adenovirus 1		1		1		
640		10541	Human adenovirus 11		12		12		
641		10560	Bovine papillomavirus type 2	15		15			
642		10562	Bovine papillomavirus type 4	10	3	10	3		
643		10566	Human papillomavirus	3	1	3	1		
644		10573	Human papillomavirus type 13	1	1	1	1		
646		10580	Human papillomavirus type 11	9	43	9	43		
647		10583	Human papillomavirus type 1a	8	15	8	15		
648		10585	Human papillomavirus type 31	13	7	13	7		
649		10586	Human papillomavirus type 33	6	9	6	9		
650		10587	Human papillomavirus type 35	1	1	1	1		
651		10588	Human papillomavirus type 39	1	1	1	1		
652		10589	Human papillomavirus type 41		1		1		
653		10592	Human papillomavirus type 44		1		1		
654		10593	Human papillomavirus type 45	2	9	2	9		
655		10595	Human papillomavirus type 51	1	1	1	1		
656		10596	Human papillomavirus type 56	1	5	1	5		
657		10598	Human papillomavirus type 58	49	34	49	34		
658		10600	Human papillomavirus type 6b	11	29	11	29		
659		10611	Human papillomavirus type 30	1		1			
660		10614	Human papillomavirus 3		3		3		
661		10615	Human papillomavirus type 40	1	1	1	1		
662		10617	Human papillomavirus 4		4		4		
663		10618	Human papillomavirus type 52	1	36	1	36		
664		10620	Human papillomavirus type 7	1	3	1	3		

665		10623	Kappapapillomavirus 2	5	7	5	7		
666		10631	BK virus strain AS		1		1		
667		10632	JC polyomavirus	9	78	9	78		
668		10636	Murine polyomavirus strain A2		3		3		
669		10638	Kilham polyomavirus		1		1		
670		10665	Escherichia virus T4	10	20	10	20		
671	X	10678	Escherichia virus P1				6		6
672	X	10703	Corynephage beta			2		2	
673		10710	Escherichia virus Lambda		6		6		
674		10754	Salmonella virus P22	5		5			
675		10760	Escherichia phage T7	1		1			
676		10783	Aleutian mink disease parvovirus (STRAIN G)	3		3			
677		10786	Feline panleukopenia virus		4		4		
678		10788	Canine parvovirus	23	20	23	20		
679		10790	Canine parvovirus strain CPV-D CORNELL 320	1		1			
680		10791	Canine parvovirus strain N	47		47			
681		10793	Mink enteritis virus strain Abashiri	1		1			
682		10796	Porcine parvovirus	40		40			
683		10798	Human parvovirus B19	93	44	94	44	1	
684		10804	Adeno-associated virus - 2	42	153	42	153		
685		10847	Escherichia virus phiX174	1		1			
686		10863	Enterobacteria phage f1	1	1	1	1		
687		10864	Enterobacteria phage fd	7	1	7	1		
688		10879	Pseudomonas virus phi6	7		7			
689		10884	Mammalian orthoreovirus 1 Lang	3		3			
690		10886	Mammalian orthoreovirus 3 Dearing	1		1			
691		10891	Reovirus sp.		2		2		
692		10900	Bluetongue virus (serotype 10 / American isolate)	3		3			
693		10903	Bluetongue virus 17	4		4			
694		10904	Bluetongue virus (serotype 1 / isolate Australia)	7		7			
695		10906	Bluetongue virus 10	3		3			
696		10915	Porcine rotavirus serotype 5/strain OSU	1		1			
697		10917	Porcine rotavirus strain Gottfried	2		2			
698		10919	Porcine rotavirus strain YM	2	1	2	1		
699		10923	Simian rotavirus A/SA11	8	5	8	5		
700		10927	Bovine rotavirus	9	1	9	1		
701		10933	Bovine rotavirus strain RF	12	7	12	7		
702		10934	Bovine rotavirus strain UK/G6		1		1		
703		10941	Human rotavirus A	14	84	14	84		
704		10950	Human rotavirus (SEROTYPE 2 / STRAIN DS1)	1		1			
705		10952	Human rotavirus strain KU	9		9			

706		10957	Human rotavirus strain P	1	4	1	4		
707		10958	Human rotavirus strain RRV	1		1			
708		10960	Human rotavirus G4 strain St. Thomas 3	6		6			
709		10962	Human rotavirus strain WA	10	7	10	7		
710		10995	Infectious bursal disease virus	12		12			
711		10996	Infectious bursal disease virus 52/70		10		10		
712		10997	Infectious bursal disease virus 002-73/AUS	1		1			
713		11002	Infectious pancreatic necrosis virus	1		1			
714		11021	Eastern equine encephalitis virus	42	2	47	2	5	
715		11022	Eastern equine encephalitis virus (STRAIN VA33[TEN BROECK])		1		1		
716		11029	Ross River virus		1		1		
717		11032	Ross river virus (STRAIN T48)	3		3			
718		11033	Semliki Forest virus	36	5	36	5		
719		11034	Sindbis virus	26		26			
720		11036	Venezuelan equine encephalitis virus	2	5	2	5		
721		11037	Venezuelan equine encephalitis virus (strain TC-83)	25		25			
722		11038	Venezuelan equine encephalitis virus (strain Trinidad donkey)	15		15			
723		11039	Western equine encephalitis virus		1		1		
724		11041	Rubella virus	81	100	81	100		
725		11043	Rubella virus strain M33	3	11	3	11		
726		11044	Rubella virus vaccine strain RA27/3	2	6	2	6		
727		11045	Rubella virus strain Therien	20	35	20	35		
728		11047	Equine arteritis virus	3		3			
729		11048	Lactate dehydrogenase-elevating virus	14		14			
730		11049	Lelystad virus	66	12	66	12		
731		11053	Dengue virus 1	51	559	90	625	39	66
732		11057	Dengue virus 1 Thailand/AHF 82-80/1980		1		1		
733		11059	Dengue virus 1 Nauru/West Pac/1974	4	50	4	50		
734		11060	Dengue virus 2	184	713	191	739	7	26
735		11062	Dengue virus 2 Malaysia M2	1		1			
736		11064	Dengue virus 2 Jamaica/1409/1983	264	1254	264	1254		
737		11065	Dengue virus 2 Thailand/NGS-C/1944	20	37	20	146		109
738		11066	Dengue virus 2 Puerto Rico/PR159-S1/1969	32	21	32	21		
739		11067	Dengue virus 2 Tonga/EKB194/1974		3		3		
740		11069	Dengue virus 3	76	621	129	674	53	53
741		11070	Dengue virus 4	80	429	83	461	3	32
742		11072	Japanese encephalitis virus	49	143	49	143		
743		11073	Japanese encephalitis virus strain SA-14	6	1	6	1		
744		11075	Japanese encephalitis virus strain JAOARS982	4	4	4	4		

745		11076	Japanese encephalitis virus strain Nakayama	2	2	2	2		
746		11077	Kunjin virus	12	1	12	1		
747		11078	Kunjin virus (STRAIN MRM61C)		4		4		
748		11079	Murray Valley encephalitis virus	21	9	21	9		
749		11080	Saint Louis encephalitis virus	9	1	9	1		
750		11081	St. Louis encephalitis virus (strain MS1-7)	7		7			
751		11082	West Nile virus	51	442	51	442		
752		11083	Powassan virus	1	3	1	3		
753		11084	Tick-borne encephalitis virus	14	137	18	146	4	9
754		11085	Langat virus		1		1		
755	X	11086	Louping ill virus			1		1	
756		11087	Tick-borne encephalitis virus (STRAIN SOFJIN)	6		6			
757		11089	Yellow fever virus		1352		1352		
758		11090	Yellow fever virus 17D		364	2	364	2	
759		11092	Kumlinge virus	26		26			
760		11096	Classical swine fever virus	15	4	15	4		
761		11098	Classical swine fever virus - Brescia	4		4			
762		11099	Bovine viral diarrhea virus 1	1	12	1	12		
763		11100	Bovine viral diarrhea virus 1-NADL	4	3	4	3		
764		11103	Hepacivirus C	682	1129	693	1147	11	18
765		11104	Hepatitis C virus (isolate 1)	37	256	37	256		
766		11105	Hepatitis C virus (isolate BK)	3	90	3	90		
767		11108	Hepatitis C virus (isolate H)	161	84	163	84	2	
768		11110	Hepatitis C virus HCT18	1		1			
769		11113	Hepatitis C virus isolate HC-J6	8	3	8	3		
770		11115	Hepatitis C virus isolate HC-J8	1	1	1	1		
771		11116	Hepatitis C virus (isolate Japanese)	6	19	6	19		
772		11120	Infectious bronchitis virus	10	5	10	5		
773		11127	Avian infectious bronchitis virus (strain M41)	4	3	4	3		
774		11128	Bovine coronavirus	7		7			
775		11137	Human coronavirus 229E		2		2		
776		11138	Murine hepatitis virus	3	31	3	31		
777		11142	Murine hepatitis virus strain A59	26	4	26	4		
778		11144	Murine hepatitis virus strain JHM	25	21	25	21		
779		11149	Transmissible gastroenteritis virus	15	1	15	1		
780		11150	Porcine transmissible gastroenteritis coronavirus strain FS772/70	2		2			
781		11151	Porcine transmissible gastroenteritis coronavirus strain Purdue	14		14			
782		11152	Turkey coronavirus	1		1			
783		11169	Mumps virus strain Kilham	1		1			
784		11173	Mumps virus strain SBL-1	6		6			
785		11176	Avian avulavirus 1	20	5	21	5	1	

786		11177	Newcastle disease virus (STRAIN AUSTRALIA-VICTORIA/32)	4		4			
787		11178	Newcastle disease virus strain Beaudette C/45	12		12			
788		11180	Newcastle disease virus strain D26/76	4		4			
789		11186	Newcastle disease virus strain Queensland/66	4		4			
790		11191	Murine respirovirus	63	10	63	10		
791		11194	Sendai virus (strain Enders)	7	11	7	11		
792		11195	Sendai virus (strain Fushimi)		1		1		
793		11196	Sendai virus (strain Harris)	2		2			
794		11198	Sendai virus (Z)		1		2		1
795		11214	Human parainfluenza virus 2 (strain Toshiba)	3		3			
796		11215	Bovine respirovirus 3	3	1	3	1		
797		11216	Human respirovirus 3	2		3		1	
798		11217	Human parainfluenza 3 virus (strain NIH 47885)	8		8			
799		11232	Canine morbillivirus	14	9	14	9		
800		11233	Canine distemper virus strain Onderstepoort	6	34	6	34		
801		11234	Measles morbillivirus	64	39	64	39		
802		11235	Measles virus strain Edmonston	167	210	167	210		
803		11236	Measles virus strain Halle		34		34		
804		11241	Rinderpest morbillivirus	2	3	2	3		
805		11243	Rinderpest virus (strain L)	6		6			
806		11246	Bovine orthopneumovirus	3	2	3	2		
807		11249	Bovine respiratory syncytial virus (strain RB94)	4		4			
808		11250	Human orthopneumovirus	34	206	35	207	1	1
809		11251	Human respiratory syncytial virus (subgroup B / strain 18537)	2	1	2	1		
810		11252	Human respiratory syncytial virus (strain RSB642)	2		2			
812		11255	Human respiratory syncytial virus (strain RSB6190)	6		6			
813		11256	Human respiratory syncytial virus (strain RSB6256)	11		11			
814		11259	Human respiratory syncytial virus A2	91	136	94	211	3	75
815		11260	Human respiratory syncytial virus A strain Long	128	31	129	31	1	
816		11263	Murine orthopneumovirus		14		14		
817		11269	Marburg marburgvirus	5	95	5	104		9
818		11276	Vesicular stomatitis virus		10		10		
819		11277	Vesicular stomatitis Indiana virus	9	7	9	7		
820		11278	Vesicular stomatitis Indiana virus strain Glasgow		1		1		
821		11279	Vesicular stomatitis Indiana virus strain Mudd-Summers	1		1			
823		11285	Vesicular stomatitis Indiana virus strain San Juan		1		1		
824		11288	Viral hemorrhagic septicemia virus 07-71	12	1	12	1		
825		11290	Infectious hematopoietic necrosis virus	8		8			

826		11292	Rabies lyssavirus	13	26	14	26	1	
827		11293	Rabies virus AVO1		3		3		
828		11294	Rabies virus CVS-11	2		3		1	
829		11295	Rabies virus ERA	10	27	10	27		
830		11296	Rabies virus HEP-FLURY	7	1	7	1		
831		11298	Rabies virus Nishigahara RCEH	1		1			
832		11307	Sonchus yellow net nucleorhabdovirus		1		1		
833		11318	Dhori thogotovirus	1		1			
834		11320	Influenza A virus	74	533	74	592		59
836		11384	Influenza A virus (A/chicken/FPV/Weybridge(H7N7))		2		2		
837		11408	Influenza A virus (STRAIN A/EQUINE/NEW MARKET/76)		1		1		
838		11448	Influenza A virus (A/parrot/Ulster/73(H7N1))		1		1		
839		11484	Influenza A virus (A/whale/Maine/1/84(H13N9))	3		3			
840		11520	Influenza B virus	4	6	4	452		446
841		11521	Influenza B virus (B/Ann Arbor/1/1986)		3		3		
842		11532	Influenza B virus (STRAIN B/HT/84)		1		1		
843		11541	Influenza B virus (B/Oregon/5/80)	16		16			
844		11550	Influenza B virus (B/Yamagata/1/73)		3		3		
845		11552	Influenza C virus		1		1		
846		11553	Influenza C virus (C/Ann Arbor/1/50)	16		16			
847		11577	La Crosse virus	2	1	2	1		
848		11578	La Crosse virus L74		2		2		
849		11583	HoJo virus		1		1		
850		11588	Rift Valley fever virus	5	27	13	27	8	
851		11589	Rift valley fever virus (STRAIN ZH- 548 M12)		2		2		
852		11602	Hantaan virus 76-118	14	132	14	132		
853		11605	Puumala virus Hallnas B1		1		1		
854		11607	Sapporo rat virus	1	4	1	4		
855		11610	Seoul virus SR11	1		1			
856		11618	Arenavirus		2		2		
857		11620	Lassa mammarenavirus	13	670	15	706	2	36
858		11621	Lassa virus GA391		54		55		1
859		11622	Lassa virus Josiah	10	409	10	409		
860		11623	Lymphocytic choriomeningitis mammarenavirus	5	654	5	655		1
861		11624	Lymphocytic choriomeningitis virus (strain Armstrong)		1158		1158		
862		11625	Lymphocytic choriomeningitis virus (strain Pasteur)		5		5		
863		11626	Lymphocytic choriomeningitis virus (strain Traub)		3		3		
864		11627	Lymphocytic choriomeningitis virus (strain WE)		69		74		5
865		11628	Machupo mammarenavirus	1	800	1	800		

866		11629	Mopeia mammarenavirus		14		14		
867		11631	Tacaribe mammarenavirus		106		106		
868		11636	Reticuloendotheliosis virus	2	5	2	5		
869		11660	Caprine arthritis encephalitis virus	14	1	14	1		
870		11661	Caprine arthritis encephalitis virus strain Cork	9		9			
871		11662	Caprine arthritis encephalitis virus G63	6		6			
872		11665	Equine infectious anemia virus	93	112	93	112		
873		11670	Equine infectious anemia virus (CLONE 1369)		1		1		
874		11671	Equine infectious anemia virus (STRAIN WSU5)		19		19		
875		11673	Feline immunodeficiency virus		30		30		
876		11674	Feline immunodeficiency virus (isolate Petaluma)	2	4	2	4		
877		11675	Feline immunodeficiency virus (isolate San Diego)		1		1		
878		11676	Human immunodeficiency virus 1	236	499	276	514	40	15
879		11678	Human immunodeficiency virus type 1 BH10	2	27	2	27		
880		11679	Human immunodeficiency virus type 1 (CLONE 12)		7		7		
882		11682	Human immunodeficiency virus type 1 (BH5 ISOLATE)		1		1		
883		11683	Human immunodeficiency virus type 1 (Z2/CDC-Z34 ISOLATE)		1		1		
885		11685	HIV-1 M:B_ARV2/SF2	1	44	1	44		
886		11686	Human immunodeficiency virus type 1 (BRU ISOLATE)	1	4	1	4		
887		11687	Human immunodeficiency virus type 1 (CDC-451 ISOLATE)		3		3		
888		11688	Human immunodeficiency virus type 1 (JRCSF ISOLATE)	4	37	4	37		
889		11689	Human immunodeficiency virus type 1 (ELI ISOLATE)		7		7		
890		11690	Human immunodeficiency virus type 1 (SF33 ISOLATE)		3		3		
891		11691	Human immunodeficiency virus type 1 (SF162 ISOLATE)	2	1	2	1		
892		11694	Human immunodeficiency virus type 1 (JH3 ISOLATE)		4		4		
893		11695	Human immunodeficiency virus type 1 (NDK ISOLATE)		8		8		
894		11696	HIV-1 M:B_MN	11	27	11	27		
895		11697	Human immunodeficiency virus type 1 (MAL ISOLATE)		8		8		
896		11698	Human immunodeficiency virus type 1 (NEW YORK-5 ISOLATE)	2	2	2	2		
897		11699	Human immunodeficiency virus type 1 (OYI ISOLATE)		3		3		
898		11701	Human immunodeficiency virus type 1 (RF/HAT ISOLATE)	1	19	1	19		
899		11703	Human immunodeficiency virus type 1 (STRAIN UGANDAN / ISOLATE U455)		15		15		
900		11704	Human immunodeficiency virus type 1 (MFA ISOLATE)		2		2		
901		11705	Human immunodeficiency virus type 1 (WMJ2 ISOLATE)		1		1		
902		11706	HIV-1 M:B_HXB2R	13	17	15	17	2	

903		11708	Human immunodeficiency virus type 1 (ZAIRO 6 ISOLATE)		1		1		
904		11709	Human immunodeficiency virus 2	1	8	1	8		
905		11711	Simian immunodeficiency virus - mac		1		1		
906		11713	Human immunodeficiency virus type 2 (ISOLATE D194)		1		1		
907		11714	Human immunodeficiency virus type 2 (ISOLATE BEN)		12		12		
908		11715	Human immunodeficiency virus type 2 (ISOLATE CAM2)		2		2		
909		11716	Human immunodeficiency virus type 2 (ISOLATE D205,7)		2		2		
910		11717	Human immunodeficiency virus type 2 (ISOLATE GHANA-1)		7		7		
911		11718	Human immunodeficiency virus type 2 (ISOLATE SBLISY)		2		2		
912		11720	Human immunodeficiency virus type 2 (ISOLATE ROD)		2		2		
913		11723	Simian immunodeficiency virus		238		239		1
914		11730	Simian immunodeficiency virus (AGM3 ISOLATE)		1		1		
917		11733	Simian immunodeficiency virus (MM142-83 ISOLATE)		102		102		
918		11734	Simian immunodeficiency virus (MM251 ISOLATE)		1		1		
919		11735	Simian immunodeficiency virus - mac K6W		125		125		
920		11736	Simian immunodeficiency virus (K78 ISOLATE)		29		29		
921		11737	Simian immunodeficiency virus (F236/SMH4 ISOLATE) (SOOTY MANGABEY)		17		17		
922		11738	Simian immunodeficiency virus (PBJ/BC13 ISOLATE) (SOOTY MANGABEY)		2		2		
923		11742	Visna lentivirus (strain 1514)	1		1			
924		11743	Visna lentivirus (strain 1514 / clone LV1-1KS1)	4		4			
925		11746	Jaagsiekte sheep retrovirus	1		1			
926		11757	Mouse mammary tumor virus		12		12		
927		11764	Baboon endogenous virus strain M7	1		1			
928		11769	Feline leukemia virus strain A/Glasgow-1	6		6			
929		11780	Snyder-Theilen feline sarcoma virus	1		1			
930		11786	Murine leukemia virus	1	23	1	23		
931		11790	AKT8 murine leukemia virus	1		1			
932		11791	AKR (endogenous) murine leukemia virus		12		13		1
933		11795	Friend murine leukemia virus	6	53	6	53		
934		11801	Moloney murine leukemia virus		5		5		
935		11812	Murine sarcoma virus 3611	4		4			
936		11824	Gardner-Arnstein feline leukemia oncovirus B	13		13			
937		11827	Human endogenous retrovirus	1	1	1	1		
938		11861	Avian erythroblastosis virus	1		1			
939		11864	Avian leukosis virus	4		4			
940		11886	Rous sarcoma virus	4	4	4	4		

941		11901	Bovine leukemia virus	108	40	108	40		
943		11908	Human T-cell leukemia virus type I	236	280	236	280		
944		11909	Human T-lymphotropic virus 2	63	2	63	2		
945		11926	Human T-cell lymphotrophic virus type 1 (strain ATK)	30	118	30	118		
946		11927	Human T-cell lymphotrophic virus type 1 (Caribbean isolate)		6		6		
947		11928	Human T-cell lymphotrophic virus type 1 (isolate MT-2)	1		1			
948		11942	Simian retrovirus 1	1		1			
949	X	11963	Human spumaretrovirus			1		1	
950		11966	Aids-associated retrovirus		2		2		
951		11976	Rabbit hemorrhagic disease virus	4		4			
952		11978	Feline calicivirus	4	1	4	1		
953		11980	Feline calicivirus strain Japanese F4	6		6			
954		11981	Feline calicivirus strain F9	2		2			
955		11983	Norwalk virus	4	1	4	1		
956		11984	Southampton virus	1		1			
957		12022	Enterobacteria phage MS2	1		1			
958		12060	Echovirus E9	1		1			
959		12063	Human parechovirus 1	7		7			
960		12064	Enterovirus E	13		17		4	
961		12065	Bovine enterovirus strain VG-5-27	6		6			
962		12066	Coxsackievirus	1		1			
963		12067	Coxsackievirus A9	30		30			
964		12071	Coxsackievirus B1	12		12			
965		12072	Coxsackievirus B3	7	15	7	15		
966		12073	Coxsackievirus B4	17	51	17	51		
967		12075	Swine vesicular disease virus	1		1			
968		12076	Swine vesicular disease virus (STRAIN H/3 '76)	5		5			
969		12077	Swine vesicular disease virus (STRAIN UKG/27/72)	3		3			
970		12078	Echovirus E11	1		1			
971		12080	Human poliovirus 1	6	1	6	1		
972		12081	Human poliovirus 1 Mahoney	62	31	62	31		
973		12082	Human poliovirus 1 strain Sabin	7		7			
974		12086	Human poliovirus 3	5	2	5	2		
975		12088	Poliovirus type 3 (strains P3/LEON/37 AND P3/LEON 12A[1]B)	4	15	4	15		
976		12092	Hepatovirus A	26	22	26	22		
977		12098	Human hepatitis A virus Hu/Australia/HM175/1976	86	83	87	83	1	
978		12104	Encephalomyocarditis virus		1		1		
979		12107	Mengo virus	5	13	5	13		
980		12110	Foot-and-mouth disease virus	25	5	30	5	5	
981		12111	Foot-and-mouth disease virus - type A	3	6	3	6		

982		12112	Foot-and-mouth disease virus (strain A10-61)	8		8			
983		12113	Foot-and-mouth disease virus (strain A5)	3		3			
984		12114	Foot-and-mouth disease virus (strain A12)	21	1	21	1		
985		12115	Foot-and-mouth disease virus (strain A24 Cruzeiro)	17	32	17	32		
986		12116	Foot-and-mouth disease virus - type C	6	26	6	26		
987		12117	Foot-and-mouth disease virus (strain C3 Indaial)	2		2			
988		12118	Foot-and-mouth disease virus - type O	44	8	45	8	1	
989		12120	Foot-and-mouth disease virus (strain C1-Santa Pau)	1		1			
990		12121	Foot-and-mouth disease virus C1	1	4	1	4		
991		12123	Foot-and-mouth disease virus - type SAT 3		1		1		
992		12124	Theiler's encephalomyelitis virus	1	18	1	18		
993		12125	Theiler's encephalomyelitis virus (STRAIN BEAN 8386)	16	52	16	52		
994		12126	Theiler's encephalomyelitis virus (STRAIN DA)	3	2	3	2		
995		12130	Human rhinovirus A2	11		11			
996		12131	Rhinovirus B14	15	1	15	1		
997		12132	Human rhinovirus A89	3		3			
998		12134	Human rhinovirus 1A		19		19		
999		12146	Tomato bushy stunt virus (STRAIN BS-3)	3		3			
1000		12161	Beet yellows virus	5		5			
1001		12162	Citrus tristeza virus	8		8			
1002		12211	Plum pox virus	1		1			
1003		12213	Plum pox virus isolate NAT		1		1		
1004		12216	Potato virus Y	2		2			
1005		12219	Potato virus Y strain N	1		1			
1006		12220	Potato virus Y strain O	7		7			
1007		12232	Zucchini yellow mosaic virus	1		1			
1008		12242	Tobacco mosaic virus	36	13	142	13	106	
1009		12243	Tobacco mosaic virus (vulgare)	1		1			
1010		12246	Tobacco mosaic virus strain Dahlemense	2		2			
1011		12260	Bean pod mottle virus	2		2			
1012		12264	Cowpea mosaic virus		1		1		
1013		12305	Cucumber mosaic virus	1		1			
1014		12455	Borna disease virus	8	4	8	4		
1015		12461	Hepatitis E virus	153	76	153	91		15
1016		12475	Hepatitis delta virus	56	19	56	66		47
1017		12509	Human herpesvirus 4 type 2	2	10	2	10		
1018		12557	Seoul virus 80-39		3		3		
1019		12618	Chicken anemia virus	3		3			
1020		12637	Dengue virus	51	553	52	588	1	35

1021		12639	Duck hepatitis B virus	262	20	262	20		
1022		12643	Ectromelia virus		6		45		39
1023		12663	Feline coronavirus		1		1		
1024		12701	Human astrovirus 2	2		2			
1025		12750	Visna/maedi virus EV1	1		1			
1026		12760	Murine hepatitis virus strain 4		5		5		
1027		12814	Respiratory syncytial virus		2	5	5	5	3
1028		12870	Variola major virus		17		17		
1029		13101	Juniperus ashei	13		13			
1030		13187	Parietaria officinalis	2		2			
1031		13286	Theromyzon tessulatum	1		1			
1032		13373	Burkholderia mallei	1	49	3	49	2	
1033		13415	Chamaecyparis obtusa	5	68	5	68		
1034		13451	Corylus avellana	27	57	27	57		
1035		13469	Cupressus sempervirens		8		8		
1036		13557	Hapalemur griseus		1		1		
1037		13616	Monodelphis domestica	1	4	1	4		
1038		13618	Myrmecia pilosula	2		2			
1039	X	13677	Scomber scombrus			1		1	
1040		13687	Sphingomonas	1	4	1	4		
1042		15368	Brachypodium distachyon	1		1			
1043		15957	Phleum pratense	64	1158	64	1158		
1044		16719	Juglans nigra	1		1			
1045		27990	Plasmodium vivax-like sp.	3	1	3	1		
1046		28038	Lactobacillus curvatus		1		1		
1047		28080	Campylobacter upsaliensis	3		3			
1048		28108	Alteromonas macleodii		1		1		
1049		28130	Prevotella disiens		1		1		
1050	X	28131	Prevotella intermedia				2		2
1052	X	28172	Vibrio metschnikovii			1		1	
1053		28227	Mycoplasma penetrans	40		40			
1054		28276	Human adenovirus 15	1		1			
1055		28280	Human adenovirus E4	1		1			
1056		28282	Human adenovirus 12	11	3	11	3		
1057		28284	Human adenovirus 40	2	1	2	1		
1058		28285	Human adenovirus 5	26	185	27	186	1	1
1059		28295	Porcine epidemic diarrhea virus	5		13		8	
1060		28300	Heron hepatitis B virus		1		1		
1061		28314	Aleutian mink disease virus	10		10			
1062		28327	Murine rotavirus		3		3		
1063		28344	Porcine reproductive and respiratory syndrome virus	87	95	90	95	3	
1064		28375	Soil-borne wheat mosaic virus	1		1			
1065		28448	Komagataeibacter xylinus		1		1		

1066		28450	Burkholderia pseudomallei	14	9	19	9	5	
1067		28479	Phalaris aquatica		12		12		
1068		28869	Ovine respiratory syncytial virus	1		1			
1069		28871	Taterapox virus		4		4		
1070		28873	Camelpox virus		2		2		
1071		28875	Rotavirus A	1		2		1	
1072		28901	Salmonella enterica		141		141		
1073		28903	Mycoplasma bovis	21		21			
1074		28909	Cynodon dactylon	27	48	27	48		
1075	X	29159	Crassostrea gigas			7		7	
1076		29176	Neospora caninum	2	17	2	17		
1077		29271	Dasheen mosaic virus	1		1			
1078		29292	Pyrococcus abyssi		1		1		
1079		29320	Paenarthrobacter nicotinovorans	1		1			
1080		29339	Bacillus thuringiensis serovar kurstaki	3		3			
1081		29362	Ruminiclostridium papyrosolvens		1		1		
1082		29371	Ruminiclostridium cellobioparum subsp. termitidis	1		1			
1083		29388	Staphylococcus capitis	1		1			
1084		29430	Acinetobacter haemolyticus	1		1			
1085		29442	Pseudomonas tolasi		1		1		
1086		29447	Xanthomonas albilineans		1		1		
1087		29459	Brucella melitensis	17	94	19	95	2	1
1088		29461	Brucella suis	1	8	1	8		
1089		29477	Salmonella enterica subsp. enterica serovar Essen	1		1			
1090		29491	Aeromonas salmonicida subsp. salmonicida		1		1		
1091		29507	Leptospira kirschneri	1		1			
1092		29518	Borreliella afzelii	5	1	6	1	1	
1093		29519	Borreliella garinii	6	29	6	29		
1094		29661	Anthoxanthum odoratum		3		3		
1095		29679	Holcus lanatus	14	3	14	3		
1096		29715	Ambrosia psilostachya		10		10		
1097		29760	Vitis vinifera	1		1			
1098		29780	Mangifera indica	1		1			
1099	X	29916	Fusarium sp.			3		3	
1100		29918	Cladosporium herbarum		18		18		
1101		29960	Penaeus indicus	2		2			
1102		30069	Anopheles stephensi	1		1			
1104		30538	Vicugna pacos	1		1			
1105		31271	Plasmodium chabaudi chabaudi		3		3		
1106		31273	Plasmodium vivax strain Belem	6	31	6	31		
1107		31276	Perkinsus marinus		1		1		
1108		31285	Trypanosoma brucei gambiense	2		2			

1109		31286	Trypanosoma brucei rhodesiense	1	9	1	9		
1110		31330	Ephydatia fluviatilis		1		1		
1111		31512	Hepatitis B virus adr/mutant		1		1		
1112		31525	Human herpesvirus 4 strain CAO		1		1		
1113		31531	Vaccinia virus L-IPV		8		8		
1114		31545	Human adenovirus D8	1	1	1	1		
1115		31552	Human papillomavirus type 6	12	4	12	4		
1116		31560	Infectious bursal disease virus E	1		1			
1117		31569	Human rotavirus (serotype 2 / strain RV-5)	1		1			
1118		31604	Small ruminant morbillivirus	13	31	13	31		
1119		31608	Simian virus 5 (isolate canine/CPI+)	1		1			
1120		31611	Bovine respiratory syncytial virus (strain 391-2)	3		3			
1121		31615	Tacaribe virus strain V5		1		1		
1122		31616	Tacaribe virus strain V7		1		1		
1123		31621	Four Corners hantavirus	2	8	2	8		
1124		31631	Human coronavirus OC43		1		1		
1125		31634	Dengue virus 2 Thailand/16681/84	32	62	32	62		
1126		31635	Dengue virus 2 16681-PDK53	4	32	4	80		48
1127	X	31636	Dengue virus 2 China/D2-04				5		5
1128	X	31637	Dengue virus 2 Thailand/TH-36/1958				4		4
1129		31641	Yellow fever virus 1899/81		36		36		
1130		31644	Hepatitis C virus HCV-KF	1	1	1	1		
1131		31645	Hepatitis C virus (isolate Taiwan)	3	15	3	15		
1132		31646	Hepatitis C virus subtype 1a	202	399	206	399	4	
1133		31647	Hepatitis C virus subtype 1b	608	293	608	293		
1134		31649	Hepatitis C virus subtype 2a	80	22	80	22		
1135		31650	Hepatitis C virus subtype 2b	103	4	103	4		
1136		31653	Hepatitis C virus subtype 4a	1	1	1	1		
1137		31654	Hepatitis C virus subtype 5a	1	1	1	1		
1138		31655	Hepatitis C virus subtype 6a		1		1		
1139		31678	Human immunodeficiency virus type 1 (WMJ1 isolate)		16		16		
1141		31682	Simian immunodeficiency virus - mac1A11		18		18		
1142		31683	Simian immunodeficiency virus - stm		7		7		
1143		31684	Simian immunodeficiency virus (isolate AGM / clone GRI-1)		2		2		
1145		31704	Coxsackievirus A16	4		4			
1146		31708	Human rhinovirus A16		30	9	30	9	
1147		31715	Bean-pod mottle virus (strain Kentucky G7)	9	1	9	1		
1148		31721	Beet necrotic yellow vein virus	10		10			
1149		31767	Hepatitis E virus (strain Burma)	160		160			
1150		31768	Hepatitis E virus (strain Mexico)	31		31			
1151		32008	Burkholderia	1		1			

1152		32019	Campylobacter fetus subsp. fetus	3		3			
1153		32022	Campylobacter jejuni subsp. jejuni	2		2			
1154		32025	Helicobacter hepaticus		1		1		
1155		32049	Synechococcus sp. PCC 7002		1		1		
1156		32201	Carya illinoiensis	19		19			
1157		32278	Metapenaeus ensis	1	6	1	6		
1158		32603	Human betaherpesvirus 6A	2	7	2	7		
1159		32604	Human betaherpesvirus 6B	2	1394	2	4483		3089
1160		32605	Buffalopox virus		1		1		
1161		32606	Rabbitpox virus		2		2		
1162		32614	Convict Creek 107 virus	1	3	1	3		
1163	X	32630	synthetic construct				1		1
1164		32644	unidentified		22073		22559		486
1165	X	33090	Viriplantae			1		1	
1166		33127	Parietaria judaica	65	2	65	2		
1167		33178	Aspergillus terreus	2		2			
1168		33703	Suid herpesvirus 1 strain Kaplan	4		4			
1169		33706	Caviid betaherpesvirus 2	3	3	3	3		
1170		33708	Murid gammaherpesvirus 4	1	53	1	53		
1171		33717	Bluetongue virus (serotype 13 / isolate USA)	2		2			
1172		33718	Bluetongue virus (serotype 17 / isolate USA)	4		4			
1173		33727	Marburg virus - Musoke, Kenya, 1980	3	84	3	84		
1174		33728	Lake Victoria marburgvirus - Popp	2	15	3	15	1	
1175		33734	Feline infectious peritonitis virus (strain 79-1146)	15	14	15	14		
1176		33741	Dengue virus 1 Singapore/S275/1990		245		245		
1177		33745	Hepatitis C virus genotype 4	1	10	1	10		
1178		33746	Hepatitis C virus genotype 5		2		2		
1179		33747	Simian T-lymphotropic virus 1		14		14		
1180		33758	Echovirus		1		1		
1181		33892	Mycobacterium tuberculosis variant bovis BCG	12	146	12	147		1
1182		33934	Anoxybacillus flavithermus		1		1		
1184		33990	Rickettsia bellii	1		1			
1185		34054	Yersinia enterocolitica (type O:8)		1		1		
1186		34245	Zinnia elegans		1		1		
1187	X	34613	Ixodes ricinus			1		1	
1188		34631	Rhipicephalus appendiculatus	1		1			
1189		34632	Rhipicephalus sanguineus	1		1			
1190		34828	Eulemur mongoz	1		1			
1191		34862	Otospermophilus beecheyi		1		1		
1192		35241	Lactococcus phage Tuc2009	1		1			
1193		35258	Lambdapapillomavirus 2		25		25		

1194		35269	Woodchuck hepatitis virus	4	6	4	6		
1195		35275	Murine endogenous retrovirus		13		13		
1196		35288	Grapevine virus A	12		12			
1197		35292	Foot-and-mouth disease virus - type SAT 2	1	1	1	1		
1198		35297	Striped jack nervous necrosis virus	1		1			
1199		35305	California encephalitis virus		1		1		
1200		35327	Bluetongue virus 1	4		4			
1201		35329	Bluetongue virus 11	6		6			
1202		35330	Bluetongue virus 13	1		1			
1203		35331	Bluetongue virus 15	7		7			
1204		35336	Rotavirus G4		1		1		
1205		35345	Lactococcus phage TP901-1	3		3			
1206		35670	Naja naja	3		3			
1207		35725	Macrophomina phaseolina		1		1		
1208		35788	Rickettsia africae		1		1		
1209		35791	Rickettsia massiliae		1		1		
1210		35793	Rickettsia sibirica		4		4		
1211		35795	Ehrlichia muris	2	3	2	3		
1212		36329	Plasmodium falciparum 3D7	225	270	1166	270	941	
1213		36351	Human herpesvirus 6 strain Z29	1	146	1	146		
1214		36352	Human herpesvirus 4 type 1	4	14	4	14		
1215		36372	Feline immunodeficiency virus (strain UK8)		1		1		
1216		36374	Visna/maedi virus EV1 KV1772	2		2			
1217		36375	Human immunodeficiency virus type 1 (KB-1 isolate)		2		2		
1218		36382	Venezuelan equine encephalitis virus (strain 3880)		1		1		
1219		36386	Louping ill virus (strain 31)	1		1			
1220		36409	Rinderpest virus (strain RBOK)	33	5	33	5		
1221		36412	Human parainfluenza 1 virus (strains A1426 / 86-315 / 62M-753)		1		1		
1222		36418	Influenza A virus (A/chicken/Brescia/1902(H7N7))		1		1		
1223		36420	H1N1 swine influenza virus		13		13		
1224		36421	African horse sickness virus 4	42	4	42	4		
1225		36439	Bovine rotavirus strain NCDV/G6	1		1			
1226		36470	Streptococcus sp. 'group A'	21		21			
1227		36596	Prunus armeniaca	4		4			
1228		36809	Mycobacteroides abscessus		19		19		
1229		36826	Clostridium botulinum A	46		46			
1230		36827	Clostridium botulinum B	29		29			
1231		36829	Clostridium botulinum D	2		2			
1232		36830	Clostridium botulinum E	3	3	3	3		
1233		36831	Clostridium botulinum F	3		3			
1234		36855	Brucella canis		4		4		

1235		36911	Clavispora lusitaniae	1		1			
1236		36936	Lepidoglyphus destructor	5	10	5	10		
1238		37111	Human papillomavirus 28		1		1		
1239		37112	Human papillomavirus 29		1		1		
1240		37115	Human papillomavirus type 59	2	1	2	1		
1241		37120	Human papillomavirus type 67	2		2			
1242		37121	Human papillomavirus type 69		1		1		
1243		37124	Chikungunya virus	78	10	78	22		12
1244		37128	Potato mop-top virus	8		8			
1245		37132	Rabies virus Ontario fox	3		3			
1246		37137	Simian rotavirus A/SA11-both	20	2	20	2		
1247		37207	Rio Segundo hantavirus	1		1			
1248		37296	Human gammaherpesvirus 8	26	488	26	488		
1249		37325	Muscovy duck parvovirus	11		11			
1250		37326	Nocardia brasiliensis	6		6			
1251		37329	Nocardia farcinica		1		1		
1252		37347	Tupaia belangeri		1		1		
1253		37546	Glossina morsitans morsitans	2		2			
1255		37762	Escherichia coli B	1	1	1	1		
1256		38020	marmosets	3		3			
1257		38033	Chaetomium globosum	1		1			
1258		38171	Avian reovirus strain S1133	5		6		1	
1259		38251	Goose parvovirus	9		9			
1260		38323	Bartonella henselae	1		1			
1261	X	38347	Leptospira interrogans serovar Hardjo-prajitno			1		1	
1262		38832	Micromonas		1		1		
1263		38873	Fraxinus excelsior		3		3		
1264		38973	Influenza A virus (A/Memphis/4/1973(H3N2))		1		2		1
1265		39002	Puumala virus sotkamo/v-2969/81	196		196			
1266		39015	Human T-cell lymphotropic virus type 1 (african isolate)		2		2		
1267		39054	Enterovirus A71	111	1	128	1	17	
1269		39113	Hepatitis GB virus B		4		4		
1270		39152	Methanococcus maripaludis	1		1			
1271		39414	Plantago lanceolata		2		2		
1272		39442	Mus musculus musculus		1		1		
1273		39457	Human papillomavirus type 70		1		1		
1275		39803	Escherichia virus Qbeta		2		2		
1276		39947	Oryza sativa Japonica Group	5	1	5	1		
1277		40051	Bluetongue virus	12	1	12	1		
1278		40214	Acinetobacter johnsonii		1		1		
1279		40271	Hepatitis C virus genotype 2	41	6	42	6	1	
1280		40674	Mammalia	6		6	2		2

1281		40697	Blomia tropicalis	19	6	19	6		
1282		41514	Salmonella enterica subsp. arizonae serovar 62:z4,z23:-		4		4		
1283		41856	Hepatitis C virus genotype 1	4	177	4	177		
1284		41857	Influenza A virus H3N2	2	50	3	50	1	
1285	X	41858	Simian foamy virus-gorilla			1		1	
1286		41953	Pseudo-nitzschia	1		1			
1287		42097	Isla Vista hantavirus	1	2	1	2		
1288		42182	Hepatitis C virus genotype 6		7		7		
1289		42229	Prunus avium	3	1	3	1		
1290		42345	Phoenix dactylifera		3		3		
1291		42358	Hantavirus Monongahela-3		5		5		
1292		42764	Oliveros mammarenavirus		2		2		
1293	X	42769	Coxsackievirus A10			3		3	
1294		42782	Coxsackievirus A20	1		1			
1295		42789	Enterovirus D68	1		3		2	
1296		42792	Hepatitis C virus subtype 3g	1		1			
1297		42862	Rickettsia felis		1		1		
1298		42897	Shigella flexneri 2a	35		35			
1299		43304	Mycobacterium peregrinum	2		2			
1300		43765	Corynebacterium amycolatum		1		1		
1301		43767	Rhodococcus hoagii	18	3	18	3		
1302		43852	Toxicodendron	1	1	1	1		
1303	X	43853	Toxicodendron radicans			1		1	
1304		44026	Sepik virus		1		1		
1305		44088	Canarypox virus		8		8		
1306		44104	Vibrio cholerae 569B	37		37			
1307		44271	Leishmania chagasi	3		3			
1308		44275	Leptospira interrogans serovar Copenhageni	2		2			
1309		44276	Leptospira interrogans serovar Pomona	2	3	2	3		
1310		44561	Murine type C retrovirus		1		1		
1311		44689	Dictyostelium discoideum	1	1	1	1		
1312		44755	New York hantavirus		2		2		
1313		45029	Bluetongue virus 16	3		3			
1314		45201	Mannheimia haemolytica serotype 1	82		82			
1315		45219	Guanarito mammarenavirus		842		842		
1316		45240	Human papillomavirus type 68		1		1		
1317		45409	Feline immunodeficiency virus (isolate wo)	3		3			
1318		45410	Hepatitis B virus adw4/Brazil/isolate w4b		12		12		
1319		45455	Macacine gammaherpesvirus 4		27		27		
1320		45582	[Candida] saitoana	1		1			
1321		45617	Human endogenous retrovirus K	14		14			
1322		45659	Human adenovirus B3	29	2	29	2		

1324		46015	Autographa californica nucleopolyhedrovirus		1		1		
1325		46221	Porcine circovirus	1	49	1	49		
1326		46242	Spodoptera litura nucleopolyhedrovirus		2		2		
1327		46245	Drosophila pseudoobscura pseudoobscura	1		1			
1328		46290	Foot-and-mouth disease virus C3	4	1	4	1		
1329		46457	Cycloclasticus oligotrophus		1		1		
1331		46506	Bacteroides stercoris		1		1		
1332		46771	Simian virus 12	1		1			
1333		46835	Fasciola gigantica	3		3			
1334		46919	Whitewater Arroyo mammarenavirus		349		349		
1335		46920	Rio Mamore hantavirus	1	1	1	1		
1336		46921	Human adenovirus D13	1		1			
1337		46941	Human adenovirus 46	1		1			
1340		47929	Macacine betaherpesvirus 3		99		99		
1341		48409	Salmonella enterica subsp. enterica serovar Virchow		1		1		
1342		48483	Reclinomonas americana		1		1		
1343		48935	Novosphingobium aromaticivorans		1		1		
1344		49011	Hesperocyparis arizonica	2	6	2	6		
1346		50557	Insecta	7		7			
1347		51031	Necator americanus	17		17			
1348		51033	Human papillomavirus type 73		1		1		
1349		51240	Juglans regia	34	19	34	19		
1350		53179	Porcine rubulavirus	3		3			
1351		53182	Feline foamy virus	7		7			
1352		53258	Variola minor virus		93		93		
1353		53751	Echinacea purpurea	1		1			
1354		54290	GB virus C	16		16			
1355		54315	Bovine viral diarrhea virus 2	1		1			
1356		54388	Salmonella enterica subsp. enterica serovar Paratyphi A		1		4		3
1357		54390	Micrurus corallinus	123		125		2	
1358		55097	Mobala mammarenavirus	1		1			
1360		55429	Megathura crenulata	1		1			
1361		55513	Pistacia vera		6		6		
1362		55532	Influenza A virus (A/swine/Quebec/1192/1986(H1))		1		1		
1363		55601	Vibrio anguillarum	1		1			
1364		55635	Inula helenium		1		1		
1365		55951	Grapevine leafroll-associated virus 3	1		1			
1366		56636	Aeropyrum pernix	3	2	3	2		
1367		57068	Acanthisitta chloris		1		1		
1368		57266	Plasmodium falciparum 7G8	42	52	42	52		
1369		57270	Plasmodium falciparum Palo Alto/Uganda	38		38			

1370		57278	Human herpesvirus 7 strain JI		1		1		
1372		57372	Mycoplasma suis	3		3			
1373		57482	European bat 1 lyssavirus		1		1		
1374		57486	Mus musculus molossinus		1		1		
1375		57667	Simian-Human immunodeficiency virus	1		1			
1376		57678	Leptospira interrogans serovar Lai	10	10	10	10		
1377		58024	Spermatophyta	4	1	4	1		
1378		58216	Loxosceles gaucho	1		1			
1379		58217	Loxosceles laeta	2		2			
1380		58218	Loxosceles intermedia	83		83			
1381		59201	Salmonella enterica subsp. enterica		18		18		
1382		59202	Salmonella enterica subsp. salamae		1		1		
1383		59203	Salmonella enterica subsp. arizonae		1		1		
1384		59205	Salmonella enterica subsp. houtenae		1		1		
1385		59375	Influenza A virus (A/South Carolina/1/1918(H1N1))	8	1	9	1	1	
1386		59538	Pantholops hodgsonii		1		1		
1387		59729	Taeniopygia guttata		1		1		
1388		59799	Angomonas deanei		2		2		
1389		60189	Rhipicephalus decoloratus	5		5			
1391		60552	Burkholderia vietnamiensis		2		2		
1392		60876	Pixuna virus		1		1		
1393		60879	Cabassou virus		1		1		
1394		60893	Desulfobacca acetoxidans		1		1		
1395		61466	Gnathostoma binucleatum	10		10			
1396		61673	Porcine endogenous retrovirus	2	11	2	11		
1397		62319	Halococcus saccharolyticus		1		1		
1398		62330	Fagopyrum tataricum	5		5			
1399		62446	Influenza A virus (A/Argentina/3779/94(H3N2))		1		1		
1400		62478	Influenza A virus (A/Kitakyushu/93(H3N2))		1		1		
1401		62488	Influenza A virus (A/Nanchang/58/1993(H3N2))		1		1		
1402		62496	Influenza A virus (A/New_York/17/94(H3N2))		1		1		
1403		62503	Influenza A virus (A/Ohio/3/95(H3N2))		1		1		
1404		62512	Influenza A virus (A/Shangdong/5/94(H3N2))		1		1		
1405		62541	Influenza A virus (A/Christchurch/2/1988(H3N2))		1		1		
1406		62549	Influenza A virus (A/Fukuoka/C29/1985(H3N2))	5		5			
1407		62559	Influenza A virus (A/Los Angeles/1987(H3N2))	5		5			
1408		62564	Influenza A virus (A/New_York/15/94(H3N2))		1		1		
1409		62575	Influenza A virus (A/Sichuan/2/1987(H3N2))		5		5		
1410		62596	Influenza A virus (A/USSR/26/1985(H3N2))		1		1		

1412		63106	Influenza A virus (A/Wuhan/359/1995(H3N2))	5		5			
1413		63221	Homo sapiens neanderthalensis		1		1		
1414		63330	Hendra henipavirus	9	2	9	2		
1415		63363	Aquifex aeolicus	2	3	2	3		
1416		63421	Swine hepatitis E virus	10		10			
1417		63673	Turbo cornutus	2		2			
1418		63737	Nostoc punctiforme PCC 73102		2		2		
1419		63746	Hepatitis C virus (isolate H77)	150	208	165	208	15	
1420		64284	Saboya virus		1		1		
1421		64289	Carey Island virus		2		2		
1422		64293	Tembusu virus	2	10	2	10		
1423		64320	Zika virus	53	193	112	630	59	437
1424		64382	Human Endogenous Retrovirus IDDMK1,2-22	3		3			
1425		64495	Rhizopus oryzae	4	1	4	1		
1426		65690	AK7 murine leukemia virus		1		1		
1427		65699	Neisseria meningitidis serogroup A	5		5			
1428		65743	Blackcurrant reversion virus	2		2			
1429		66692	Bacillus clausii KSM-K16		1		1		
1430	X	67351	Streptomyces californicus			1		1	
1431		68621	Classical swine fever virus strain Riems		5		5		
1432		68887	Torque teno virus	5	94	5	94		
1433		68909	Deinococcus geothermalis	1		1			
1434		69008	Juniperus oxycedrus		3		3		
1435		69153	Human enterovirus 71 (strain BCR)	1		1			
1436		69156	Murine cytomegalovirus (strain K181)	2	14	2	14		
1437		69245	Lechiguanas virus		9		9		
1439		69247	Oran virus		2		2		
1440		69248	Pergamino virus		1		1		
1441		70146	Measles virus strain Edmonston-B	2	78	2	78		
1442		70149	Measles virus strain Edmonston- Zagreb	1		1			
1443		70175	Androctonus australis hector	24		24			
1444		70203	Vibrio virus fs1		1		1		
1445		70865	Murine rotavirus EDIM		27		27		
1446		71238	Pseudomonas sp. G-179		1		1		
1447		71421	Haemophilus influenzae Rd KW20		3		3		
1450		72132	Rotavirus G1	1	1	1	1		
1451		72539	Physalis mottle virus	2		2			
1452		72556	Achromobacter piechaudii	1		1			
1453		72590	Salmonella sp. 'group B'	6		6			
1454		72664	Eutrema salsugineum	2		2			
1455		73036	Rotavirus G3		1		1		

1456		73239	Plasmodium yoelii yoelii	22	42	22	42		
1457		73482	Foot-and-mouth disease virus (strain O1)	38	1	38	1		
1458		73484	Human immunodeficiency virus type 2 (isolate KR)		3		3		
1459		74138	Pseudomonas sp. DJ-12		1		1		
1460		74537	Vladivostok virus	1		1			
1462		74722	Stachybotrys chartarum	11		11			
1463		74942	Hantavirus CRF355		1		1		
1465		75922	Mycolicibacterium tusciae		2		2		
1468		76777	Malassezia sympodialis	1		1			
1469		76832	Myroides odoratimimus		1		1		
1470		76869	Pseudomonas putida GB-1		1		1		
1472		77009	Hordeum vulgare subsp. spontaneum		2		2		
1473	X	77095	Prevotella bryantii				2		2
1474	X	77153	Muscovy duck reovirus			1		1	
1475	X	77643	Mycobacterium tuberculosis complex				5		5
1476		78245	Xanthobacter autotrophicus Py2		1		1		
1477		79692	Human respiratory syncytial virus B1	1	25	1	25		
1478		79695	Influenza A virus (A/Memphis/1/71H-A/Bellamy/42N)		1		1		
1479	X	79698	Merluccius bilinearis			1		1	
1480		79889	Bovine herpesvirus type 1.1	2		2			
1481		79923	Clonorchis sinensis	2	1	2	1		
1482		80365	Laminaria digitata	2		2			
1483		80859	Streptomyces ribosidificus		1		1		
1484		80956	Pomacentrus moluccensis		1		1		
1485		81475	Frateuria aurantia	1		1			
1486		81847	Trichophyton quinckeanum	1		1			
1487		81985	Capsella rubella	1		1			
1488	X	82070	Drimia maritima			1		1	
1489		82300	Adeno-associated virus - 5	9		9			
1490		82372	Influenza A virus (A/Sydney/05/97-like(H3N2))		1		1		
1491		82470	Bovine viral diarrhea virus strain Oregon C24V	5	3	5	3		
1492		82639	Coxsackievirus B2	2		2			
1493		82659	Sapporo virus-Manchester		1		1		
1494		82823	Bovine respiratory syncytial virus strain lelystad	1		1			
1495		82824	Bovine respiratory syncytial virus strain snook	1	75	1	75		
1496		82830	Epstein-barr virus strain ag876	14	1	16	1	2	
1497		82831	Equid herpesvirus type 2 strain 86/87	1		1			
1499		83192	Topografov hantavirus	1		1			
1500		83206	Influenza A virus (A/swine/Scotland/410440/94(H1N2))		5		5		

1501		83262	Mycobacteroides immunogenum		5		5		
1502		83331	Mycobacterium tuberculosis CDC1551		42		42		
1503		83332	Mycobacterium tuberculosis H37Rv	62	964	62	973		9
1504		83333	Escherichia coli K-12	28	19	33	19	5	
1505		83334	Escherichia coli O157:H7		123	3	123	3	
1506		83455	Myxococcus stipitatus		1		1		
1507		83554	Chlamydia psittaci	86	2	102	6	16	4
1508		83555	Chlamydia abortus	12		32		20	
1509		83556	Chlamydia felis	3		12		9	
1510		83557	Chlamydia caviae	6		14		8	
1511		83558	Chlamydia pneumoniae	84	24	110	24	26	
1512		83559	Chlamydia suis	4		19		15	
1513		83560	Chlamydia muridarum	12	3	17	3	5	
1514		83810	Thosea asigna virus		1		1		
1515		85106	Adeno-associated virus - 1		11		11		
1516		85223	Laurus nobilis		1		1		
1517		85552	Scylla paramamosain	7		88		81	
1518		85569	Salmonella enterica subsp. enterica serovar Typhimurium str. DT104	1		1			
1519		85698	Achromobacter xylosoxidans	1		1			
1520		85708	Porcine circovirus 2	33	1	34	1	1	
1521		85709	Porcine circovirus type 2-B	6		6			
1522		85777	Agelas mauritiana		1		1		
1523		85962	Helicobacter pylori 26695	40	10	40	10		
1524		85963	Helicobacter pylori J99		53		53		
1525		85991	Chlamydia pecorum	116		142		26	
1526		86107	Coxsackievirus A6	1		1			
1527		86600	Discosoma sp.		1		1		
1528		86782	Amur virus		35		35		
1530		87883	Burkholderia multivorans	1	2	1	2		
1531		88036	Selaginella moellendorffii		1		1		
1532		88085	Lachesis stenophrys	13		13			
1533		88086	Protobothrops elegans	7		7			
1534		88087	Protobothrops flavoviridis	3		3			
1535		88103	Influenza A virus (A/Hong Kong/532/1997(H5N1))		1		1		
1536		88104	Influenza A virus (A/Hong Kong/483/1997(H5N1))	3	10	3	10		
1537		88776	Influenza A virus (A/Brevig Mission/1/1918(H1N1))		1		1		
1538		89169	Influenza A virus (A/Chicken/Pennsylvania/13552-1/98 (H7N2NSB))	1		1			
1539		89172	Influenza A virus (A/quail/Arkansas/16309-7/94 (H7N3NSA))	1		1			
1541		89462	Bubalus bubalis	7	1	7	1		
1543		90370	Salmonella enterica subsp. enterica serovar Typhi	15	111	15	112		1

1544		90371	Salmonella enterica subsp. enterica serovar Typhimurium	16	76	16	76		
1545		91465	Pseudomonas sp. MIS38		1		1		
1546	X	92050	Macruronus magellanicus			2		2	
1547		92652	Shrimp white spot syndrome virus	3		3			
1548		93061	Staphylococcus aureus subsp. aureus NCTC 8325	5	1	5	1		
1549		93062	Staphylococcus aureus subsp. aureus COL	17	1	17	1		
1550		93621	Heteropneustes fossilis		1		1		
1551		93678	TTV-like mini virus		1		1		
1552		93838	Influenza A virus (A/goose/Guangdong/1/1996(H5N1))	1	9	1	9		
1553		94432	Human rotavirus MP409	1	1	1	1		
1554		94966	Bluetongue virus 12	15		15			
1555		94967	Bluetongue virus 4	7		7			
1557		95486	Burkholderia cenocepacia	1	1	1	1		
1558		95602	Eriocheir sinensis	10		10			
1559		95888	Influenza A virus (A/mallard duck/PA/10218/84(H5N2))	8		8			
1563		97348	Influenza A virus (A/Chicken/Hong Kong/G23/97(H9N2))		1		1		
1564		97353	Influenza A virus (A/Chicken/Hong Kong/739/94(H9N2))		1		1		
1565		97477	Acetomicrobium mobile		1		1		
1566		98360	Salmonella enterica subsp. enterica serovar Dublin		2		2		
1567		99287	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2		77		78		1
1568		99586	Echis ocellatus	5		5			
1569		99875	Leishmania donovani donovani	1		1			
1570		99883	Tetraodon nigroviridis		2		2		
1571		100226	Streptomyces coelicolor A3(2)	1	1	1	1		
1572		100835	Influenza A virus (A/Chicken/Hong Kong/258/97 (H5N1))	1		1			
1573		101350	Porcine rotavirus strain A253	2		2			
1574		102617	Helicobacter pylori SS1	3	3	4	3	1	
1575		102793	H5N1 subtype	27	36	27	36		
1576		102796	H9N2 subtype	1		2		1	
1577		102862	Proteus penneri	1		1			
1578		103448	Pleistophora sp. LS		1		1		
1579		103903	Coxsackievirus B3 (strain Nancy)	13	30	13	30		
1580		103905	Coxsackievirus B4 (strain E2)	7	41	7	41		
1581		103906	Coxsackievirus B4 (strain JVB / Benschoten / New York/51)		76		76		
1582		103920	Guinea pig cytomegalovirus (strain 22122 / ATCC VR682) (GPCMV)	1		1			
1583		103929	Rabies virus strain Pasteur vaccin	2	1	2	1		
1584		103930	Rhesus cytomegalovirus strain 68-1		18		18		
1585		104102	Acetobacter tropicalis		1		1		
1586		105751	Aeromonas bestiarum		1		1		

1587		106820	Hepatitis B virus subtype adr	23	25	23	25		
1588		106821	Hepatitis B virus subtype adw	17	75	17	76		1
1589		107404	Influenza B virus (B/Beijing/184/93)		1		1		
1590		107406	Influenza B virus (B/Chiba/447/98)		1		1		
1591		107493	Influenza A virus (A/Cordoba/3278/96(H3N2))		1		1		
1592		107558	Influenza A virus (A/France/75/97(H3N2))		1		1		
1593		107819	Clostridium perfringens D	44		45		1	
1594		108098	Human mastadenovirus B	1		1			
1595		110195	Foot-and-mouth disease virus - type Asia 1	10	3	10	3		
1596		112509	Hordeum vulgare subsp. vulgare		18		18		
1597		114727	H1N1 subtype	15	44	16	49	1	5
1598		114729	H2N2 subtype		1		1		
1599		114742	Pythium insidiosum	2		2			
1600		115711	Chlamydia pneumoniae AR39	1		1			
1601		115713	Chlamydia pneumoniae CWL029		48	34	48	34	
1602		117125	Cucumber mosaic virus (strain Pepo)	1		1			
1603	X	117187	Fusarium verticillioides			1		1	
1604		117204	African horse sickness virus 3	21		21			
1605		119210	H3N2 subtype	5	23	6	23	1	
1606		119211	H3N8 subtype	1		1			
1607		119218	H7N7 subtype		1		1		
1608	X	119220	H5N2 subtype			1		1	
1609		119602	Streptococcus dysgalactiae subsp. equisimilis	21		21			
1610		119856	Francisella tularensis subsp. tularensis		5		5		
1611		119912	Salmonella enterica subsp. enterica serovar Choleraesuis		3		3		
1612		120505	Baboon cytomegalovirus		1		1		
1613		121224	Pediculus humanus corporis	2		2			
1614		121723	Photobacterium sp. SKA34		1		1		
1615		121759	Paracoccidioides brasiliensis	4	16	4	16		
1616		121791	Nipah henipavirus	5		5			
1617		122291	Kappapapillomavirus 1	2		2			
1618		122355	Pseudomonas psychrophila	1		1			
1619		122586	Neisseria meningitidis MC58	17		17			
1620		122928	Norovirus GI	2		2			
1621		122929	Norovirus GII	2		2			
1622		126283	Herpes simplex virus unknown type		1		1		
1623		126793	Plasmodium vivax Sal-1	17		22		5	
1624		126794	Vaccinia virus Ankara		127		127		
1625		127906	Vibrio cholerae O1	9		9			
1626		127999	Tanacetum parthenium		1		1		
1627		128947	Ebola virus - Gabon (1994-1997)		18		18		

1628		128948	Sudan virus - Boniface, Sudan,1976	2	1	2	1		
1629		128949	Sudan ebolavirus - Maleo (1979)		30		30		
1630		128951	Ebola virus - Zaire (1995)		1		3		2
1631		128952	Ebola virus - Mayinga, Zaire, 1976	36	13	37	13	1	
1632		128982	Influenza A virus (A/Swine/Indiana/9K035/99 (H1N2))		2		2		
1633		128987	Grass carp reovirus		1		1		
1634		128999	Tai Forest virus - Cote d'Ivoire, Cote d'Ivoire, 1994	1	3	1	3		
1635		129000	Ebola virus - Eckron (Zaire, 1976)		12		12		
1636		129003	Reston ebolavirus - Reston	2	27	2	27		
1637		129052	Catelliglobosispora koreensis		1		1		
1638		129138	Pseudomonas amygdali pv. morsprunorum	2		2			
1639		129727	Bovine papular stomatitis virus		2		2		
1640		129875	Human mastadenovirus A		1		1		
1641		129951	Human mastadenovirus C	1	3	1	3		
1642		130663	Fowl aviadenovirus 4	3		3			
1643		130760	Influenza A virus (A/Hong Kong/1073/99(H9N2))	1	25	1	25		
1644		130763	Influenza A virus (A/Hong Kong/156/97(H5N1))	2	26	4	26	2	
1645		132475	Yaba-like disease virus		3		3		
1646		132487	Measles virus strain Schwarz	1	1	1	1		
1647		132504	Influenza A virus (A/X-31(H3N2))	77	189	78	189	1	
1649		132783	Influenza A virus (A/Netherlands/626/89 (H3N2))		1		1		
1650		132841	Influenza A virus (A/Netherlands/785e/90 (H3N2))		1		1		
1651		132884	Influenza A virus (A/Netherlands/458/98 (H3N2))		1		1		
1652		133704	Porcine circovirus 1	5		5			
1653		134537	Paraburkholderia fungorum	1		1			
1655		135661	Influenza A virus (A/environment/Hong Kong/437-10/99 (H5N1))		1		1		
1656		135720	Neisseria meningitidis serogroup C	3		3			
1657		136371	Umbilicaria papulosa	1		1			
1658		136474	Influenza A virus (A/Swine/Colorado/23619/99(H3N2))		1		1		
1659		136966	SEN virus		7		7		
1660		137578	Influenza A virus (A/England/939/69 x A/PR/8/34)		2		2		
1661		137885	Influenza A virus (A/parakeet/Chiba/1/97(H9N2))		4		4		
1662		137886	Influenza A virus (A/parakeet/Narita/92A/98(H9N2))		2		2		
1663		138948	Enterovirus A	1		1			
1664		138950	Enterovirus C	6	3	6	3		
1666	X	142786	Norovirus				1		1
1667		142948	Influenza A virus (A/ruddy turnstone/Delaware/67/1998(H12N4))		1		1		

1668		144549	Mycolicibacterium fortuitum subsp. fortuitum		1		1		
1669		145262	Methanothermobacter thermautotrophicus		1		1		
1670		145306	Influenza A virus (A/swine/Hong Kong/10/98(H9N2))	5		5			
1671		145307	Influenza A virus (A/swine/Hong Kong/9/98(H9N2))	2		2			
1672		147095	Influenza A virus (A/Swine/Italy/25823/94(H3N2))		2		2		
1673		147272	Paspalum notatum		16		16		
1674		148360	Watermelon mosaic virus 2 (isolate USA)	2		2			
1675		148363	Helicoverpa armigera nucleopolyhedrovirus G4	2		2			
1676		149539	Salmonella enterica subsp. enterica serovar Enteritidis	1	2	1	3		1
1677		150080	Norovirus isolates	1		1			
1678		150127	Influenza B virus (B/Osaka/983/97-V3)	1		1			
1679		150340	Vibrio antiquarius		15		15		
1680		150396	Pseudomonas sp. MT-1		1		1		
1681		150846	Enterovirus 5865/sin/000009	2		2			
1682		151250	Kali turgidum		22	1	22		1
1683		152219	Menangle virus	2		2			
1684		152794	Corynebacterium efficiens		5		5		
1685		153969	Influenza A virus (A/Hong Kong/497/97(H3N2))		1		1		
1686		154540	Influenza A virus (A/Kayano/57(H2N2))		1		1		
1687		155017	Anogeissus	1		1			
1688		155091	Secale cereale subsp. afghanicum		2		2		
1689		155218	Influenza A virus (A/Hong Kong/482/97(H5N1))	7	1	7	1		
1690		155220	Influenza A virus (A/Hong Kong/542/97(H5N1))	1		1			
1691		155222	Influenza A virus (A/Hong Kong/488/97(H5N1))		1		1		
1692		155225	Influenza A virus (A/Hong Kong/507/97(H5N1))		5		5		
1693		155226	Influenza A virus (A/Hong Kong/514/97(H5N1))		1		1		
1694		155227	Influenza A virus (A/Hong Kong/516/97(H5N1))		2		2		
1695		155864	Escherichia coli O157:H7 str. EDL933	4	32	4	32		
1696		155917	Influenza A virus (A/NWS/33HA-A/tern/Australia/G70C/75NA(H1N9))	1		1			
1697		156230	Karenia brevis	1		1			
1698		156586	Flavobacteria bacterium BBFL7		1		1		
1700		157703	Murine polyomavirus strain A3		4		4		
1701		157914	Ziziphus mauritiana	4		4			
1702		158306	Influenza A virus (A/swine/Cotes d'Armor/800/00(H1N2))		1		1		
1703		158465	Human calicivirus Hu/NLV/GII/MD145-12/1987/US	1		1			
1704		158474	Bovine viral diarrhea virus strain Trangie Y546	1		1			
1705		158879	Staphylococcus aureus subsp. aureus N315		5		5		

1706		159091	Pseudomonas sp. KIE171		1		1		
1707		159449	Streptomyces scabrisporus	1		1			
1708		159471	Influenza A virus (A/eq/Sussex/89/(H3N8))	4		4			
1709		159479	Saaremaa hantavirus		21		21		
1710		160490	Streptococcus pyogenes M1 GAS	13	2	13	2		
1711		160491	Streptococcus pyogenes str. Manfredo	3	35	3	35		
1712		160753	Simian immunodeficiency virus 17E-Fr		2		2		
1713		161502	Influenza A virus (A/swine/Italy/1509-6/97(H1N1))		15		15		
1714		161600	Yellow grouper nervous necrosis virus	1		1			
1715		161727	Foot-and-mouth disease virus A10/Holland	11	14	11	14		
1716		161934	Beta vulgaris	5		5			
1717		162145	Human metapneumovirus	8	130	8	130		
1718		162326	Influenza A virus (A/Hong Kong/1143/99(H3N2))	1		1			
1719		163164	Wolbachia endosymbiont of <i>Drosophila melanogaster</i>		1		1		
1720		164326	Influenza A virus (A/Hong Kong/1131/1998(H1N1))	1	1	1	1		
1721		164756	Mycobacterium sp. MCS		73		73		
1722		164757	Mycobacterium sp. JLS		77		77		
1723		165420	Influenza A virus (A/Turkey/MO/24093/99(H1N2))		4		4		
1724		165512	Influenza A virus (A/goose/Guangdong/3/1997(H5N1) )	3	1	3	1		
1726		167758	TTV-like virus DXL1		10		10		
1727		168278	Influenza A virus (A/swine/Finistere/127/99(H3N2))		4		4		
1728		168807	Escherichia coli O127:H6	1		1			
1729		169166	Influenza A virus (A/swine/Italy/1521/98(H1N2))		4		4		
1730		169169	Influenza A virus (A/swine/Cotes d'Armor/1482/1999(H1N1))		1		1		
1731		169173	Choclo virus		3		3		
1733		169963	Listeria monocytogenes EGD-e	5	64	5	64		
1735		170187	Streptococcus pneumoniae TIGR4		2		2		
1736		170325	Canid alphaherpesvirus 1		1		1		
1737		170342	Influenza A virus (A/swine/Italy/1654-1/99(H1N2))		1		1		
1738		170500	H1N9 subtype	1		1			
1739		170525	Measles virus genotype D4	1		1			
1740		170529	Measles virus genotype D7	1		1			
1741		170955	Amur virus Solovey/AP63/1999		2		2		
1742		171101	Streptococcus pneumoniae R6	1	12	1	12		
1743		171264	Measles virus genotype D3	1		1			
1744		171425	Influenza B virus (B/Kobe/87/2001)	1		1			
1745	X	171631	Fusarium oxysporum species complex			8		8	
1746		171929	Anacardium occidentale	64	10	64	10		

1747		172148	Alkhumra hemorrhagic fever virus		4		4		
1748		172149	Influenza A virus (A/swine/Quebec/192/81(H1N1))	1		1			
1749		172851	Avian hepatitis E virus	20		20			
1750		173473	Influenza A virus (A/swine/Hong Kong/2106/98(H9N2))		2		2		
1751		173477	Influenza A virus (A/swine/Hong Kong/3297/98(H9N2))		3		3		
1752		176672	Influenza A virus (A/Duck/Hong Kong/ww461/2000(H5N1))		1		1		
1754		177128	Influenza A virus (A/SW/MN/12883/00(H1N2))		2		2		
1755		177131	Influenza A virus (A/SW/KS/13481-T/00(H1N2))		1		1		
1756		177188	Influenza A virus (A/SW/MN/3227/00(H1N2))		1		1		
1757		177416	Francisella tularensis subsp. tularensis SCHU S4		92		92		
1758		178876	Cryptococcus neoformans var. grubii	1		1			
1759		180454	Anopheles gambiae str. PEST	6	2	6	2		
1760		180498	Jatropha curcas	6		6			
1761		182082	Chlamydia pneumoniae TW-183	7		7			
1762		182781	Influenza A virus (A/Goose/Hong Kong/385.3/2000(H5N1))		1		1		
1763		182785	Mycobacterium tuberculosis subsp. tuberculosis		1		1		
1764		183741	Influenza A virus (A/Chicken/Shanghai/F/98(H9N2))	5		5			
1765		183764	Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))	7	100	7	100		
1766		183778	Influenza A virus (A/quail/Hong Kong/SF550/00(H6N1))		2		2		
1767		183783	Influenza A virus (A/duck/Hong Kong/3096/99(H6N2))		2		2		
1768		184816	Influenza B virus (B/Kadoma/122/99)	2		2			
1769		184922	Giardia lamblia ATCC 50803		249		249		
1770		185431	Trypanosoma brucei brucei TREU927		1		1		
1771		185579	Hepatitis E virus type 1	3		3			
1772		185580	Hepatitis E virus type 4	1		1			
1773		185794	Influenza A virus (A/mallard/NZ/1/97(H5N2))		1		1		
1774		185905	Human rhinovirus A34		54		54		
1775		185907	Human rhinovirus A39		1		1		
1776		185949	Sphingomonas aurantiaca		1		1		
1777		186460	Influenza A virus (A/swine/New Jersey/11/1976(H1N1))	1		1			
1778		186536	Ebolavirus	61	1	61	1		
1779		186538	Zaire ebolavirus	99	886	124	897	25	11
1780		186539	Reston ebolavirus	1	11	1	11		
1781		186540	Sudan ebolavirus	4	292	4	292		
1782		186541	Tai Forest ebolavirus		1		1		
1783		187164	Influenza A virus (A/Swine/Minnesota/55551/2000(H1 N2))		1		1		
1784		187410	Yersinia pestis KIM10+		11		11		

1785		187420	Methanothermobacter thermautotrophicus str. Delta H		1		1		
1786		188763	Panine betaherpesvirus 2		4		4		
1787		189518	Leptospira interrogans serovar Lai str. 56601	1		1			
1788		189918	Mycobacterium sp. KMS		69		69		
1789		191090	Influenza A virus (A/Weiss/1943(H1N1))		1		1		
1790		191218	Bacillus anthracis str. A2012		29		29		
1791		192087	Pseudomonas syringae pv. atrofaciens	4		4			
1792		192222	Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819	10	22	10	22		
1793		192535	Influenza A virus (A/Saudi Arabia/7971/2000(H1N1))		1		1		
1794		192549	Influenza A virus (A/Egypt/96/2002(H1N2))		1		1		
1795		192720	Influenza A virus (A/Saudi Arabia/2581/2001(H1N2))		1		1		
1796		194601	Vipera aspis aspis	3		3			
1797		194958	Porcine endogenous retrovirus A	2		2			
1798		194959	Porcine endogenous retrovirus B	1		1			
1799	X	195055	Human parechovirus 3			1		1	
1800		195099	Campylobacter jejuni RM1221		13		13		
1801		195102	Clostridium perfringens str. 13		1		1		
1802		195700	Avian rotavirus PO-13	6		6			
1803		196164	Corynebacterium efficiens YS-314		4		4		
1804		196403	Baboon endogenous virus	1	1	1	1		
1805		196462	Influenza A virus (A/chicken/California/1002a/00(H6N2))	1	1	1	1		
1806		196600	Vibrio vulnificus YJ016		75		75		
1807		196620	Staphylococcus aureus subsp. aureus MW2		7		7		
1808		196627	Corynebacterium glutamicum ATCC 13032		14		14		
1809		197575	Haemophilus aegyptius	1		1			
1810		197579	Influenza A virus (A/Chicken/Guangdong/11/97(H9N2))		1		1		
1811		197585	Influenza A virus (A/Chicken/Shandong/6/96(H9N2))	1		1			
1812		197589	Influenza A virus (A/Quail/Shanghai/8/96(H9N2))		1		1		
1813		197780	Bluetongue virus 8	2	21	2	21		
1814		198059	Influenza A virus (A/England/627/01(H1N2))		2		2		
1815		198094	Bacillus anthracis str. Ames		2		2		
1816		198214	Shigella flexneri 2a str. 301		4		4		
1817		198215	Shigella flexneri 2a str. 2457T		2		2		
1818		199306	Coccidioides posadasii		9		10		1
1819		199310	Escherichia coli CFT073	1	2	1	2		
1820		199738	uncultured Chlamydia sp.	2		2			
1821		201444	Aracatuba virus		5		5		
1822		202812	Adeno-associated virus - 7		2		2		

1823		202813	Adeno-associated virus - 8	17	14	17	14		
1824		202950	Acinetobacter baylyi		2		2		
1825		203119	Hungateiclostridium thermocellum ATCC 27405		1		1		
1826		203124	Trichodesmium erythraeum IMS101		2		2		
1827		203126	Influenza A virus (A/Kamata/14/91(H3N2))	1		1			
1828		203129	Influenza A virus (A/Aichi/2/1994(H3N2))		1		1		
1829		203172	Camelpox virus CMS		28		28		
1830		203173	Camelpox virus M-96		133		133		
1831		203174	Camelpox virus CP1		1		1		
1833		204428	Chlamydiae	16		16			
1834		204711	Theilovirus		10		10		
1835		204722	Brucella suis 1330	1	29	1	29		
1837		205488	Ebola virus sp.		2		2		
1838		205913	Bifidobacterium longum DJO10A		2		2		
1839		205914	Histophilus somni 129PT		2		2		
1840		205920	Ehrlichia chaffeensis str. Arkansas	23		23			
1841		205946	Influenza A virus (A/Chicken/Beijing/1/95(H9N2))		1		1		
1843		206203	Influenza B virus (B/Hong Kong/330/2001)		23		23		
1844		207401	Influenza A virus (A/finch/Canada/NS1301/2001(H3N8))		1		1		
1845		208435	Streptococcus agalactiae 2603V/R	1	2	1	2		
1846		208726	Human hepatitis A virus	4	1	4	1		
1847		208893	Human respiratory syncytial virus A	30	4	30	4		
1849		208899	Cupixi mammarenavirus		1		1		
1850		208963	Pseudomonas aeruginosa UCBPP-PA14		23		23		
1851		208964	Pseudomonas aeruginosa PAO1	2	39	2	39		
1852		209261	Salmonella enterica subsp. enterica serovar Typhi str. Ty2		16		16		
1853		209841	Actinobacillus pleuropneumoniae serovar 7	1		1			
1854		209882	Fusobacterium nucleatum subsp. vincentii ATCC 49256		2		2		
1855		210655	Influenza A virus (A/Duck/Shantou/2144/00(H9N2))		1		1		
1856		210656	Influenza A virus (A/Duck/Shantou/1881/00(H9N2))		1		1		
1857		210659	Influenza A virus (A/Duck/Shantou/2088/01(H9N2))		1		1		
1858		210663	Influenza A virus (A/Duck/Shantou/2134/00(H9N2))		1		1		
1859		211044	Influenza A virus (A/Puerto Rico/8/1934(H1N1))	33	504	36	538	3	34
1860		211110	Streptococcus agalactiae NEM316		1		1		
1861		211882	Leptospira interrogans serovar Australis	2		2			
1862		212042	Anaplasma phagocytophilum str. HZ	21		21			
1863		212045	Bacillus anthracis str. Western North America USA6153		1		1		
1864	X	212361	Anabaena aequalis			1		1	

1865		212717	Clostridium tetani E88		16		16		
1866		214092	Yersinia pestis CO92	39	22	39	22		
1867	X	214675	Leptospira interrogans serovar Manilae			1		1	
1868		214697	Musa acuminata AAA Group	1		1			
1870		214856	Alistipes finegoldii		1		1		
1871		215862	Influenza A virus (A/Chicken/Nanchang/2-220/2001(H3N6))		1		1		
1873		216466	Streptococcus agalactiae serogroup V	1		1			
1874		216495	Streptococcus agalactiae serogroup III	12		12			
1875		216592	Escherichia coli 042	2		2			
1876		216594	Mycobacterium marinum M		29		29		
1877		216597	Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344		2		2		
1878		216600	Streptococcus pneumoniae 23F	6		6			
1879		216877	Influenza A virus (A/quail/Hong Kong/FY298/00(H9N2))		4		4		
1880		216895	Vibrio vulnificus CMCP6		53		53		
1881		217686	Little cherry virus 1		1		1		
1882		217992	Escherichia coli O6		7		7		
1883	X	218497	Chlamydia abortus S26/3			29		29	
1884		219334	Lactobacillus casei subsp. casei ATCC 393	2		2			
1885		220341	Salmonella enterica subsp. enterica serovar Typhi str. CT18		92		92		
1886		220837	Cryptosporidium sp. MNJ-1		1		1		
1887		220977	Influenza A virus (A/England/10/67(H2N2))		1		1		
1888		221012	Influenza A virus (A/Rio/6/69(H3N2))		1		1		
1889	X	221703	Simian foamy virus Pongo pygmaeus pygmaeus			2		2	
1890		221918	Bovine viral diarrhea virus VEDEVAC	6		6			
1891		221988	[Mannheimia] succiniciproducens MBEL55E		2		2		
1892		222523	Bacillus cereus ATCC 10987		1		1		
1893		223337	Tobacco leaf curl Zimbabwe virus		1		1		
1894		223926	Vibrio parahaemolyticus RIMD 2210633	2	17	2	17		
1895		223931	Influenza A virus (A/Bangkok/10/1983(H1N1))		1		1		
1897		223935	Influenza A virus (A/Okuda/1957(H2N2))	1	9	1	9		
1898		223947	Influenza A virus (A/Hokkaido/20/89(H3N2))		3		3		
1899		223997	Murine norovirus 1	4	1	4	1		
1900		224197	Influenza C virus (C/Nara/1/85)		1		1		
1901		224206	Simian immunodeficiency virus - mon		1		1		
1902		224308	Bacillus subtilis subsp. subtilis str. 168		1		1		
1903		224324	Aquifex aeolicus VF5	1	1	2	1	1	
1904		224326	Borrelia burgdorferi B31	107	10	113	10	6	

1905		224819	Influenza A virus (A/Nagasaki/76/98(H3N2))		1		1		
1906		224914	Brucella melitensis bv. 1 str. 16M	6	14	6	14		
1907		224964	Influenza B virus (B/Johannesburg/5/99)	1		1			
1908		225071	Influenza A virus (A/Tokyo/1566/98(H3N2))		1		1		
1909	X	225085	Influenza A virus (A/Aichi/2/68 (Ao))				9		9
1910		225088	Influenza A virus (A/Kitakyushu/159/93(H3N2))		1		1		
1911		225089	Influenza A virus (A/equine/NewMarket/D64/79(H3N8 ))		1		1		
1912		226186	Bacteroides thetaiotaomicron VPI-5482		1		1		
1913		226900	Bacillus cereus ATCC 14579		2		2		
1914		227377	Coxiella burnetii RSA 493		13		13		
1915	X	227941	Chlamydia caviae GPIC				11		11
1916		227984	SARS coronavirus Tor2	171	2205	171	2205		
1917		228330	SARS coronavirus Urbani	26	52	26	52		
1918		228399	Actinobacillus pleuropneumoniae serovar 1 str. 4074	2	1	2	1		
1919		228400	Histophilus somni 2336	1		1			
1921		228407	SARS coronavirus BJ01	64	28	64	28		
1922		228928	Influenza A virus (A/Memphis/31/98(H3N2))	6		6			
1923		229032	Porcine epidemic diarrhea virus CV777	5		5			
1924		229051	Influenza A virus (A/81/HO)		6		6		
1925		229992	SARS coronavirus Frankfurt 1	5	26	5	26		
1926		231428	Avian infectious bronchitis virus (strain Vic S)	11	8	11	8		
1927		231455	Dyella japonica	1		1			
1928		231851	Influenza A virus (A/Hong Kong/1774/99(H3N2))		1		1		
1929		233262	Bovine enteric coronavirus (strain 98TXSF-110-ENT)		1		1		
1930		233412	[Haemophilus] ducreyi 35000HP	1		1			
1931		233413	Mycobacterium tuberculosis variant bovis AF2122/97		54		54		
1932		234267	Candidatus Solibacter usitatus Ellin6076		2		2		
1933		234603	Sapovirus Mc114		1		1		
1934		234826	Anaplasma marginale str. St. Maries	16	28	16	28		
1935		235279	Helicobacter hepaticus ATCC 51449	2		2			
1936		235455	Adeno-associated virus 9	10		10			
1938		237561	Candida albicans SC5314		3		3		
1939		237609	Pseudomonas alkylphenolica		1		1		
1940		237631	Ustilago maydis 521		2		2		
1941		237895	Cryptosporidium hominis		3		3		
1943		240426	Squirrelpox virus		1		1		
1945		242619	Porphyromonas gingivalis W83	4		4			
1946		243160	Burkholderia mallei ATCC 23344		40		40		

1947		243161	Chlamydia muridarum str. Nigg		42	11	42	<b>11</b>	
1948		243164	Dehalococcoides mccartyi 195		1		1		
1949		243230	Deinococcus radiodurans R1	1		2		<b>1</b>	
1950		243232	Methanocaldococcus jannaschii DSM 2661	3	1	3	1		
1951		243243	Mycobacterium avium 104		43		43		
1952		243273	Mycoplasma genitalium G37	8	1	8	1		
<b>1953</b>	<b>X</b>	<b>243274</b>	<b>Thermotoga maritima MSB8</b>			<b>1</b>		<b>1</b>	
1954		243276	Treponema pallidum subsp. pallidum str. Nichols	283	9	283	9		
1955		243277	Vibrio cholerae O1 biovar El Tor str. N16961	4	3	4	3		
1956		244320	Escherichia coli O55:H7		1		1		
1957		244367	Foot-and-mouth disease virus C-S8c1	15	17	15	17		
1958		246196	Mycolicibacterium smegmatis MC2 155		61		61		
1959		246202	Streptococcus sobrinus 6715	4	4	4	4		
1960		246437	Tupaia chinensis	1		1			
1961		246618	Bifidobacterium thermacidophilum	1		1			
1962		246878	Canine parvovirus 2	3		3			
1963		249372	Influenza A virus (A/duck/Hokkaido/13/00(H9N2))	2		2			
1964		251297	Influenza A virus (A/Netherlands/127/03(H7N7))		1		1		
1965		253182	Human Respiratory syncytial virus 9320	1		1			
<b>1966</b>	<b>X</b>	<b>253446</b>	<b>Avian orthoreovirus strain 1017-1</b>			<b>1</b>		<b>1</b>	
1967		253682	Influenza A virus (A/swine/Hong Kong/5190/99(H3N2))		3		3		
1968		253686	Influenza A virus (A/swine/Hong Kong/74/02(H3N2))		1		1		
1969		254252	Lactococcus virus P2	2		2			
1970		254355	Small ruminant lentivirus	1		1			
1971		255681	Influenza A virus (A/Yokohama/22/2002(H1N2))		2		2		
1972		255682	Influenza A virus (A/Yokohama/47/2002(H1N2))		1		1		
1973		256045	Influenza A virus (A/swine/Chiai/77-10/2001(H3N1))		1		1		
1974		256080	Influenza B virus (B/Kobe/1/2003)	1		1			
1975		257313	Bordetella pertussis Tohama I		11		11		
1976		257363	Rickettsia typhi str. Wilmington		6		6		
1977		260799	Bacillus anthracis str. Sterne	5	4	5	4		
1978		260806	Influenza A virus (A/FPV/Dutch/1927(H7N7))	1		1			
1979		260965	Cercopithecine herpesvirus 1 (strain E2490)	18		18			
1980		261202	Alto Paraguay hantavirus		3		3		
1981		261204	Itapua hantavirus		10		10		
1982		261594	Bacillus anthracis str. 'Ames Ancestor'		1		1		
1983		261658	Cavenderia fasciculata		1		1		
1984		262307	Measles virus genotype A	4		4			

1985		262316	Mycobacterium avium subsp. paratuberculosis K-10	4	58	4	58		
1986		262698	Brucella abortus bv. 1 str. 9-941		1		1		
1987		262722	Mycoplasma hyopneumoniae 7448	1		1			
1988	X	262724	<b>Thermus thermophilus HB27</b>			1		1	
1989		262727	Haemophilus influenzae R2846		6		6		
1990		262728	Haemophilus influenzae R2866		2		2		
1991		263683	Bovine herpesvirus 5 strain TX89	2		2			
1992		263815	Pneumocystis murina	3		3			
1993	X	264202	<b>Chlamydia felis Fe/C-56</b>			14		14	
1994		264510	Influenza A virus (A/chicken/Thailand/LV1NF/2004(H 5N1))		1		1		
1996		264635	Acholeplasma granularum	1		1			
1997		264730	Pseudomonas savastanoi pv. phaseolicola 1448A		1		1		
1998		264732	Moorella thermoacetica ATCC 39073		1		1		
1999		265120	Influenza A virus (A/turkey/Italy/214845/2002(H7N3))	1		1			
2000		265619	Ornithodoros erraticus	22		22			
2001		265669	Listeria monocytogenes serotype 4b str. F2365		7		7		
2002		265872	Cowpox virus (Brighton Red)		1		1		
2003		266093	Influenza A virus (A/chicken/Yamaguchi/7/2004(H5N 1))	3		3			
2004		266264	Cupriavidus metallidurans CH34		3		3		
2005		266779	Chelativorans sp. BNC1		4		4		
2006		266827	Influenza A virus (A/Thailand/1(KAN-1)/2004(H5N1))	4		4			
2007		266834	Sinorhizobium meliloti 1021		3		3		
2008		266940	Kineococcus radiotolerans SRS30216 = ATCC BAA-149		2		2		
2009	X	267212	<b>Neisseria bacilliformis</b>			1		1	
2010	X	267377	<b>Methanococcus maripaludis S2</b>			1		1	
2011		267409	Listeria monocytogenes serotype 1/2a str. F6854		3		3		
2012		267410	Listeria monocytogenes serotype 4b str. H7858		25		25		
2013		267671	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	11		11			
2014		269482	Burkholderia vietnamiensis G4		9		9		
2015		269484	Ehrlichia canis str. Jake	16		16			
2016	X	269638	<b>Bovine enterovirus type 2</b>			2		2	
2017		269798	Cytophaga hutchinsonii ATCC 33406		1		1		
2019		269801	Bacillus cereus G9241		41		41		
2020		270338	Human poliovirus 3 strain Sabin	80	1	80	1		
2021		270473	Pneumonia virus of mice J3666		10		10		
2022		270478	Zantedeschia mild mosaic virus	1		1			
2023		270484	Influenza A virus (A/tiger/Thailand/CU-LV/2004(H5N1))		2		2		

2024		270490	Influenza A virus (A/chicken/Nakorn- Patom/Thailand/CU- K3/2004(H5N1))		1		1		
2025		270510	Influenza A virus (A/chicken/Vietnam/HD1/2004(H5N 1))		3		3		
2026		270945	Influenza A virus (A/Thailand/4(SP- 528)/2004(H5N1))		21		21		
2027		271108	Bombyx mori nucleopolyhedrovirus	2		2			
2028		271848	Burkholderia thailandensis E264		2		2		
2029		272560	Burkholderia pseudomallei K96243	3	735	3	735		
2030		272561	Chlamydia trachomatis D/UW-3/CX	1	26	51	26	50	
2031		272562	Clostridium acetobutylicum ATCC 824		1		1		
2032		272564	Desulfitobacterium hafniense DCB- 2		3		3		
2033		272620	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	28		28			
2035		272624	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	1		1			
2036		272627	Magnetospirillum magnetotacticum MS-1		5		5		
2037		272631	Mycobacterium leprae TN		30		30		
2038		272634	Mycoplasma pneumoniae M129	9		9			
2039		272636	Adeno-associated virus		18		18		
2040		272831	Neisseria meningitidis FAM18	1		1			
2041		272843	Pasteurella multocida subsp. multocida str. Pm70		5		5		
2042		272943	Rhodobacter sphaeroides 2.4.1		1		1		
2043		272944	Rickettsia conorii str. Malish 7		5		5		
2044		272947	Rickettsia prowazekii str. Madrid E		8		8		
2045		272951	Rickettsia sibirica 246		27		27		
2046	X	272989	Salmonella enterica subsp. enterica serovar Enteritidis str. LK5				1		1
2047		273123	Yersinia pseudotuberculosis IP 32953		1		1		
2049		274828	Influenza A virus (A/duck/Fujian/13/2002(H5N1))		1		1		
2050		274829	Influenza A virus (A/duck/Fujian/17/2001(H5N1))		1		1		
2051		278137	Mycobacterium gilvum Spry1		53		53		
2052		279150	Classical swine fever virus 96TD	2		2			
2053	X	279329	Influenza B virus (B/Shandong/7/97)			1	1	1	1
2054		279797	Influenza A virus (A/egret/Hong Kong/757.3/2002(H5N1))		3		3		
2056		279889	Triticum spelta var. arduini		3		3		
2057		280240	Nocardiopsis baichengensis	1		1			
2058		280463	Emiliania huxleyi CCMP1516		1		1		
2060		281310	Haemophilus influenzae 86-028NP	13		13			
2061		281689	Desulfuromonas acetoxidans DSM 684		1		1		
2062		282124	Influenza A virus (A/mallard/Alberta/127/00(H3N8))		1		1		
2063		282458	Staphylococcus aureus subsp. aureus MRSA252	86		86			
2064		283166	Bartonella henselae str. Houston-1		1		1		

2065		283643	Cryptococcus neoformans var. neoformans B-3501A	1	3	1	3		
2066		284168	Influenza A virus (A/Ck/HK/2133.1/2003(H5N1))		1		1		
2067		284177	Influenza A virus (A/Ck/HK/YU22/2002(H5N1))	1		1			
2068		284190	Influenza A virus (A/Ck/Viet Nam/36/2004(H5N1))	1		1			
2069		284195	Influenza A virus (A/Ck/YN/115/2004(H5N1))		1		1		
2070		284202	Influenza A virus (A/Dk/ST/5048/2001(H3N8))	1		1			
2071		284218	Influenza A virus (A/Viet Nam/1203/2004(H5N1))	73	134	74	134	1	
2072		284672	SARS coronavirus TJF		14		14		
2073		284813	Encephalitozoon cuniculi GB-M1		28		28		
2074		285006	Saccharomyces cerevisiae RM11- 1a		2		2		
2075		286239	Influenza A virus (A/red knot/Delaware/2561/1987(H10N5))		1		1		
2076		286542	Soochong virus-2		1		1		
2077		286636	Streptococcus pyogenes MGAS10394		1		1		
2078		286783	Salmonella enterica subsp. enterica serovar Indiana		1		1		
2079		287752	Aurantimonas manganoxydans SI85-9A1		1		1		
2080	X	288118	Mandrillus leucophaeus foamy virus			1		1	
2082		289338	Influenza B virus (B/Nanchang/12/98)		1		1		
2083		289365	Human parvovirus 4		3		3		
2085		290512	Prosthecochloris aestuarii DSM 271		1		1		
2086		291592	Influenza A virus (A/crow/Kyoto/53/2004(H5N1))	1		1			
2087		292039	Influenza A virus (A/chicken/HongKong/SF1/03(H9N2 ))	1		1			
2088		292045	Influenza A virus (A/chicken/HongKong/YU427/03(H9 N2))	1		1			
2089		292348	Canine calicivirus (strain 48)	2		2			
2090		292349	Feline calicivirus (strain Urbana)	1		1			
2091		292590	Influenza A virus (A/swine/Ontario/42729A/01(H3N3))	1		1			
2092		292633	Dragon grouper nervous necrosis virus	20		20			
2093		293054	Influenza A virus (A/turkey/Ontario/6213/66(H5N?))	1		1			
2094		293055	Influenza A virus (A/mallard/Ohio/556/1987(H5N9))		1		1		
2095		293090	Influenza A virus (A/Fujian/411/2002(H3N2))		1		1		
2096		293614	Rickettsia akari str. Hartford		1		1		
2097		294381	Entamoeba histolytica HM-1:IMSS		103		103		
2098		295027	Human herpesvirus 5 strain Merlin	2	3	2	3		
2099		295319	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150		3		3		
2100		295358	Mycoplasma hyopneumoniae 232	21		21			
2101	X	298339	Pan troglodytes foamy virus			1		1	
2102		298653	Frankia sp. EAN1pec		2		2		

2103		298713	Influenza A virus (A/chicken/Korea/SNU0091/00(H9N2))		1		1		
2104		298716	Influenza A virus (A/chicken/Korea/SNU1035C/00(H9N2))		1		1		
2105		299386	Equine arteritis virus Bucyrus	2		2			
2106		299390	Influenza A virus (A/Viet Nam/HN/2004(H5N1))		6		6		
2107		299730	Influenza A virus (A/chicken/Viet Nam/AG-010/2004(H5N1))		1		1		
2109		300015	Lactate dehydrogenase elevating virus C	1		1			
2110		300016	Lactate dehydrogenase elevating virus Plagemann	1		1			
2111		300180	Mopeia Lassa virus reassortant 29		4		4		
2112		300267	Shigella dysenteriae Sd197		5		5		
2113		300268	Shigella boydii Sb227		5		5		
2114		300269	Shigella sonnei Ss046		9		9		
2115		300559	PRRSV VR2332	21	7	21	7		
2116		300563	PRRSV HB-1(sh)/2002	1		1			
2117		300748	Influenza A virus (A/swine/Korea/S190/2004(H9N2))		3		3		
2118		300749	Influenza A virus (A/swine/Korea/S452/2004(H9N2))		1		1		
2119		300750	Influenza A virus (A/chicken/Korea/S1/2003(H9N2))		1		1		
2120		300852	Thermus thermophilus HB8		1		1		
2121		301448	Streptococcus pyogenes serotype M3	1		1			
2122		301449	Streptococcus pyogenes serotype M5	56	57	56	57		
2123		301450	Streptococcus pyogenes serotype M6	9	7	9	7		
2124		301451	Streptococcus pyogenes serotype M18	1		1			
2125		301452	Streptococcus pyogenes serotype M49	1		1			
2126		301478	Murray valley encephalitis virus (strain MVE-1-51)	11	14	11	14		
2127		301964	CY1014 virus		1		1		
2128		302272	Sendai virus (strain Ohita)	1		1			
2129		303316	Influenza A virus (A/Hatay/2004/(H5N1))	3		3			
2130		304883	Influenza A virus (A/Belfast/53582/2004(H3N?))		2		2		
2131		304895	Catenulispora acidiphila		1		1		
2132		305674	Deerpox virus W-848-83		2		2		
2133		306061	Influenza A virus (A/swine/IDT/Bakum1832/2000(H1N2))		1		1		
2134		306254	Campylobacter coli RM2228		3		3		
2135		306263	Campylobacter lari RM2100		1		1		
2136		306264	Campylobacter upsaliensis RM3195		1		1		
2137		306537	Corynebacterium jeikeium K411		1		1		
2138		307044	West Nile virus strain 385-99	22	12	22	12		
2139	X	307685	Merluccius australis polylepis			1		1	

2140		307819	Influenza A virus (A/Jiangsu/38/2004(H3N2))		1		1		
2141		308061	Hantavirus HPR/02-73		1		1		
2142		308159	Araucaria virus		6		6		
2143		310542	Chimpanzee adenovirus	2		2			
2144		311169	Influenza A virus (A/duck/Korea/S10/03(H3N2))		1		1		
2145		311339	Human herpesvirus 5 strain Toledo	9		9			
2146	X	311596	Influenza A virus (A/New York/18/2003(H3N2))				9		9
2147		311695	Influenza A virus (A/New York/124/2001(H3N2))		1		1		
2149		311775	Influenza A virus (A/New York/205/2001(H1N1))		12		12		
2150		313589	Janibacter sp. HTCC2649		1		1		
2151		313596	Robiginitalea biformata HTCC2501		1		1		
2152		313606	Microscilla marina ATCC 23134		1		1		
2153		313627	Bacillus sp. NRRL B-14911		2		2		
2154		314262	Roseobacter sp. MED193		1		1		
2155		314275	Alteromonas mediterranea		1		1		
2156		314278	Nitrococcus mobilis Nb-231		1		1		
2157		314283	Reinekea blandensis MED297		1		1		
2158		314285	Congregibacter litoralis KT71		1		1		
2159		314288	Vibrio alginolyticus 12G01		3		3		
2160		314291	Vibrio splendidus 12B01		2		2		
2161		314292	Photobacterium angustum S14		1		1		
2162		315277	Chlamydia trachomatis A/HAR-13	6	1	6	1		
2163		315456	Rickettsia felis URRWXCal2		7		7		
2164		315730	Bacillus mycoides KBAB4		5		5		
2165		315749	Bacillus cytotoxicus NVH 391-98		3		3		
2166		316056	Rhodopseudomonas palustris BisB18		1		1		
2167		316068	Leadbetterella byssophila		1		1		
2168		316287	Ceratogyrus marshalli	1		1			
2169		316385	Escherichia coli str. K-12 substr. DH10B		3		3		
2170		316401	Escherichia coli ETEC H10407	64	31	64	31		
2171		316407	Escherichia coli str. K-12 substr. W3110		1		1		
2172		317652	Influenza A virus (A/Hong Kong/2/68(H3N2))		4		4		
2173		317655	Sphingopyxis alaskensis RB2256		1		1		
2174		318586	Paracoccus denitrificans PD1222		2		2		
2175		319224	Shewanella putrefaciens CN-32		1		1		
2176		320306	Influenza A virus (A/crested eagle/Belgium/01/2004(H5N1))	2		2			
2177		320372	Burkholderia pseudomallei 1710b		4		4		
2178		320373	Burkholderia pseudomallei 668		10		10		
2179		320374	Burkholderia pseudomallei S13		2		2		
2180		320388	Burkholderia mallei SAVP1		29		29		

2181		320390	Burkholderia mallei GB8 horse 4		1		1		
2182		320483	Anaplasma marginale str. Florida	19	61	19	61		
2183		320667	Trichosanthes dioica	1		1			
2184		321314	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67		5		5		
2185		322053	Konjac mosaic virus	1		1			
2186		322564	Influenza A virus (A/tiger/Thailand/CU-T4/04(H5N1))		5		5		
2187		322566	Influenza A virus (A/tiger/Thailand/CU-T6/04(H5N1))		1		1		
2188		322710	Azotobacter vinelandii DJ		2		2		
2190		325240	Shewanella baltica OS155		2		2		
2191		327105	HIV-1 O_ANT70	1		1			
2192		327205	Influenza A virus (A/New York/348/2003(H1N1))		149		150		1
2193		327310	Influenza A virus (A/Kinmen/645/04(H3N2))		1		1		
2194		327311	Influenza A virus (A/Yilan/515/03(H3N2))		1		1		
2195		328670	Banana streak GF virus	4		4			
2196		328671	Banana streak OL virus	4		4			
2198		329389	Hepatitis C virus (isolate Glasgow)	3	4	3	4		
2199		329593	Influenza A virus (A/chicken/Fujian/25/00(H9N2))		6		6		
2200		329854	Bacteroides intestinalis		1		1		
2201		330879	Aspergillus fumigatus Af293		18		18		
2202		331111	Escherichia coli O139:H28 str. E24377A		36		36		
2203		331112	Escherichia coli HS		14		14		
2204		331271	Burkholderia cenocepacia AU 1054		7		7		
2205		331272	Burkholderia cenocepacia HI2424		1		1		
2206		331635	Chlamydia pecorum E58	1		29		28	
2207		331636	Chlamydia psittaci 6BC	1		1			
2208		331978	Burkholderia pseudomallei Pasteur 52237		1		1		
2209		332193	Vaccinia Virus Acambis 3000 MVA		20		20		
2211		332747	Influenza A virus (A/swine/Tennessee/25/1977(H1N1))	1		1			
2212		333278	H7N9 subtype	3	26	7	26	4	
2213		333284	Hepatitis C virus (isolate Con1)	4	3	4	3		
2214		333367	[Clostridium] asparagiforme		1		1		
2215		333668	Theileria parva strain Muguga	14	19	14	19		
2216		333751	Human papillomavirus type 2		7		7		
2217		333754	Alphapapillomavirus 10	4		4			
2218		333760	Human papillomavirus type 16	349	463	349	492		29
2219		333761	Human papillomavirus type 18	26	104	26	104		
2220		333762	Human papillomavirus type 26		1		1		
2221		333763	Human papillomavirus type 32	1	1	1	1		
2222		333765	Human papillomavirus type 53		1		1		
2223		333849	Enterococcus faecium DO		1		1		

2224		333923	Human papillomavirus 5	1		1			
2225	X	333990	Carnobacterium sp. AT7			1		1	
2226		334203	Mupapillomavirus 1	1	38	1	38		
2227		334380	Orientia tsutsugamushi str. Ikeda		1		1		
2228		334426	Angiostrongylus costaricensis	1	1	1	1		
2230		334590	Influenza A virus (A/Moscow/343/2003(H3N2))		1		1		
2231		334802	Burkholderia mallei FMH		1		1		
2232		334803	Burkholderia mallei JHU		2		2		
2233		335333	Influenza A virus (A/New York/384/2005(H3N2))		64		64		
2234		335337	Influenza A virus (A/New York/388/2005(H3N2))		14		14		
2235		335358	Influenza A virus (A/New York/232/2004(H3N2))		110		110		
2236		335812	Influenza B virus (B/Shanghai/361/2002)	1		1			
2237		336092	Influenza A virus (A/black-headed goose/Qinghai/1/2005(H5N1))	2		2			
2238		336205	Influenza A virus (A/swine/Bakum/5/95(H1N1))		2		2		
2239		336207	Influenza A virus (A/swine/Bakum/1832/2000(H1N2))		3		3		
2240		336238	Influenza A virus (A/Bar-headed Goose/Qinghai/61/05(H5N1))		8		8		
2241		336407	Rickettsia bellii RML369-C		7		7		
2242		336794	Influenza A virus (A/equine/Massachusetts/213/2003(H3N8))		1		1		
2243		336800	Influenza A virus (A/equine/New York/1/1999(H3N8))		3		3		
2244		336982	Mycobacterium tuberculosis F11		24		24		
2245		337042	Alphapapillomavirus 7	11		11			
2246		337043	Alphapapillomavirus 4		1		1		
2247		337052	Deltapapillomavirus 4	24		24			
2248		337090	Chlorobium chlorochromatii		1		1		
2249	X	338079	African green monkey simian foamy virus			3		3	
2250		338188	Bacteroides finegoldii		1		1		
2251	X	338478	Macaque simian foamy virus			1		1	
2252		338966	Pelobacter propionicus DSM 2379		3		3		
2253		339670	Burkholderia ambifaria AMMD		4		4		
2254		339854	Bacillus thuringiensis serovar israelensis ATCC 35646		6		6		
2255		340177	Chlorobium chlorochromatii CaD3		1		1		
2256		340184	Escherichia coli B7A		5		5		
2257		340185	Escherichia coli E22		13		13		
2258		340186	Escherichia coli E110019		2		2		
2259		340197	Escherichia coli F11		12		12		
2261		341663	Aspergillus terreus NIH2624	2		2			
2262		341946	Woodchuck hepatitis virus 2	4		4			
2263		341980	Human herpesvirus 3 strain Oka vaccine	3	62	3	62		

2264		342023	Streptococcus pyogenes serotype M12	3	1	3	1		
2265		342137	Influenza A virus (A/chicken/CA/375TR/2002(H6N2))		1		1		
2266		342145	Influenza A virus (A/turkey/MN/735/79(H6N2))		2		2		
2267		342207	Influenza A virus (A/shorebird/Delaware/141/2002(H9 N9))		1		1		
2268		342210	Influenza A virus (A/shorebird/Delaware/275/2001(H9 N7))		1		1		
2269		342221	Influenza A virus (A/chicken/Korea/S4/2003(H9N2))		1		1		
2270		342396	Influenza A virus (A/turkey/Canada-Ontario/NS-01839-1/05(H3))		1		1		
2271		342508	Influenza A virus (A/New York/444/2001(H1N1))		25		25		
2273		342610	Pseudoalteromonas atlantica T6c		1		1		
2274		342613	Streptococcus agalactiae 18RS21	2		2			
2275		342614	Streptococcus agalactiae 515	1		1			
2276		342615	Streptococcus agalactiae H36B	1		1			
2277		342617	Streptococcus agalactiae CJB111	2		2			
2278		343462	Human adenovirus 11p	7		7			
2279		343463	Human adenovirus 11a	1		1			
2280		344598	Influenza A virus (A/whooper swan/Mongolia/6/05(H5N1))		1		1		
2281		344601	Escherichia coli B171		25		25		
2282		344609	Shigella boydii CDC 3083-94		20		20		
2283		344610	Escherichia coli 53638		1		1		
2284		345072	Vibrio cholerae MO10		1		1		
2285		345073	Vibrio cholerae O395		4		4		
2286		345074	Vibrio cholerae RC385		2		2		
2287		345075	Vibrio cholerae V51		3		3		
2288		345076	Vibrio cholerae V52		32		32		
2290		347257	Mycoplasma agalactiae PG2	3		3			
2291		347495	Bacillus cereus F837/76		1		1		
2292		347515	Leishmania major strain Friedlin	29	38	29	38		
2293		348776	Mycobacterium tuberculosis C		177		177		
2294		349101	Rhodobacter sphaeroides ATCC 17029		1		1		
2295		349163	Acidiphilum cryptum JF-5		1		1		
2296		349344	Bat SARS CoV Rp3/2004		1		1		
2297		349746	Yersinia pestis Angola		3		3		
2298		349747	Yersinia pseudotuberculosis IP 31758		9		9		
2299		349966	Yersinia frederiksenii ATCC 33641		2		2		
2300		349967	Yersinia mollaretii ATCC 43969		3		3		
2301		349968	Yersinia bercoieri ATCC 43970		5		5		
2302		350054	Mycolicibacterium gilvum PYR-GCK		64		64		
2303		350058	Mycolicibacterium vanbaalenii PYR-1		55		55		
2304		350702	Burkholderia cenocepacia PC184		1		1		

2305		350703	Pseudomonas aeruginosa 2192		2		2		
2306		350704	Pseudomonas aeruginosa C3719		2		2		
2307		351071	Newcastle disease virus AF2240	1		1			
2308		351073	Mammalian orthoreovirus		1		1		
2309		351277	Influenza A virus (A/Nanchang/0058/1994(H3N2))		1		1		
2310		351581	Francisella tularensis subsp. holarctica FSC200		1		1		
2311		351607	Acidothermus cellulolyticus 11B		2		2		
2312		351627	Caldicellulosiruptor saccharolyticus DSM 8903		1		1		
2313		351745	Shewanella sp. W3-18-1		1		1		
2314		351746	Pseudomonas putida F1		6		6		
2315		352034	Influenza A virus (A/duck/Potsdam/1402- 6/1986(H5N2))	1		1			
2316		352348	Influenza A virus (A/chicken/Hong Kong/17/1977(H6N1))		1		1		
2317		352520	Influenza A virus (A/mallard/Alberta/35/1976(H1N1))	1	6	1	6		
2318		352561	Influenza A virus (A/duck/Australia/341/1983(H15N8) )		1		1		
2319		352564	Influenza A virus (A/mallard/Astrakhan/263/1982(H14 N5))	1		1			
2320		352764	Influenza A virus (A/mallard/Alberta/202/1996(H2N5))	1		1			
2321		352914	Plasmodium yoelii yoelii 17XNL	6	3	6	3		
2322		352963	Influenza A virus (A/California/7/2004(H3N2))		1		1		
2323		353152	Cryptosporidium parvum Iowa II		84		84		
2324		353153	Trypanosoma cruzi strain CL Brener	2058	10	2059	10	1	
2325		353154	Theileria annulata strain Ankara		4		4		
2326		353253	Influenza A virus (A/duck/Novosibirsk/56/2005(H5N1) )	6	2	6	2		
2327		353466	Influenza A virus (A/Canterbury/236/2005(H3N2))		1		1		
2328		354228	Influenza A virus (A/Gf/HK/SSP607/2003(H9N2))		1		1		
2329		354235	Influenza A virus (A/Ck/HK/CSW161/2003(H9N2))		1		1		
2330		354242	Campylobacter jejuni subsp. jejuni 81-176		4		4		
2331		355315	Streptococcus agalactiae serogroup Ia	1		1			
2333		356114	Hepatitis C virus genotype 3	121	17	121	20		3
2334		356386	Hepatitis C virus (isolate India)		1		1		
2335		356391	Hepatitis C virus (isolate 6a33)		11		11		
2336		356410	Hepatitis C virus (isolate HC-G9)	1	1	1	1		
2337		356411	Hepatitis C virus JFH-1	8	5	8	5		
2338		356413	Hepatitis C virus (isolate BEBE1)		14		14		
2339		356415	Hepatitis C virus (isolate NZL1)	1	3	1	3		
2340		356416	Hepatitis C virus (isolate HCV- K3a/650)		21		21		
2341		356417	Hepatitis C virus (isolate JK049)		6		6		

2342		356418	Hepatitis C virus ED43		1	3	1	3	
2343		356419	Hepatitis C virus (isolate EUH1480)		5		5		
2344		356421	Hepatitis C virus (isolate Th580)		7		7		
2345		356424	Hepatitis C virus (isolate VN004)		1		1		
2346		356426	Hepatitis C virus subtype 3a	12	105	12	105		
2347		357205	Influenza A virus (A/chicken/Hong Kong/3123.1/2002(H5N1))		1		1		
2348		357208	Influenza A virus (A/Vietnam/CL26/2004(H5N1))		79		79		
2349		357210	Influenza A virus (A/Vietnam/CL100/2004(H5N1))	1		1			
2350		357244	Orientia tsutsugamushi str. Boryong	2	2	2	2		
2351		357348	Burkholderia pseudomallei 1106a		2		2		
2352		357355	Hepatitis C virus (isolate Tr Kj)		3		3		
2353		358708	Shigella dysenteriae 1012		1		1		
2354		358709	Escherichia coli 101-1		5		5		
2355		358769	Classical swine fever virus - Alfort/187	70		70			
2356		358805	Classical swine fever virus - Alfort/Tuebingen	5		5			
2357		358812	Classical swine fever virus - C	2		2			
2358		359391	Brucella abortus 2308		31		31		
2359	X	359787	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> JH1			1	1	1	1
2360		359921	Influenza A virus (A/Australian shelduck/Western Australia/1756/1983(H15N2))	1		1			
2361		360095	Bartonella bacilliformis KC583		1		1		
2362		360102	Yersinia pestis Antiqua		36		36		
2363		360112	Campylobacter jejuni subsp. <i>jejuni</i> HB93-13		2		2		
2364		360115	Coxiella burnetii RSA 331		8		8		
2365		360116	Coxiella burnetii 'MSU Goat Q177'		7		7		
2366		360117	Coxiella burnetii Q321		14		14		
2367		360118	Burkholderia pseudomallei 406e		2		2		
2368		360549	Themiste hennahi	1		1			
2369		360910	Bordetella avium 197N		1		1		
2370		362242	Mycobacterium ulcerans Agy99		16		16		
2371		362651	Human immunodeficiency virus type 1 (isolate YU2)	16	21	16	21		
2372		362663	Escherichia coli 536		65		65		
2373		363020	Avian leukosis virus HPRS103	1		1			
2374		364106	Escherichia coli UTI89		2		2		
2375		364132	Influenza A virus (A/New York/504/1998(H3N2))		1		1		
2376		365044	Polaromonas naphthalenivorans CJ2		2		2		
2378		365078	Influenza A virus (A/duck/Guangxi/1586/2004(H5N1))		1		1		
2379		365080	Influenza A virus (A/duck/Guangxi/1793/2004(H5N1))		1		1		
2380		365129	Influenza A virus (A/chicken/Vietnam/DT171/2004(H5 N1))		1		1		

2382		366394	Sinorhizobium medicae WSM419		1		1			
2384		367120	Influenza A virus (A/Fort Monmouth/1/1947(H1N1))	1		1				
2385		367400	Neembucu hantavirus		5		5			
2386	X	367737	<i>Arcobacter butzleri RM4018</i>			1		1		
2387		367830	Staphylococcus aureus subsp. aureus USA300	1		1				
2388		368445	Crocodilepox virus		2		2			
2389		370127	Influenza A virus (A/Victoria/1968(H3N2))		1		1			
2390		370128	Influenza A virus (A/Northern Territory/60/1968(H3N2))		3		3			
2391		370354	Entamoeba dispar SAW760		19		19			
2392		370810	Influenza A virus (A/Anhui/1/2005(H5N1))	6		7		1		
2393		370811	Influenza A virus (A/Anhui/2/2005(H5N1))	1		1				
2394		370813	Influenza A virus (A/duck/IT/701/2005(H10N7))		1		1			
2395		370830	Hantaan virus Q32		4		4			
2396		371082	Influenza A virus (A/Taiwan/2/2006(H1N1))		7		7			
2397		371094	Chikungunya virus strain S27-African prototype	24		24				
2398		371214	Influenza A virus (A/chicken/Taiwan/0329/01(H6N1))	5		5				
2399		373098	Gambierdiscus toxicus	6		6				
2401		373153	Streptococcus pneumoniae D39		61		61			
2402		373384	Shigella flexneri 5 str. 8401		23		23			
2403		373665	Yersinia pestis biovar Orientalis str. IP275		1		1			
2404		374405	Influenza C virus (C/Yamagata/15/2004)	2		2				
2405		374507	Human rotavirus G9 isolate F45	7		7				
2406		374927	Haemophilus influenzae 22.1-21		3		3			
2407		374928	Haemophilus influenzae PittAA		2		2			
2408		374931	Haemophilus influenzae PittGG		1		1			
2409		374932	Haemophilus influenzae PittHH	1		1				
2410		374933	Haemophilus influenzae PittII		3		3			
2411		375177	Haemophilus influenzae 3655		1	6	1	6		
2412		375432	Haemophilus influenzae R3021		2		2			
2413		375450	Yersinia pestis FV-1		2		2			
2414		376619	Francisella tularensis subsp. holarktica LVS	10	291	10	291			
2415		376721	Influenza A virus (A/chicken/Kurgan/05/2005(H5N1))	1		1				
2416		377628	Yersinia pestis Nepal516		135		135			
2417		378131	Influenza A virus (A/Memphis/13/1978(H1N1))		1		1			
2418		378139	Influenza A virus (A/Memphis/1/1978(H1N1))		7		7			
2419		378809	Ravn virus - Ravn, Kenya, 1987	2	32	2	32			
2420		378830	Lake Victoria marburgvirus - Angola2005	6	18	6	18			
2422		380210	Influenza A virus (A/England/333/1980(H1N1))	1	1	1	1			

2423		380213	Influenza A virus (A/Taiwan/1/1986(H1N1))		1		1		
2424		380217	Influenza A virus (A/swine/Hong Kong/4/1976(H3N2))		1		1		
2425		380282	Influenza A virus (A/Fort Monmouth/1/1947-mouse adapted(H1N1))		47		47		
2426		380284	Influenza A virus (A/England/268/1996(H7N7))	1	1	1	1		
2427		380285	Influenza A virus (A/turkey/Ireland/1378/1983(H5N8))		1		1		
2428		380299	Influenza A virus (A/turkey/Wisconsin/1968(H5N9))		1		1		
2429		380301	Influenza A virus (A/turkey/Ontario/7732/1966(H5N9))	5	8	5	8		
2430		380330	Influenza A virus (A/goose/Hong Kong/8/1976(H1N1))		2		2		
2431		380332	Influenza A virus (A/swine/Hong Kong/273/1994(H1N1))		1		1		
2432		380337	Influenza A virus (A/equine/Prague/1/1956(H7N7))		1		1		
2433		380339	Influenza A virus (A/equine/Tennessee/5/1986(H3N8))		1		1		
2434		380340	Influenza A virus (A/equine/London/1416/1973(H7N7))	1	1	1	1		
2435		380342	Influenza A virus (A/swine/Iowa/15/1930(H1N1))	1		1			
2436		380343	Influenza A virus (A/ruddy turnstone/New Jersey/47/1985(H4N6))		2		2		
2437		380346	Influenza A virus (A/Wisconsin/3523/1988(H1N1))	2		2			
2439		380836	Influenza A virus (A/chicken/Vietnam/5/2003(H5N1))		1		1		
2440		380842	Influenza A virus (A/duck/Vietnam/15/2003(H5N1))		3		3		
2441		380905	Influenza A virus (A/X-47(H3N2))	3	2	3	2		
2442		380950	Influenza A virus (A/Beijing/32/1992(H3N2))		54		54		
2443		380951	Influenza A virus (A/Hebei/19/1995(H3N2))	1		1			
2444		380960	Influenza A virus (A/Tokyo/3/1967(H2N2))	2		2			
2445		380964	Influenza A virus (A/Texas/36/1991(H1N1))		1		1		
2446		380978	Influenza A virus (A/Wisconsin/4755/1994(H1N1))		5		5		
2447		380979	Influenza A virus (A/Wisconsin/4754/1994(H1N1))		1		1		
2448		380982	Influenza A virus (A/WSN(H1N1))		1		1		
2449		380984	Influenza A virus (A/Leningrad/134/17/1957(H2N2))		2		2		
2450		380985	Influenza A virus (A/Chile/1/1983(H1N1))		4		4		
2451		381512	Influenza A virus (A/New Caledonia/20/1999(H1N1))	39	236	39	243		7
2452		381513	Influenza A virus (A/Panama/2007/1999(H3N2))	10	14	10	14		
2453		381516	Influenza A virus (A/USSR/90/1977(H1N1))	12		12			
2454		381517	Influenza A virus (A/Udorn/307/1972(H3N2))		5		5		
2455		381518	Influenza A virus (A/Wilson-Smith/1933(H1N1))	1	149	1	150		1

2456		381666	Cupriavidus necator H16		1		1		
2457		382781	Influenza A virus (A/Singapore/1/1957(H2N2))	1	32	1	32		
2458		382813	Influenza A virus (A/Japan/305+/1957(H2N2))	2		2			
2459		382825	Influenza A virus (A/Philippines/2/1982(H3N2))	1	1	1	1		
2460		382828	Influenza A virus (A/RI/5- /1957(H2N2))		1		1		
2461		382832	Influenza A virus (A/VM113- V1(H1N1))	1		1			
2462		382835	Influenza A virus (A/WSN/1933(H1N1))	7	3	13	3	6	
2463		382842	Influenza A virus (A/swine/29/1937(H1N1))		2		2		
2464		382848	Influenza A virus (A/swine/Hong Kong/126/1982(H3N2))		1		1		
2465		383028	Influenza A virus (A/New York/687/1995(H3N2))	1		1			
2466		383121	Influenza A virus (A/Waikato/7/2000(H3N2))		2		2		
2467		383152	Influenza A virus (A/Wellington/22/2001(H3N2))		1		1		
2468		383231	Influenza A virus (A/Wellington/8/2004(H3N2))		2		2		
2469		383281	Influenza A virus (A/Otago/5/2005(H1N1))		1		1		
2470		383379	Toxoplasma gondii RH	27	23	27	23		
2471		383531	Influenza A virus (A/swine/Italy/2/1979(H1N1))		4		4		
2472		383537	Influenza A virus (A/swine/Iowa/1946(H1N1))		1		1		
2473		383550	Influenza A virus (A/duck/England/1/1956(H1N6))		2		2		
2475		383561	Influenza A virus (A/swine/Italy/1850/1977(H3N2))		1		1		
2476		383566	Influenza A virus (A/swine/Italy/425/1976(H1N1))		1		1		
2477		383568	Influenza A virus (A/Shanghai/11/1987(H3N2))		1		1		
2478		383571	Influenza A virus (A/Memphis/6/1986(H3N2))	4	1	4	1		
2479		383574	Influenza A virus (A/Memphis/2/1985(H3N2))	1		1			
2480		383577	Influenza A virus (A/Memphis/1/1990(H3N2))		1		1		
2481		383578	Influenza A virus (A/Memphis/4/1980(H3N2))		1		1		
2482		383586	Influenza A virus (A/Memphis/1/1971(H3N2))	19	11	19	11		
2483		383602	Influenza A virus (A/Anas acuta/Primorje/695/1976(H2N3))		17		17		
2484		383603	Influenza A virus (A/turkey/Minnesota/833/1980(H4N 2))		1		1		
2486		384483	Influenza A virus (A/swine/Hong Kong/127/1982(H3N2))		1		1		
2487		384484	Influenza A virus (A/swine/Hong Kong/81/1978(H3N2))		12		12		
2488		384487	Influenza A virus (A/Swine/Indiana/1726/1988(H1N1) )		2		2		
2489		384493	Influenza A virus (A/seal/Mass/1/1980(H7N7))	1	1	1	1		
2490		384495	Influenza A virus (A/Kiev/59/1979(H1N1))		5		5		

2491		384498	Influenza A virus (A/Ann Arbor/6/1960(H2N2))		270		270		
2492		384499	Influenza A virus (A/gull/Maryland/704/1977(H13N6))		1		1		
2493		384500	Influenza A virus (A/Beijing/11/1956(H1N1))		30		30		
2495		384505	Influenza A virus (A/nt/60/1968(H3N2))		69	1	69	1	
2496		384509	Influenza A virus (A/tern/Australia/G70C/1975(H11N9))	9		9			
2497		384510	Influenza A virus (A/tern/South Africa/1961(H5N3))	1		1			
2498		384527	Influenza A virus (A/Cameron/1946(H1N1))		1		1		
2499		384676	Pseudomonas entomophila L48		1		1		
2500		384946	Influenza A virus (A/duck/Hungary/1/1970(H6N2))		1		1		
2501		385576	Influenza A virus (A/Alaska/6/1977(H3N2))		2		2		
2502		385580	Influenza A virus (A/duck/Ukraine/1/1963(H3N8))	3		3			
2503		385583	Influenza A virus (A/Denver/1957(H1N1))		2		2		
2504		385585	Influenza A virus (A/equine/Jilin/1/1989(H3N8))	1		1			
2505		385586	Influenza A virus (A/chicken/Pennsylvania/1/1983(H5 N2))		1		1		
2506		385587	Influenza A virus (A/budgerigar/Hokkaido/1/1977(H4 N6))		10		10		
2507		385599	Influenza A virus (A/udorn/1972(H3N2))		1		1		
2508		385600	Influenza A virus (A/Puerto Rico/8/1934(Cambridge)(H1N1))	1		1			
2509		385605	Influenza A virus (A/equine/Kentucky/2/1986(H3N8))		3		3		
2510		385616	Influenza A virus (A/ruddy turnstone/NJ/60/1985(N9))		1		1		
2511		385617	Influenza A virus (A/chicken/Pennsylvania/1370/1983 (H5N2))	1		1			
2512		385624	Influenza A virus (A/Port Chalmers/1/1973(H3N2))	7	1	7	1		
2513		385630	Influenza A virus (A/Bangkok/1/1979(H3N2))	1	7	1	7		
2514		385640	Influenza A virus (A/Memphis/102/1972(H3N2))		8		8		
2515		385644	Influenza A virus (A/swine/Ukkel/1/1984(H3N2))		1		1		
2516		386032	Reston ebolavirus - Reston (1989)		4		4		
2517		386033	Sudan ebolavirus - Uganda (2000)	1	6	1	6		
2518		386043	Listeria welshimeri serovar 6b str. SLCC5334		3		3		
2519		386056	Paraburkholderia ferrariae		1		1		
2520		386415	Clostridium novyi NT		2		2		
2521		386585	Escherichia coli O157:H7 str. Sakai		17		17		
2522		386656	Yersinia pestis Pestoides F		2		2		
2523		387093	Sulfurovum sp. NBC37-1		1		1		
2524		387139	Influenza A virus (A/Aichi/2/1968(H3N2))	10	11	12	11	2	
2525		387147	Influenza A virus (A/England/878/1969(H3N2))	1	2	1	2		

2526		387156	Influenza A virus (A/Harbin/1/1988(H1N2))		17		17		
2527		387161	Influenza A virus (A/Japan/305/1957(H2N2))	4	29	4	29		
2528		387191	Influenza A virus (A/camel/Mongolia/1982(H1N1))		8		8		
2529		387203	Influenza A virus (A/duck/Bavaria/2/1977(H1N1))		1		1		
2530		387207	Influenza A virus (A/duck/Hokkaido/8/1980(H3N8))		6		6		
2532		387213	Influenza A virus (A/equine/Alaska/1/1991(H3N8))		1		1		
2533		387223	Influenza A virus (A/equine/Miami/1963(H3N8))	5		5			
2534		387239	Influenza A virus (A/gull/Delaware/475/1986(H2N2))		1		1		
2535		387243	Influenza A virus (A/herring gull/DE/677/1988(H2N8))		1		1		
2536		388041	Influenza A virus (A/bar-headed goose/Qinghai/1A/2005(H5N1))	1		1			
2537		388272	Pseudomonas aeruginosa PACS2		12		12		
2538		388634	Bombyx mandarina nuclear polyhedrosis virus		1		1		
2539		388799	HIV-1 group O	1		1			
2540		389259	Influenza A virus (A/Nagasaki/N03/2005(H3N2))		1		1		
2541		390236	Borrelia afzelii PKo	2		2			
2542		391646	Hepatitis B virus ayw3	1		1			
2543		391647	Hepatitis B virus ayw2	8		8			
2544		391650	Hepatitis B virus ayw4	1		1			
2545		391896	Rickettsia bellii OSU 85-389		3		3		
2546		392021	Rickettsia rickettsii str. 'Sheila Smith'	1	9	1	9		
2547		392734	Terriglobus roseus		1		1		
2548		392809	Influenza A virus (A/Victoria/3/1975(H3N2))	45	9	45	9		
2549		392810	Influenza A virus (A/chicken/Rostock/8/1934(H7N1))	2	4	2	4		
2550		392811	Influenza A virus (A/Udorn/8/1972(H3N2))	1		1			
2551		393011	Francisella tularensis subsp. holartica OSU18		6		6		
2552		393115	Francisella tularensis subsp. tularensis FSC198		85		85		
2553		393117	Listeria monocytogenes FSL J1-194		2		2		
2554		393124	Listeria monocytogenes FSL N3- 165		2		2		
2555		393125	Listeria monocytogenes FSL R2- 503		1		1		
2556		393126	Listeria monocytogenes FSL R2- 561		1		1		
2557		393128	Listeria monocytogenes F6900		1		1		
2558		393130	Listeria monocytogenes J0161		6		6		
2559		393133	Listeria monocytogenes 10403S		4		4		
2560		393305	Yersinia enterocolitica subsp. enterocolitica 8081		16		16		
2562		393548	Influenza A virus (A/chicken/Tula/Russia/Oct- 5/2005(H5N1))		1		1		
2563		393557	Influenza A virus (A/Leningrad/1954/1(H1N1))		8		8		

2564		393697	Influenza A virus (A/Liaoning/25/2000(H1N1))		1		1		
2565		393902	Influenza A virus (A/Wisconsin/67/2005(H3N2))	1	5	1	5		
2566		395095	Mycobacterium tuberculosis str. Haarlem		127		127		
2567		395494	Gallionella capsiferriformans ES-2		1		1		
2568		395841	Influenza A virus (A/duck/Hokkaido/1130/01(H1N1))		1		1		
2569		395842	Influenza A virus (A/tern/Australia/1/04(H2N5))		1		1		
2570		397342	Horsepox virus		6		6		
2572		398031	Toxoplasma gondii type III		1		1		
2573		398812	TGEV virulent Purdue	4		4			
2575		399741	Serratia proteamaculans 568		1		1		
2576		400331	Influenza A virus (A/New South Wales/15/1999(H3N2))		1		1		
2577		400667	Acinetobacter baumannii ATCC 17978	10	13	10	13		
2578		400788	Influenza A virus (A/Indonesia/5/2005(H5N1))	1	3	1	3		
2579		400810	Influenza A virus (A/Indonesia/CDC594/2006(H5N1))	1		1			
2580		400828	Influenza A virus (A/Indonesia/CDC669/2006(H5N1))	5		5			
2581		400830	Influenza A virus (A/Indonesia/CDC699/2006(H5N1))	2		2			
2583		401650	Listeria monocytogenes HPB2262		3		3		
2584		401671	HIV-1 M:B_89.6		1		1		
2585		402194	Influenza A virus (A/Istanbul/CTF/10/2004(H3N2))		1		1		
2586		402464	Influenza A virus (A/gray teal/Australia/2/1979(H4N4))		1		1		
2587		402489	Influenza A virus (A/turkey/Minnesota/1200/1980(H7 N3))		1		1		
2588		402518	Influenza A virus (A/Canada/rv504/2004(H7N3))	1		1			
2589		402527	Influenza A virus (A/chicken/Scotland/1959(H5N1))		1		1		
2590		402938	Influenza A virus (A/Michigan/2/2003(H1N2))	1		1			
2591		404137	Influenza A virus (A/chicken/Beijing/nl/2002(H9N2))		1		1		
2593		404150	Influenza A virus (A/chicken/Hubei/wk/1997(H5N1))		2		2		
2595		404155	Influenza A virus (A/chicken/Hunan/fg/2004(H5N1))		2		2		
2596		404163	Influenza A virus (A/chicken/Jilin/hg/2002(H5N1))		1		1		
2597		404330	Streptococcus pyogenes serotype M2	2		2			
2598		404331	Streptococcus pyogenes serotype M4	2		2			
2599		404408	Influenza A virus (A/chicken/Shanxi/2/2006(H5N1))	1		1			
2600		404573	Influenza A virus (A/chicken/Netherlands/03010132/0 3(H7N7))	1		1			
2601		404974	Vibrio cholerae AM-19226		1		1		
2602		405050	Influenza A virus (A/tern/Australia/1402/2004(H2N5))		1		1		
2603		405531	Bacillus cereus G9842		3		3		

2604		405532	Bacillus cereus B4264		1		1		
2605		405533	Bacillus cereus AH1134		3		3		
2606		405536	Bacillus anthracis str. Tsiankovskii-I		1		1		
2607		405917	Bacillus cereus W		1		1		
2608		405955	Escherichia coli APEC O1		8		8		
2609		406269	West Nile virus strain PTRoxo		12		12		
2610		407134	Yellow fever virus strain Ghana/Asibi/1927		5		5		
2611		407141	Yellow fever virus isolate Ethiopia/Couma/1961		2		2		
2612		407148	Campylobacter jejuni subsp. jejuni 81116		14		14		
2613		407418	Influenza A virus (A/chicken/Guiyang/2147/2005(H5N1))		1		1		
2614		408599	Human rotavirus G9P[8]	1		1			
2615		408685	Dengue virus 1 Brazil/97-11/1997		1058		1058		
2616		408686	Dengue virus 4 Philippines/H241/1956	4	947	4	947		
2617		408687	Dengue virus 4 Singapore/8976/1995		5		5		
2618		408688	Dengue virus 4 Thailand/0348/1991		15		15		
2619		408689	Dengue virus 4 Thailand/0476/1997		3		3		
2620		408690	Dengue virus 3 China/80-2/1980		84		84		
2621		408691	Dengue virus 3 Martinique/1243/1999		889		889		
2622		408692	Dengue virus 3 Sri Lanka/1266/2000		66		66		
2623		408693	Dengue virus 3 Singapore/8120/1995		69		69		
2624		408694	Dengue virus 2 Peru/IQT2913/1996		87		87		
2625		408870	Dengue virus 3 Philippines/H87/1956	8	13	8	13		
2626		408871	Dengue virus 4 Dominica/814669/1981	1	256	1	256		
2627		410069	Streptococcus pyogenes serotype M80	1		1			
2628		410072	Coprococcus comes	1		1			
2629		410078	Human respiratory syncytial virus S2	1		1			
2630		410289	Mycobacterium tuberculosis variant bovis BCG str. Pasteur 1173P2	1	229	1	229		
2631		411157	Influenza A virus (A/Thailand/271/2005(H1N1))	1		1			
2632		411167	Influenza A virus (A/Queensland/11/2001(H3N2))		1		1		
2633		411662	Influenza A virus (A/Hanoi/TN405/2005(H3N2))		1		1		
2634		412022	Burkholderia mallei NCTC 10229		9		9		
2635		412419	Borrelia duttonii Ly	12		12			
2636		412420	Yersinia pestis CA88-4125		21		21		
2637		412614	Vibrio cholerae 2740-80		44		44		
2638		412694	Bacillus thuringiensis str. Al Hakam		8		8		
2639		412883	Vibrio cholerae MZO-3		1		1		
2640		412966	Vibrio cholerae 1587		3		3		
2641		412967	Vibrio cholerae MAK 757		9		9		

2642	X	413502	Cronobacter turicensis			1		1	
2643		413999	Clostridium botulinum A str. ATCC 3502		3		3		
2644		414044	Influenza A virus (A/Thailand/1(KAN-1A)/2004(H5N1))	1		1			
2645		415166	Influenza A virus(A/swine/Henan/2/2004(H9N2))		2		2		
2646		415167	Influenza A virus(A/swine/Henan/3/2004(H9N2))		1		1		
2647		415169	Influenza A virus(A/swine/Henan/5/2004(H9N2))		1		1		
2648		415172	Influenza A virus(A/swine/Henan/8/2004(H9N2))		2		2		
2649		415176	Influenza A virus(A/swine/Shandong/fNY/2003(H9N2))		3		3		
2650		415177	Influenza A virus(A/swine/Shandong/fZC/2003(H9N2))		7		7		
2651		416035	Norovirus Hu/GII.4/DenHaag89/2006/NL	1		1			
2652		416276	Rickettsia massiliae MTU5		2		2		
2653		416674	Influenza B virus (B/Yamagata/16/1988)	4		4	1		1
2654		416730	Influenza A virus (A/Memphis/10/1996(H1N1))		1		1		
2655		417398	Vibrio cholerae MZO-2		2		2		
2656		417399	Vibrio cholerae NCTC 8457		1		1		
2657		417400	Vibrio cholerae B33		5		5		
2658		417758	Influenza A virus (A/quail/Shantou/1475/2004(H9N2))	1		1			
2659		418136	Francisella tularensis subsp. tularensis WY96-3418		2		2		
2660		418868	Influenza A virus (A/Egypt/14724-NAMRU3/2006(H5N1))	1		1			
2661		419109	Vibrio parahaemolyticus AQ3810		38		38		
2662		419947	Mycobacterium tuberculosis H37Ra		130		130		
2663		420174	Hepatitis C virus isolate HC-J4	23	160	23	163		3
2664		420245	Leishmania braziliensis MHOM/BR/75/M2904	14	8	14	8		
2665		420246	Geobacillus thermodenitrificans NG80-2	1		2		1	
2666		420521	Expression vector pNIC-NHT-CF	1		1			
2667		420662	Methylibium petroleiphilum PM1		1		1		
2668		421472	Influenza A virus (A/Indonesia/CDC1032N/2007(H5N1))	1		1			
2669		421877	Hepatitis C virus isolate HC-J1	3	26	3	26		
2670		421901	Influenza A virus (A/Egypt/0636-NAMRU3/2007(H5N1))	2	1	2	1		
2671		423368	Salmonella enterica subsp. enterica serovar Newport str. SL254		1		1		
2672		424717	Shigella flexneri 3a	4		4			
2673		424718	Shigella flexneri 5a	2		2			
2674		424720	Shigella flexneri Y	8		8			
2675		425067	Burkholderia pseudomallei 305		2		2		
2676		425088	Tanganya virus		1		1		

2677		425551	Influenza A virus (A/AA/Huston/1945(H1N1))	1		1			
2678		425557	Influenza A virus (A/California/10/1978(H1N1))		1		1		
2679		426430	Staphylococcus aureus subsp. aureus str. Newman	7		7			
2680		426738	Influenza A virus (A/swine/Miyagi/5/2003(H1N2))		2		2		
2681		427773	Influenza A virus (A/Thailand/SP83/2004(H5N1))	1		1			
2682		427826	Influenza B virus (B/Hong Kong/8/1973)		1		1		
2683		427890	Influenza A virus (A/Viet Nam/JP4207/2005(H5N1))	1		1			
2685		430066	Brucella abortus S19		15		15		
2686		430417	Influenza A virus (A/Wyoming/3e5/2003(H3))	1		1			
2687		430511	Juquitiba virus		2		2		
2688		430557	Francisella tularensis subsp. tularensis FSC033		27		27		
2689		431944	Magnetospirillum gryphiswaldense MSR-1		1		1		
2690		431947	Porphyromonas gingivalis ATCC 33277	20	4	20	4		
2691		432070	Influenza A virus (A/Hong Kong/213/2003(H5N1))	1	4	1	4		
2692		432094	Influenza A virus (A/Wyoming/3/2003-X-147(H3N2))		1		1		
2693		432359	Toxoplasma gondii VEG	14		14			
2694		434922	Coxiella burnetii Dugway 5J108-111		8		8		
2695		434923	Coxiella burnetii CbuG_Q212		1		1		
2696		434924	Coxiella burnetii CbuK_Q154		1		1		
2697		435258	Leishmania infantum JPCM5	28	5	28	15		10
2698		435359	Influenza A virus (A/chicken/Hebei/706/2005(H5N1))		2		2		
2699		436004	Influenza A virus (A/kunke/1/71(H3N2))		1		1		
2700	X	439184	Escherichia coli RS218			1		1	
2701		439235	Desulfatibacillum alkenivorans AK-01		1		1		
2702		439843	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633		1		1		
2703		439847	Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29		1		1		
2704		440534	Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701		1		1		
2705		441158	Burkholderia pseudomallei 9		1		1		
2706		441159	Burkholderia pseudomallei 91		2		2		
2707		441160	Burkholderia pseudomallei 14		1		1		
2708		441769	Bacillus coahuilensis m4-4		1		1		
2709		441771	Clostridium botulinum A str. Hall	44		45		1	
2710		441962	Influenza A virus (A/duck/Mongolia/47/2001(H7N1))		3		3		
2711	X	443149	Mycobacterium tuberculosis CCDC5079				3		3
2712		444178	Brucella ovis ATCC 25840		8		8		
2713		444185	Simian rotavirus A strain RRV	10	1	10	1		
2714		444186	Simian rotavirus A strain TUCH		5		5		

2715		444318	Influenza A virus (A/Texas/1/1977(H3N2))	1	15	1	15		
2716		444793	Influenza A virus (A/Auckland/590/2000(H1N1))		1		1		
2717	X	444922	<b>Psychromonas ossibalaenae</b>				<b>1</b>		<b>1</b>
2718		445335	Clostridium botulinum NCTC 2916		2		2		
2719		445338	Clostridium botulinum str. Iwanei E	6		6			
2720		445983	Borreliella burgdorferi 156a	1		1			
2721		445985	Borreliella burgdorferi ZS7	3	45	3	45		
2722		446023	Influenza A virus (A/Hong Kong/68(H3N2))	1		1			
2724		447095	Blastomyces dermatitidis ATCC 26199		1		1		
2725		447133	Influenza A virus (A/chicken/Japan/1925(H7N7))	1		1			
2726		447188	Influenza A virus (A/duck/Tasmania/277/2007(H7N2))	1		1			
2727		448058	Influenza A virus (A/swine/Guangdong/01/2005(H3N2))		1		1		
2728		449278	West Nile virus SPU116/89		1		1		
2729		449656	Influenza A virus (A/chicken/Taiwan/2838V/00(H6N1))	15		15			
2731		451707	Bacillus cereus NVH0597-99		7		7		
2732		451708	Bacillus cereus H3081.97		12		12		
2733		451709	Bacillus cereus 03BB108		8		8		
2734		451804	Aspergillus fumigatus A1163		13		13		
2735		452646	Neovison vison		1		1		
2736		452652	Kitasatospora setae KM-6054		1		1		
2737		452659	Rickettsia rickettsii str. Iowa		1		1		
2738		453057	Influenza A virus (A/Indonesia/CDC540/2006(H5N1))	1		1			
2739		453927	Juniperus formosana	1		1			
2741		458234	Francisella tularensis subsp. holarctica FTNF002-00		1		1		
2742		458678	Hantaanvirus CGRn93P8		2		2		
2743		461739	Influenza B virus (B/Florida/4/2006)	1		1			
2744		461772	Influenza A virus (A/Wisconsin/43/2006(H3N2))	1		1			
2745		462695	Influenza A virus (A/Hiroshima/52/2005(H3))	2		2			
2746		463722	Murine norovirus GV/CR6/2005/USA		1		1		
2747		464314	Influenza A virus (A/Anhui/T2/2006(H5N1))	1		1			
2748		464417	Influenza B virus (B/Malaysia/2506/2004)	1		1			
2749		464622	Influenza A virus (A/Solomon Islands/3/2006 (Egg passage)(H1N1))	1		1			
2750		464623	Influenza A virus (A/Solomon Islands/3/2006(H1N1))	12		14		<b>2</b>	
2751		465541	Streptomyces sp. Mg1		1		1		
2752		467144	Modified Vaccinia Ankara virus		22		23		<b>1</b>
2753		468968	Influenza A virus (A/Indonesia/560H/2006(H5N1))	1		1			

2754		470137	Brucella suis ATCC 23445	1	5	1	5		
2755		471223	Geobacillus sp. WCH70		2		2		
2756		471721	HIV-1 CRF01_AE	1		1			
2757		472511	Influenza A virus (A/Indonesia/TLL007/2006(H5N1))	1		1			
2758		475478	Influenza A virus (A/equine/New Market/1/1979(H3N8))	1		1			
2759		475493	Influenza A virus (A/equine/California/8560/2002(H3 N8))		2		2		
2760	X	476176	Moraea pallida			1		1	
2761		476294	Influenza A virus (A/Brisbane/10/2007(H3N2))	5		5			
2762		476303	Influenza A virus (A/California/04/2007(H1N1))		1		1		
2763		478005	Escherichia coli O157:H7 str. EC4486		1		1		
2764		478006	Escherichia coli O157:H7 str. EC4501		2		2		
2765		478008	Escherichia coli O157:H7 str. EC869		13		13		
2766	X	479022	Influenza A virus (A/chicken/Korea/IS/2006(H5N1))			1		1	
2767		480019	Influenza A virus (A/Moscow/10/1999(H3N2))		2		2		
2768		480024	Influenza A virus (A/Wyoming/03/2003(H3N2))		8		8		
2769		481805	Escherichia coli ATCC 8739		1		1		
2770		482134	Hepatitis B virus adw/Japan/Nishioka/1983		1		1		
2771		482628	Campylobacter jejuni subsp. jejuni BH-01-0142		1		1		
2772		482957	Burkholderia lata		2		2		
2773		483179	Brucella canis ATCC 23365		9		9		
2774		484021	Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044		1		1		
2775		486280	Torque teno virus VT416		3		3		
2776		486619	Bacillus anthracis str. A0193		3		3		
2777		486620	Bacillus anthracis str. A0465		5		5		
2778		486621	Bacillus anthracis str. A0442		1		1		
2779		486623	Bacillus anthracis str. A0389		5		5		
2780		486624	Bacillus anthracis str. A0488		91		91		
2781		487067	Torque teno virus Human/Ghana/GH1/1996		3		3		
2782		487521	Mycobacterium intracellulare ATCC 13950	1		1			
2783		488233	Influenza A virus (A/Iran/1/1957(H2N2))		1		1		
2784		488241	Influenza A virus (A/Korea/426/1968(H2N2))		2		2		
2785		489455	HBV genotype A	1		1			
2786		489460	HBV genotype B	1		1	5		5
2787		489466	HBV genotype C	10	11	10	21		10
2788		489469	Hepatitis B virus ayw/China/Tibet127/2002	1		1			
2789		489483	HBV genotype D	1	3	1	3		
2790		489821	Norovirus GII.4	2	11	2	11		

2791		489822	Norovirus Hu/Houston/TCH186/2002/US	2		2			
2792		490039	Norovirus GII.2	1		1			
2793		490041	Norovirus GII.3	1		1			
2794		490133	Hepatitis B virus ayw/France/Tiollais/1979		4		4		
2795		493803	Merkel cell polyomavirus	2	2	2	12		10
2796		496036	Influenza A virus (A/duck/Vietnam/37/2007(H5N1))		1		1		
2797		497976	Salmonella enterica subsp. enterica serovar Typhi str. E00-7866		1		1		
2798		497977	Salmonella enterica subsp. enterica serovar Typhi str. 404ty		1		1		
2799		499191	Norovirus GII.1	1		1			
2800		499286	Influenza A virus (A/Hong Kong/ CUHK13527/2003(H3N2))		2		2		
2801		502057	Vaccinia virus GLV-1h68		2		2		
2802		502780	Paracoccidioides brasiliensis Pb18	1	1	1	1		
2803		502790	Aeromonas diversa		1		1		
2804		503386	Influenza B virus (B/Kobe/3/2004)	1		1			
2805		504660	Influenza B virus (B/Kobe/67/2005)	1		1			
2806		504662	Influenza B virus (B/Kobe/39/2005)	1		1			
2807		504664	Influenza B virus (B/Kobe/113/2005)	1		1			
2808		504666	Influenza B virus (B/Kobe/115/2005- T1)	1		1			
2809		504697	Influenza A virus (A/Cygnus olor/Czech Republic/10732/07(H5N1))		1		1		
2810		504904	Influenza A virus (A/Brisbane/59/2007(H1N1))	26	13	26	14		1
2811		504910	Influenza A virus (A/Wellington/75/2006(H1N1))		1		1		
2812		505184	HIV-1 M:A	9	1	9	1		
2813		505185	HIV-1 M:B	8	1	8	25		24
2814		505186	HIV-1 M:C	10		11		1	
2815		505228	HIV-1 M:G	4		4			
2816		506282	Influenza A virus (A/unknown/New York/11646-5/2005(H7N2))	1		1			
2817		506350	Influenza A virus (A/Hong Kong/1/1968(H3N2))	18	3	22	3	4	
2819	X	506380	Influenza A virus (A/Hong Kong/1-4- MA21-1/1968(H3N2))			1		1	
2820		507601	Toxoplasma gondii GT1		205		205		
2821		508767	Clostridium botulinum E3 str. Alaska E43		1		1		
2822		508771	Toxoplasma gondii ME49	21	89	21	89		
2823		508775	Norovirus GII.9	1	1	1	1		
2824		509173	Acinetobacter baumannii AYE		1		1		
2825	X	509628	Hepatitis E virus type 3				1		1
2826		510222	Influenza A virus (A/duck/Vietnam/NCVD- 9/2007(H5N1))	1		1			
2827	X	510670	Hepatitis delta virus dTk6				1		1
2828		511145	Escherichia coli str. K-12 substr. MG1655		31		31		

2829		511839	Influenza A virus (A/turkey/England/N28/1973(H5N2))	1		1			
2831		514193	Influenza A virus (A/CHU/2-524/2005(H3N2))		2		2		
2832		515581	Influenza A virus (A/swine/Ohio/24366/2007(H1N1))		2		2		
2834		515817	Amphioctopus fangsiao	1		1			
2835		518922	Influenza A virus (A/Beijing/262/1995(H1N1))	1		1			
2836		518968	Influenza A virus (A/X-31B(Puerto Rico/8/1934-Aichi/2/1968)(H3N2))	1		1			
2837		518987	Influenza B virus (B/Lee/1940)	5	3	5	3		
2838	X	519082	Influenza A virus (A/New York/107/2003(H7N2))			1		1	
2840		520450	Brucella abortus bv. 2 str. 86/8/59		1		1		
2841		520464	Brucella melitensis bv. 1 str. Rev.1	1		1			
2842		520963	Norovirus GII.11	1		1			
2843		520964	Norovirus GII.18	1		1			
2844		521004	Haemophilus influenzae 6P18H1		1		1		
2845		521005	Haemophilus influenzae 7P49H1		1		1		
2846		521007	Borrelia burgdorferi N40	4	3	4	3		
2847		522740	Influenza A virus (A/swine/Hannover/1/1981(H1N1))		12		12		
2848		524364	Norovirus Hu/1968/US	3	1	6	1	3	
2849		525281	Escherichia coli 83972		3		3		
2850		525368	Mycobacterium parascrofulaceum ATCC BAA-614		35		35		
2851		525374	Staphylococcus epidermidis BCM-HMP0060		1		1		
2852		526974	Bacillus cereus BDRD-ST24		1		1		
2853		526977	Bacillus cereus ATCC 4342		1		1		
2855		527024	Bacillus thuringiensis serovar tochiensis BGSC 4Y1		1		1		
2856		527026	Bacillus thuringiensis serovar sotto str. T04001		1		1		
2858		528354	Neisseria gonorrhoeae MS11	8		8			
2859		529058	Influenza A virus (A/Uruguay/716/2007(H3N2))	1		1			
2860		529507	Proteus mirabilis HI4320	1		1			
2861		533026	Influenza A virus (A/turkey/Ohio/313053/2004(H3N2))	1	2	1	2		
2862		535026	Bacillus subtilis subsp. subtilis NCIB 3610 = ATCC 6051		1		1		
2863		535852	Influenza A virus (A/California/06/2008(H1N1))		1		1		
2864		538555	Influenza A virus (A/swine/Korea/Hongsong2/2004(H1N2))		2		2		
2865		543153	Mycobacterium phage Predator		1		1		
2866		543824	Synechocystis aquatilis		2		2		
2867		546980	Norovirus Hu/GII-4/Saga1/2006/JP	1		1			
2868		548470	Staphylococcus aureus subsp. aureus MN8	11		11			
2869		549169	Pseudogulbenkiania ferrooxidans		1		1		
2870		552536	Listeria monocytogenes HCC23		2		2		

2871		553345	Influenza A virus (A/Aichi/72/2007(H3N2))	1		1			
2872		553583	Staphylococcus aureus A9635	1		1			
2873		554290	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601		3		3		
2874	X	556277	Influenza A virus (A/swine/Guangdong/02/2005(H3N2))			1		1	
2875		557433	Lactobacillus reuteri JCM 1112	3		3			
2876		557599	Mycobacterium kansasii ATCC 12478	1		1			
2877		558177	Influenza A virus (A/mallard/Bavaria/10/2007(H5N1))		1		1		
2878		559292	Saccharomyces cerevisiae S288C	16	1	16	2		1
2879		560463	Influenza A virus (A/Taiwan/VGHYM0325-06/2002(H3N2))		1		1		
2882		562988	Influenza A virus (A/Egypt/2289-NAMRU3/2008(H5N1))	1		1			
2883		562992	Influenza A virus (A/Egypt/3300-NAMRU3/2008(H5N1))	1		1			
2884		563041	Helicobacter pylori G27	2		2			
2885		563773	Vibrio parahaemolyticus AN-5034		4		4		
2886		565995	Bundibugyo ebolavirus	14		15		1	
2888		566466	gamma proteobacterium NOR5-3		1		1		
2889		567106	Campylobacter jejuni subsp. jejuni IA3902		1		1		
2890		568206	Bacillus anthracis str. CDC 684		3		3		
2891		568819	Listeria monocytogenes serotype 4b str. CLIP 80459		6		6		
2892		571800	Psychrobacter sp. G	1		1			
2893		572264	Bacillus cereus 03BB102		2		2		
2894		572307	Neospora caninum Liverpool		1		1		
2895	X	573729	Thermothelomyces thermophilus ATCC 42464			1		1	
2896		573797	Influenza A virus (A/England/654/2007(H1N1))		1		1		
2897		573977	Human bocavirus 2	4		4			
2898		574556	Anaplasma centrale str. Israel		2		2		
2899		575590	Bacteroidetes oral taxon 274 str. F0058	1		1			
2900		575591	Brucella abortus NCTC 8038		1		1		
2901		575788	Vibrio tasmaniensis LGP32		1		1		
2903		577543	Influenza A virus (A/Xinjiang/1/2006(H5N1))	4		4			
2904		578079	Influenza A virus (A/ferret/Maryland/P10-UMD/2008(H9N2))		1		1		
2905		580047	Chlamydia trachomatis A2497	1		3		2	
2906		585034	Escherichia coli IAI1	3		3			
2907		585544	Bacteroides sp. D22	1		1			
2908	X	586029	Fowl adenovirus 8b			2		2	
2909		587200	Variola virus human/India/Ind3/1967		4		4		
2910		587884	Influenza A virus (A/Sydney/5/1997(H3N2))	7		7			

2911		588533	Norovirus Hu/GII/GZ-1/2008/CHN	1		1			
2912		591020	Shigella flexneri 2002017		1		1		
2913		592021	Bacillus anthracis str. A0248		1		1		
2914		592313	Vibrio cholerae 12129(1)		1		1		
2915	X	595609	Recombinant Hepatitis C virus HK6a/JFH-1			3		3	
2916		598745	Giardia intestinalis ATCC 50581		7		7		
2917		604436	Influenza B virus (B/Brisbane/60/2008)	2		8		6	
2918		614035	Influenza A virus (A/swine/Belgium/1/1998(H1N1))	1		1			
2919		616922	Influenza A virus (A/chicken/Anhui/1/1998(H9N2))		1		1		
2920		617102	Yellow fever virus 17D/Tiantan	4	5	4	5		
2921		619693	Prevotella sp. oral taxon 472 str. F0295	1		1			
2922		627442	SARS coronavirus P2	1		1			
2923		627611	Vibrio parahaemolyticus K5030		22		22		
2924		630277	Tarsius larhang		1		1		
2925		632134	Influenza A virus (A/chicken/Pakistan/UDL-01/2008(H9N2))	7		7			
2926		633557	Infectious bronchitis virus CK/CH/LHLJ/04V	1		1			
2927		634464	Chlamydia trachomatis Sweden2	1		1			
2928		637383	Helicobacter pylori NCTC 11639		8		8		
2929		638313	Human bocavirus 3	6		6			
2930		641140	Brucella abortus str. 2308 A		1		1		
2931		641501	Influenza A virus (A/California/04/2009(H1N1))	74	127	74	128		1
2932		641809	Influenza A virus (A/California/07/2009(H1N1))	30	14	35	50	5	36
2933		641812	Influenza A virus (A/Texas/05/2009(H1N1))	1		1			
2934		642261	Influenza A virus (A/California/08/2009(H1N1))	8		8			
2935		642794	Influenza A virus (A/Auckland/1/2009(H1N1))		1		1		
2936		643212	Influenza A virus (A/Netherlands/602/2009(H1N1))	2	14	2	14		
2937		643680	Saccharomyces cerevisiae EC1118		1		1		
2938		644289	Influenza A virus (A/Korea/01/2009(H1N1))	3		4		1	
2939		644788	Influenza A virus (A/Vietnam/1194/2004(H5N1))	14	9	14	9		
2940		645463	Clostridiooides difficile R20291	1		1			
2941		645724	Influenza A virus (A/Hong Kong/01/2009(H1N1))	3		3			
2942		645771	Influenza A virus (A/Catalonia/63/2009(H1N1))		1		1		
2943		647096	Influenza A virus (A/Beijing/01/2009(H1N1))		27		35		8
2944		647514	Norovirus GI.1	1		1			
2945		647515	Norovirus GI.2	1		1			
2946		647516	Norovirus GI.3		1		1		
2947		647519	Norovirus GI.5	1		1			
2948		647521	Norovirus GI.7	1		1			

2949		647923	Influenza A virus (A/reassortant/NYMC X-179A(California/07/2009 x NYMC X-157)(H1N1))	16		16			
2950		648194	Neisseria meningitidis serogroup Y	3		3			
2951		648856	Influenza A virus (A/Beijing/501/2009(H1N1))	1		1			
2952		650131	Equine rhinitis B virus 1 strain P1436/71	6		6			
2953		652616	Mycobacterium tuberculosis str. Erdman = ATCC 35801	15	19	15	19		
2954		654811	Influenza A virus (A/Perth/16/2009(H3N2))	3		3			
2955		655288	Influenza A virus (A/mallard/Quebec/10969/2006(H2 N3))		1		1		
2956		655827	Metarhizium acridum CQMa 102	1		1			
2957		655863	Grosmannia clavigera kw1407		1		1		
2958		657165	Influenza A virus (A/Hong Kong/213/03)	2	2	2	2		
2959		658578	Influenza A virus (A/duck/Beijing/MG0617/2005(H9N 2))		1		1		
2960		658655	Lachnospiraceae bacterium 1_4_56FAA		1		1		
2961		658858	Giardia lamblia P15		1		1		
2962		661367	Legionella longbeachae NSW150		1		1		
2964		667015	Bacteroides salanitronis DSM 18170		1		1		
2965		672161	Chlamydia trachomatis B/TZ1A828/OT	3		3			
2966		673446	Influenza A virus (A/reassortant/NYMC X-181(California/07/2009 x NYMC X-157)(H1N1))	1		1			
2967		679206	Escherichia coli MS 119-7		1		1		
2968		679716	Trypanosoma brucei gambiense DAL972		1		1		
2969		680689	Influenza A virus (A/England/AV877/1996(H7N7))		1		1		
2970		680690	Influenza A virus (A/Hong Kong/1074/1999(H9N2))	2	1	2	1		
2971		680692	Influenza A virus (A/Hong Kong/485/1997(H5N1))	1	1	1	1		
2972		680693	Influenza A virus (A/Netherlands/219/2003(H7N7))	1		1			
2973		680729	Influenza A virus (A/chicken/Italy/1067/1999(H7N1))		17		20		3
2974		680739	Influenza A virus (A/chicken/Mexico/37821-771/1996(H5N2))		1		1		
2975		680767	Influenza A virus (A/duck/Hong Kong/140/1998(H5N1))		1		1		
2976		680785	Influenza A virus (A/environment/Hong Kong/156/1997(H5N1))	1		1			
2977		680789	Influenza A virus (A/environment/Viet Nam/1203/2004(H5N1))	1		1			
2978		680799	Influenza A virus (A/goose/Hong Kong/437-6/1999(H5N1))		1		1		
2979		680803	Influenza A virus (A/goose/Hong Kong/739.2/2002(H5N1))		1		1		
2981		682728	Influenza A virus (A/Quebec/144147/2009(H1N1))	10		10			

2982	X	683780	Influenza A virus (A/wild bird/Korea/A81/2009(H5N2))			1		1	
2983		687340	Torque teno virus 1		3		3		
2984		687341	Torque teno virus 2		4		4		
2985		687342	Torque teno virus 3		4		4		
2986		687343	Torque teno virus 4		6		6		
2987		687345	Torque teno virus 6		2		2		
2988		687346	Torque teno virus 7		3		3		
2989		687347	Torque teno virus 8		6		6		
2990		687350	Torque teno virus 11		1		1		
2991		687353	Torque teno virus 14		5		5		
2992		687354	Torque teno virus 15		3		3		
2993		687355	Torque teno virus 16		4		4		
2994		687358	Torque teno virus 19		5		5		
2995		687359	Torque teno virus 20		2		2		
2996		687360	Torque teno virus 21		2		2		
2997		687362	Torque teno virus 23		2		2		
2998		687363	Torque teno virus 24		3		3		
2999		687364	Torque teno virus 25		3		3		
3000		687365	Torque teno virus 26		5		5		
3001		687366	Torque teno virus 27		5		5		
3002		687367	Torque teno virus 28		3		3		
3003		687368	Torque teno virus 29		4		4		
3004		687369	Torque teno mini virus 1		1		1		
3005		687371	Torque teno mini virus 3		2		2		
3006		687375	Torque teno mini virus 7		2		2		
3007		687376	Torque teno mini virus 8		2		2		
3008		687382	Torque teno tamarin virus		2		2		
3009		687383	Torque teno douroucouli virus		5		5		
3010		687384	Torque teno felis virus		1		1		
3011		687385	Torque teno canis virus		1		1		
3012		687386	Torque teno sus virus 1a	12	1	12	1		
3013		689403	Human bocavirus 1	8		8			
3016		694009	Severe acute respiratory syndrome-related coronavirus	170	502	171	505	1	3
3017		696871	Vaccinia virus Western Reserve		4		31		27
3018		697610	Influenza A virus (A/India/GWMH05/2009(H1N1))		1		1		
3019		703352	Brucella melitensis M5-90	5	26	5	26		
3021		714978	Human adenovirus 55	4		4			
3022		715091	Influenza A virus (A/Roma/ISS1941/2009(H1N1))		1		1		
3023		715494	Influenza A virus (A/Hong Kong/33982/2009(H9N2))		3		3		
3024		722438	Mycoplasma pneumoniae FH	3		3			
3025		742305	Influenza A virus (A/slaty-backed gull/Japan/6KS0185/2006(H4N8))		1		1		

3026		742503	Tokudaia muenninki		1		1		
3027		743722	Sphingobacterium sp. 21	1		1			
3028		743973	Taylorella equigenitalis ATCC 35865	1		1			
3029		744533	Naegleria gruberi strain NEG-M	1		1			
3030		746128	Aspergillus fumigatus	126	86	127	87	1	1
3031		747305	Norovirus GII.10	7		7			
3032		754027	Treponema phagedenis F0421		1		1		
3033		754366	Influenza A virus (A/Ontario/309862/2009(H1N1))	1		1			
3034		754503	Mycoplasma hyopneumoniae 7422	1		1			
3035		759272	Chaetomium thermophilum var. thermophilum DSM 1495	1		1			
3036	X	759363	Chlamydia trachomatis D-EC			3		3	
3037	X	760591	Influenza A virus (A/Egypt/N03072/2010(H5N1))			1		1	
3038		761193	Runella slithyformis DSM 19594		1		1		
3039		761251	Influenza A virus (A/Mexico City/WR1704T/2009(H1N1))		1		1		
3040		762378	Influenza A virus (A/bar-headed goose/Qinghai/3/2005(H5N1))		1		1		
3042		763552	Mus musculus papillomavirus type 1		4		4		
3043		768646	Influenza A virus (A/chicken/Uchal/8293/2006(H9N2))		1		1		
3044		768647	Influenza A virus (A/chicken/Uchal/8286/2006(H9N2))		1		1		
3045		857099	Streptococcus mutans OMZ175	2	1	2	1		
3046		857571	Moraxella catarrhalis O35E	27		27			
3047	X	862909	Trichodysplasia spinulosa-associated polyomavirus			2		2	
3050		868597	Stenotrophomonas maltophilia JV3	1		1			
3051		870484	Nonlabens agnitus		1		1		
3052		871575	Ogataea parapolymerpha DL-1		1		1		
3053		875328	Mycolicibacter sinensis		10		10		
3055		885311	Entamoeba histolytica KU27		1		1		
3056		887118	Influenza A virus (A/Mexico/UASLP-012/2008(H3N2))		1		1		
3057		908203	Influenza A virus (A/Thailand/CU-H126/2009(H1N1))		1		1		
3058		909420	Neisseria meningitidis H44/76	2		2			
3059		913028	Yersinia enterocolitica W22703		1		1		
3060	X	914129	Streptococcus pneumoniae 2061376				1		1
3061		915014	Influenza A virus (A/swine/Heilongjiang/44/2009(H1N1))	1		1			
3062		928301	Fowlpox virus strain NVSL		3		3		
3063		928313	Tacaribe virus strain Franze-Fernandez		6		6		
3064		929439	Leishmania mexicana MHOM/GT/2001/U1103		1		1		
3065		932622	Influenza A virus (A/chicken/Huadong/4/2008(H5N1))	1		1			
3066		935198	Clostridium botulinum B str. Eklund 17B (NRP)		1		1		
3067		936115	Influenza A virus (A/Netherlands/18/1994(H3N2))		1		1		

3068		940614	Granulicella mallensis		1		1		
3069		947939	Influenza A virus (A/aquatic bird/Korea/w44/2005(H7N3))		1		1		
3070		981087	Leishmania donovani BPK282A1		9		9		
3071		986174	Influenza A virus (A/swine/Korea/4382/2009(H1N2))		1		1		
3072		991335	Influenza A virus (A/swine/Hong Kong/71/2009(H1N1))		1		1		
3073		992121	Helicobacter pylori Hp M5	1		1			
3074		996581	Influenza A virus (A/chicken/Shanghai/Q0808-1/2008(H9N2))		1		1		
3075		1003835	Severe fever with thrombocytopenia virus	1		1			
3076		1004253	Cyberlindnera mrakii	1	1	1	1		
3077		1005048	Collimonas fungivorans Ter331		2		2		
3078		1005962	Ogataea parapolymerpha		1		1		
3079	X	1006061	Duck hepatitis A virus 1			1		1	
3080		1006581	Mycoplasma gallisepticum S6	1		1			
3081		1009714	Pseudomonas aeruginosa PAK	7	3	7	3		
3082		1016852	Banana streak CA virus	5		5			
3083		1016853	Banana streak IM virus	10		10			
3084		1016998	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7		11		11		
3085		1035514	Plasmodium vivax North Korean	1		1			
3086		1041522	Mycobacterium colombiense CECT 3035		20		20		
3087		1041990	Influenza A virus (A/Guangdong/15/2007(H3N2))	3		3			
3088		1045775	Paenibacillus catalpae	1		1			
3089		1050221	Chlamydia psittaci NJ1	10		10			
3090		1053141	Recombinant Hepatitis C virus J6/JFH1-J6	2		2			
3091	X	1055687	Trypanosoma vivax Y486			1		1	
3092		1068705	Influenza A virus (A/swine/Guangdong/221/2009(H1 N1))		1		1		
3093		1077587	Influenza B virus (B/Victoria/2/1987)	2	4	2	4		
3094		1081253	Influenza A virus (A/Indiana/08/2011(H3N2))		6		6		
3095		1082519	Influenza A virus (A/chicken/Taixing/10/2010(H9N2))	2		2			
3096		1086859	Influenza A virus (A/Bilthoven/4791/1981(H3N2))		3		3		
3097		1091045	Cutibacterium acnes subsp. defendens ATCC 11828	5		5			
3098		1093545	Influenza A virus (A/shorebird/Delaware Bay/277/2000(H9N7))		1		1		
3099	X	1112244	Chlamydia psittaci 06-1683			3		3	
3100		1112253	Chlamydia psittaci 02DC14	1		1			
3101	X	1112254	Chlamydia psittaci 02DC15			19		19	
3102		1112258	Chlamydia psittaci 02DC22	1		2		1	
3103		1112262	Chlamydia psittaci 03DC29	1		1			
3104	X	1112269	Chlamydia psittaci 09DC78			1		1	

3105		1117322	Glaesserella parasuis str. Nagasaki	1		1			
3106		1122279	Influenza A virus (A/equine/Guangxi/3/2011(H9N2))		1		1		
3107		1125722	Porphyromonas gingivalis W50		36		36		
3108		1126212	Macrophomina phaseolina MS6		1		1		
3109	X	1129345	Influenza A virus (A/little yellow-shouldered bat/Guatemala/153/2009(H17N10))				3		3
3111		1133363	Schmallenberg virus	6		6			
3112		1133968	Babesia microti strain RI	3		3			
3113		1144025	Influenza A virus (A/Shandong/9/1993(H3N2))	13		13			
3114		1146883	Blastococcus saxobsidens DD2		1		1		
3115		1156983	Norovirus Hu/GII.4/Minerva/CS1258/2006/US A	1		1			
3116		1163697	Influenza A virus (A/Oklahoma/309/2006(H3N2))	4	3	4	3		
3117		1169127	Clostridioides difficile genomovar ribotype_087	1		1			
3119		1171336	Influenza A virus (A/swine/Nebraska/A01116984/201 1(H3N2))		1		1		
3120		1172206	Neisseria meningitidis NMB	1		1			
3121		1176042	Influenza A virus (A/swine/Italy/1513-1/1998(H1N1))		1		1		
3122		1178016	Encephalitozoon romaleae SJ-2008		1		1		
3123	X	1182143	Norovirus Hu/GII.4/Farmington Hills/2004/USA			2		2	
3124		1182144	Norovirus Hu/GII.4/Minerva/2006/USA	2		2			
3125		1184252	Streptococcus suis S735	2		2			
3126		1186058	Trichosporon asahii var. asahii CBS 2479		1		1		
3127		1197131	Escherichia coli F576	1		1			
3128		1198627	Mycobacteroides abscessus subsp. massiliense str. GO 06		1		1		
3129		1198676	Streptococcus mutans GS-5		14		14		
3130		1207470	Streptococcus pyogenes M1 476	1		1			
3131		1209523	Toxoplasma gondii type II		2		2		
3132		1209525	Toxoplasma gondii type I		2		2		
3133		1214154	Streptococcus suis 2651	1		1			
3134		1214159	Streptococcus suis 13730	2		2			
3135		1214225	Acidocella sp. MX-AZ02	1		1			
3136		1218488	Torque teno sus virus k2	11		11			
3137		1219377	Human rhinovirus C3		52		52		
3138		1225860	Porcine torque teno virus 1	2		2			
3139		1229831	Chlamydia avium 10DC88	2		2			
3142		1235996	Human betacoronavirus 2c EMC/2012	7		7	12		12
3143		1236978	Staphylococcus epidermidis JCM 2414	1		1			
3144		1239567	Mamastrovirus 3	2		2			

3145		1241973	Norovirus Hu/GII.4/Sydney/NSW0514/2012/A U	3		4		<b>1</b>	
3146		1263102	Prevotella copri CAG:164		1		1		
3147		1263720	Betacoronavirus England 1	9		10		<b>1</b>	
3148		1268303	Rhodococcus sp. AW25M09	1	1	1	1		
3149		1268360	Influenza A virus (A/Victoria/361/2011(H3N2))	5		5			
3150		1278073	Myxococcus stipitatus DSM 14675		1		1		
<b>3151</b>	X	<b>1285028</b>	<b>Influenza A virus (A/American black duck/New Brunswick/00464/2010(H4N6))</b>			<b>1</b>		<b>1</b>	
3152		1285600	Nile crocodilepox virus		2		2		
3153		1285902	Artificial vector pGEX-2T	1		1			
3154		1286616	Norovirus Hu/GII.3/693/425/2008/AU	6		6			
3155		1286635	Desulfotignum phosphitoxidans DSM 13687		1		1		
3156		1288825	Shigella flexneri 2b	2		2			
3157		1289562	Influenza A virus (A/swine/Spain/SF11131/2007(H1N 1))		3		3		
<b>3158</b>	X	<b>1291361</b>	<b>Leptospira interrogans serovar Naam str. Naam</b>			<b>1</b>		<b>1</b>	
<b>3161</b>	X	<b>1303514</b>	<b>Diaporthe toxica</b>			<b>1</b>		<b>1</b>	
3162		1310532	Influenza A virus (A/chicken/West Java/Sbg-29/2007(H5N1))	7		7			
3163		1318439	Influenza A virus (A/Washington/05/2011(H1N1))	1		1			
<b>3164</b>	X	<b>1318464</b>	<b>Bovine Schmallenberg virus BH80/Germany/2011</b>			<b>2</b>		<b>2</b>	
3165		1321009	Influenza A virus (A/Texas/50/2012(H3N2))	1		2		<b>1</b>	
<b>3167</b>	X	<b>1330520</b>	<b>Enterovirus F</b>			<b>1</b>		<b>1</b>	
3168		1332244	Influenza A virus (A/Shanghai/02/2013(H7N9))	9		11		<b>2</b>	
3169		1335626	Middle East respiratory syndrome- related coronavirus	6	12	11	21	<b>5</b>	<b>9</b>
3170		1337063	Puumala virus bank vole/CG1820/Russia/1984		1		1		
3171		1337393	Helicobacter pylori PZ5056	1		1			
3172		1342397	Influenza A virus (A/chicken/Hong Kong/TP38/2003(H9N2))		3		3		
3173		1342434	Influenza A virus (A/turkey/Minnesota/511/1978(H9N 2))		1		1		
3174		1345266	HIV-1 M:CRF01_AE	1		1			
3175		1346336	Influenza A virus (A/Fort Monmouth/1-JY2/1947(H1N1))		1		1		
3176		1352357	Helicobacter pylori SouthAfrica50	1		1			
3177		1355477	Bradyrhizobium diazoefficiens		1		1		
3178		1380386	Mycobacterium sp. URHB0044		1		1		
3179		1389959	Mycobacterium tuberculosis variant bovis AN5	9	28	9	28		
3180		1391655	Influenza A virus (A/Aichi/2- 1/1968(H3N2))	1		1			
<b>3181</b>	X	<b>1391998</b>	<b>Mycobacterium avium subsp. paratuberculosis 08-8281</b>			<b>1</b>		<b>1</b>	
3182		1392869	Escherichia coli K1		1		1		

3184	X	1395982	Influenza A virus (A/tree sparrow/Shanghai/01/2013(H7N9))			1		1	
3185		1398154	Sporothrix brasiliensis 5110		4		4		
3186		1399582	Duck Tembusu virus	7		7			
3187		1401444	Avian leukosis virus ev/J	5		5			
3188		1403335	Porphyromonas gingivalis 381	71	55	71	55		
3189		1403514	Influenza A virus (A/chicken/Jiangsu/x1/2004(H9N2))	7		7			
3190		1405296	Chlamydia suis MD56	1		1			
3191	X	1406148	Norovirus Hu/GII.3/Jingzhou/2013402/CHN			2		2	
3192		1408475	Taylorella asinigenitalis ATCC 700933	1		1			
3193		1413188	Influenza A virus (A/Anhui/PA-1/2013(H7N9))	1	3	1	3		
3194		1416333	Trypanosoma cruzi Dm28c	2		2			
3195		1420840	Influenza A virus (A/Luxembourg/46/2009(H1N1))		1		1		
3196		1427371	Chlamydia pecorum VR629	5		5			
3197	X	1432052	Eisenbergiella tayi				3		3
3198		1432555	Escherichia coli ISC7		1		1		
3199		1440122	Murid herpesvirus 68		2		2		
3200		1447813	Influenza A virus (A/Shanghai/5190T/2013(H7N9))		6		6		
3201		1451093	Influenza A virus (A/chicken/Taiwan/67/2013(H6N1))		5		5		
3202		1457141	Chlamydia avium	1		1			
3203		1457153	Chlamydia gallinacea	3		3			
3204		1458279	Staphylococcus aureus USA300-ISMMS1	1		1			
3205		1463841	Streptomyces sp. NRRL F-2580		1		1		
3206		1464048	Micromonospora parva		1		1		
3207		1470614	Influenza A virus (A/swine/Thailand/CU-S3673N/2012(H3N2))		1		1		
3208		1476909	Banana streak MY virus	39		39			
3209		1481964	Influenza A virus (A/Anhui/1-DEWH730/2013(H7N9))	1	35	1	35		
3210	X	1481966	Influenza A virus (A/Anhui/1-JCVI1_RG2/2013(H7N9))			3		3	
3211		1498499	Legionella norlandica		1		1		
3212		1507381	Influenza A virus (A/Minnesota/11/2010(H3N2))	11		19		8	
3215	X	1566298	Paraiso Escondido virus				1		1
3216	X	1570291	Ebola virus			3		3	
3217		1581419	Amblyomma sculptum	1		1			
3218		1634342	Norovirus Hu/GII/JP/2015/GII.P17_GII.17/Kawasaki308	1		1			
3219		1663864	Influenza A virus (A/Anhui/1-YK_RG134/2013(H7N9))		1		1		
3220		1663934	Influenza A virus (A/Anhui/1-YK_RG64/2013(H7N9))		2		2		
3221		1663996	Influenza A virus (A/Anhui/1-YK_RG01/2013(H7N9))	1		1			
3222		1665645	Norovirus GI/Hu/NL/2012/GI.6/Groningen		1		1		

3223		1671798	Human papillomavirus type 54		1		1		
3224		1727172	Influenza A virus (A/duck/Bavaria/1/1977(H1N1))		2		2		
3225	X	1763596	Guertu virus			32		32	
3226		1835656	Rotavirus A RVA/Cow- tc/USA/B223/1983/G10P[11]	2		2			
3227	X	1855372	bacterium JGI 053				1		1
3228	X	1885248	Variegated squirrel bornavirus 1				1		1
3229		1891187	Zaire ebolavirus Makona		34		57		23
3230		1891729	Mesocricetus auratus polyomavirus 1	11		11			
3231		1891730	Mus musculus polyomavirus 1	4	30	4	30		
3232		1891762	Human polyomavirus 1	3	52	4	52	1	
3233		1891767	Macaca mulatta polyomavirus 1	16	42	16	42		
3234		1898104	Bacteroidetes bacterium		1		1		
3235	X	1898203	Lachnospiraceae bacterium				1		1
3236		1933300	Watermelon silver mottle tospovirus	3		3			
3237	X	1972699	Norovirus Hu/GII.3/3- 34/2015/HNZZ/CHN			11		11	
3238		1979160	Human rubulavirus 2	10		10			
3239		1979162	Mammalian rubulavirus 5	1	1	1	1		
3240		1979165	Mumps rubulavirus	3		3	1		1
3241		1980442	Orthohantavirus		15		15		
3242		1980456	Andes orthohantavirus	2	77	2	77		
3243		1980459	Bayou orthohantavirus	1		1			
3244		1980463	Cano Delgadito orthohantavirus		1		1		
3245		1980467	Dobrava-Belgrade orthohantavirus		25		25		
3246		1980468	El Moro Canyon orthohantavirus		2		2		
3247		1980471	Hantaan orthohantavirus	2	60	2	60		
3248		1980475	Khabarovsk orthohantavirus		1		1		
3249		1980476	Laguna Negra orthohantavirus		12		12		
3250		1980481	Montano orthohantavirus	3		3			
3251		1980485	Prospect Hill orthohantavirus	1	2	1	2		
3252		1980486	Puumala orthohantavirus	32	20	32	20		
3253		1980489	Sangassou orthohantavirus		6		6		
3254		1980490	Seoul orthohantavirus		5		5		
3255		1980491	Sin Nombre orthohantavirus	1	35	1	35		
3256		1980494	Tula orthohantavirus	1	14	1	14		
3257		1980519	Crimean-Congo hemorrhagic fever orthonairovirus	82	18	82	18		
3259	X	2029108	Bacillus sp. UMB0899			1		1	
3260		2043570	Zika virus ZIKV/H. sapiens/FrenchPolynesia/10087PF/ 2013		54	6	54	6	
3262		2070132	Influenza A virus (A/chicken/Jiangsu/W1- 8/2015(H7N9))	6		6			
3263	X	2115988	Swine acute diarrhea syndrome related coronavirus			1		1	
3264		2116544	Synechococcus lacustris	1		1			

3265		2169971	Visna-maedi virus	5	7	5	7		
3266		2169986	Barley yellow dwarf virus PAV	1		1			
3267		2169991	Argentinian mammarenavirus	8	873	8	873		
3268		2169992	Brazilian mammarenavirus		879		879		
3269		2169993	Cali mammarenavirus		11		11		
3270		2169994	Paraguayan mammarenavirus		1		1		
3271		2169996	Serra do Navio mammarenavirus		3		3		
3272	X	2170197	Guenon simian foamy virus			1		1	
3273	X	2170200	Spider monkey simian foamy virus			1		1	
3274	X	2170201	Squirrel monkey simian foamy virus			1		1	
3275	X	2170206	Yellow-breasted capuchin simian foamy virus			1		1	
3276	X	2316109	Zika virus ZIKV/Human/Cambodia/FSS13025/ 2010				2		2
3277	X	2487134	Clostridium sp. E02				1		1
3278		2678873	Trimerodentes annularis	1		1			
3279		10000000	Mus musculus BALB/c		3		3		
3280		10000055	Mus musculus DBA/2	1		1			
3281		10000067	Mus musculus C57BL/6		6005		6005		
3282		10000187	Sus scrofa Landrace X Large White	1		1			
3283		10000291	Bacillus anthracis str. Sterne 34F2	1		1			
3284		10000293	Clostridium botulinum A 1	1		1			
3285		10000294	Clostridium botulinum A 2	2		2			
3286		10000295	Clostridium botulinum B 111	2		2			
3287		10000296	Clostridium botulinum D 1873	2		2			
3288		10000297	Clostridium botulinum C 92-13	5		5			
3289		10000299	Clostridium botulinum E Beluga	2		2			
3290		10000301	Clostridium botulinum A str. Hall hyper	3		3			
3291		10000302	Clostridium botulinum A Kyoto-F	1		1			
3292		10000303	Clostridium botulinum B Lamman	1		1			
3293		10000304	Clostridium botulinum F NCTC 10281	1		1			
3294		10000305	Clostridium botulinum B Okra	3		3			
3295		10000306	Clostridium botulinum C Stockholm	2		2			
3296		10000307	Clostridium difficile BART'S W1	1		1			
3297		10000308	Listeria monocytogenes ATCC 35967		1		1		
3298		10000309	Listeria monocytogenes ATCC 43251		3		3		
3299		10000313	Mycobacterium avium serovar 1	1		1			
3300		10000314	Mycobacterium avium serovar 2	1		1			
3301		10000316	Mycobacterium avium serovar 25	1		1			
3302		10000317	Mycobacterium avium serovar 26	1		1			
3303		10000318	Mycobacterium avium serovar 4	2		2			
3304		10000319	Mycobacterium avium serovar 8	1	1	1	1		
3305		10000320	Mycobacterium avium serovar 9	1		1			

3306		10000323	Mycobacterium bovis T/91/1378		6		6		
3307		10000328	Mycobacterium avium subsp. paratuberculosis Strain Ben		1		1		
3308		10000329	Mycobacterium tuberculosis 103	1		1			
3309		10000331	Mycobacterium gastri W471	1		1			
3310		10000335	Candida albicans A-9 (serotype B)	1		1			
3311		10000337	Candida albicans KIT 1113	1		1			
3312		10000339	Candida albicans serotype A	1		1			
3313		10000341	Leishmania donovani donovani 1S2D	1		1			
3314		10000345	Leishmania infantum LEM 75	14		14			
3315		10000348	Trypanosoma cruzi G	1		1			
3316		10000351	Trypanosoma cruzi Y	1		1			
3317		10000352	Entamoeba histolytica YS-27	1		1			
3318		10000353	Toxoplasma gondii 76K	5	5	5	5		
3319		10000354	Toxoplasma gondii BK	1	1	1	1		
3320		10000355	Toxoplasma gondii Prugniaud		1		1		
3321		10000356	Plasmodium berghei NK65	2	2	2	2		
3322		10000357	Plasmodium chabaudi adami DS	2	37	2	37		
3323		10000358	Plasmodium falciparum 366		1		1		
3327		10000363	Plasmodium falciparum Brazil-608	1	1	1	1		
3328		10000366	Plasmodium falciparum FCB-2	1		1			
3329		10000369	Plasmodium falciparum FVO		5		5		
3330		10000370	Plasmodium falciparum GAM5		1		1		
3331		10000371	Plasmodium falciparum Indochina I/CDC	32		32			
3332		10000373	Plasmodium falciparum ItG2G1		1		1		
3333		10000375	Plasmodium falciparum RO71	1	1	1	1		
3334		10000376	Plasmodium falciparum UF-5	2		2			
3335		10000378	Plasmodium vivax NK		2		2		
3336		10000381	Plasmodium yoelii yoelii YM	1	5	1	5		
3337		10000382	Babesia bovis Mexico	1	4	1	4		
3338		10000383	Babesia bovis Mexico Mo7	1	33	1	33		
3339		10000385	Schistosoma mansoni Puerto Rico	20	7	20	7		
3340		10000386	Monkeypox virus USA_2003_039		1		1		
3341		10000388	Vaccinia virus NYCBH - Dryvax		29		29		
3342		10000390	Variola major virus India-1967		1		1		
3343		10000391	Equid herpesvirus 2 ER32	1		1			
3344		10000394	Human herpesvirus 1 103/65	1		1			
3345		10000396	Human herpesvirus 1 McIntrye		1		1		
3346		10000398	Human herpesvirus 1 NS	1		1			
3347		10000404	Bovine herpesvirus 1 Lam	1		1			
3348		10000405	Equid herpesvirus 4 TH20	2		2			
3349		10000406	Human herpesvirus 3 H-551	26	15	26	15		
3350		10000408	Human herpesvirus 5 TB40		1		1		

3351		10000411	Murid herpesvirus 1 deltaMS94.5		2		2		
3352		10000412	Murid herpesvirus 1 Isolate G4		1		1		
3353		10000413	Murid herpesvirus 1 Isolate K6		1		1		
3355		10000420	Human herpesvirus 4 BL74		1		1		
3356		10000421	Human herpesvirus 4 CKL		10		10		
3357		10000424	Human herpesvirus 4 GD1	4	1	4	1		
3358		10000427	Human herpesvirus 4 type A		5		5		
3360		10000435	Hepatitis B virus genotype D		6		6		
3361		10000436	Hepatitis B virus subtype AY	7		7			
3362		10000437	Hepatitis B virus subtype AYR		1		1		
3363		10000438	Human parvovirus B19 genotype 1	1		1			
3364		10000439	Eastern equine encephalitis virus SV	8		8			
3365		10000440	Dengue virus type 1 Hawaii	29	22	29	22		
3366		10000442	Dengue virus type 3 CH53489		7		7		
3367		10000444	Japanese encephalitis virus CH2195LA	1		1			
3368		10000445	Japanese encephalitis virus JaOH0566	1		1			
3369		10000447	West Nile virus 3000.0259	2		2			
3370		10000449	Tick-borne encephalitis virus (WESTERN SUBTYPE) - Neudoerfl	10		10			
3371		10000451	Classical swine fever virus Shimen	16		16			
3372		10000453	Hepatitis C virus subtype 1a (isolate Gla)	5		5			
3373		10000455	Hepatitis C virus subtype 1a 1/910		18		18		
3374		10000456	Hepatitis C virus subtype 1b AD78	71		71			
3375		10000457	Hepatitis C virus subtype 1a Chiron Corp.	1	1	1	1		
3377		10000460	Hepatitis C virus subtype 1b JK1	13		13			
3378		10000462	Measles virus CAM/RB		1		1		
3379		10000463	Phocine distemper virus 2558/Han 88	5		5			
3380		10000465	Rinderpest virus LATC	2		2			
3381		10000467	Rabies virus CVS	14		14			
3382		10000470	Rabies virus Flury LEP		1		1		
3383		10000471	Rabies virus RC-HL	4		4			
3384		10000472	Bovine ephemeral fever virus BB7721	2		2			
3385		10000474	Influenza A virus H3N2 (A/Resvir-9 (H3N2))		10		10		
3386		10000477	H1N1 subtype Influenza A virus (A/Netherlands/306/00 (H1N1))		1		1		
3387		10000482	Rift Valley fever virus ZH501	2		2			
3388		10000483	Puumala virus CG18-20	4		4			
3389		10000484	Puumala virus Kazan	26	7	26	7		
3390		10000485	Puumala virus (STRAIN HALLNAS B1) Vranica/Hallnas	4		4			
3391		10000487	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 4)	1		1			
3392		10000488	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 53b)		61		61		

3393		10000490	Lymphocytic choriomeningitis virus A22.2b		1		1		
3394		10000491	Lymphocytic choriomeningitis virus Docile		2		2		
3395		10000494	Lymphocytic choriomeningitis virus (strain WE) variant 8.7		1		1		
3396		10000495	Lymphocytic choriomeningitis virus (strain WE) WE CL1.2		1		1		
3397		10000496	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 3)		1		1		
3398		10000497	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 5)	1		1			
3399		10000499	Equine infectious anemia virus PV		2		2		
3400		10000500	Human immunodeficiency virus 1 IIIB	1	2	1	2		
3401		10000501	Simian immunodeficiency virus - mac - mac 239		474	1	474	1	
3402		10000502	Simian immunodeficiency virus - mac - mac 32H		9		9		
3403		10000503	Simian immunodeficiency virus - mac - mac BK28		4		4		
3404		10000504	Simian immunodeficiency virus - mac - mac F965		2		2		
3406		10000506	Simian immunodeficiency virus - sm - sm PT573		3		3		
3407		10000507	Rabbit hemorrhagic disease virus Olot/89	1		1			
3408		10000513	Foot-and-mouth disease virus (strain O1) (O1 Kaufbeuren)	43	8	43	8		
3409		10000514	Foot-and-mouth disease virus (strain O1) (O1BFS 1860)	9		9			
3410		10000515	Foot-and-mouth disease virus (strain O1) (O1BFS)	5		5			
3411		10000516	Foot-and-mouth disease virus (strain O1) (O1 Campos)	18	19	18	19		
3412		10000518	Borna disease virus Giessen strain He/80	6		6			
3413		10000519	Hepatitis E virus China Xinjiang	1		1			
3414		10000520	Hepatitis E virus SAR-55	2	6	2	6		
3415		10000523	Hepatitis delta virus TW2667		5		5		
3416		10000524	Equid herpesvirus 2 691	1		1			
3417		10000525	Equid herpesvirus 2 16V	1		1			
3418		10000526	Equid herpesvirus 2 5FN	1		1			
3419		10000527	Equid herpesvirus 2 FIN60	1		1			
3420		10000528	Porcine respiratory and reproductive syndrome virus BJ-4	1		1			
3421		10000529	Porcine respiratory and reproductive syndrome virus CH-1a	7	1	7	1		
3422		10000530	Borrelia garinii IP90	3		3			
3423		10000535	Human herpesvirus 6B HST	1		1			
3424		10000536	Murid herpesvirus 4 G2.4		3		3		
3425		10000537	Murid herpesvirus 4 WUMS		19		19		
3426		10000542	Streptococcus pyogenes serotype M3 D58	4		4			
3427		10000544	Sin Nombre virus NM H10	4		4			
3428		10000547	Human enterovirus 71 Subgenogroup B5	12		12			
3429		10000548	Human enterovirus 71 Subgenogroup C2	19		19			
3430		10000549	Human enterovirus 71 Subgenogroup C4	11		11			

3431		10000550	Influenza A virus H3N2 (A/Netherlands/9/03 (H3N2))		1		1		
3432		10000553	Andes virus CHI-7913	53		53			
3433		10000554	Salmonella enterica subsp. enterica serovar Minnesota R595	2		2			
3434		10000555	Plasmodium yoelii yoelii 265BY		1		1		
3435		10000556	Foot-and-mouth disease virus (strain O1) Kaufbeuren	44	12	44	12		
3436		10000559	Chlamydophila abortus B-577	11		11			
3437		10000560	Norovirus genogroup 3 Bo/Jena/1980/DE	1		1			
3438		10000566	Paracoccidioides brasiliensis B339		8		8		
3439		10000567	Vibrio cholerae O1 serotype Inaba	1		1			
3440		10000568	Vibrio cholerae O1 serotype Ogawa	6		6			
3441		10000571	Cowpox virus (Brighton Red) White-pock		1		1		
3442		10000662	Rattus norvegicus Lewis		1		1		
3443		10000675	Borrelia burgdorferi CA12		6		6		
3444		10000679	Campylobacter jejuni subsp. jejuni 16971.94GSH (O:41)	2		2			
3445		10000718	Helicobacter pylori J223	2		2			
3446		10000720	Helicobacter pylori UA948	2		2			
3447		10000721	Helicobacter pylori UA955	1		1			
3448		10000723	Pseudomonas aeruginosa Immunotype 4	4		4			
3449		10000727	Escherichia coli 180/C3	1		1			
3450		10000728	Escherichia coli B B/r CM6		1		1		
3451		10000733	Escherichia coli O5:K4:H4	1		1			
3452		10000734	Escherichia coli O65:K:-H-	1		1			
3453		10000738	Salmonella typhimurium PL5 (O9,12)	1		1			
3454		10000739	Salmonella typhi 620Ty	1		1			
3455		10000740	Salmonella typhi Ty21a		6		6		
3456		10000742	Salmonella typhimurium SH 4809	4		4			
3457		10000743	Salmonella typhimurium SL3261		4		4		
3458		10000748	Shigella dysenteriae serotype 1	3		3			
3459		10000749	Shigella dysenteriae serotype 1 114Sd	1		1			
3460		10000752	Shigella flexneri 5b	1		1			
3461		10000754	Shigella flexneri X	1		1			
3462		10000756	Yersinia pestis KIM 5	21		21			
3463		10000757	Yersinia pestis 195/P	5		5			
3464		10000759	Pasteurella multocida X-73	2		2			
3465		10000760	Anaplasma marginale South Idaho		2		2		
3466		10000761	Orientia tsutsugamushi Karp	1		1			
3467		10000763	Chlamydia trachomatis Serovar C	16	1	16	1		
3468		10000764	Chlamydia trachomatis Serovar E	19	2	19	2		
3469		10000765	Chlamydia trachomatis Serovar H	7		7			
3470		10000766	Chlamydia trachomatis Serovar I	10		10			
3471		10000767	Chlamydia trachomatis serovar K	14		14			

3472		10000768	Chlamydia trachomatis Serovar L2	15	12	15	12		
3473		10000769	Chlamydia trachomatis Serovar L3	2		2			
3474		10000773	Streptococcus mutans MT 8148	40	12	40	12		
3475		10000775	Streptococcus pyogenes 156	1		1			
3476		10000776	Streptococcus pyogenes 88/25	1		1			
3477		10000777	Streptococcus pyogenes 88/30	1		1			
3478		10000778	Streptococcus pyogenes 88/544	1		1			
3479		10000779	Streptococcus pyogenes 90/85	1		1			
3480		10000780	Streptococcus pyogenes serotype M12 A374	1		1			
3481		10000781	Streptococcus pyogenes BSA10	3		3			
3482		10000782	Streptococcus pyogenes NS1	1		1			
3483		10000783	Streptococcus pyogenes NS14	1		1			
3484		10000784	Streptococcus pyogenes NS27	1		1			
3485		10000785	Streptococcus pyogenes NS5	1		1			
3486		10000786	Streptococcus pyogenes serotype M11	2		2			
3487		10000787	Streptococcus pyogenes serotype M13	1		1			
3488		10000788	Streptococcus pyogenes serotype M22	1		1			
3489		10000789	Streptococcus pyogenes serotype M24	6	2	6	2		
3490		10000790	Streptococcus pyogenes serotype M30	1		1			
3491		10000791	Streptococcus pyogenes serotype M41	1		1			
3492		10000792	Streptococcus pyogenes serotype M52	1		1			
3493		10000793	Streptococcus pyogenes serotype M54	1		1			
3494		10000794	Streptococcus pyogenes serotype M55	1		1			
3495		10000795	Streptococcus pyogenes serotype M57	1		1			
3496		10000796	Streptococcus pyogenes serotype M60	1		1			
3497		10000797	Streptococcus pyogenes serotype M75	1		1			
3498		10000798	Streptococcus pyogenes serotype M8	1		1			
3499		10000801	Foot-and-mouth disease virus - type O (O/SKR/2002)	1		1			
3500		10000802	Taenia crassiceps Strain ORF	3	3	3	3		
3501		10000804	Chlamydia trachomatis Serovar B	47	5	47	5		
3502		10000806	Foot-and-mouth disease virus (strain O1) (O1 Manisa)	5		6	1	1	1
3503		10000807	Haemophilus influenzae NTHi UC19	2	2	2	2		
3504		10000809	Swine vesicular disease virus ITL/1/66	1		1			
3505		10000814	Leptospira interrogans serovar Lai str. HY-1	1		1			
3506		10000815	Pseudomonas aeruginosa PAO	2	2	2	2		
3507		10000816	Plasmodium falciparum T9/96	1	1	1	1		
3508		10000817	Pseudomonas aeruginosa KB7	2		2			
3509		10000818	Pseudomonas aeruginosa P1	1		1			

3510		10000820	Foot-and-mouth disease virus (strain O1) (O/Taiwan/1/97)	1		1			
3511		10000822	Pseudomonas aeruginosa Immunotype 3	1		1			
3512		10000824	Streptococcus pyogenes serotype M6 strain D471	4		4			
3513		10000825	Infectious bronchitis virus Avian strain D207	11		11			
3514		10000828	Ajellomyces dermatitidis ATCC 60636		2		2		
3515		10000829	Norovirus genogroup 2 Mexico type strain 36	3		3			
3516		10000832	Norovirus genogroup 2 Camberwell 1890	1		1			
3517		10000833	Haemophilus influenzae NTHi 1128	6		6			
3518		10000835	Equine rhinitis A virus 393/76	4		4			
3519		10000836	Foot-and-mouth disease virus C1 CS8	22	24	22	24		
3520		10000840	Foot-and-mouth disease virus C1 Brescia It/64	2		2			
3521		10000842	Swine vesicular disease virus NET/1/92	1		1			
3522		10000843	Neisseria meningitidis serogroup B H44/76	74	22	74	22		
3523		10000845	Chlamydia trachomatis Serovar F	3		3			
3524		10000848	Theileria sergenti Type B1		1		1		
3525		10000849	Theileria sergenti Type B2		2		2		
3526		10000850	Theileria sergenti Type C		5		5		
3527		10000851	Theileria sergenti Type I		1		1		
3528		10000852	Chlamydophila pneumoniae Kajaani 6		7		7		
3529		10000853	Chlamydia trachomatis Serovar L1	21	3	21	3		
3530		10000855	Theiler's murine encephalomyelitis virus (strain BeAn 8386) (variant M2)		1		1		
3531		10000856	Foot-and-mouth disease virus - type O isolate O/UKG/35/2001		14		14		
3533		10000858	Chlamydia trachomatis B/Jali-20/OT	2		2			
3534		10000859	Porcine respiratory and reproductive syndrome virus JA142	1		1			
3535		10000860	Haemophilus influenzae Serotype B	18	9	18	9		
3536		10000861	Haemophilus influenzae Variant d1	18		18			
3537		10000862	Plasmodium vivax VK247	1		1			
3538		10000863	Neisseria gonorrhoeae 4505	1		1			
3539		10000864	Porcine respiratory and reproductive syndrome virus MD-001	2		2			
3540		10000865	Influenza A virus H3N2 (A/Kiev/301/94)	3		3			
3541		10000888	Porcine respiratory and reproductive syndrome virus Olot/91	3	5	3	5		
3542		10000890	Porcine respiratory and reproductive syndrome virus SD92-23983		33		33		
3543		10000960	Human respiratory syncytial virus A Mon/3/88	6		6			
3544		10000961	Dengue virus type 1 strain 16007	15		15			
3545		10000964	Foot-and-mouth disease virus (strain O1) (O1 Brugge)	2		2			

3546		10000965	Dengue virus type 1 FGA/89	4		4			
3547		10000968	Hepatitis C virus subtype 1b isolate BE-11	3		3			
3548		10000969	Porcine respiratory and reproductive syndrome virus 111/92	9		9			
3549		10000971	West Nile virus NY-99	15	21	15	21		
3550		10000972	Neisseria meningitidis serogroup B Strain B16.B6	1		1			
3551		10000979	Neisseria meningitidis serogroup B Strain 8047	4		4			
3552		10000980	Arcanobacterium pyogenes Strain 42	4		4			
3553		10000986	Foot-and-mouth disease virus C1 CS30	1		1			
3554		10000987	Human rhinovirus 2 Vienna	5		5			
3555		10000989	Foot-and-mouth disease virus - type A (strain A22)	8	6	8	6		
3556		10000991	Foot-and-mouth disease virus - type A (strain A22 Iraq)	5	1	5	1		
3557		10000992	Foot-and-mouth disease virus - type SAT 1 (Strain Bot 1/68)	1		1			
3558		10000993	Foot-and-mouth disease virus - type SAT 2 (Strain Ken 3/57)	1		1			
3559		10000994	Foot-and-mouth disease virus - type SAT 3 (Strain Bec 1/65)	1		1			
3560		10000995	Foot-and-mouth disease virus - type Asia 1 Pakistan	1		1			
3561		10001000	Foot-and-mouth disease virus - type SAT 2 (strain Rho 1/48)	4		4			
3562		10001002	Swine vesicular disease virus SPA/1/93	16		16			
3563		10001003	Neisseria meningitidis serogroup B CU385	2		2			
3564		10001004	Human T-cell lymphotropic virus type 1 (Caribbean isolate) (Strain HS35)	1		1			
3565		10001006	Proteus mirabilis CFT322	1		1			
3566		10001008	Chlamydia trachomatis Serovar J	6		6			
3567		10001019	Mus musculus B10.D2		1		1		
3568		10001020	Peste-des-petits-ruminants virus (strain Nigeria 75/1)		1		1		
3569		10001021	Treponema pallidum subsp. pallidum (strain Chicago)	19		19			
3570		10001025	Classical swine fever virus Glentorf		26		26		
3571		10001027	Vaccinia virus Connaught	1		1			
3572		10001028	Human poliovirus 2 (strain MEF-1)	1		1			
3573		10001032	Newcastle disease virus (strain La Sota)	1		17		16	
3574		10001039	Foot-and-mouth disease virus C3 (strain Resendne-Br/55)	1		1			
3575		10001040	Human poliovirus 2 (strain Sabin)	2	7	2	7		
3576		10001042	Haemophilus influenzae NTHi 1479	12	4	12	4		
3577		10001044	Neisseria meningitidis serogroup C MC51	1		1			
3578		10001047	West Nile virus strain 2741	32		32			
3579		10001049	Neisseria meningitidis serogroup B Strain S3446	1		1			
3580		10001050	Neisseria meningitidis serogroup B Strain 7967	1		1			
3581		10001051	Neisseria meningitidis serogroup A Strain 8659	1		1			

3582		10001053	Haemophilus influenzae MinnA	9		9			
3583		10001055	Haemophilus influenzae 6U	2		2			
3584		10001056	Haemophilus influenzae ATCC 9795	2		2			
3585		10001057	Pseudomonas aeruginosa CD4	1		1			
3586		10001058	Pseudomonas aeruginosa K122-4	1		1			
3587		10001077	Neisseria gonorrhoeae SU89	1		1			
3588		10001078	Neisseria gonorrhoeae SU96	3		3			
3589		10001081	Porphyromonas gingivalis HG66	2		2			
3590		10001085	Chlamydia trachomatis Serovar D	3		3			
3591		10001091	Borrelia burgdorferi BEP4	1		1			
3592		10001097	Sus scrofa Yorkshire	1		1			
3593		10001100	Plum pox virus (strain W)	6		6			
3594		10001102	Foot-and-mouth disease virus (strain O1) O/UKG/11/2001	1	1	1	1		
3595		10001116	Norovirus genogroup 1 isolates 96-908	4		4			
3596		10001118	Foot-and-mouth disease virus - type O (strain HKN/14/82)	2		2			
3597		10001120	Cryptococcus neoformans var. neoformans Serotype D	1		1			
3598		10001121	Chlamydia trachomatis Serovar Da	1		1			
3599		10001130	Feline leukemia virus subtype A	2		2			
3600		10001132	Cryptococcus neoformans var. neoformans Serotype A	1		1			
3601		10001133	Rattus norvegicus DA		3		3		
3602		10001138	Newcastle disease virus (strain Eaves)	1		1			
3603		10001140	Newcastle disease virus (strain WA2116)	1		1			
3604		10001141	Chlamydia trachomatis Serovar A	22	8	22	8		
3605		10001145	Escherichia coli 1471	2		2			
3606		10001149	Haemophilus influenzae Subtype 1H	23		23			
3607		10001150	Haemophilus influenzae Strain Eagan	58		58			
3608		10001154	Transmissible gastroenteritis virus MAD88	8	1	8	1		
3609		10001155	Haemophilus influenzae strain 1479	2		2			
3610		10001156	Hepatitis B virus subtype AD	3	2	3	2		
3611		10001157	H3N2 subtype Influenza A virus (A/Hong Kong(H3N2))		15		15		
3612		10001161	Neisseria meningitidis serogroup B Strain 2996	1		1			
3613		10001162	Neisseria meningitidis serogroup B Strain M1239	4		4			
3614		10001207	Murine leukemia virus LP-BM5		1		1		
3615		10001209	Tobacco mosaic virus (strain PM5)	1		1			
3616		10001210	Tobacco mosaic virus (strain Ni568)	1		1			
3617		10001213	Human coxsackievirus B3 (strain RK)	1		1			
3618		10001215	Human rotavirus G9 WI61	1		1			
3619		10001216	Rotavirus G3 strain RV-3	1		1			
3620		10001223	Porphyromonas gingivalis OMZ 409	23		23			

3621		10001225	H1N1 subtype Influenza A/Oklahoma/7485/01		5		5		
3622		10001238	Puumala virus (strain Umea/hu)	1		1			
3623		10001239	Porcine circovirus strain ISU31	7		7			
3624		10001243	Theileria parva strain Markebuni		1		1		
3625		10001307	Small ruminant lentivirus strain It-561	1		1			
3626		10001308	Small ruminant lentivirus strain It-Pt1	1		1			
3627		10001315	H1N1 swine influenza virus (A/swine/Korea/S10/2004(H1N1))		3		3		
3628		10001316	H1N1 swine influenza virus (A/swine/Korea/S175/2004(H1N1))		1		1		
3629		10001317	H9N2 subtype Influenza A virus (A/swine/Korea/S81/2004(H9N2))		1		1		
3630		10001318	H9N2 subtype Influenza A virus (A/swine/Korea/S83/2004(H9N2))		2		2		
3631		10001335	Japanese encephalitis virus Vellore P20778	1	1	1	1		
3632		10001392	Human adenovirus B strain Harbin04B	5		5			
3633		10001396	Murine cytomegalovirus (strain Smith) MW97.01		5		5		
3634		10001412	Rattus norvegicus Wistar-Furth		11		11		
3635		10001424	Brucella abortus W99	1		1			
3636		10001431	Infectious bronchitis virus CK/CH/LDL/97I	1		1			
3637		10001439	Streptococcus sanguinis strain BD113-20		6		6		
3638		10001456	Human respiratory syncytial virus A strain RGH	1		1			
3639		10001459	Babesia bovis Argentina R1A	4		4			
3640		10001484	Norovirus genogroup 1 GI.12	1		1			
3641		10001485	Norovirus genogroup 3 GIII.1	1		1			
3642		10001489	Proteus vulgaris Strain 5/43	1		1			
3643		10001490	Proteus mirabilis O24	1		1			
3644		10001491	Proteus mirabilis O29	1		1			
3645		10001492	Salmonella enterica subsp. enterica serovar Enteritidis SH1262	3		3			
3647		10001498	Proteus mirabilis O23	1		1			
3648		10001499	Proteus mirabilis O6	1		1			
3649		10001500	Proteus mirabilis O43	1		1			
3650		10001501	Proteus penneri ATCC 33519	1		1			
3651		10001502	Escherichia coli J-5	1		1			
3652		10001503	Acinetobacter lwoffii F78	1		1			
3653		10001504	Yokenella regensburgei PCM 2476	1		1			
3654		10001505	Yokenella regensburgei PCM 2477	1		1			
3655		10001511	Salmonella 'group A'	2		2			
3656		10001514	Providencia stuartii O33	1		1			
3657		10001519	Pseudomonas aeruginosa serotype O11	1		1			
3658		10001520	Haemophilus influenzae strain RM7004	1		1			
3659		10001523	Haemophilus influenzae strain I-69 Rd-/b+	4		4			

3660		10001524	Neisseria meningitidis strain 3006	1		1			
3661		10001526	Salmonella thompson C1 strain IS40	1		1			
3662		10001528	Escherichia coli F515	1		1			
3663		10001530	Acinetobacter haemolyticus strain 57	1		1			
3664		10001531	Acinetobacter haemolyticus strain 61	1		1			
3665		10001556	Moraxella catarrhalis 26404	1		1			
3666		10001558	Neisseria gonorrhoeae 15253	1		1			
3667		10001560	Neisseria meningitidis M982B	2		5		3	
3668		10001569	Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 11	1		1			
3669		10001570	Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 77	1		1			
3670		10001573	Anatid herpesvirus 1 Clone-03	1		1			
3671		10001578	Classical swine fever virus LPC/AHRI	4		4			
3672		10001581	Proteus penneri 8 (O67)	1		1			
3673		10001582	Dengue virus 1 Mochizuki	4		4			
3674		10001583	Dengue virus 2 New Guinea C	1	4	1	38		34
3675		10001586	Porcine reproductive and respiratory syndrome virus 07V063	3		3			
3676		10001587	Porcine reproductive and respiratory syndrome virus 08V204	2		2			
3677		10001588	Providencia stuartii O4	1		1			
3679		10001606	Norovirus genogroup 2 Hu/NoV/Farmington Hills/2002/USA	1	2	1	2		
3680		10001614	Junin virus strain MC2		1		1		
3681		10001615	Machupo virus strain Carvallo		1		1		
3682		10001616	Guanarito virus strain INH-95551		1		1		
3683		10001617	Whitewater Arroyo virus strain AV9310135		1		1		
3684		10001618	Pichinde virus strain Munchique		1		1		
3685		10001619	Dengue virus 3 strain 16652	16		16			
3686		10001624	Feline infectious peritonitis virus (strain KU-2)	22	43	22	43		
3687		10001627	Human herpesvirus 5 (strain RV798)		6		6		
3688		10001628	Aggregatibacter actinomycetemcomitans serotype b str. Y4	1		1			
3689		10001633	Escherichia coli 055:B5	3		3			
3690		10001635	Dengue virus 2 PL046		7		7		
3691		10001636	Dengue virus 2 S221		42		42		
3692		10001638	Streptococcus pneumoniae type 27	2		2			
3693		10001641	Streptococcus dysgalactiae subsp. equisimilis D181	1		1			
3694		10001642	Foot-and-mouth disease virus - type O Wuppertal/FRG/82		1		1		
3695		10001644	Streptococcus pneumoniae CCUG 1378	1		1			
3696		10001645	Streptococcus pneumoniae CSR-SCS-2	1		1			
3697		10001646	Streptococcus pneumoniae type 37	2		2			
3698		10001648	Japanese encephalitis virus strain SA-14 -14-2	2		2			

3699		10001649	West Nile virus strain 956	1		1			
3700		10001651	Streptococcus pneumoniae type 14	19		19			
3701		10001652	Candida albicans NIH B-792 (serotype B)	1		1			
3702		10001659	Escherichia coli O125	1		1			
3703		10001662	Staphylococcus aureus Cowan 1	2		2			
3704		10001663	Streptococcus anginosus K214-2K	4		4			
3705		10001667	Helicobacter pylori 487	1		1			
3706		10001676	Streptococcus dysgalactiae subsp. equisimilis ATCC 12388	2		2			
3707		10001686	Streptococcus pneumoniae type 6A	2		2			
3708		10001687	Streptococcus pneumoniae type 6B	5		5			
3709		10001688	Pseudomonas syringae pv. atrofaciens str. IMV 7836	1		1			
3710		10001689	Pseudomonas syringae pv. atrofaciens str. IMV K-1025	1		1			
3711		10001690	Pseudomonas syringae pv. atrofaciens str. IMV 4394	1		1			
3712		10001693	Pseudomonas syringae pv. tagetis str. ICMP 6370	1		1			
3713		10001697	Pseudomonas syringae pv. phaseolicola str. IMV 120a	1		1			
3714		10001698	Pseudomonas syringae pv. morsprunorum str. GSPB 883	1		1			
3715		10001700	Pseudomonas syringae pv. morsprunorum str. CFBP 1650	1		1			
3716		10001705	Dengue virus 2 strain 43	1		2		1	
3717		10001713	Neisseria meningitidis serogroup W- 135	1		1			
3718		10001722	Salmonella 'group D'	3		3			
3719		10001730	Streptococcus pneumoniae type 6C	1		1			
3720		10001731	Streptococcus pneumoniae type 2	8		8			
3722		10001740	Candida glabrata IFO 0622	1		1			
3723		10001747	Candida parapsilosis M1015	1		1			
3724		10001761	BK polyomavirus strain Dunlop		1		1		
3725		10001762	JC polyomavirus strain MAD1		1		1		
3726		10001763	Simian virus 40 strain 776		1		1		
3727		10001764	Classical swine fever virus Margarita (AJ704817)	4	1	4	1		
3728		10001768	Dengue virus 2 S-16803	1		1			
3729		10001771	Porcine reproductive and respiratory syndrome virus HuN4- F112	4	1	4	1		
3730		10001783	Neisseria meningitidis serogroup C strain C11	1	1	1	1		
3731		10001792	Streptococcus pneumoniae type 3	6		6			
3732		10001794	Helicobacter pylori B128 Gerbil- adapted variant 7.13	1		1			
3734		10001797	Neisseria meningitidis serogroup C strain MC19	1		1			
3735		10001798	Porcine transmissible gastroenteritis coronavirus strain Pur46-MAD	4		4			
3736		10001800	Porcine reproductive and respiratory syndrome virus HuN4	1	4	4	4	3	
3737		10001801	Streptococcus pneumoniae type 8	10		10			
3738		10001831	Moraxella catarrhalis serotype B	1		1			

3740		10001835	Proteus penneri 7 (O61)	2		2			
3741		10001836	Proteus penneri 14 (O59)	2		2			
3742		10001837	Proteus penneri 15 (O52)	2		2			
3743		10001847	Clostridium difficile BI / NAP1/ 027	1		1			
3744		10001849	Moraxella catarrhalis serotype A	3		3			
3745		10001851	Moraxella catarrhalis serotype C	1		1			
3746		10001860	Neisseria meningitidis serogroup X	3		3			
3747		10001879	West Nile virus strain 68856	2		2			
3748		10001881	Porcine circovirus 2 -A	3		3			
3750		10001886	Brucella ovis 020	2		2			
3751		10001887	Brucella ovis Reo 198	1		1			
3752		10001888	Brucella ovis 63/290	1		1			
3754		10001895	Yersinia pseudotuberculosis str. 32777		1		1		
3755		10001900	Streptococcus agalactiae serogroup III M781	1	1	1	1		
3756		10001902	Human enterovirus 71 NUH0083/SIN/08	4		4			
3757		10001913	Lactobacillus johnsonii JCM 1022	3		3			
3758		10001918	Muscovy duck reovirus S12	2		4		2	
3759		10001929	Equine rhinitis B virus 2 strain 313/75	5		5			
3760		10001930	Equine rhinitis B virus 3 isolate 2225AS	5		5			
3761		10001934	Chikungunya virus Singapore/11/2008	3		3			
3762		10001943	Dengue virus 4 Burma/63632/1976	3		3			
3763		10001944	Dengue virus 3 Thailand/PaH881/1988	2		2			
3764		10001945	Dengue virus 1 PVP159	2		2			
3765		10001946	Foot-and-mouth disease virus - type Asia 1 YS/CHA/05	4		4			
3766		10001964	Porcine circovirus 1 strain 1/G	7		7			
3767		10001965	Avian leukosis virus strain NX0101	1		1			
3768		10001967	Avian leukosis virus isolate CAUHM01	1		1			
3769		10001973	Vaccinia virus Acambis 2000	8		8			
3770		10001975	Streptococcus salivarius JCM 5707	1		1			
3771		10001997	Chikungunya virus strain LR2006OPY1 IMT/Reunion Island/2006	1		1			
3772		10001999	Reticuloendotheliosis virus strain HLJ07I	1		1			
3773		10002000	Porcine epidemic diarrhea virus CH/SHH/06	1		1			
3774		10002003	Campylobacter jejuni subsp. jejuni serotype HS:15	1		1			
3775		10002006	Bluetongue virus 16 BN96/16	2		2			
3776		10002007	Plasmodium falciparum isolate UAS22	4		4			
3777		10002008	Plasmodium falciparum isolate UAS31	1		1			
3778		10002009	Plasmodium falciparum isolate UAS29	2		2			
3779		10002010	Dengue virus 2 D2/SG/05K4155DK1/2005		49		49		

3780		10002011	Plasmodium falciparum R29/IT4	1		1			
3781		10002015	Human coxsackievirus A16 shzh05-1	92		92			
3782		10002018	Bovine coronavirus Kakegawa	1		1			
3783		10002020	Foot-and-mouth disease virus - type Asia 1 Nepal 29/97	4		4			
3784		10002022	Escherichia coli O6 O6:K15:H31		1		1		
3785		10002026	Murine norovirus 1 Mu/NoV/GV/MNV1/2002/USA		1		1		
3786		10002027	Bluetongue virus 16 Kumamoto/1985	2		2			
3787		10002028	Bluetongue virus 16 Beatrice Hill/1987	2		2			
3788		10002034	Fish	4		4			
3789		10002052	Toxoplasma gondii Gansu Jingtai	27		27			
3790		10002056	Enterovirus A71 TW/2086/98	1		1			
3791		10002069	Bordetella pertussis 509		7		7		
3792		10002079	Clostridium difficile VPI 10463	2		2			
3793		10002082	Rhesus rotavirus MMU 18006		3		3		
3794		10002089	Porcine reproductive and respiratory syndrome virus SY0608	17		17			
3795		10002090	Influenza A virus (A/swine/Denmark/101310-1/2011(H1N1))		7		7		
3796		10002111	Dengue virus 4 TVP-376	1		1			
3797		10002112	Dengue virus 4 1036	1		1			
3798		10002121	Staphylococcus aureus Reynolds	2		2			
3799		10002122	Staphylococcus aureus Becker	2		2			
3800		10002123	Peste-des-petits-ruminants virus China/Tibet/Geg/07-30	53		53			
3801		10002127	Escherichia coli O86:B7	1		1			
3802		10002129	Staphylococcus aureus RN4850	1		1			
3803		10002132	Duck hepatitis A virus 1 HP-1	2		2			
3805		10002148	Dengue virus 4 Mexico/BC287/1997	1		1			
3806		10002151	Duck hepatitis A virus 1 LY0801	1		1			
3807		10002152	Duck hepatitis A virus 3 SD1201	1		1			
3808		10002161	Streptococcus pneumoniae type 1	5		5			
3809		10002165	Avian infectious bronchitis virus (strain CHINA/Sczy3/09)	2		2			
3810		10002169	Avian infectious bronchitis virus (strain Holte)		2		2		
3812		10002183	ZIKV/H. sapiens/French Polynesia/PF13/2013	4		4			
3813	X	10002188	ZIKV/H. sapiens/PRI/PRVABC59/2015				5		5
3814		10002190	ZIKV/H. sapiens/Uganda/MR-766/1947	4		4			
3815		10002192	Streptococcus suis 1178027	2		2			
3817		10002196	Hepatitis E virus type 4 JAK-Sai	1		1			
3818		10002197	Chikungunya virus MY/08/065	15		15			
3820		10002238	Influenza A virus (A/swan/Poland/305-135V08/2006(H5N1))	1		1			
3821		10002272	Streptococcus pneumoniae 7F	5		5			

3822		10002273	Influenza A virus (A/Hong Kong/4801/2014(H3N2))		1		1		
3823	X	10002285	Yellow fever virus CNYF01/2016			1		1	
3824	X	10002287	Salmonella enterica subsp. enterica serovar Typhi str. Quailes				1		1
3825		10002289	Enterobacteria phage PRD1	2		2			
<b>Total</b>				50617	461348	55918	541508	5301	80160

## 2 Website Features

In 2019, the IEDB adopted an agile, continuous deployment methodology, whereby weekly, iterative updates were deployed to the IEDB external website (3.10). Changes of note include:

- Updated finders to have close and expand/shrink tree buttons
- Updated Banner Messages to “Upcoming Events” to allow displaying a calendar of events for the year
- Updated Allele Finder to use full display names for the search results tables, so users can more clearly identify search hits
- Redesigned CSV Export delivery by providing a new download page that allows the export to run in the background window, making the export file link available for 24 hours
- Revised CSV Export design to retrieve data in segments, allowing epitope/assay exports to function on very large sets of data
- Updated Assay Details pages to move carrier information into comments fields
- Upgraded external build and searches to support new standard finder design for Disease Finder
- Removed/consolidated fields from Details pages that were previously removed from curation since the fields were rarely used

In addition to feature updates and improvements, many outstanding bugs and defects were also addressed throughout the contract year.

In addition, there were two major releases (Releases 2.21 and 2.22) of the Analysis Resource since the 2018 Annual Compendium plus numerous smaller updates made throughout the year. Changes of note include:

- Launch of new structure tool - Structural Complexes of Epitope Receptor (SCEptRe)
- Incorporation of new structure tool - Docktope
- Performance enhancements for CD4episcore
- Performance enhancements for the Deimmunization tool
- Improved sequence format detection for MHC I binding, MHC II binding, Deimmunization and Tepitool
- NetMHCpan 4.0 EL mode has been added to the class I binding predictor (web, API, standalone), as well as an option in MHCNP
- Class II binding predictor now allows prediction for various lengths (11-30)
- NetMHCIIPan 3.2 and NetMHCIIPan 2.3 have been added to the class II binding predictor (web, API, standalone)
- DNA fasta sequences input detection and reminder on web page and standalone tool
- Additional input validation added to APIs
- Optimization of automated benchmark dataset downloads
- Stability improvements and performance enhancements throughout

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

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

## 2.1 Home Page

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

The top box in the left column contains a welcome statement that briefly describes the content of the database. It also has a “Learn More” link that brings the user to a web page containing more information about the support and user help features available, about the data itself, and about the IEDB program. This page is described in detail in Section 2.6. The Summary Metrics are displayed in the bottom box of this column. These numbers are intended to be a gauge of the volume of data available in the system. The Summary Metrics provide the number of epitopes (peptidic and non-peptidic), assays (T cell, B cell, and MHC ligand assays), epitope source organisms, restricting MHC alleles, and references. A middle box may appear (as shown in Figure 2.1) when there are special messages to convey to users. The text will appear in red. The middle column contains the initial search interface that is described in detail in Section 2.2.1. This section includes several finders on the search interface, thus enabling more complete queries without the need for further filtering of the results. The rightmost column has links to the most frequently used tools in the Analysis Resource.

The screenshot shows the IEDB 3.10 Home page with the following layout:

- Welcome:** Contains a brief introduction to the IEDB, mentioning it is a freely available resource funded by NIAID, and a "Learn More" link.
- Upcoming Events:** Lists events such as a virtual tour on June 17, a webinar recording, a FOCIS Booth on Oct 28-31, and a User Workshop on Nov 5-6, with a link to register.
- Summary Metrics:** Displays various statistics:

Peptidic Epitopes	738,607
Non-Peptidic Epitopes	3,002
T Cell Assays	377,701
B Cell Assays	544,776
MHC Ligand Assays	1,629,184
Epitope Source Organisms	3,943
Restricting MHC Alleles	829
References	21,325
- START YOUR SEARCH HERE:** A search interface with four main sections:
  - Epitope:** Options for Any Epitopes, Linear Epitope, Discontinuous Epitopes, Non-peptidic Epitopes, and a search field (Exact Match) with example "SIINFEKL".
  - Assay:** Options for Positive Assays Only, T Cell Assays, B Cell Assays, and MHC Ligand Assays, with a search field (Exact Match) for "neutralization" and a "Find" button.
  - Antigen:** Options for Organism (example: influenza, peanut) and Antigen Name (example: core, capsid, myosin).
  - MHC Restriction:** Options for Any MHC Restriction, MHC Class I, MHC Class II, MHC Nonclassical, and a search field (Exact Match) for "HLA-A\*02:01" with a "Find" button.
- Epitope Analysis Resource:** A column of links to various tools:
  - T Cell Epitope Prediction:** Scan an antigen sequence for amino acid patterns indicative of: MHC I Binding, MHC II Binding, MHC I Processing (Proteasome, TAP), and MHC I Immunogenicity.
  - B Cell Epitope Prediction:** Predict linear B cell epitopes using: Antigen Sequence Properties, Predict discontinuous B cell epitopes using antigen structure via: Discotope, ElliPro.
  - Epitope Analysis Tools:** Analyze epitope sets of: Population Coverage, Conservation Across Antigens, Clusters with Similar Sequences.

At the bottom, there are links for "Provide Feedback", "Help Request", "Solutions Center", "Tool Licensing Information", and "Last Updated: July 19, 2020".

Figure 2.1 IEDB 3.10 Home page

## 2.2 *Query*

There are several ways users can find information in the IEDB. A simplified search that is especially designed for the needs of most immunologists appears on the home page. This document will refer to this particular query as the Simple Search or Home Page Search. A family of advanced query-by-example searches can be accessed on the Search pull-down menu and consist of “Epitope Details”, “T Cell Assay Details”, “B Cell Assay Details”, “MHC Assay Details”, “Identifier Search”, and “Browse by 3D Structure”. This group of queries are referred to as Specialized Searches. All of these methods return results in a common format, as described in Section 2.2.3. These methods are elaborated in the subsections below.

### 2.2.1 Perform a Home Page Search

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

The results of the query are displayed in five tabs – Epitopes, Antigens, Assays, Receptors, and References. The Epitopes tab lists the epitope description, such as the amino acid sequence for linear epitopes, its associated antigen and source organism, the number of references in which it appears, and the number of assays in which it is used. The Antigen tab lists the antigen, its source organism, and the number of related epitopes, assays, and references. The Assays tab contains three tabs, one each for T cell, B cell, and MHC ligand assays. The Receptors tab details the receptor types alongside the sequences of each chain component, and is divided into two separate tabs for T Cell Receptors (TCRs) and B Cell Receptors (BCRs). The References tab lists the IEDB-specific reference identifier, the authors, title, abstract, and year of publication or submission. A user can cross-query specific criteria from any of these five tabs; for example, filtering on a specific assay would refresh the results to display data across all tabs which is only relevant to that assay. Additionally, a user can click on the IEDB-specific identifier link to drill down to get additional information about the epitope, assay, receptor or reference.

**START YOUR SEARCH HERE ?**

<b>Epitope ?</b>	<b>Assay ?</b>
<input checked="" type="radio"/> Any Epitopes <input type="radio"/> Linear Epitope <input type="radio"/> Discontinuous Epitopes <input type="radio"/> Non-peptidic Epitopes Exact M ▾ Ex: SIINFEKL <input type="button" value="Find"/>	<input checked="" type="checkbox"/> Positive Assays Only <input checked="" type="checkbox"/> T Cell Assays <input checked="" type="checkbox"/> B Cell Assays <input checked="" type="checkbox"/> MHC Ligand Assays Ex: neutralization <input type="button" value="Find"/>
<b>Antigen ?</b>	<b>MHC Restriction ?</b>
Organism Ex: influenza, peanut Antigen Name Ex: core, capsid, myosin	<input checked="" type="radio"/> Any MHC Restriction <input type="radio"/> MHC Class I <input type="radio"/> MHC Class II <input type="radio"/> MHC Nonclassical Ex: HLA-A*02:01 <input type="button" value="Find"/>
<b>Host ?</b>	<b>Disease ?</b>
<input checked="" type="radio"/> Any Host <input type="radio"/> Humans <input type="radio"/> Mice <input type="radio"/> Non-human Primates Ex: dog, camel <input type="button" value="Find"/>	<input checked="" type="radio"/> Any Disease <input type="radio"/> Infectious Disease <input type="radio"/> Allergic Disease <input type="radio"/> Autoimmune Disease Ex: asthma, diabet <input type="button" value="Find"/>
<input type="button" value="Reset"/> <input type="button" value="Search"/>	

**Figure 2.2** Home page simple search

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

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

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

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

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

Epitopes (5)		Antigens (1)		Assays (10)		Receptors (0)		References (7)	
<a href="#">Go To Records Starting At 1200</a> <a href="#">GO</a> <a href="#">Export Results</a>									
5 Records Found <a href="#">Page 1 of 1</a> <a href="#">25 Per Page</a>									
Details	Epitope	Antigen	Organism	# References	# Assays				
1055	AELLVALEN	Hemagglutinin	Influenza A virus	2	5				
1056	AELLVALENQHTIDL	Hemagglutinin	Influenza A virus	2	2				
50489	QDLEKYVEDTKIDLWSYNAEL LVALENQHTIDLTS	Hemagglutinin	Influenza A virus	1	1				
124806	VALENQHTI	Hemagglutinin	Influenza A virus	1	1				
130384	YNAELLVALENQHTIDL	Hemagglutinin	Influenza A virus	1	1				

5 Records Found [Page 1 of 1](#) [25 Per Page](#) [Go To Records Starting At 1200](#) [GO](#) [Export Results](#)

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

## 2.2.2 Specialized Searches

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

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

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

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

Details	Epitope	Antigen	Organism	# References	# Assays
123885	cardiolipin			327	1228
44920	NLVPMVATV	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	314	786
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	236	644
58560	SINFEKL	Gal α 2	Gallus gallus (chicken)	194	516
113645	MEVGWYRSPFSSRVRVHLRNGK	Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	192	1054
4602	ASNEENMETM	Nucleoprotein	Influenza A virus	155	481
20788	GLCTLVAML	mRNA export factor ICP27 homolog	Human herpesvirus 4 (Epstein Barr virus)	149	329
112741	2,4-dinitrophenyl group			142	576
130694	1-O-(alpha-D-galactosyl)-N-hexacosanoylphytosphingosine			131	634
48237	PKYVKQNTLKLAT	Hemagglutinin	Influenza A virus	125	484
24786	HSLGKWLGHFDK:F	Myelin proteolipid protein	Mus musculus (mouse)	122	799
6435	CINGVCWTW	Genome polyprotein	Hepatitis C virus	116	340
112742	2,4,6-trinitrophenyl group			110	353
53112	RAHYNIVTF	Protein E7	Alphapapillomavirus 9	108	292
130649	alpha-D-Galp(1->3)-beta-D-Galp-(1->4)-D-GlcNAc-yl group	N-glycan		108	458
32208	KLVALGINAV	Genome polyprotein	Hepatitis C virus	104	333
65748	TPRVTGGGAM	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	102	206
16833	FLPSDFPPSV	Capsid protein	Hepatitis B virus (hepatitis B virus (HBV))	98	307
61086	SSIEFARL	Envelope glycoprotein B	Human herpesvirus 1	97	339
6568	CLGGLLTMV	Latent membrane protein 2	Human herpesvirus 4 (Epstein Barr virus)	95	281
30001	KAVYNFATC	Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus (Lymphocytic choriomeningitis virus)	92	284
61151	SSLENFRAYV	Polymerase acidic protein	Influenza A virus	91	288
16878	FLRGRAYGL	Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	89	276
17516	FQPQNQFQI	Nucleoprotein	Lymphocytic choriomeningitis mammarenavirus (Lymphocytic choriomeningitis virus)	88	224
67436	TYQRTRALV	Nucleoprotein	Influenza A virus	85	203

Figure 2.4 Epitope Specialized Search input screen

**Epitope** 

Epitope ID	Ex: 44920	
Structure Type - Any Epitopes		
Organism	Ex: influenza, Peanut	
Antigen Name	Ex: core, capsid, myosin	
<b>Epitope Reference Details</b>		
Epitope Structure Defines	Select Multiple Options	
Evidence Code for Source...	Select Multiple Options	
Epitope Name	Ex: Fab-12 epitope	
Reference Start Position	Ex: 124	to Ex: 130
Reference End Position	Ex: 130	to Ex: 130
Reference Region	Ex: Reference Region	
Comments	Ex: comments	
Data Location in Reference	Ex: location_of_data_in_reference	
<b>Epitope Related Object</b>		
Related Object	Select Multiple Options	
Type - Any Type		
Organism	Ex: influenza, Peanut	
Antigen Name	Ex: core, capsid, myosin	

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

**Epitope** 

Epitope ID	Ex: 44920	
Structure Type - Linear Epitopes		
Linear Sequence	Ex: SIINFEKL	
Match	Exact Matches	
Modified Residue(s)	Ex: T10	
Modification(s)	Select Multiple Options	
Organism	Ex: influenza, Peanut	
Antigen Name	Ex: core, capsid, myosin	
Starting Position	Ex: 124	to Ex: 124
Ending Position	Ex: 130	to Ex: 130
<b>Epitope Reference Details</b>		
<b>Epitope Related Object</b>		

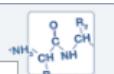
**Figure 2.6** Epitope query fields in the Advanced Search for Linear peptide epitopes

**Epitope** 

Epitope ID	Ex: 44920	
Structure Type - Discontinuous Epitopes		
Discontinuous Residues	Ex: E170, E172	
Modified Residue(s)	Ex: T10	
Modification(s)	Select Multiple Options	
Organism	Ex: influenza, Peanut	
Antigen Name	Ex: core, capsid, myosin	
 Epitope Reference Details		
 Epitope Related Object		

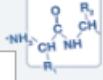
**Figure 2.7** Epitope query fields in the Advanced Search for Discontinuous peptide epitopes

**Epitope** 

Epitope ID	Ex: 44920	
Structure Type - Discontinuous Peptides on Multi Chain		
Molecule Name	Ex: Vascular endothelial growth factor	
Discontinuous Residues	Ex: E170, E172	
 Chain 1		
Modified Residue(s)	Ex: T10	
Modification(s)	Select Multiple Options	
Organism	Ex: influenza, Peanut	
 Chain 2		
Modified Residue(s)	Ex: T10	
Modification(s)	Select Multiple Options	
Organism	Ex: influenza, Peanut	
 Epitope Reference Details		
 Epitope Related Object		

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

**Epitope**

Epitope ID	Ex: 44920	
Structure Type - Non-peptidic Epitopes		
Non-peptidic	Ex: penicillin	
Organism	Ex: influenza, Peanut	
Antigen Name	Ex: core, capsid, myosin	
<a href="#"> Epitope Reference Details</a> <a href="#"> Epitope Related Object</a>		

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

There are five other Specialized Search queries that can be used to select search criteria for references, epitopes, and assays. These are T Cell Assay Details, B Cell Assay Details, MHC Assay Details, Identifier Search, and Browse by 3D Structure. As an example, the MHC Assay Detailed Search page is shown in Figure 2.10. As is the case for all three assay search pages, the Epitope and Reference criteria fields are listed first and last, respectively, with the other relevant filter criteria specific for each assay type listed between them.

Help | More iEDB

**MHC Assay Detailed Search**

Reset    Search

**Epitope** (590144)

Epitope ID  
Structure Type - Any  
Organism  
Antigen Name  
Epitope Reference...  
Epitope Related ...

**Host** (590144)

Host Organism  
Host Details  
In Vivo Process  
In Vivo Processed...  
In Vitro Administra...  
In Vitro Processe...  
Antigen Processin...

**Assay** (590144)

Qualitative Measurement  
Assay  
Measurement Det...  
MHC Allele  
Antigen Presentin...  
3D Structure of C...  
Assay Reference ...

**Reference** (590144)

Author  
Title  
Reference Details  
Reference ID  
Abstract  
Affiliations  
Date (Year)  
Type - Any

No Filters Set

Epitopes (590144)    Antigens (45312)    Assays (1629184)    References (2816)

Go To Records Starting At 1200    Export Results

590144 Records Found    Page 1 of 23606    25 Per Page

Details	Epitope	Antigen	Organism	# References	# Assays
48237	PKYVKQNTLKLAT	Hemagglutinin	Influenza A virus	87	323
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	80	115
58560	SIINFEKL	Gal d 2	Gallus gallus (chicken)	60	107
27201	ILMEHIIHLK	60S ribosomal protein L19	Homo sapiens (human)	50	78
4602	ASNENMETM	Nucleoprotein	Influenza A virus	48	69
156807	AIVDIKVPSV	Coatomer subunit gamma-1	Homo sapiens (human)	43	69
69922	VMAPRTLV	HLA class I histocompatibility antigen, A-2 alpha chain	Homo sapiens (human)	42	81
162865	KIYEGQVEV	60S ribosomal protein L5 (UniProt:P46777)	Homo sapiens (human)	41	60
16833	FLPSDFPPSV	Capsid protein	Hepatitis B virus (hepatitis B virus (HBV))	40	87
58547	SIIGRLLEV	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit (UniProt:P62136)	Homo sapiens (human)	40	78
74794	YLLPAIVHI	Probable ATP-dependent RNA helicase DDX5 (UniProt:P17844)	Homo sapiens (human)	40	64
120106	NEIEDTFRQF	V-type proton ATPase subunit F	Homo sapiens (human)	40	52
27000	ILDKKVEKV	Heat shock protein HSP 90-beta	Homo sapiens (human)	39	56
30620	KESTLHLVL	Ubiquitin-60S ribosomal protein L40 (UniProt:P62987)	Homo sapiens (human)	39	54
37182	LLDVPTAAV	Gamma-interferon-inducible lysosomal thiol reductase	Homo sapiens (human)	39	64
55785	RRYOKSTEL	Histone H3.1	Homo sapiens (human)	39	68
55556	RRFFPYYYV	Proteasome subunit beta type-1	Homo sapiens (human)	38	84
163959	YQFTGIKKY	Up-regulated during skeletal muscle growth protein 5	Homo sapiens (human)	38	62
69939	VMDSKIVQV	Importin subunit alpha-6	Homo sapiens (human)	37	57
101382	VMAPRTLLL	HLA class I histocompatibility antigen, A-29 alpha chain	Homo sapiens (human)	37	62
162178	FASGLIHRV	Other Homo sapiens (human) protein	Homo sapiens (human)	37	59
44920	NLVPMPMVT	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	36	51
134316	AETPDIKLF	40S ribosomal protein S5 (UniProt:P46782)	Homo sapiens (human)	36	47
134356	EEVHDLERKY	Nucleosome assembly protein 1-like 4	Homo sapiens (human)	36	48
161927	ALADGVQKV	Apolipoprotein L1 (UniProt:O14791)	Homo sapiens (human)	36	56

590144 Records Found    Page 1 of 23606    25 Per Page

Go To Records Starting At 1200    Export Results

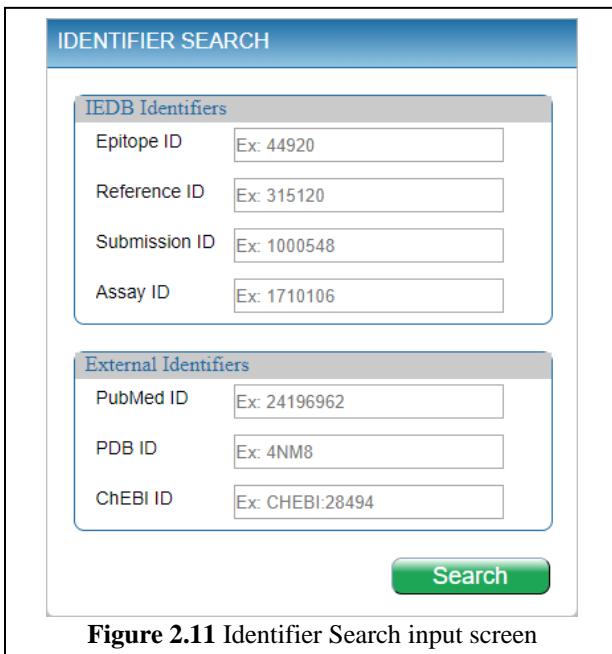
**Figure 2.10 MHC Assay Detailed Search web page**

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

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

The MHC Ligand assay category combines assays that were previously in the MHC Binding and MHC Ligand Elution assay categories. As such, the MHC Ligand category captures details relating to the in vitro

interaction of the epitope with specific MHC molecules along with available Epitope-MHC complex structure details, that is the epitope's binding capacity to the MHC molecule. It also captures data related to epitopes that are naturally processed and presented on the surface of an antigen presenting cell. The MHC Ligand Elution subcategory differs from the MHC Binding subcategory in that for the former, antigen bound to the MHC molecule on the cell surface has been taken up and processed internally for presentation by the antigen presenting cell, whilst 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 a web-based form titled "IDENTIFIER SEARCH". It contains two main sections: "IEDB Identifiers" and "External Identifiers".

**IEDB Identifiers:**

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

**External Identifiers:**

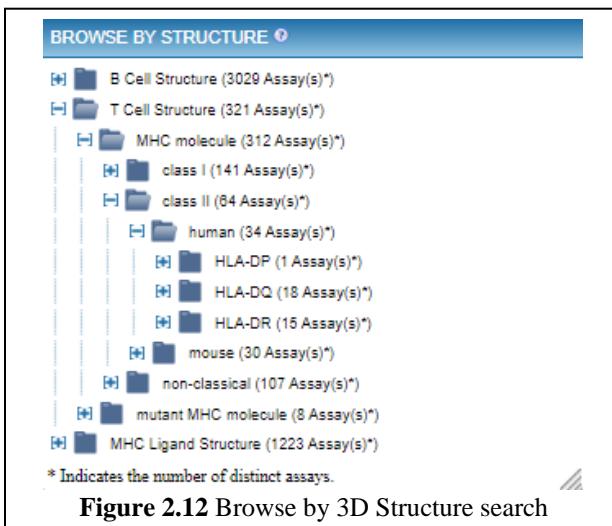
- PubMed ID: Ex: 24196962
- PDB ID: Ex: 4NM8
- ChEBI ID: Ex: CHEBI:28494

A green "Search" button is located at the bottom right of the form.

**Figure 2.11** Identifier Search input screen

The Identifier Search input screen is shown in Figure 2.11. If users know the epitope, reference, submission, or assay identifier they are seeking, they can enter that information into one of the four IEDB Identifiers fields.

The Browse by 3D Structure selection screen is shown in Figure 2.12. Users can select 3D structure of interest to them based on available structures within the database.



The Browse by 3D Structure search screen is a hierarchical tree view titled "BROWSE BY STRUCTURE".

- B Cell Structure (3029 Assay(s)\*)
- T Cell Structure (321 Assay(s)\*)
  - MHC molecule (312 Assay(s)\*)
    - class I (141 Assay(s)\*)
    - class II (64 Assay(s)\*)
      - human (34 Assay(s))
        - HLA-DP (1 Assay(s))
        - HLA-DQ (18 Assay(s))
        - HLA-DR (15 Assay(s))
      - mouse (30 Assay(s))
      - non-classical (107 Assay(s))
      - mutant MHC molecule (8 Assay(s))
  - MHC Ligand Structure (1223 Assay(s)\*)

\* Indicates the number of distinct assays.

**Figure 2.12** Browse by 3D Structure search

## 2.2.3 Search Results Page

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

The screenshot shows the search results page with the following interface elements:

- Pending Filters:** On the left, there are several filter panels:
  - Epitope:** Radio buttons for Any Epitopes, Linear Epitope, Discontinuous Epitopes, Non-peptidic Epitopes, 3D structure available, and Amino Acid Modification.
  - Antigen:** Filter by Organism (e.g., Ex: influenza, peanut) and Antigen Name (e.g., Ex: core, capsid, myosin).
  - Receptor:** Filter by Type (Any Type), Chain (Any Type), and Sequence (Exact Match).
  - Assay:** Checkboxes for Positive Assays Only, T Cell Assays, B Cell Assays, and MHC Ligand Assays.
  - MHC Restriction:** Radio buttons for Any MHC Restriction and MHC Class I.
- Current Filters:** A dropdown menu showing "Positive Assays Only".
- Table Headers:** Epitopes (741609), Antigens (49386), Assays (1846090), Receptors (67022), References (21206).
- Table Content:** A grid of 741609 rows, each representing an epitope record. Columns include Details, Epitope, Antigen, Organism, # References, and # Assays. Each row has a link to the epitope detail page (e.g., 123885, 44920, 20354, ...).
- Page Navigation:** Go To Records Starting At 1200, Page 1 of 29665, Export Results.
- Bottom Section:** 741609 Records Found, Go To Records Starting At 1200, Page 1 of 29665, Export Results.

Figure 2.13 The Epitope tab of the search results page



## EPITOPE SUMMARY

GILGFVFTL is a linear peptide epitope (epitope ID 20351) studied as part of Matrix protein 1 from Influenza A virus. This epitope has been studied for immune reactivity in 236 publication(s), tested in 524 T cell assays, 5 B cell assays, 115 MHC ligand assays and has 3D structure(s) 1OIGA, 5JHD, 5TEZ, 2VLU, 5ISZ, 5E6I, 5EUO, 2VLK, 2VLL, 2VLR, 1HHI and 4NT6.

## COMPILED DATA

## MHC Ligand Assay(s) 115

MHC molecule	Positive / All
HLA-A*02:01	75 / 75
HLA-A2	10 / 10
HLA-A*02:06	4 / 5
HLA-A*02:02	4 / 4
HLA-A*02:03	4 / 4
HLA-C*08:01	4 / 4
HLA-A*68:02	1 / 3
HLA-E	0 / 2
HLA-E*01:03	1 / 1
SLA-3*02:02	1 / 1
HLA-A*01:01	0 / 1
HLA-A*03:01	0 / 1
HLA-A*11:01	0 / 1
HLA-A*21:02	0 / 1
HLA-A3	0 / 1
HLA-DRA*01:01/DRB1*01:01	0 / 1

## B Cell Assay(s) 5

Assay Type	Positive / All
qualitative binding	4 / 4
complement-dependent cytotoxicity	1 / 1

## T Cell Assay(s) 524

Assay Type	Positive / All
IFNg release	155 / 160
qualitative binding	124 / 126
cytotoxicity	79 / 83
dissociation constant KD	28 / 36
off rate	14 / 14
on rate	14 / 14
proliferation	13 / 14
TNF $\alpha$ release	12 / 13
activation	10 / 10
3D structure	9 / 9
CCL4/MIP-1 $\beta$ release	6 / 6
pathogen burden after challenge	6 / 6
survival from challenge	5 / 6
degranulation	4 / 5
IL-2 release	4 / 5
perforin release	4 / 4
TNF release	3 / 4
granzyme B release	3 / 3
CXCL9/MIG release	1 / 1
decreased disease	1 / 1
IL-12 release	1 / 1
T cell-APC binding	1 / 1
IL-10 release	0 / 1
IL-1 release	0 / 1

## EXTERNAL RESOURCES

Resource	Link
IEDB-AR: MHC-I Processing <a href="#">↗</a>	Predict MHC class I processing <a href="#">↗</a>
IEDB-AR: MHC-I <a href="#">↗</a>	Predict MHC class I binding affinity <a href="#">↗</a>
IEDB-AR: B cell scales <a href="#">↗</a>	Predict B cell epitopes <a href="#">↗</a>
IRD <a href="#">↗</a>	View sequence feature Influenza A_M1_experimentally-determined-epitope_58(9) details at IRD <a href="#">↗</a>
IRD <a href="#">↗</a>	View sequence feature Influenza A_M1_monoclonal-antibody-binding-site_58(9) details at IRD <a href="#">↗</a>

Figure 2.14 An example of the epitope detail page

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

This screenshot shows the search results page for the Immune Epitope Database. The top navigation bar includes links for Home, Specialized Searches, and Analysis Resource, along with Help and More IEDB options. The main content area features a Pending Filters sidebar on the left containing sections for Epitope, Antigen, Receptor, Assay, and MHC Restriction. The current filters are set to Positive Assays Only and Antigen: Nucleoprotein. The main table displays 49388 records found, with columns for Antigen, Organism, # Epitopes, # Assays, and # References. A blue arrow points to the Antigen column header. The table lists various antigens such as Hemagglutinin, Genome polyprotein, Nucleoprotein, and Matrix protein 1, each with their respective organism, number of epitopes, assays, and references. The bottom of the table shows a summary of 1 record found for Nucleoprotein from Influenza A virus.

Antigen	Organism	# Epitopes	# Assays	# References
Hemagglutinin	Influenza A virus	1901	8067	706
Genome polyprotein	Hepatitis C virus	4715	14077	627
Nucleoprotein	Influenza A virus	652	3139	513
65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	374	2306	401
Matrix protein 1	Influenza A virus	349	1737	370
Other Homo sapiens (human) protein	Homo sapiens (human)	20025	32216	357
Large envelope protein	Hepatitis B virus (hepatitis B virus (HBV))	711	3139	341
Gal d 2	Gallus gallus (chicken)	123	973	306
Amyloid beta A4 protein	Homo sapiens (human)	355	1963	302
Genome polyprotein	Dengue virus	7454	20648	297
Envelope glycoprotein gp160	Human immunodeficiency virus 1 (human immunodeficiency virus 1 (HIV-1))	487	2021	293
Myelin basic protein (UniProt P02686)	Homo sapiens (human)	442	2198	252
Protein E7	Alphapapillomavirus 9	266	1285	236
Circumsporozoite (CS) protein	Plasmodium falciparum (malaria parasite P. falciparum)	449	2107	227
Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus (Lymphocytic choriomeningitis virus)	347	1839	206
Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	74	1235	206
Immunoglobulin	Homo sapiens (human)	3211	5211	201
Capsid protein	Hepatitis B virus (hepatitis B virus (HBV))	268	1096	190
Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	254	1010	186
Glutamate decarboxylase 2	Homo sapiens (human)	409	1705	176
Polymerase acidic protein	Influenza A virus	250	1038	167
Nucleoprotein	Lymphocytic choriomeningitis mammarenavirus (Lymphocytic choriomeningitis virus)	226	1137	160
Latent membrane protein 2	Human herpesvirus 4 (Epstein Barr virus)	156	847	153
Myelin proteolipid protein	Mus musculus (mouse)	56	1082	153
Vimentin	Homo sapiens (human)	973	3172	151

**Figure 2.15** The Antigens tab of the search results page

This screenshot shows the search results page for the Immune Epitope Database, similar to Figure 2.15 but with a specific filter applied. The Pending Filters sidebar shows the filter 'Antigen: Nucleoprotein' is selected. The main table displays 1 record found for Nucleoprotein from Influenza A virus. A red arrow points to the Antigen column header. The table shows the same structure as Figure 2.15, with columns for Antigen, Organism, # Epitopes, # Assays, and # References. The bottom of the table shows a summary of 1 record found for Nucleoprotein from Influenza A virus.

Antigen	Organism	# Epitopes	# Assays	# References
Nucleoprotein	Influenza A virus	577	2821	485

**Figure 2.16** The Results filtered by the Nucleoprotein of the Influenza A virus. This was achieved by clicking on the filter icon in the antigen column. The content of the other tabs contain data specific to this antigen.

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

ID	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	MHC Restriction	Assay Description
1505273	P Chong; Infect Immun 1992	AGFYIYRETFCITTY KTGQPAADHYSK VTA Pertussis toxin subunit 3 precursor (106-136) Bordetella pertussis	Mus musculus BALB/c	Administration in vivo with Pertussis toxin subunit 3 precursor (Source Antigen)	AGFYIYRETFCITTY KTGQPAADHYSK VTA Pertussis toxin subunit 3 precursor (106-136) Bordetella pertussis	Epitope	H2-d class II	3H-thymidine proliferation Positive-High
1481451	Gerald E Hancock; J Med Virol 2003	AICKRIPNKKPGKKA Major surface glycoprotein G (184-198) Human respiratory syncytial virus A2	Mus musculus BALB/c	Administration in vivo with Major surface glycoprotein G (Source Antigen)	AICKRIPNKKPGKKA Major surface glycoprotein G (184-198) Human respiratory syncytial virus A2	Epitope	H2-IE <sub>d</sub>	3H-thymidine proliferation Positive-High
1810409	Xuefeng Wang; Parasit Vectors 2010	AKQYNICCKFKELL D 22.6 kDa tegumental antigen (111-125) Schistosoma japonicum	Mus musculus C57BL/6	Administration in vivo with AKQYNICCKFKELL D (Epitope)	AKQYNICCKFKELL D 22.6 kDa tegumental antigen (111-125) Schistosoma japonicum	Epitope	H2-b class II	3H-thymidine proliferation Positive-High
1737052	S Ghosh; Int Immunol 1999	ALNNRFQIKGVEL KS hemagglutinin (511-525) Influenza A virus	Mus musculus BALB/c	Administration in vivo with ALNNRFQIKGVEL KS (Epitope)	ALNNRFQIKGVEL KS hemagglutinin (511-525) Influenza A virus	Epitope	H2-d class II	3H-thymidine proliferation Positive-High
1648562	A G Paul; Int Immunol 2000	ALSTLVVNIK 60 kDa chaperonin 2 (256-265) Mycobacterium tuberculosis	Rattus norvegicus	Administration in vivo with ALSTLVVNIK (Fragment of Source Antigen) followed by restimulation in vitro	ALSTLVVNIK 60 kDa chaperonin 2 (256-265) Mycobacterium tuberculosis	Epitope	RT1-B <sub>i</sub>	3H-thymidine proliferation Positive-High
1648483	A G Paul; J Immunol 2000	ALSTLVVNIK 60 kDa chaperonin 2 (256-265) Mycobacterium tuberculosis H37Ra	Rattus norvegicus Lewis	Administration in vivo with ALSTLVVNIK (Fragment of Source Antigen) followed by restimulation in vitro	ALSTLVVNIK 60 kDa chaperonin 2 (256-265) Mycobacterium tuberculosis H37Ra	Epitope	rat class II	3H-thymidine proliferation Positive-High
1506620	Maria M Garcia-Briones; Virology 2004	ANHCS DAMNIMF EV polyprotein (2103-2117) Foot-and-mouth	Sus scrofa Landrace X Large White	Administration in vivo with Foot-and-mouth disease virus C-S6c1 (Source Organism)	ANHCS DAMNIMF EV polyprotein (2103-2117) Foot-and-mouth disease virus C-	Epitope	SLA class II	3H-thymidine proliferation Positive-High

**Figure 2.17** The Assays tab of the search results page. The page contains three additional tabs for T Cell, B Cell, and MHC Ligand Assays

T Cell Assay	
Qualitative Measurement	Positive-High
Method/Technique	3H-thymidine
Measurement of	proliferation
Effector Cells	
Effector Cell Tissue Type	Spleen
Effector Cell Type	T cell
Effector Cell Culture Conditions	Direct Ex Vivo
Antigen Presenting Cells	
Cell Tissue Type	Spleen
Cell Type	Splenocyte
Cell Culture Conditions	Direct Ex Vivo
Autologous or Syngeneic	Y
MHC Allele	
MHC Allele Name	H2-b class II
MHC Evidence Code	T cell assay -Biological process measured
Antigen	
Epitope Relation	Epitope
Chemical Type	Linear peptide
Linear Sequence	LFAAFPSFAGLRPTFDTRLM
Starting Position	21
Ending Position	40
Source Molecule Name	14 kDa antigen
Source Accession	P0A5B7.2 
Source Organism ID	1773
Source Organism	Mycobacterium tuberculosis
Antigen Details	
Antigen Evidence Code	Exact match to reference information
Assay Reference Details	
Assay Comments by IEDB Curator	Spleen T cells from heat-killed H37Ra immunized mice or LNC cells from soluble H37Ra extracts immunized mice proliferated in response to the epitope.
Location of Assay Data in Reference	Figures 3 and 5

**Figure 2.18** The top three sections of a sample T cell assay detail page.

The fourth tab on the results page is the Receptors tab (Figure 2.19). The Receptors tab indicates the distinct receptor group, the species, and the receptor types alongside the sequences of each chain component. The display is subdivided into two separate tabs for TCRs and BCRs. Clicking on the Group ID links brings the user to a receptor specific details page.

Group ID	Species	Type	Chain 1 CDR3	Chain 2 CDR3
47	Homo sapiens (human)	αβ	IVRSSNTGKLI	ASSQDRDTQY
49	Mus musculus (mouse)	αβ	AASANSGYQR	ASGDAGGGYEQY
50	Mus musculus C57BL/6	αβ	AAS	ASSL
57	Homo sapiens (human)	αβ	ALIQQGAQKLV	ASTYHGTGQY
94	Homo sapiens (human)	αβ	AVRPLLDGTYIPT	ASSYLGNTGELF
102	Mus musculus (mouse)	αβ	ALSENLYNEKIT	ASGDASGAETLY
103	Mus musculus (mouse)	αβ	ALSENYGNEKIT	ASGDASGGNTLY
104	Mus musculus (mouse)	αβ	AANSGYQR	ASGDFWIGDTLY
109	Homo sapiens (human)	αβ	IVWGGYQKV	ASRYRDDSNEQF
110	Homo sapiens (human)	αβ	AVTTDSWIGKLQ	ASRPGLAGGRPEQY
111	Homo sapiens (human)	αβ	AVTTDSWIGKLQ	ASRPGLMSAQPEQY
114	Mus musculus (mouse)	αβ	AVSDPPPLT	ASGGGGTLY
115	Mus musculus (mouse)	αβ	AVSLERPYLT	ASGGGGTLY
116	Homo sapiens (human)	αβ	ALSGFYNTDKLI	ASPLLAGEYEQY
117	Homo sapiens (human)	αβ	AVRPTSGGSYIPT	ASSYVGNTGELF
118	Mus musculus (mouse)	αβ	ALFLASSFSKLV	ASSDWVSYEQY
125	Homo sapiens (human)	αβ	ATDTTSGTYKYI	SARDLTSGANNEQF
140	Mus musculus (mouse)	αβ	VVGDGRGSALGRLH	ASGDAGGNIAEQF
141	Mus musculus (mouse)	αβ	VVGDGRGSALGRLH	ASSSTGLDTQY
142	Mus musculus (mouse)	αβ	VVGDGRGSALGRLH	ASGSLLDVREVF
143	Homo sapiens (human)	αβ	VVSDRGSTLGRLY	ASSGLRDRGLYEQY
144	Homo sapiens (human)	αβ	VVSDRGSTLGRLY	ASSEEGALKESVGTOY
227	Homo sapiens (human)	αβ	AVNIVAGKST	AWSETGLGTGELF
237	Mus musculus (mouse)	αβ	AAEDGGSGNKLI	ASSWIDRAGNTLY
246	Mus musculus (mouse)	αβ	AVSHQGRYL	ASGGGGTLY

Figure 2.19 The Receptors tab of the search results page

The fifth tab on the results page is the References tab (Figure 2.20). Results are initially sorted by the year of publication or submission, the most recent references first. Again, the user can click on the column header to change the sort order. The table includes the IEDB-assigned reference ID, the PubMed ID, authors, article title, abstract, and the date. For journal articles, the information is downloaded directly from PubMed. Clicking on the Ref ID in the far-left lane will take the user to a Reference Detail page. An example is given in Figure 2.21.

**IMMUNE EPITOPE DATABASE  
AND ANALYSIS RESOURCE**

Home | Specialized Searches | Analysis Resource | Help | More IEDB

**Pending Filters**

**Epitope** 

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

3D structure available

Amino Acid Modification

**Antigen** 

Organism  
Ex: influenza, peanut

Antigen Name  
Ex: core, capsid, myosin

**Receptor** 

Has receptor sequence

Type: Any Type

Chain: Any Type

Sequence: Exact Matches

**Assay** 

Positive Assays Only

T Cell Assays

B Cell Assays

MHC Ligand Assays

**Current Filters:**  Positive Assays Only

**Epitopes** (741609)    **Antigens** (49388)    **Assays** (1846090)    **Receptors** (67022)    **References** (21205)

Go To Records Starting At: 1982 [60] Export Results

21205 Records Found Page 1 of 849 [25] Per Page

Ref ID	PMID	Author	Title	Abstract	Date
1036848	32314731	Kenji Murata; Munehide Nakatsugawa; Mohammed A. Rahman; Linh T. Nguyen; Douglas G. Miller; David T. Mulder; Kenji Sugata; Hiroshi Saito; Yukio Matsunaga; Yuki Kagoya; Tingxi Guo; Mark Anzurowski; Chung-Hsi Wang; Brian O. Burt; Dalam Ly; Kayoko Saeki; Alimurad Easim; David P. Goldstein; Michael Reedijk; Danny Ghazarian; Trevor J. Pugh; Marcus O. Butler; Tak W. Mak; Pamela S. Ohashi; Naoto Hirano	Landscape mapping of shared antigenic epitopes and their cognate TCRs of tumor-infiltrating T lymphocytes in melanoma.	HLA-restricted T cell responses can induce antitumor effects in cancer patients. Previous human T cell research has largely focused on the few HLA alleles prevalent in a subset of ethnic groups. Here, ... <a href="#">more...</a>	2020
1036421	31848261	Martine Solleder; Philippe Guillame; Julien Radle; Justine Michaux; Hui-Song Pak; Markus Müller; George Coukos; Michal Bassani-Sternberg; David Gfeller	Mass Spectrometry Based Immunopeptidomics Leads to Robust Predictions of Phosphorylated HLA Class I Ligands.	The presentation of peptides on class I human leukocyte antigen (HLA-I) molecules plays a central role in immune recognition of infected or malignant cells. In cancer, non-self HLA-I ligands can arise ... <a href="#">more...</a>	2020
1036600	31844290	Siranush Sarkisova; Susan Klaeger; Phuong M. Le; Letitia W. Li; Giacomo Oliveira; Hasmik Keshishian; Christina R. Hartigan; Wandi Zhang; David A. Braun; Keith L. Ligon; Pavani Bachireddy; Ioannis K. Zervantarakis; Jennifer M. Rosenbluth; Tamara Ovsyannikova; Daniel L. Levy; Sune Justesen; Jonathan Stevens; William J. Lane; Thomas Eisenhauer; Guang Lan Zhang; Karl R. Clouser; Nir Hacohen; Steven A. Carr; Catherine J. Wu; Derin B. Keskin	A large peptidome dataset improves HLA class I epitope prediction across most of the human population.	Prediction of HLA epitopes is important for the development of cancer immunotherapies and vaccines. However, current prediction algorithms have limited predictive power, in part because they were not ... <a href="#">more...</a>	2020
1036769	32217358	Xiaoling Chen; Shufeng Wang; Yi Huang; Xia Zhao; Xu Jia; Gang Meng; Qian Zheng; Mengjun Zhang; Yuzhang Wu; Li Wang	Obesity Reshapes Visceral Fat-Derived MHC I Associated-Immunopeptidomes and Generates Antigenic Peptides to Drive CD8 <sup>+</sup> T Cell Responses.	Adaptive CD8 <sup>+</sup> T cells were observed to contribute to the initiation and progression of obesity-induced visceral adipose tissue (VAT) chronic inflammation that is critically linked to metabo ... <a href="#">more...</a>	2020

**Figure 2.20** The References tab of the search results page

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE		Help	More IEDB
<a href="#">Home</a> <a href="#">Specialized Searches</a> <a href="#">Analysis Resource</a>			
<b>Reference</b>			
<b>Article Authors</b>		Shira Yair-Sabag; Valentina Tedeschi; Carolina Vitulano; Eilon Barnea; Fabian Glaser; Dganit Melamed Kadosh; Joel D Taurog; Maria Teresa Fiorillo; Rosa Sorrentino; Arie Admon	
<b>Article Title</b>		The Peptide Repertoire of HLA-B27 may include Ligands with Lysine at P2 Anchor Position.	
<b>Reference Detail</b>			
<b>Reference ID</b>		1033511	
<b>Abstract</b>		The HLA-B*27 peptidome has drawn significant attention due to the genetic association between some of the HLA-B*27 alleles and the inflammatory rheumatic disease ankylosing spondylitis (AS), for which a comprehensive biological explanation is still lacking. This study aims to expand the known limits of the HLA-B*27 peptidome to facilitate selection and testing of new peptides, possibly involved in the disease. The HLA peptidomes of HeLa and C1R cell lines stably transfected with the AS-associated HLA-B*27:05 allele, the nonassociated HLA-B*27:09 allele, or their cysteine 67 to serine mutants (C67S), are analyzed on a very large scale. In addition, the peptidomes of HLA-B*27:05 and HLA-B*27:05-C67S are analyzed from the spleens of rats transgenic for these alleles. The results indicate that C67S mutation increases the percentage of peptides with glutamine or lysine at their P2 position (P2-Lys), in both HLA-B*27:05 and HLA-B*27:09. Furthermore, a small fraction of HLA-B*27 peptides contains lysine at their second position (P2), in addition to the more commonly found peptides with arginine (P2-Arg) or the less common glutamine (P2-Gln) located at this anchor position. Overall these data indicate that peptides with P2-Lys should be considered as real ligands of HLA-B*27 molecules and taken into account while looking for putative peptides implicated in the AS.	
<b>Affiliations</b>		Department of Biology, Technion-Israel Institute of Technology, Haifa, Israel; Department of Biology and Biotechnology "C. Darwin", Sapienza University of Rome, Rome, Italy; Bioinformatics Knowledge Unit, The Lorry I. Lokey Interdisciplinary Center for Life Sciences and Engineering, Technion-Israel Institute of Technology, Haifa, Israel; Department of Internal Medicine, University of Texas Southwestern Medical Center, Dallas, USA.	
<b>Date</b>		2018	
<b>Reference Type</b>		Literature	
<b>PubMed ID</b>		29393594 <a href="#">[link]</a>	
<b>Journal</b>		Proteomics	
<b>Journal Volume</b>		18	
<b>Article Pages</b>		e1700249	
<b>Journal ISSN</b>		1615-9861	
<b>Curation Last Updated</b>		2019-01-03 23:39:42	
<b>Related Information</b>			
<b>Epitopes</b>		<a href="#">34798 (Click for related results)</a>	
<b>Bcell Assays</b>		0	
<b>Tcell Assays</b>		0	
<b>MHC Ligand Assays</b>		<a href="#">42431 (Click for related results)</a>	

**Figure 2.21** An example of the Reference detail page

### 2.2.3.1 Peptide MHC Binding Motif Displays

A display of peptide MHC binding motif diagrams and amino acid binding charts for a subset of MHC allele records appears on the MHC Allele Details page. Clicking on the allele name in the MHC Restriction column on the Assays tab for T Cells and MHC Ligand will bring the user to an MHC Allele Details page (Figure 2.22). As can be seen by the tabs in the binding motif display, the Peptide MHC Binding Motif diagrams on MHC Allele Information pages support diagrams for multiple lengths.

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

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

**Peptide MHC Binding Motif** [\(?\)](#)

[9-length](#) [10-length](#)

Preferred F Y      Position 2 Anchor FM W      W Y      F W      C-terminal Anchor Preferred ILV

Position 1      Preferred LM      3 4 5 6 7 8      Tolerated ILV

Deleterious DEP      Preferred LM      Tolerated IQV      EKR      KR      GKR      Preferred ILV      Tolerated AM

[Amino Acid Binding Chart](#)

**Figure 2.22** Sample MHC Allele Details page with Peptide MHC Binding Motif diagram for HLA-A\*02:01. Note the link to the corresponding Amino Acid Binding Chart on the bottom left of the diagram

The Peptide MHC Binding Motif diagram summarizes the results of the amino acid binding for each position, which is shown in Figure 2.23. The amino acids are color-coded for each position, where green indicates the residue is preferred for binding, purple indicates it is deleterious for binding, and white indicates the residue is tolerated at that position. The motif diagram shows which residues are preferred and tolerated at the anchor positions, and which residues are preferred and deleterious at the non-anchor positions.

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

For anchor position:

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

3. if a residue's value in this column of the SMM matrix is within 10-fold of the best value, designate this residue as tolerated
4. The remaining residues are designated as deleterious

HLA-A-0201 Motif Amino Acid Binding Chart									
AMINO ACID	PEPTIDE BINDING MOTIF POSITION								
	1	2	3	4	5	6	7	8	9
A	-0.11	<b>-0.20</b>	-0.17	-0.12	0.073	0.077	-0.06	0.008	-0.93
C	0.048	<b>0.479</b>	0.121	-0.13	-0.27	-0.14	-0.04	-0.01	<b>0.071</b>
D	<b>0.834</b>	<b>0.522</b>	-0.11	-0.38	-0.02	0.188	0.252	0.349	<b>0.579</b>
E	<b>0.867</b>	<b>0.607</b>	<b>0.587</b>	-0.33	0.193	0.188	0.195	-0.16	<b>0.737</b>
F	-0.85	<b>0.014</b>	<b>-0.47</b>	0.033	-0.21	-0.23	<b>-0.63</b>	-0.29	<b>0.018</b>
G	0.011	<b>0.374</b>	0.248	-0.04	0.057	0.307	<b>0.451</b>	-0.02	<b>0.361</b>
H	0.096	<b>0.773</b>	0.266	0.068	0.016	0.217	-0.13	0.121	<b>0.780</b>
I	-0.18	-0.85	-0.28	0.158	-0.12	-0.36	-0.18	0.144	<b>-1.13</b>
K	-0.27	<b>0.656</b>	<b>0.740</b>	0.140	0.233	<b>0.500</b>	<b>0.653</b>	0.217	<b>0.540</b>
L	-0.17	<b>-1.54</b>	-0.34	0.182	-0.06	-0.35	-0.11	-0.15	<b>-1.16</b>
M	-0.43	<b>-1.58</b>	<b>-0.74</b>	0.077	-0.01	-0.20	<b>-0.17</b>	0.081	-0.66
N	0.216	<b>0.693</b>	0.061	0.031	0.148	-0.03	0.227	0.158	<b>0.474</b>
P	<b>0.838</b>	<b>0.627</b>	0.173	-0.01	0.356	-0.07	-0.20	-0.21	<b>0.474</b>
Q	0.267	-0.73	0.132	0.118	0.206	0.057	0.277	0.124	<b>0.538</b>
R	-0.08	<b>1.017</b>	<b>0.612</b>	0.243	0.191	<b>0.442</b>	<b>0.452</b>	0.136	<b>0.439</b>
S	-0.06	<b>0.095</b>	-0.00	-0.06	0.132	-0.04	0.195	-0.02	<b>0.053</b>
T	0.125	<b>-0.36</b>	0.207	0.014	0.156	-0.13	0.009	0.001	<b>-0.37</b>
V	-0.11	-0.67	0.040	0.164	-0.08	-0.30	-0.07	0.157	<b>-1.60</b>
W	-0.19	<b>-0.15</b>	<b>-0.66</b>	-0.16	<b>-0.47</b>	-0.08	<b>-0.62</b>	-0.18	<b>0.332</b>
Y	-0.81	<b>0.247</b>	-0.38	0.021	<b>-0.48</b>	0.014	-0.47	-0.42	<b>0.475</b>

(ROW HEADER) Indicates anchor positions.
(MATRIX BODY) Indicates that the residue is a preferred residue 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 2.23** Amino acid binding matrix for MHC allele HLA-A\*02:01

For non-anchor position:

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

### 2.2.3.2 Immunome Browser

The Immunome Browser is a feature integrated into the IEDB to more efficiently display large sets of immune epitope data. The purpose of the tool is to allow users to explore how often each protein region has been studied in immune assays and in how many assays the immune response was positive or negative. The Immunome Browser “maps” query results from the IEDB onto a reference proteome. A reference proteome

is used because (1) epitopes reported in IEDB were identified for different strains and protein isoforms – mapping to the reference protein allows to visualize and study such epitopes as they would have the same antigen; (2) different mutant variants of the same epitope were tested and reported; and (3) immune response varies among studies and assays due to heterogeneity of samples and complexity of immune response. The Immunome Browser presents the mapped data along with calculated ‘epitope prominence scores’ that rank known epitopes based on how frequently subjects responded to each epitope, allowing identification of immunodominance. Both linear and discontinuous linear peptide epitopes with T cell or B cell responses are supported for viewing using the Immunome Browser. It is accessible via the Immunome Browser icon on the Antigen tab on the results page, as seen in Figure 2.24.

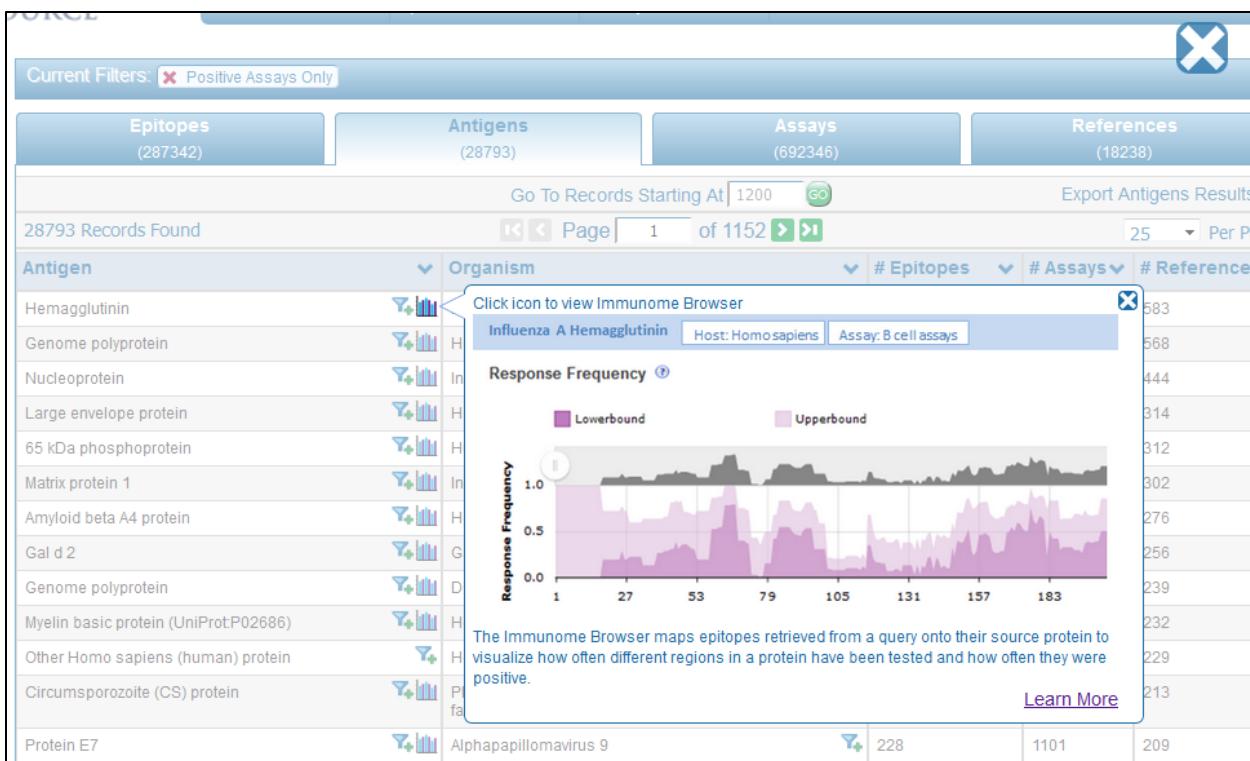
The screenshot shows the Immunome Browser interface with the following details:

- Current Filters:** Epitope Structure: Linear Sequence, Positive Assays Only, No B cell assays, No MHC ligand assays, Organism: Hepatitis C virus (ID:11103, Hepatitis C), Host: Homo sapiens (human).
- Tab Headers:** Epitopes (1472), Antigens (3), Assays (3505), References (226).
- Search Bar:** Go To Records Starting At Ex: 1200, Export Antigens Results.
- Data Table Headers:** Antigen, Organism, # Epitopes, # Assays, # References.
- Data Rows:**

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

**Figure 2.24** The Immunome Browser is accessed by clicking on the icon shown on the Antigen tab on the results page of a query

In order to make the Immunome Browser capability more prominent, a pop-up window was added that appears the first time a user goes to the Antigen tab after making a search, as seen in Figure 2.25. It can be easily dismissed by clicking on the large X in the upper right-hand corner or clicking anywhere else on the window.



**Figure 2.25** A pop-up window appears each time the user clicks on the Antigen tab on the Results page. It highlights the Immunoome Browser icon and briefly explains the Immunoome Browser's functionality.

In the Immunoome Browser, each selected antigen is considered to be a target protein, and the tool by default maps and visualizes all epitopes in the query result that are from the source antigen, which is the target protein or any of its taxonomic child. The mapping is done using the alignment between the source antigen and the target protein, and matching the epitope positions in the source antigen with the residue positions in the target protein. By default, epitopes that were tested as negative for the correspondent query will be mapped as well, even if the user queried only for positive assays. Also, the epitopes that failed to satisfy the default mapping criteria won't be mapped and visualized. The Immunoome Browser output for query criteria of T cell assays, linear epitopes, Hepatitis C virus, and human host is shown in Figure 2.26.



**Figure 2.26** Immunome Browser graphical output displaying assay results mapped onto a reference proteome by residue position

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

Results Returned: 3464 | Displaying: 3464  Display Graphe Residue Positions

Export Results 

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

**Figure 2.27** Immunome Browser tabular output.

In addition to the plots, a table is generated that displays the epitope ID, sequence, position, and identity, as well as the number of subjects tested, the number who responded, and number of positive and negative assays, and the response frequency (Figure 2.27). The user can interactively zoom in and out on the plots to a specific protein region and, if the check box for the table to correspond the plots is selected, the table is automatically updated to show only epitope from the selected region. Alternatively, the user can specify the residue start and end positions at the bottom of plots and click Update Display.

## 2.2.4 Finders Overview

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

### 2.2.4.1 Allele Finder

The MHC Allele Finder facilitates the selection of one or more MHC alleles. The finder consists of four sections as shown in Figure 2.28. The top section lists the alleles that the user selects. The selections can be removed by clicking on the red X of an allele name or by clicking on the Reset button to delete all selected alleles. When the user has completed the selection process, the user needs to click the green Apply button. The middle left section of the finder contains the “Search By” panel. Users can search by allele name, source organism, and/or class (I, II, or non-classical). After the user supplies their search criteria and clicks the Search button, the system will filter the list of MHC alleles using the organism, class, and allele provided. The allele finder uses wild card characters by default on both ends of criteria entered into the allele field. The system then returns in the bottom “Search Results” panel a list of any alleles that contain the value in the name field and match the class selected. Users can click on the green “+” icon to select an allele. Users can also click on the yellow highlighter icon to highlight the allele in the allele tree in the middle right section of the finder. Alternatively, a user can browse the hierarchical allele tree. Clicking on a node in this tree will add the allele to the Current Selections section of the finder.

The screenshot shows the Allele Finder interface. At the top, there is a search bar with the text "Current Selection(s) Papa-A\*06:01". Below the search bar are two buttons: "Reset" and "Apply".

**Search By:**

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

Buttons: Clear, Search.

**Browse by Tree (Click to Select):**

- MHC
  - MHC molecule
    - class I
    - bonobo
      - Papa-A
        - Papa-A\*06:01
  - cattle
  - chicken
  - chimpanzee

**Search Results (Click to Select):**

3 Records Found

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

3 Records Found

**Figure 2.28** Allele Finder. Alleles are displayed in a tree structure and users can search by allele name, source organism, and MHC class (I, II, or non-classical)

### 2.2.4.2 Assay Finder

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

The Assay Finder is used to facilitate the selection of one or more assay types and lists all assay types in the selected assay category. The Assay Finder for T Cell, B cell, and MHC Ligand assays can be found in the Assay section on the home page search interface, the left-hand side of the Results page, and on their respective Specialized Search pages. These versions of the Assay Finder organize and display assays in a tree structure, as seen in Figure 2.29 for the T Cell assays. Users can also search for assays by their method/technique and by the characters within the assay's name. The figure shows the results for ELISA type assays for "CCL1/TCA-3 release". Users can click on the green "+" icon to select an assay. Users can also click on the yellow highlighter icon to highlight the assay in the assay tree in the middle right section

of the finder, as is shown in the figure. Alternatively, a user can browse the hierarchical assay tree. Clicking on a node in this tree will add the assay to the Current Selections section of the finder.

The screenshot shows the 'ASSAY FINDER' interface. On the left, there is a 'Search By' panel with fields for Name (Ex: IL-2, Release), Method/Technique (ELISA), Measurement Of (CCL1/TCA-3 release), and Units. Below these are 'Clear' and 'Search' buttons. To the right is a 'Browse by Tree (Click to Select)' panel showing a hierarchical tree structure under 'T cell assay'. The tree includes nodes for 3D structure, binding constant, biological activity (activation, cytokine release, CCL1/TCA-3, ELISA), and CCL2/MCP-1. The 'ELISA' node under 'CCL1/TCA-3' is highlighted. At the bottom is a 'Search Results (Click to Select)' table with one record found:

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

**Figure 2.29** Assay Finder on the T Cell Advanced Search page. Assays are displayed in a tree structure and users can find displays by their method/technique and by the characters with which the assay name starts

### 2.2.4.3 Disease Finder

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

Figure 2.30 shows the Disease Tree with diabetes highlighted. DOID refers to the Disease Ontology identifier. The DTREE designates an IEKB-specific identifier that will be updated later with a DOID number when the Disease Ontology incorporates the terms.

**DISEASE FINDER**

Current Selection(s) [diabetes mellitus](#)

**Search By**

Disease Name:	diabetes
Disease ID:	Ex: 9415
ID Source:	<input type="button" value="▼"/>

**Browse by Tree (Click to Select)**

- + [additional diseases by category](#)
- + [disease of anatomical entity](#)
- + [disease of mental health](#)
- + [disease of metabolism](#)
- + [acquired metabolic disease](#)
  - + [amyloidosis](#)
  - + [carbohydrate metabolism ...](#)
  - + [glucose metabolism ...](#)
  - + [diabetes mellitus](#)

**Search Results (Click to Select)**

4 Records Found

Disease Name	Synonyms	Disease ID
diabetes mellitus		<a href="#">DOID [DOID:9351]</a>
prediabetes syndrome	prediabetic state, Prediabetes	<a href="#">DOID [DOID:11716]</a>
type 1 diabetes mellitus	type I diabetes mellitus, insulin-dependent diabetes mellitus, IDDM	<a href="#">DOID [DOID:9744]</a>
type 2 diabetes mellitus	type 2 diabetes, non-insulin-dependent diabetes mellitus, type II diabetes mellitus, NIDDM	<a href="#">DOID [DOID:9352]</a>

4 Records Found

**Figure 2.30** The disease finder is particularly helpful in specifying epitopes related to autoimmune diseases. In the example shown, diabetes is highlighted and selected.

#### 2.2.4.4 Molecule Finder

The Molecule Finder is used to facilitate the selection of source antigens, immunogens, and epitopes. There are two versions of the Molecule Finder – one specifically for non-peptidic molecules found in the Epitope box in the results page, and another that includes peptidic and non-peptidic branches, found in the Antigen box in the results page. The former contains the structures curated by the Chemical Entities of Biological Interest (ChEBI) database. An example of the non-peptidic finder is shown in Figure 2.31.

**NON-PEPTIDIC MOLECULE FINDER ?**

Current Selection(s)  penicillin

**Reset** **Apply**

**Search By**

Name:	penicillin
Molecule ID:	Ex: 17334
<b>Search</b>	

**Browse by Tree (Click to Select)**

- gatifloxacin
- indometacin
- lomefloxacin
- methotrexate
- monocarboxylic acid
- norfloxacin
- ochratoxin A
- oxolinic acid
- penicillin

**Search Results (Click to Select)**

18 Records Found      Page  of 4      Per Page

Molecule Name	Synonyms	Database ID	Organism Name
penicillin	Penicillin, penicillins, penicillins	ChEBI:17334	
benzylpenicillin	2,2-dimethyl-6beta-(phenylacetamido)penam-3alpha-carboxylic acid, Benzylpenicillin, PENICILLIN G, (2S,5R,6R)-3,3-dimethyl-7-oxo-6-(phenylacetamido)-4-thia-1-azabicyclo[3.2.0]heptane-2-carboxylic acid, ...more...	ChEBI:18208	
penicillin O	6beta-[(prop-2-en-1-ylsulfanyl)acetamido]-2,2-dimethylpenam-3alpha-carboxylic acid, almeccilene, (2S,5R,6R)-6-[(allylsulfanyl)acetyl]amino]-3,3-dimethyl-7-oxo-4-thia-1-azabicyclo[3.2.0]heptane-2-carb...more...	ChEBI:51207	

**Figure 2.31** The non-peptidic version of the Molecule Finder. This finder is accessed in the Epitope filter on the search results page.

With regard to the protein or peptidic branch of the Molecule Finder, individual GenPept proteins utilized by IEDB data are assigned to parent proteins from reference proteomes by sequence homology. These reference proteomes are graded by a star system described below that reflects the quality and completeness of each. An example of the star system and the protein tree can be seen in Figure 2.32.

The screenshot shows the MOLECULE FINDER application window. At the top, there is a search bar with the text "Current Selection(s) Voltage-gated potassium channel ★★". Below the search bar are two panels: "Search By" on the left and "Browse by Tree (Click to Select)" on the right. The "Search By" panel contains fields for Name (potassium channel), Molecule ID (Ex: P69710), and Source Organism (Ex: influenza, peanut). It also has a "Finder" button and "Clear" and "Search" buttons. The "Browse by Tree" panel shows a hierarchical tree structure under the "protein" category, with "Archeobacterium protein" expanded. A node labeled "Voltage-gated potassium channel ★★" is selected and highlighted with a green dashed border. Below these panels is a "Search Results (Click to Select)" section. It displays a table with 87 records found, showing columns for Molecule Name, Synonyms, Database ID, and Organism Name. The first three rows of the table are shown below:

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

**Figure 2.32** An example of the protein branch of the Molecule Finder

## Proteomes

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

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

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

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

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

## Proteins

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

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

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

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

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

As one can see in Figure 2.32, a user can search the molecule tree by entering text, including synonyms, in the Name field in the upper left-hand corner of the finder. The user can also specify the source organism of the molecule of interest using the autocomplete field or the organism finder. For example, this can facilitate the specification of a hemagglutinin in a particular strain of Influenza.

### 2.2.4.5 Organism Finder

The organism finder is used to facilitate the selection of a species or strain from the NCBI Taxonomy Database. The Organism finder allows the user to find species using their name, synonyms, or taxonomy identifier (assigned by NCBI). When the user performs a search, the system will display a tree structure. The user can search for a name or Organism ID in the "Search By" panel in the upper left-hand portion of the Finder. In the example shown in

Figure 2.33, a search for "dengue" is performed, which results in 47 items being found. The user can select one or more of the items by clicking on the green "+" icon or clicking a branch in the tree. The user can also choose to highlight the item in the tree, as shown in the figure, by clicking the corresponding yellow highlighter icon. Synonyms for a selection are listed next to the organism name column in the search results table. When the Organism Finder is adjacent to a Host Organism field, only the source organisms for which data exist in the IEDB are displayed in the tree structure.

The screenshot shows the Organism Finder interface. At the top, there is a search bar with 'Current Selection(s) Dengue virus' and buttons for 'Reset' and 'Apply'. Below the search bar is a 'Search By' section with fields for 'Name' (dengue) and 'Organism ID' (Ex: 10002045), and a 'Search' button. To the right is a 'Browse by Tree (Click to Select)' panel showing a hierarchical tree of viruses. The 'Dengue virus' node is highlighted in yellow. The tree includes nodes for Coronavirus, DNA virus, Filovirus, Flaviviridae family virus, Flavivirus, CY1014 virus, Carey Island virus, Dengue virus, and Dengue virus 1. Below the tree is a 'Search Results (Click to Select)' table with 47 records. The columns are 'Organism Name', 'Synonyms', and 'Organism ID'. The results include entries for Dengue virus, Dengue virus 1, Dengue virus 2, Dengue virus 3, and Dengue virus 4, each with its corresponding synonym and ID.

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

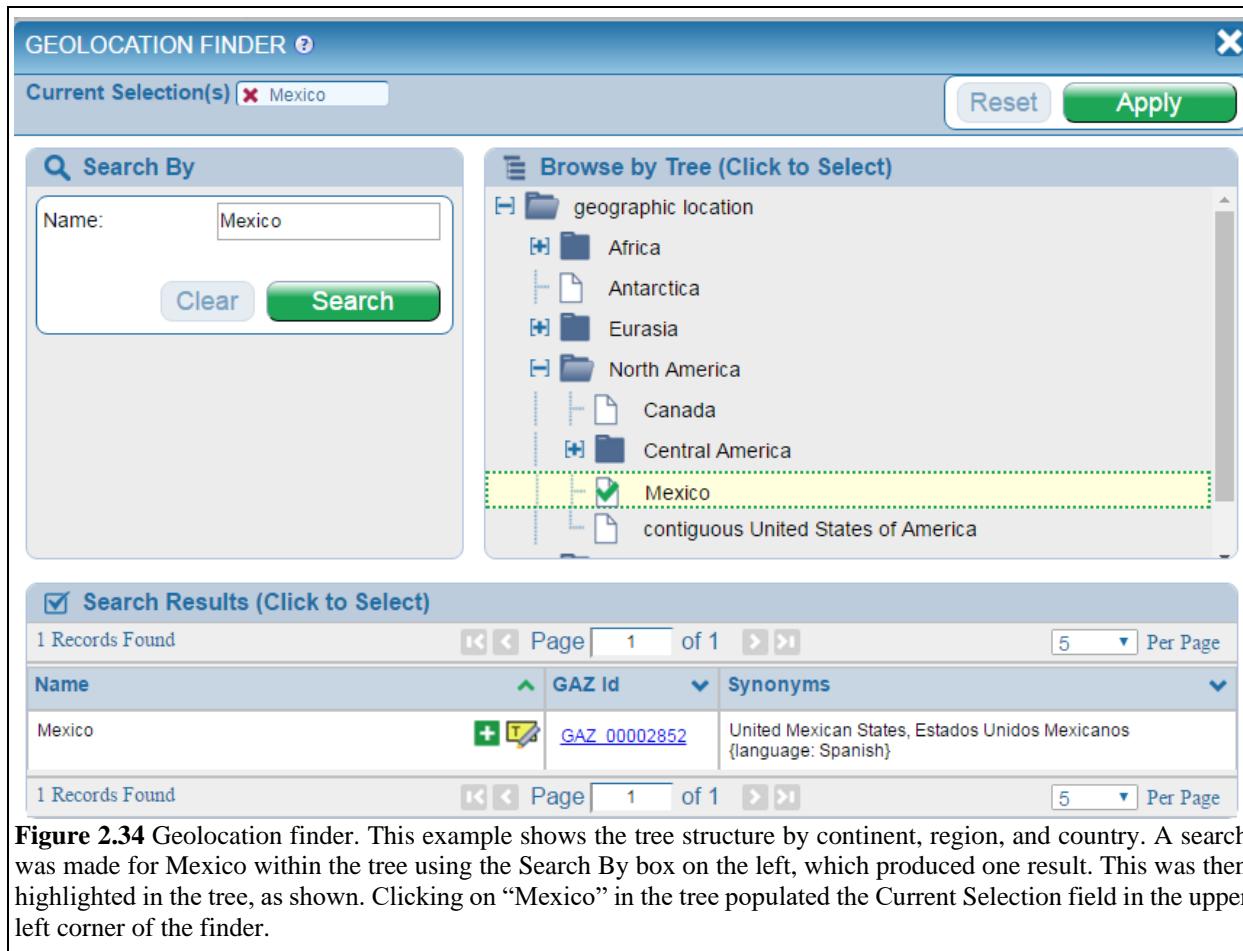
**Figure 2.33** Organism Finder showing a search for dengue with dengue highlighted in the tree

#### 2.2.4.6 Geolocation Finder

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

To use the Finder, simply navigate the tree by clicking open the continent of choice to find the country(ies) where study subjects were exposed to the immunogen tested in the immune epitope assays. Alternatively, one may use the "Search By" feature and type free text to search the tree. The Search By feature accepts synonyms as search criteria. Its use is shown in Figure 2.34 for the term "Mexico".

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



**Figure 2.34** Geolocation finder. This example shows the tree structure by continent, region, and country. A search was made for Mexico within the tree using the Search By box on the left, which produced one result. This was then highlighted in the tree, as shown. Clicking on “Mexico” in the tree populated the Current Selection field in the upper left corner of the finder.

## 2.3 Tools

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

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

For prediction tools, it is important to differentiate between the **tool** making predictions, and the **method** used to generate that tool, given a set of training data. For example, the artificial neural network (ANN) 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.

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

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

### 2.3.1 T Cell and B Cell Prediction Tools

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

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

#### 2.3.1.1 T Cell Epitopes - MHC binding prediction

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

combinatorial peptide libraries (Comblib\_Sidney2008), Consensus, NetMHCpan, PickPocket, NetMHCcons, and NetMHCstabpan. The Consensus method is derived from the ANN, SMM, and CombLib methods. For class II binding predictions, users can select IEDB Recommended, the Combinatorial Library method, the NN\_align, the SMM\_align method, a method devised by Sturniolo et al. and used in TEPITOPE, NetMHCIIpan, and a consensus method derived from the NN-align, SMM\_align, Sturniolo methods, and the Combinatorial Library. Tutorials and example data are available for both the class I and II tools.

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

#### **2.3.1.1.1 Peptide Binding to MHC Class I Molecules**

Users can select from ten different methods for predicting class I epitopes – ANN, SMM, SMMPMBEC, Comblib\_Sidney2008, Consensus, NetMHCpan, NetMHCcons, PickPocket, NetMHCstabpan, and IEDB recommended, which are described further below. A check box can be used to show only frequently occurring alleles. This allows the selection of only those alleles that occur in at least 1% of the human population or allele frequency of 1% or higher. However, un-checking the check-box will allow selection of all the alleles and corresponding peptide lengths for a particular species. Users can also upload an allele file instead of entering allele on the page one at a time.

#### **Artificial Neural Network**

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

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

#### **Stabilized Matrix Method (SMM)**

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

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

#### **Scoring matrices derived from combinatorial peptide libraries (Comblib\_Sidney2008)**

Comblib\_Sidney2008 refers to a set of predictors (i.e. scoring matrices) that were derived from binding affinity measurements of combinatorial peptide libraries against a panel of MHC alleles. This work is

described in Sidney et al. (Immunome Res. 2008). This class of predictors is unique in that average binding energy contribution of a given residue at a position is directly measured, without worrying about limited peptide sequence coverage.

### **Consensus**

The Consensus predictor was motivated by an idea that predictions made by consulting “consensus” of individual predictions from multiple predictors may result in improved performance over that of any individual ones. For MHC-I, a work describing an early implementation can be found in Moutaftsi et al. (Nat Biotech 2006). The methods used for Consensus are ANN, SMM, and CombLib\_Sidney2008. The Consensus method uses as many of these three component methods as possible, depending on their applicability for the chosen allele and length.

### **NetMHCpan**

NetMHCpan version 4.0 predicts binding of peptides to any MHC class I molecule of known sequence using artificial neural networks (ANNs). The method is trained on binding affinity and eluted ligand data leveraging the information from both data types as described in Jurtz et al. (J Immunol, 2017). To train this method, data on all class I MHC ligand elution assays available in IEDB database were collected including the ligand sequence, details of the source protein, position of the ligand in the source protein and the restricting allele of the ligand. There were 160,527 distinct assays in total and the length of the ligands ranged from 4–37. All lengths with a count of ligands at least 0.5% of total ligands were selected for further analysis which included lengths 8–15 and comprised of 99% of the assay entries. After refinement described in Jurtz et al. (J Immunol, 2017), the final training data set had 85,217 entries in total with ligand length ranging from 8 to 15. The ligands originated from 14,797 source antigens and were restricted by 55 unique HLA molecules. Random artificial negatives were generated for each MHC molecule covered by eluted ligand data by sampling randomly  $10^*N$  peptides of each length 8–15 amino acids from the antigen source protein sequences, where N is the number of 9mer ligands for the given MHC molecule.

### **PickPocket**

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

### **NetMHCcons**

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

### **NetMHCstabpan**

NetMHCstabpan was introduced in 2016. It predicts binding stability of peptides to any known MHC molecule using artificial neural networks (ANNs). The method is trained on more than 25,000 quantitative

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

### **IEDB Recommended**

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

#### **2.3.1.1.2 Peptide Binding to MHC Class II Molecules**

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

#### **SMM-align**

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

#### **Sturniolo**

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

#### **Combinatorial Library**

The positional scanning combinatorial libraries approach utilized a pool of random peptide libraries to systematically measure the contribution to MHC binding from each amino acid at each of the nine positions at the binding peptide. Each pool in the library contains 9-mer peptides with one fixed residue at a single position. With each of the 20 naturally occurring residues represented at each position along the 9-mer backbone, the entire library consisted of 180 peptide mixtures. Competitive binding assays were then carried out to determine the IC<sub>50</sub> values for each pool. IC<sub>50</sub> values for each mixture were standardized as a ratio to the geometric mean IC<sub>50</sub> value of the entire set of 180 mixtures, and then normalized at each position so that the value associated with the optimal value at each position corresponds to 1. For each position, an average (geometric) relative binding affinity (ARB) was calculated, and then the ratio of the ARB for the entire library to the ARB for each position was derived. The final results are a set of 9 by 20 scoring matrices which could predict the binding of novel peptides to MHC molecules.

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

## **Consensus**

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

## **NN-align**

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

## **NetMHCIIpan**

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

## **IEDB Recommended**

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

### **2.3.1.1.3 Tepitool**

The tool is designed as a wizard for the prediction of T cell epitope candidates from a given set of amino acid sequences, based on predicted peptide binding to MHC class I and class II molecules, where the user is led through a series of well-defined steps to complete the task. In contrast to the independent methods described above, Tepitool guides the user step-by-step as a client-side web form that takes user input data that is in turn processed at the server-side when the user submits the entire form. All fields except sequences and alleles are filled with default recommended settings for prediction and selection of optimum peptides. The input parameters can be adjusted as per the user's specific needs, and the user can go back to previous steps to change the selection before final submission of the job. The TepiTool has six steps:

- (i) Provide sequence data.
- (ii) Select the host species and MHC allele class.
- (iii) Select the alleles for binding prediction.
- (iv) Select peptides to be included in prediction.
- (v) Select preferred methods for binding prediction and peptide selection and cutoff values.
- (vi) Review selections, enter job details and submit data.

The tool is described in Paul et al. (Curr. Protoc. Immunol., 2016).

### **2.3.1.2 T Cell Epitopes – MHC Processing Prediction**

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

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

The proteasomal cleavage predictions evaluate how efficiently a peptide or its N-terminally prolonged precursors can be liberated from its source protein. The TAP transport predictions evaluate how efficiently a peptide or its N-terminal prolonged precursors are transported into the ER by TAP (Peters et al., Immunol, 2003). When this information is taken together and combined with MHC class I binding predictions, the tool yields a prediction of the efficiency with which a peptide is presented on the cell surface. The methods available are ANN, SMM, SMMPMBEC, Complib\_Sidney2008, NetMHCpan, PickPocket, NetMHCcons, and IEDB Recommended, which are described in Section 2.3.1.1.1.

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

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

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

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

### **2.3.1.2.3 MHC-NP: Prediction of peptides naturally processed by the MHC**

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

### **2.3.1.2.4 MHC-II-NP: Prediction of peptides naturally processed by the MHC**

Although algorithms for the prediction of peptide binding affinity to MHC II molecules exist, there is a lack of methods that predict the ligands resulting from natural antigen processing. To address this gap MHC-II-NP was developed.

The training ligand dataset, obtained through IEDB database query, contained more than 14,000 naturally processed ligands identified by MS of peptides eluted from MHC class II-expressing cells (from approximately 2,600 unique protein sequences). Analysis into sequence signatures which liberate peptides from their source antigens revealed preferred amino acids surrounding both N- and C- ligand terminuses. These cleavage motifs were used to develop this method for predicting naturally processed MHC II ligands as described in Paul et al. (Front. Immunol., 2018).

### **2.3.1.3 T Cell Class I pMHC Immunogenicity Predictor**

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

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

### **2.3.1.4 Deimmunization**

The deimmunization tool is attempt to identify immunodominant regions in a given therapeutically important protein, and suggest amino-acid substitutions that create non-immunogenic versions of the proteins. Therefore, we have opted for a two steps process; 1) In the first step, the deimmunization tool will list all the immunogenic regions or peptides based on selected threshold. These peptides will be generated from the protein with 15mer window size and 10mer overlap. 2) In the second step, the user can select one or more peptides listed in the results and final result window will display the non-immunogenic substitution of each selected peptides. The default threshold is 8.5 (which is difference in the median of percentile rank from 26 reference alleles set for MHC class II). In the final result window, the tools will also take care of the fact that non-immunogenic substitution in the immunogenic peptides, should not create new

immunogenic site in the neighboring peptides. Therefore, the result window will also display the effect of substitution on the neighboring peptides.

This tool is described in Dhanda et al. (Immunology, 2018).

### **2.3.1.5 CD4 T cell immunogenicity**

The server is developed to predict the allele independent CD4 T cell immunogenicity at population level, overcoming complications related to the high level of variability of HLA molecules, potential other factors beyond HLA as well as a frequent lack of HLA typing data. With this tool, users can predict the T cell immunogenicity using 7-allele method (Paul et. al. 2015), immunogenicity method and combined method (IEDB recommended). The combined method predicts the final score that combines the predictions from 7-allele method and immunogenicity method.

This tool is described in Dhanda et al. (Front Immunol, 2018).

## **2.3.2 B Cell Epitope Prediction**

### **2.3.2.1 Prediction of linear epitopes from protein sequence**

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

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

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

### **2.3.2.2 DiscoTope - Prediction of epitopes from protein structure**

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

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

### **2.3.2.3 ElliPro - Epitope prediction based upon structural protrusion**

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

### **2.3.2.4 Methods for modeling and docking of antibody and protein 3D structures**

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

## **2.3.3 Structure Tools**

### **2.3.3.1 LYmphocyte Receptor Automated modeling (LYRA)**

The LYRA web server implements a complete and automated method for building of B- and T-cell receptor structural models starting from their amino acid sequence alone. The webserver is freely available and easy to use for non-specialists. Upon submission, LYRA automatically generates alignments using ad hoc profiles, predicts the structural class of each hypervariable loop, selects the best templates in an automatic fashion, and provides within minutes a complete 3D model that can be downloaded or inspected online. Experienced users can manually select or exclude template structures according to case specific information. LYRA is based on the canonical structure method, that in the last 30 years has been successfully used to generate antibody models of high accuracy, and in our benchmarks this approach proves to achieve similarly good results on TCR modeling, with a benchmarked average RMSD accuracy of 1.29 and 1.48 Å for B- and T-cell receptors, respectively. The tool is described in detail by Klausen et al. (Nucleic Acids Research, 2015).

### **2.3.3.2 Structural Complexes of Epitope Receptor (SCEptRe)**

SCEptRe provides weekly updated, non-redundant, user customized benchmark datasets with information on the immune receptor features for receptor-specific epitope predictions. This tool extracts weekly updated 3D complexes of antibody-antigen, TCR-pMHC and MHC-ligand from the Immune Epitope Database (IEDB) and clusters them based on antigens, receptors and epitopes to generate benchmark datasets. Users can customize structural quality and clustering parameters (e.g., resolution, R free factors, antigen or epitope sequence identity) to generate these datasets based on their need. The tool is described in detail by Mahajan et al. (BMC Bioinformatics, 2019).

### **2.3.3.3 Docktope**

Docktope is a web-based tool, based on the D1-EM-D2 approach, intended to allow the pMHC-I modeling. Some applications allowed from the pMHC-I construction include the study of the pMHC-I tridimensional structure, epitope-MHC-I interaction patterns, cross-reactivity assessment and molecular dynamics studies. The tool allows the user to construct pMHC-I structures for the following alleles: HLA-A\*02:01 (9-mer

epitopes), HLA-B\*27:05 (9-mer epitopes), H2-Db (9-mer/10-mer epitopes) and H2-Kb (8-mer epitopes). The tool is described in detail by Rigo et al. (Scientific Reports, 2015).

## 2.3.4 Epitope Analysis Tools

### 2.3.4.1 Population Coverage

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

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

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

recognized by the population, and (3) minimum number of epitope hits / HLA combinations recognized by 90% of the population (PC90).

#### **2.3.4.2 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).

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

#### **2.3.4.3 Epitope Cluster Analysis**

Version 2.0 of the Epitope Cluster Analysis tool (Dhanda et al., Immunology. 2018) was released in 2018. This new version expanded tool functionality to include graphical representation, to provide connectivity within a cluster, to generate epitope clusters based on representative or consensus sequences, and to calculate overhang sequence identity. The base functionality of the tool remained the same.

The 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.

#### **2.3.4.4 Computational Methods for Mapping Mimotopes to Protein Antigens**

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

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

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

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

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

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

#### **2.3.4.5 Restrictor Analysis Tool for Epitopes (RATE)**

RATE is an automated method that can infer HLA restriction for a set of given epitopes from large datasets of T cell responses in HLA typed subjects. The tool takes two data files, one containing the alleles expressed by the subjects and the other containing the response of the peptides in the subjects. The tool calculates the odds ratio and estimates its significance using Fisher's exact test. It also calculates a parameter called relative frequency similar to odds ratio. The tool was developed with a focus on class II alleles but can also be applied to class I alleles. A description of the tool can be found in Paul et al. (Journal of Immunology, 2015).

In 2017, RATE was validated using experimentally defined restriction data from a set of 191 tuberculosis-derived epitopes and 63 healthy individuals with MTB infection from the Western Cape Region of South Africa. Additionally, the parameters used by the RATE tool to infer restriction were optimized. New HLA restrictions were identified using the optimized RATE tool. A description of this study can be found in Paul et al. (BMC Immunol, 2017).

#### **2.3.4.6 ImmunomeBrowser**

This tool aggregates all data relevant to the user query and allows one to visualize the known immune response to a specific antigen, as well as illustrating knowledge gaps in a reference protein. It provides the immune reactivity in terms of response frequency (RF) and the number of subjects tested/responded and/or number of independent assays performed along the length of reference protein. The tool was originally implemented in the results page of the database section of the IEDB. To further extend the usability to predicted epitopes and propriety epitopes or non-IEDB data, a stand-alone version of the tool was developed in 2018 (Dhanda et. al., Bioinformatics 2018). The standalone version maps user provided peptide sets and associated response data to a user-provided protein reference sequence. This now allows the user to analyze and visualize immunodominant regions within their own dataset. The results are presented both as a user interactive JavaScript based web interface and a tabular format in a selected reference sequence.

### 2.3.5 IEDB Analysis Resource Labs

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

Of the tools described above, 8 tools are currently available under the Labs designation:

<u>Prediction LABS Tools</u>	<u>Analysis LABS Tools</u>
MHCII-NP	RATE
Deimmunization	ImmunomeBrowser
CD4 T Cell Immunogenicity	
LYRA	
SCEptRe	
Docktope	

### 2.3.6 Benchmark References and Data Sets

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

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

- Jurtz V, Paul S, Andreatta M, Marcatili P, Peters B, Nielsen M. NetMHCpan-4.0: Improved Peptide-MHC Class I Interaction Predictions Integrating Eluted Ligand and Peptide Binding Affinity Data. *J Immunol.* 2017 Nov 1;199(9):3360-3368. doi: 10.4049/jimmunol.1700893. Epub 2017 Oct 4. PMID: 28978689; PMCID: PMC5679736.
- Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M. Automated benchmarking of peptide-MHC class I binding predictions. *Bioinformatics.* 2015 Jul 1;31(13):2174-81. doi: 10.1093/bioinformatics/btv123. Epub 2015 Feb 25. PMID: 25717196; PMCID: PMC4481849
- Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B. Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. *BMC Bioinformatics.* 2014 Jul 14;15:241. doi: 10.1186/1471-2105-15-241. PMID: 25017736; PMCID: PMC4111843.
- Kim Y, Sidney J, Pinilla C, Sette A, Peters B. Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior. *BMC Bioinformatics.* 2009 Nov 30;10:394. PMID: 19948066.
- Peters B, Bui HH, Frankild S, Nielson M, Lundegaard C, Kostem E, Basch D, Lamberth K, Harndahl M, Flerl W, Wilson SS, Sidney J, Lund O, Buus S, Sette A., A community resource benchmarking predictions of peptide binding to MHC-I molecules, *PLoS Comput Biol.* 2006 Jun 9;2(6):e65. Epub 2006 Jun 9. PMID: 16789818

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

- Andreatta M, Trolle T, Yan Z, Greenbaum JA, Peters B, Nielsen M. An automated benchmarking platform for MHC class II binding prediction methods. *Bioinformatics*. 2018 May 1;34(9):1522-1528. doi: 10.1093/bioinformatics/btx820. PMID: 29281002; PMCID: PMC5925780.
- Wang P, Sidney J, Kim Y, Sette A, Lund O, Nielsen M, Peters B. Peptide binding predictions for HLA DR, DP and DQ molecules. *BMC Bioinformatics*. 2010 Nov 22;11:568. PMID: 21092157; PMCID: PMC2998531.
- Wang, P., J. Sidney, C. Dow, B. Mothe, A. Sette, B. Peters. (2008). A Systematic Assessment of MHC Class II Peptide Binding Predictions and Evaluation of a Consensus Approach. *PLoS Computational Biology* 4(4). PMID: 18389056

For the B cell predictions, the references are:

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

### 2.3.7 Other Ways to Access Tools

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

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

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

## **2.4 Help Overview**

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

### **2.4.1 Support**

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

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

### **2.4.2 Help Request**

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

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

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

### **2.4.3 Provide Feedback**

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

### **2.4.4 Video Tutorials**

There is a link to the IEDB video tutorials under the Help menu at the top of each web page. This link takes the user to the “How-to Videos” article in the Solutions Center in the Tutorials and Reference Materials folder. Most of the videos are edited versions of live presentations made at the annual IEDB User Workshops. The videos from the 2019 event are currently posted for user viewing. An overview of the

resource and information regarding the data structure and curation are presented first. The next category addresses the query and reporting features. Videos for all the tools in the Analysis Resource are listed next. Videos for the legacy website have been removed because the legacy site has been retired and can no longer be accessed by users.

## 2.5 More IEDB

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

### 2.5.1 Database Export

The contents of the Immune Epitope Database are exported weekly to files in XML format. The database export page (Figure 2.35) contains a complete database export in XML format along with exports of the various records that are referenced in the complete database export. The complete dataset export is provided as a ZIP archive (iedb\_export.zip) containing one XML file for each reference contained in the database. The export also contains ZIP archives of XML files that provide users with the full record for the various identifiers that are referenced in the full database export, such as the IEDB source organism accession identifier list, the MHC allele name list, and the organism list. The supporting XML files only contain full records when the record is not otherwise available from the original source.

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

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

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

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

### 2.5.2 Meta-Analyses

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

### **2.5.3 Citing the IEDB**

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

1. The IEDB website should be cited using the URL: <http://www.iedb.org>
2. The journal reference for the IEDB was updated in 2018; and should be cited as:

Vita R, Mahajan S, Overton JA, Dhanda SK, Martini S, Cantrell JR, Wheeler DK, Sette A, Peters B. The Immune Epitope Database (IEDB): 2018 update. Nucleic Acids Res. 2018 Oct 24. doi: 10.1093/nar/gky1006. [Epub ahead of print] PubMed PMID: 30357391.

### **2.5.4 Release Notes**

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

### **2.5.5 Links to External Sources**

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

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

## 2.6 Learn More

The Learn More web page can be accessed from the link at the bottom of the Welcome box in the upper left-hand corner of the IEDB home page. The Learn More page has five major sections, as seen in Figure 2.36. The upper left section has a carousel of content from the New and Noteworthy forum in the Solutions Center. A graphic is usually included in the forum article that is displayed in the left-hand portion of the section. Below this section are three other sections titled Support, About the Data, and About Us. The Support section has links to submit a help request or feedback. The right-hand panel of the page lists the release notes for the most recent versions of the main website and the Analysis Resource.

The screenshot shows the IEDB Learn More page. At the top, there's a navigation bar with 'Home', 'Specialized Searches', and 'Analysis Resource'. On the far right, there are 'Help' and 'More IEDB' links. The main content area is divided into several sections:

- News and Updates:** Features a photograph of a workshop audience and a text block about the 2020 IEDB User Workshop.
- Support:** Includes links to ask a question, browse support topics, watch how-to videos, get help with common searches, and browse epitope resources.
- About the Data:** Contains a figure showing the distribution of age groups (3-5, 5-18, >18) and a bar chart of frequencies versus CD4+ T-cell types (CLG, YLL, FLY, LLD).
- About Us:** Shows a group photo of the IEDB team and links to citation guidelines, publications, acknowledgments, terms of use, and annual compendia.
- Latest Release Notes:** A sidebar listing recent releases:
  - IEDB Analysis Resource v2.23 release note (2 Jul 2020)**: All code ported from Python 2 to Python 3, including standalone packages (Python 3.6 or higher is required). The 'IEDB reco...' tool is incorporated.
  - IEDB Analysis Resource v2.22 release note (4 Sep 2019)**: NEW: Docktope is incorporated as a n tool. Class II binding predictor now allows predicting for various lengths (11-30). Ne...
  - IEDB Analysis Resource v2.21 release note (26 Mar 2019)**: NEW: SCeptRe - Structural Complexes of Epitope Receptor. Improved sequence format detection added to MHC I binding, MHC II binding D...
  - IEDB v3.10.0 release notes**: IEDB v3.10.0 release notes. This topic contains the release notes for IED version 3.10.0. Redesigned receptor database tables a...

**Figure 2.35** The Learn More page, accessed from the Welcome message in the upper left corner of the IEDB home page

### 2.6.1 Support

Each link is briefly described below.

#### Ask a question or submit an idea

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

#### Browse support topics

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

### **Get help with common searches**

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

### **Browse links to epitope resources**

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

## **2.6.2 About the Data**

Each link is briefly described below.

### **Export all or part of the IEDB**

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

### **Meta-analyses**

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

### **Read about the data fields**

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

### **See how the data is entered**

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

### **Learn about the IEDB ontology**

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

## **2.6.3 About Us**

### **Citation Guidelines**

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

### **IEDB Publications**

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

### **Acknowledgements**

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

### **Terms of Use**

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

### **Annual Compendia**

An archive of the IEDB Annual Compendia can be found at this link to the IEDB Solutions Center. The list includes all Annual Compendia going back to 2005.

### 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 17 years. The second section lists references that cited the IEDB. This list was compiled by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the IEDB team authored papers.

#### 3.1 IEDB Sponsored Publications

Scientific articles written by the IEDB team members that are relevant to the IEDB are listed below (organized by year of publication) through 2019. This publication list was re-evaluated in December 2019 to ensure that the list was accurate and up to date. As a result of this review, the publication list now contains 158 IEDB sponsored publications (including book chapters) between program inception in 2003 and 31 December 2019.

Year	Type	Paper	PMID	Journal
2019	General	Comprehensive Review of Human Plasmodium falciparum-Specific CD8+ T Cell Epitopes	30949162	Frontiers in Immunology
		Human T Cell Response to Dengue Virus Infection	31552052	Frontiers in Immunology
		A survey of known immune epitopes in the enteroviruses associated with acute flaccid myelitis	31451291	Human Immunology
		Benchmark datasets of immune receptor-epitope structural complexes	31601176	BMC Bioinformatics
		The Immune Epitope Database and Analysis Resource program 2003-2019 reflections and outlook	31761977	Immunogenetics
2019	Tools	Antibody specific B-cell epitope predictions: leveraging information from antibody-antigen protein complexes	30863406	Frontiers in Immunology
		Immune Epitope Database - Analysis Resource (IEDB-AR) in 2019	31114900	Nucleic Acids Research
		TCRpMHCmodels: Structural modelling of TCR-pMHC class I complexes.	31601838	Scientific Reports
		Book Chapter: Prediction of B and T cell epitopes in proteins	N/A	Immunotechnology and Its Applications
		NNAlign_MA; MHC Peptidome Deconvolution for Accurate MHC Binding Motif Characterization and Improved T-cell Epitope Predictions	31578220	Molecular & Cellular Proteomics
2018	General	Investigation of outbreak-specific nonsynonymous mutations on Ebolavirus GP in the context of known immune reactivity	30581874	Journal of Immunology Research
		FAIR principles and the IEDB: Short-term improvements and a Long-term vision of OBO-Foundry mediated machine-actionable interoperability	29688354	Database
		A Review on T Cell Epitopes Identified Using Prediction and Cell-Mediated Immune Models for Mycobacterium tuberculosis and Bordetella pertussis	30555469	Frontiers in Immunology
		Identification of Errors in the IEDB Using Ontologies	29688357	Database

	Epitope Specific Antibodies and T Cell Receptors in the Immune Epitope Database	30515166	Frontiers in Immunology	
	The Immune Epitope Database (IEDB): 2018 update	30357391	Nucleic Acids Research	
Tools	An automated benchmarking platform for MHC class II binding prediction methods	29281002	Bioinformatics	
	Bioinformatics Tools for the Prediction of T-Cell Epitopes.	29714025	Methods Mol Biol	
	Development of a novel clustering tool for linear peptide sequences	30014462	Immunology	
	Predicting HLA CD4 immunogenicity in human populations	29963059	Frontiers in Immunology	
	Footprints of antigen processing boost MHC class II natural ligand binding predictions	30446001	Genome Medicine	
	Computational Tools for the Identification and Interpretation of Sequence Motifs in Immunopeptidomes	29327813	Proteomics	
	ImmunomeBrowser: A tool to aggregate and visualize complex and heterogeneous epitopes in reference protein	29878047	Bioinformatics	
	Improved methods for predicting peptide binding affinity to MHC class II molecules	29315598	Immunology	
	Determination of a Predictive Cleavage Motif for Eluted Major Histocompatibility Complex Class II Ligands	30127785	Frontiers in Immunology	
	Microbiota epitope similarity either dampens or enhances the immunogenicity of disease-associated antigenic epitopes	29734356	PLoS One	
General	Deciphering the MHC-associated peptidome: a review of naturally processed ligand data	28756714	Expert Rev Proteomics	
	Unconventional peptide Presentation by Major Histocompatibility Complex (MHC) Class I Allele HLA-A*02:01: Breaking Confinement	28179428	J Biol Chem	
	The Immune Epitope Database: How Data Are Entered and Retrieved	28634590	J Immunol Res	
	Better living through ontologies at the Immune Epitope Database	28365732	Database (Oxford)	
	The SysteMHC Atlas project	28985418	Nucleic Acids Res	
	The Immune Epitope Database and Analysis Resource in Epitope Discovery and Synthetic Vaccine Design	28352270	Front Immunol	
2017	Tools	Experimental validation of the RATE tool for inferring HLA restrictions of T cell epitopes	28681704	BMC Immunology
		Citrullination only infrequently impacts peptide binding to HLA class II MHC	28481943	PLoS One
		Machine learning reveals a non-canonical mode of peptide binding to MHC class II molecules	28542831	Immunology
		NNAlign: a platform to construct and evaluate artificial neural network models of receptor-ligand interactions	28407117	Nucleic Acids Res
		BepiPred-2.0: improving sequence-based B-cell epitope predictions using conformational epitopes	28472356	Nucleic Acids Res
		GibbsCluster: unsupervised clustering and alignment of peptide sequences	28407089	Nucleic Acids Res

		An introduction to Deep learning on biological sequence data - Examples and solutions	28961695	Bioinformatics
		Development of a strategy and computational application to select candidate protein analogues with reduced HLA binding and immunogenicity	28833085	Immunology
		NetMHCpan 4.0: Improved peptide-MHC class I interaction predictions integrating eluted ligand and peptide binding affinity data	28978689	J Immunol
2016	General	Ebola: an analysis of immunity at the molecular level	N/A	IEEE Xplore Digital Library
		Identifying candidate targets of immune responses in Zika virus based on homology to epitopes in other Flavivirus species	28018746	PLoS Curr
		Immune Epitope Database and Analysis Resource (IEDB)	N/A	Encyclopedia of Bioimmunology
		An Ontology for Major Histocompatibility Restriction	26759709	J Biomed Semantics
		The Ontology for Biomedical Investigations	27128319	PLoS One
	Tools	Reproducibility and Conflicts in Immune Epitope Data	26678806	Immunology
		The Length Distribution of Class I-Restricted T Cell Epitopes Is Determined by Both Peptide Supply and MHC Allele-Specific Binding Preference	26783342	J Immunol
		NetMHCpan-3.0; improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length data sets	27029192	Genome Med
		T-cell recognition is shaped by epitope sequence conservation in the host proteome and microbiome	26789414	Immunology
		TepiTool: A pipeline for computational prediction of T cell epitope candidates	27479659	Current Protocols in Immunology
2015	General	Toxoplasma gondii peptide ligands open the gate of the HLA class I binding groove	26824387	Elife
		Gapped sequence alignment using artificial neural networks: application to the MHC class I system	26515819	Bioinformatics
		Pan-Specific Prediction of Peptide-MHC Class I Complex Stability, a Correlate of T Cell Immunogenicity	27402703	J Immunol
		Analysis of Human RSV immunity at the molecular level: learning from the past and present	26001197	PLoS One
	Tools	The Use of the Immune Epitope Database (IEDB) to Study Autoimmune Epitope Data related to Alopecia Areata	26551944	Journal of Investigative Dermatology
		The immune epitope database (IEDB) 3.0	25300482	Nucleic Acids Res
		Consequences of periodic $\alpha$ -to- $\beta$ (3) residue replacement for immunological recognition of peptide epitopes	25559929	ACS Chem Biol

		Antibody specific epitope prediction - emergence of a new paradigm	25837466	Curr Opin Virol
		A population response analysis approach to assign class II HLA-epitope restrictions	25948811	J Immunol
		LYRA, a webserver for lymphocyte receptor structural modeling	26007650	Nucleic Acids Res
		Accurate pan-specific prediction of peptide-MHC class II binding affinity with improved binding core identification	26416257	Immunogenetics
2014	General	Substantial gaps in knowledge of <i>Bordetella pertussis</i> antibody and T cell epitopes relevant for natural immunity and vaccine efficacy	24530743	Human Immunology
		Conservancy of mAb epitopes in Ebolavirus glycoproteins of previous and 2014 outbreaks	25642381	PLoS Curr
		A molecular view of multiple sclerosis and experimental autoimmune encephalitis: What can we learn from the epitope data?	24365494	J Neuroimmunol
	Tools	Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions	25017736	BMC Bioinformatics
		NetTepi: an integrated method for the prediction of T-cell epitopes	24863339	Immunogenetics
		NetMHCstab - predicting stability of peptide:MHC-I complexes; impacts for CTL epitope discovery	23927693	Immunology
		Characterization of binding specificities of bovine leucocyte class I molecules: impacts for rational epitope discovery	25186069	Immunogenetics
2013	General	Navigating diabetes-related immune epitope data: resources and tools provided by the Immune Epitope Database (IEDB)	25140192	Immunome Res
		Query Enhancement through the Practical Application of Ontology: The IEDB and OBI	23734660	J Biomed Semantics
		Positional Bias of MHC Class I Restricted T-Cell Epitopes in Viral Antigens is likely due to a Bias in Conservation	23357871	PLoS Comput Biol
	Tools	Evaluating the immunogenicity of protein drugs by applying in vitro MHC binding data and the immune epitope database and analysis resource	24222776	Clin Dev Immunol
		Properties of MHC class I presented peptides that enhance immunogenicity	24204222	PLoS Comp Biol
		NetMHCIIpan-3.0, a common pan-specific MHC class II prediction method including all three human MHC class II isotypes, HLA-DR, HLA-DP and HLA-DQ	23900783	Immunogenetics
		SigniSite: Identification of residue-level genotype-phenotype correlations in protein multiple sequence alignments	23761454	Nucleic Acids Res
		Evaluation of peptide selection approaches for epitope-based vaccine design	24461003	Tissue Antigens
		HLA Class I Alleles Are Associated with Peptide-Binding Repertoires of Different Size, Affinity, and Immunogenicity	24190657	J Immunol

		Structural analysis of B-cell epitopes in antibody:protein complexes	22784991	Mol Immunol
2012	General	A meta-analysis of the existing knowledge of immunoreactivity against hepatitis C virus (HCV)	22675428	PLoS One
		The immune epitope database: a historical retrospective of the first decade	22681406	Immunology
		Strategies to query and display allergy-derived epitope data from the Immune Epitope Database (IEDB)	23172234	Int Arch Allergy Immunol
		A Comparison of Epitope Repertoires Associated with Myasthenia Gravis in Humans and Nonhuman Hosts	23243503	Autoimmune Dis
	Tools	Immune epitope database analysis resource	22610854	Nucleic Acids Res
		Predictions versus high-throughput experiments in T-cell epitope discovery: competition or synergy?	22149708	Expert Rev Vaccines
		NetMHCcons: a consensus method for the major histocompatibility complex class I predictions.	22009319	Immunogenetics
	2011	Cost sensitive hierarchical document classification to triage PubMed abstracts for manual curation	22182279	BMC Bioinformatics
		A Model for Collaborative Curation, The IEDB and ChEBI Curation of Non-peptidic Epitopes	21897450	Immunome Res
		IEDB-3D: structural data within the immune epitope database	21030437	Nucleic Acids Res
	Tools	Applications for T-cell epitope queries and tools in the Immune Epitope Database and Analysis Resource	21047510	J Immunol Methods
		Prediction of epitopes using neural network based methods	21047511	J Immunol Methods
		A computational pipeline to generate MHC binding motifs	28747991	Immunome Res
2010	General	Towards defining molecular determinants recognized by adaptive immunity in allergic disease: an inventory of the available data	21403821	J Allergy (Cairo)
		OBI consortium. Modeling biomedical experimental processes with OBI	20626927	J Biomed Semantics
		Design and utilization of epitope-based databases and predictive tools	20213141	Immunogenetics
		Meta-analysis of all immune epitope data in the Flavivirus genus: inventory of current immune epitope data status in the context of virus immunity and immunopathology	20565291	Viral Immunol
		The Immune Epitope Database 2.0	19906713	Nucleic Acids Res
		Molecular determinants of T cell epitope recognition to the common Timothy grass allergen	20554959	J Immunol
		Divergent motifs but overlapping binding repertoires of six HLA-DQ molecules frequently expressed in the worldwide human population.	20810981	J Immunol
		Five HLA-DP molecules frequently expressed in the worldwide human population share a common HLA supertypic binding specificity	20139279	J Immunol
		Uncovering the interplay between CD8, CD4 and antibody responses to complex pathogens.	20143946	Future Microbiol

		MHC class II epitope predictive algorithms	20408898	Immunology
		Peptide binding predictions for HLA DR, DP and DQ molecules	21092157	BMC Bioinformatics
	Tools	Limitations of Ab initio predictions of peptide binding to MHC class II molecules	20174654	PLoS One
		NetCTLpan: pan-specific MHC class I pathway epitope predictions	20379710	Immunogenetics
		The MHC motif viewer: a visualization tool for MHC binding motifs.	20143317	Curr Protoc Immunol
2009	General	Classification of the universe of immune epitope literature: representation and knowledge gaps	19774228	PLoS One
		Pre-existing immunity against swine-origin H1N1 influenza viruses in the general human population	19918065	Proc Natl Acad Sci
		Meta-analysis of immune epitope data for all Plasmodia: overview and applications for malarial immunobiology and vaccine-related issues	19149776	Parasite Immunol
		Two MHC class I molecules associated with elite control of immunodeficiency virus replication, Mamu-B*08 and HLA-B*2705, bind peptides with sequence similarity.	19494300	J Immunol
		Diverse recognition of conserved orthopoxvirus CD8+ T cell epitopes in vaccinated rhesus macaques.	19531389	Vaccine
	Tools	Definition of epitopes and antigens recognized by vaccinia specific immune responses: their conservation in variola virus sequences, and use as a model system to study complex pathogens	20006135	Vaccine
		NetMHCpan, a method for MHC class I binding prediction beyond humans	19002680	Immunogenetics
		Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior	19948066	BMC Bioinformatics
		The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: Application to MHC-peptide binding	19297351	Bioinformatics
		Pan-specific MHC class I predictors: a benchmark of HLA class I pan-specific prediction methods	18996943	Bioinformatics
2008	General	The Curation Guidelines of the Immune Epitope Database and Analysis Resource	18688821	Cytometry A
		Analysis of epitope information related to Bacillus anthracis and Clostridium botulinum	18251694	Expert Rev Vaccines
		Quantitative peptide binding motifs for 19 human and mouse MHC class I molecules derived using positional scanning combinatorial peptide libraries	18221540	Immunome Res
		HLA class I supertypes: a revised and updated classification	18211710	BMC Immunol
		Immunodominant epitopes in herpes simplex virus type 2 glycoprotein D are recognized by CD4 lymphocytes from both HSV-1 and HSV-2 seropositive subjects	18941251	J Immunol
	Tools	NetMHC-3.0: accurate web accessible predictions of human, mouse and monkey MHC class I affinities for peptides of length 8-11	18463140	Nucleic Acids Res

		Quantitative Predictions of Peptide Binding to Any HLA-DR Molecule of Known Sequence: NetMHCIIpan	18604266	PLoS Computational Biology
		B-cell epitope prediction		Structural Bioinformatics
		ElliPro: a new structure-based tool for the prediction of antibody epitopes	19055730	BMC Bioinformatics
		A Systematic Assessment of MHC Class II Peptide Binding Predictions and Evaluation of a Consensus Approach	18389056	PLoS Computational Biology
		Immune epitope database analysis resource (IEDB-AR)	18515843	Nucleic Acids Res
2007	General	An analysis of the epitope knowledge related to Mycobacteria	18081934	Immunome Res
		Ab and T cell epitopes of influenza A virus, knowledge and opportunities	17200302	Proc Natl Acad Sci
		Meeting Report: NIH Workshop on the Tuberculosis Immune Epitope Database	18068490	Tuberculosis (Edinb)
		Integrating epitope data into the emerging web of biomedical knowledge resources	17479127	Nat Rev Immunol
		Immune epitope mapping in the post-genomic era: lessons for vaccine development	17113275	Curr Opin Immunol
		Automating document classification for the Immune Epitope Database	17655769	BMC Bioinformatics
	Tools	Characterization of the peptide-binding specificity of the chimpanzee class I alleles A 0301 and A 0401 using a combinatorial peptide library	17701407	Immunogenetics
		Antibody-protein interactions: benchmark datasets and prediction tools evaluation.	17910770	BMC Struct Biol
		EpitopeViewer: a Java application for the visualization and analysis of immune epitopes in the Immune Epitope Database and Analysis Resource (IEDB)	17313688	Immunome Res
		Development of an epitope conservancy analysis tool to facilitate the design of epitope-based diagnostics and vaccines	17897458	BMC Bioinformatics
2006	General	Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools	17205610	J Mol Recognit
		Modeling the adaptive immune system: predictions and simulations	18045832	Bioinformatics
		NetMHCpan, a method for quantitative predictions of peptide binding to any HLA-A and -B locus protein of known sequence	17726526	PLoS One
	Tools	The biocurator: connecting and enhancing scientific data	17069454	PLoS Comput Biol
		The Immune Epitope Database and Analysis Resource	N/A	Conference Proceedings
2005	General	Curation of complex, context-dependent immunological data	16836764	BMC Bioinformatics
		Predicting population coverage of T-cell epitope-based diagnostics and vaccines	16545123	BMC Bioinformatics
	Tools	A community resource benchmarking predictions of peptide binding to MHC-I molecules	16789818	PLoS Comput Biol
		The design and implementation of the immune epitope database and analysis resource	15895191	Immunogenetics

	The Immune Epitope Database and Analysis Resource: From Vision to Blueprint	15760272	PLoS Biology	
	An ontology for immune epitopes: application to the design of a broad scope database of immune reactivities	16305755	Immunome Res	
	A Roadmap for the Immunomics of Category A–C Pathogens	15773067	Immunity	
	Characterization of the peptide-binding specificity of Mamu-A*11 results in the identification of SIV-derived epitopes and interspecies cross-reactivity	15747117	Immunogenetics	
Tools	Generating quantitative models describing the sequence specificity of biological processes with the stabilized matrix method	15927070	BMC Bioinformatics	
	A computational resource for the prediction of peptide binding to Indian rhesus macaque MHC class I molecules.	16137805	Vaccine	
2004	General	The immune epitope database and analysis resource: from vision to blueprint	16312048	Genome Inform
		Identification of seventeen new simian immunodeficiency virus-derived CD8+ T cell epitopes restricted by the high frequency molecule, Mamu-A*02, and potential escape from CTL recognition	15470050	J Immunol
2003	General	In silico prediction of peptides binding to multiple HLA-DR molecules accurately identifies immunodominant epitopes from gp43 of <i>Paracoccidioides brasiliensis</i> frequently recognized in primary peripheral blood mononuclear cell responses from sensitized individuals	15208742	Mol Med

### 3.2 Publications Citing the IEDB in 2019

In 2019, the IEDB or Analysis Resource received a total of 2,676 individual citations (2,079 total citations for IEDB publications and 597 additional inline citations). This represents an increase of 461 citations over 2,215 from the previous year (2018). The citation list includes 1,520 references that formally cited one or more of the 154 papers written by the IEDB team over the past seventeen years, and an additional 597 references that cited the IEDB in-text but did not cite a specific reference. This represents an increase of 197 references from the 1,323 references that cited the IEDB in 2018. Of note, this total may increase over time since these databases may not include references published late in 2019.

The formal citation list was compiled by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the 154 papers and excludes self-citations. In contrast, often scientific reports quote the IEDB not as a formal citation, but by simply stating in the text that the IEDB was used or listing the website address. Here we developed and implemented a plan to address in-text citations (informal mentions of the IEDB, rather than a direct citation). For this purpose, we utilized Publish or Perish, a software program that retrieves citations from Crossref, Google Scholar, Microsoft Academic, Scopus, and Web of Science, and returns output that can easily be converted to an excel file. The tool can capture citations that the document specialist's citation analysis, which includes Google Scholar and Web of Science, may have missed, and can capture references that cite the IEDB in text but do not cite a specific IEDB-related publication.

The papers have been categorized by the type of IEDB paper they cited – General IEDB (G) or Analysis Resource (AR). By reference, the General IEDB (G) papers received 529 citations in 2019 and the Analysis Resource (AR) papers received 1,550 citations. However, without redundancy, 923 unique references formally cited the IEDB and Analysis Resource, and a further 597 references informally cited the resource.

All papers listed below denote their category or categories with these abbreviations since a paper can cite several IEDB papers that belong in different categories. For example, a paper that cites an analysis resource paper may also cite the primary IEDB Nucleic Acids Res (2014) paper, and thus is listed under General IEDB and has an [AR, G] to indicate the Analysis Resource citation. Any paper that has “General” as one of its categories has been listed in the General category below.

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