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Immune Epitope Database and Analysis Resource Program

2018 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 14 January 2019. 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 2018 for which the IEDB played a contributory role.

Since the publication of last year's 2017 Annual Compendium, the quantity of data available in the IEDB continues to increase significantly. As of January 2019, the IEDB contains data for over 850,000 epitopes, 47,000 antigens, 1,900,000 assays, and 25,000 receptors from more than 19,000 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 2018, 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 2017 and 2018. Of the 3,689 species/strains listed, 74 were added in 2018. 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 2018. 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-17", "T-17", "B-18", and "T-18" indicate the cumulative number of distinct B cell and T cell epitopes in the database at the end of 2017 and 2018, respectively. The two rightmost columns display the differences in the B and T cell epitope counts from 2017 to 2018. The changes in B and T cell epitope counts are shown in red. In 2018, the number of B cell epitopes increased by 5,605 from 44,803 to 50,408 and the number of T cell epitopes increased by 72,798 from 388,409 to 461,207.

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

ID	NEW 2018	ORGANISM ID	SPECIES / STRAIN	B_17	T_17	B_18	T_18	DELTA B	DELTA T
1		2	Bacteria	45		45			
2		106	<i>Runella siltiformis</i>		1		1		
3		108	<i>Spirosoma linguale</i>		1		1		
4		139	<i>Borreliella burgdorferi</i>	65	43	78	43	13	
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>	103	29	108	29	5	
11		210	<i>Helicobacter pylori</i>	47	56	47	56		
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			
21		287	<i>Pseudomonas aeruginosa</i>	78	162	79	162	1	
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>		1	2	1	2	
37		471	<i>Acinetobacter calcoaceticus</i>		1		1		
38		480	<i>Moraxella catarrhalis</i>	10		10			
39		485	<i>Neisseria gonorrhoeae</i>	76	15	77	15	1	
40		487	<i>Neisseria meningitidis</i>	87	23	88	23	1	
41		491	<i>Neisseria meningitidis</i> serogroup B	40	1	46	1	6	
42		511	<i>Alcaligenes faecalis</i>	3	2	3	2		
43		520	<i>Bordetella pertussis</i>	338	218	338	218		
44		543	<i>Enterobacteriaceae</i>	3		4		1	
45		544	<i>Citrobacter</i>	1		1			
46		546	<i>Citrobacter freundii</i>	1		1			
47		548	<i>Klebsiella aerogenes</i>		1		1		
48		550	<i>Enterobacter cloacae</i>		9		9		
49		554	<i>Pectobacterium carotovorum</i>	2		2			
51		562	<i>Escherichia coli</i>	246	149	257	150	11	1
52		573	<i>Klebsiella pneumoniae</i>	29	9	29	9		
53		582	<i>Morganella morganii</i>	1		1			
54		583	<i>Proteus</i>	2		2			
55		584	<i>Proteus mirabilis</i>	7		7			
57		590	<i>Salmonella</i>	3		3			
58		596	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Muenchen</i>	1		1			
59		599	<i>Salmonella</i> sp.	1		1			
60		605	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Pullorum</i>		1		1		
61	X	611	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Heidelberg</i>			9		9	
62		615	<i>Serratia marcescens</i>	1	3	1	3		
63		621	<i>Shigella boydii</i>		2		2		
64		622	<i>Shigella dysenteriae</i>	6	2	6	2		
65		623	<i>Shigella flexneri</i>	77	11	77	11		
66		624	<i>Shigella sonnei</i>		1		1		
67		630	<i>Yersinia enterocolitica</i>	6	28	6	28		

68	632	<i>Yersinia pestis</i>	24	324	24	324		
69	633	<i>Yersinia pseudotuberculosis</i>		2		2		
71	644	<i>Aeromonas hydrophila</i>	7	2	9	3	2	1
72	645	<i>Aeromonas salmonicida</i>	59		59			
73	659	<i>Photobacterium phosphoreum</i>		1		1		
74	666	<i>Vibrio cholerae</i>	38	90	38	91		1
75	670	<i>Vibrio parahaemolyticus</i>		57		57		
76	671	<i>Vibrio proteolyticus</i>	1		1			
77	672	<i>Vibrio vulnificus</i>	1	66	1	66		
78	674	<i>Vibrio mimicus</i>	2		2			
79	686	<i>Vibrio cholerae O1 biovar El Tor</i>	3	1	3	1		
80	703	<i>Plesiomonas shigelloides</i>		2		2		
81	714	<i>Aggregatibacter actinomycetemcomitans</i>	1	4	1	4		
82	715	<i>Actinobacillus pleuropneumoniae</i>		2		2		
83	727	<i>Haemophilus influenzae</i>	30	68	30	68		
84	730	[<i>Haemophilus</i>] <i>ducreyi</i>	3	2	3	2		
85	738	<i>Glaesserella parasuis</i>	1		1			
86	747	<i>Pasteurella multocida</i>	1	10	1	10		
87	769	<i>Anaplasma centrale</i>		2		2		
88	770	<i>Anaplasma marginale</i>	17	14	17	14		
89	777	<i>Coxiella burnetii</i>	2	201	2	201		
90	779	<i>Ehrlichia ruminantium</i>	3		3			
91	781	<i>Rickettsia conorii</i>		13		13		
92	782	<i>Rickettsia prowazekii</i>		23		23		
93	783	<i>Rickettsia rickettsii</i>		1		1		
94	784	<i>Orientia tsutsugamushi</i>	87		87			
95	785	<i>Rickettsia typhi</i>		3		3		
96	787	<i>Rickettsia australis</i>		1		1		
97	788	<i>Rickettsia canadensis</i>		1		1		
98	813	<i>Chlamydia trachomatis</i>	128	69	178	69	50	
99	817	<i>Bacteroides fragilis</i>		3		3		
100	837	<i>Porphyromonas gingivalis</i>	91	21	91	21		
101	920	<i>Acidithiobacillus ferrooxidans</i>		1		1		
102	944	<i>Ehrlichia canis</i>	7	1	7	1		
103	945	<i>Ehrlichia chaffeensis</i>	14	1	14	1		
105	948	<i>Anaplasma phagocytophilum</i>	29		33		4	
106	955	<i>Wolbachia pipiens</i>	1		1			
107	1006	<i>Marivirga tractuosa</i>		1		1		
108	1018	<i>Capnocytophaga ochracea</i>		1		1		
109	1019	<i>Capnocytophaga sputigena</i>		1		1		
110	1022	<i>Beggiatoa alba</i>	1		1			
111	1063	<i>Rhodobacter sphaeroides</i>		1		1		
112	1076	<i>Rhodopseudomonas palustris</i>		2		2		
113	1224	<i>Proteobacteria</i>	3		3			
114	1245	<i>Leuconostoc mesenteroides</i>	1		1			
115	1254	<i>Pediococcus acidilactici</i>	1		1			
116	1260	<i>Finegoldia magna</i>		1		1		
117	1265	<i>Ruminococcus flavefaciens</i>		1		1		
118	1270	<i>Micrococcus luteus</i>	1		1			
119	1279	<i>Staphylococcus</i>	1		1			
120	1280	<i>Staphylococcus aureus</i>	132	46	134	46	2	
122	1292	<i>Staphylococcus warneri</i>	1		1			
123	1299	<i>Deinococcus radiodurans</i>	3		3			
124	1301	<i>Streptococcus</i>	5		5			
125	1303	<i>Streptococcus oralis</i>	12		12			
127	1305	<i>Streptococcus sanguinis</i>		1		1		
128	1307	<i>Streptococcus suis</i>	1		1			
129	1309	<i>Streptococcus mutans</i>	146	89	146	89		
130	1310	<i>Streptococcus sobrinus</i>	1		1			
131	1311	<i>Streptococcus agalactiae</i>	6		18		12	
132	1313	<i>Streptococcus pneumoniae</i>	87	8	90	8	3	
133	1314	<i>Streptococcus pyogenes</i>	376	115	377	115	1	
134	1317	<i>Streptococcus downei</i>	2	1	2	1		
135	1319	<i>Streptococcus</i> sp. 'group B'			1		1	
137	1324	<i>Streptococcus</i> sp. G148	14	5	14	5		
138	1334	<i>Streptococcus dysgalactiae</i>	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	399	209		
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		
150	1408	Bacillus pumilus		1		1		
151	1422	Geobacillus stearothermophilus	2	1	2	1		
152	1423	Bacillus subtilis	2	4	2	4		
153	1428	Bacillus thuringiensis	7	7	7	7		
154	1435	Bacillus thuringiensis serovar san diego		2		2		
155	1467	Bacillus lentus		1		1		
156	1491	Clostridium botulinum	194	99	196	112	2	13
157	1496	Clostridioides difficile	57	1	63	1	6	
158	1502	Clostridium perfringens	41	1	41	1		
159	1513	Clostridium tetani	78	272	79	272	1	
160	1520	Clostridium beijerinckii	1		1			
161	1585	Lactobacillus delbrueckii subsp. bulgaricus	1		1			
162	1599	Lactobacillus sakei		1		1		
163	1604	Lactobacillus amylovorus		1		1		
165	1638	Listeria ivanovii	1	1	1	1		
166	1639	Listeria monocytogenes	21	99	22	99	1	
167	1641	Listeria grayi		1		1		
168	1642	Listeria innocua	2	3	2	3		
169	1646	Renibacterium salmoninarum	12		12			
170	1661	Trueperella pyogenes	7		7			
171	1681	Bifidobacterium bifidum		1		1		
172	1717	Corynebacterium diphtheriae	15	52	15	52		
173	1718	Corynebacterium glutamicum		26		26		
174	1747	Cutibacterium acnes		2		2		
175	1752	Propionibacterium freudenreichii subsp. shermanii		1		1		
176	1763	Mycobacterium	3	19	29	20	26	1
177	1764	Mycobacterium avium	6	16	6	17		1
178	1765	Mycobacterium tuberculosis variant bovis	48	326	49	326	1	
179	1766	Mycobacterium fortuitum		1		1		
180	1767	Mycobacterium intracellulare		1		1		
181	1768	Mycobacterium kansasii	9	13	9	13		
182	1769	Mycobacterium leprae	119	409	120	409	1	
183	1770	Mycobacterium avium subsp. paratuberculosis	105	15	105	15		
184	1771	Mycobacterium phlei		1		1		
185	1772	Mycobacterium smegmatis		24		28	4	
186	1773	Mycobacterium tuberculosis	622	2522	642	2530	20	8
187	1774	Mycobacteroides chelonae	1		1			
188	1778	Mycobacterium gordoneae	1		1			
189	1781	Mycobacterium marinum		1		1		
190	1783	Mycobacterium scrofulaceum	4		4			
191	1795	Mycobacterium neoaurum		1		1		
192	1804	Mycobacterium gilvum		1		1		
193	1809	Mycobacterium ulcerans		10		10		
195	1828	Rhodococcus fascians		2		2		
196	1830	Rhodococcus ruber		1		1		
197	1833	Rhodococcus erythropolis		2		2		
198	X 1836	Saccharopolyspora erythraea			1		1	
199	X 1895	Streptomyces avidinii			1		1	
200	1902	Streptomyces coelicolor		2		2		
201	1916	Streptomyces lividans	10		10			
202	1946	Streptomyces kasugaensis			1		1	
203	2039	Tropheryma whipplei		1		1		
204	2097	Mycoplasma genitalium			1		1	
205	2099	Mycoplasma hyopneumoniae	2		2			
206	2104	Mycoplasma pneumoniae	12	2	16	2	4	

208	2133	Spiroplasma citri		1	1	1	
209	2147	Acholeplasma		1	1	2	
210	2148	Acholeplasma laidlawii		2		2	
211	2190	Methanocaldococcus jannaschii		1		1	
212	2234	Archaeoglobus fulgidus		1	1	1	1
213	2242	Halobacterium salinarum		1		1	
214	2287	Saccharolobus solfataricus		1		1	
215	2439	Plasmid ColB2		1		1	
216	2465	Plasmid F		1		1	
218	2759	Eukaryota		1		1	
219	X 2864	Dinophyceae			1		1
220	2903	Emiliania huxleyi		1		1	
221	3039	Euglena gracilis		1		1	
222	3068	Volvox carteri f. nagariensis			1		1
223	3318	Pinaceae		2		2	
224	3352	Pinus taeda		4		4	
225	3369	Cryptomeria japonica		44	299	45	299
226	3469	Papaver somniferum		1		1	
227	3505	Betula pendula		76	335	85	335
228	3513	Quercus alba			5	5	
229	3517	Alnus glutinosa			17		17
230	3562	Spinacia oleracea		4		4	
232	3617	Fagopyrum esculentum		40		40	
233	3645	Bertholletia excelsa		7	24	7	24
234	3656	Cucumis melo			13		13
235	3677	Trichosanthes kirilowii		3		4	
236	3702	Arabidopsis thaliana		2	10	3	10
237	3704	Armoracia rusticana			5	5	
238	3707	Brassica juncea			9	9	
240	X 3711	Brassica rapa			1		1
241	3726	Raphanus sativus		1		1	
242	3728	Sinapis alba		2		2	
243	3750	Malus domestica		27	48	27	48
244	3755	Prunus dulcis		19		19	
245	3758	Prunus domestica		4		4	
246	3760	Prunus persica		18	51	18	51
247	3816	Abrus precatorius			1	1	
248	3818	Arachis hypogaea			455	193	458
249	3847	Glycine max			193	2	195
250	3864	Lens culinaris			19		19
251	3885	Phaseolus vulgaris			5	1	10
253	3972	Viscum album			17		17
254	3981	Hevea brasiliensis			170	43	170
255	3988	Ricinus communis			52	6	61
256	4012	Rhus				1	1
257	4026	Acer pseudoplatanus			1		1
258	4039	Daucus carota				46	46
259	4045	Apium graveolens				14	14
260	4081	Solanum lycopersicum			3		3
261	4097	Nicotiana tabacum			5		5
262	4100	Nicotiana benthamiana			5		5
264	4146	Olea europaea			70	19	70
265	4163	Digitalis			1		1
266	4182	Sesamum indicum			11		11
267	4212	Ambrosia artemisiifolia			4	215	4
268	4214	Ambrosia trifida				10	10
269	4215	Ambrosia artemisiifolia var. elatior			9	12	9
270	4220	Artemisia vulgaris			1	70	1
271	4232	Helianthus annuus			18		18
272	4498	Avena sativa				16	16
273	4509	Dactylis glomerata				12	12
274	4513	Hordeum vulgare				26	26
275	4522	Lolium perenne			44	122	44
276	4530	Oryza sativa				2	2
277	4545	Poa pratensis			34	35	34
278	4550	Secale cereale			51	42	51
							42

279	4558	Sorghum bicolor		1		1	
280	4565	Triticum aestivum	649	577	649	577	
281	4567	Triticum turgidum subsp. durum		1		1	
282	4568	Triticum monococcum		1		1	
284	4577	Zea mays	3	1	3	1	
285	4606	Festuca arundinacea	1		1		
286	4615	Ananas comosus	3		3		
287	4641	Musa acuminata	50	1	50	1	
288	X	4751 Fungi			2		2
289	4754	Pneumocystis carinii	2	1	2	1	
290	4903	Cyberlindnera jadinii	12		12		
291	4932	Saccharomyces cerevisiae	28	14	29	14	1
292	5039	Blastomyces dermatitidis		1		1	
293	5061	Aspergillus niger		1		1	
294	5064	Aspergillus restrictus	1		1		
295	5067	Aspergillus parasiticus		1		1	
296	5076	Penicillium chrysogenum	45	19	45	19	
297	5077	Penicillium citrinum	13		13		
298	5141	Neurospora crassa	6	3	6	3	
299	5207	Cryptococcus neoformans	2	2	2	2	
300	5334	Schizophyllum commune		1	1	1	1
301	5476	Candida albicans	107	80	107	80	
302	5480	Candida parapsilosis	1		1		
303	5501	Coccidioides immitis		1		1	
304	5503	Curvularia lunata	20	10	20	10	
305	5551	Trichophyton rubrum	2	27	2	27	
306	5554	Cutaneotrichosporon cutaneum	1		1		
307	5599	Alternaria alternata	5	36	5	36	
308	5658	Leishmania	4		4		
309	5659	Leishmania amazonensis		15		15	
310	5660	Leishmania braziliensis	6		6		
311	5661	Leishmania donovani	16	55	25	84	9
312	5664	Leishmania major	18	184	25	184	7
313	5665	Leishmania mexicana	2	3	2	3	
314	5667	Leishmania aethiopica	16		16		
315	5671	Leishmania infantum	99	9	102	9	3
316	5679	Leishmania panamensis	3	7	3	7	
317	5682	Leishmania pifanoi		20		20	
318	5691	Trypanosoma brucei	13	6	13	6	
319	5692	Trypanosoma congolense	1		1		
320	5693	Trypanosoma cruzi	159	454	161	454	2
321	5702	Trypanosoma brucei brucei	5		5		
322	5722	Trichomonas vaginalis	75	1	75	1	
323	5741	Giardia intestinalis	1	13	1	13	
324	5755	Acanthamoeba castellanii	14	3	14	3	
325	5759	Entamoeba histolytica	30	14	30	14	
326	5801	Eimeria acervulina	1		1		
327	5802	Eimeria tenella	6		6		
328	5807	Cryptosporidium parvum	4	31	4	31	
329	5811	Toxoplasma gondii	78	99	83	103	5
330	5820	Plasmodium	3	4	3	4	
331	5821	Plasmodium berghei	14	50	14	50	
332	5823	Plasmodium berghei ANKA	7	64	7	65	1
333	5824	Plasmodium brasilianum	2		2		
334	5825	Plasmodium chabaudi	4	4	4	4	
335	5827	Plasmodium cynomolgi	2		2		
337	5833	Plasmodium falciparum	762	813	778	813	16
338	5834	Plasmodium falciparum RO-33	8	1	8	1	
339	5835	Plasmodium falciparum CAMP/Malaysia	36	3	36	3	
340	5836	Plasmodium falciparum CDC/Honduras	18		18		
341	5837	Plasmodium falciparum FC27/Papua New Guinea	47	60	47	60	
342	5838	Plasmodium falciparum FCR-3/Gambia	94		94		
343	5839	Plasmodium falciparum K1	18	19	18	19	
344	5840	Plasmodium falciparum LE5		2		2	
345	5841	Plasmodium falciparum Mad20/Papua New Guinea	8	47	8	47	
346	5842	Plasmodium falciparum NF7/Ghana	5		5		

347	5843	Plasmodium falciparum NF54	13	31	20	31	7
348	5846	Plasmodium falciparum T4/Thailand	25	1	25	1	
349	5848	Plasmodium falciparum isolate WELLCOME	25	51	25	51	
350	5850	Plasmodium knowlesi	2	17	2	17	
351	5851	Plasmodium knowlesi strain H	41	10	41	10	
352	5852	Plasmodium knowlesi strain Nuri		10		10	
353	5855	Plasmodium vivax	127	156	138	176	11 20
354	5857	Plasmodium fragile		5		5	
355	5858	Plasmodium malariae	1		1		
356	5861	Plasmodium yoelii	17	39	17	39	
357	5865	Babesia bovis	3	8	3	8	
358	5866	Babesia bigemina		3		3	
359	5868	Babesia microti	2		5		3
360	5872	Theileria equi	8		8		
361	5874	Theileria annulata	1		1		
362	5875	Theileria parva	28	20	28	20	
364	6035	Encephalitozoon cuniculi		5		5	
365	6100	Aequorea victoria	3	5	3	5	
366	6181	Schistosoma	3		3		
367	6182	Schistosoma japonicum	43	53	43	53	
368	6183	Schistosoma mansoni	82	50	99	52	17 2
369	6184	Schistosoma bovis	2		2		
370	6192	Fasciola hepatica	272	28	298	28	26
371	6203	Taenia ovis	8		8		
372	6204	Taenia solium	28	4	28	4	
373	6206	Taenia saginata	7		13		6
374	6207	Taenia crassiceps	11	1	11	1	
375	6210	Echinococcus granulosus	39		41	2	2 2
376	6211	Echinococcus multilocularis	6		6		
377	6238	Caenorhabditis briggsae	1		1		
378	6239	Caenorhabditis elegans	2	10	2	10	
380	6253	Ascaris suum	1	1	1	1	
381	6265	Toxocara canis	3		3		
382	6269	Anisakis simplex	38	28	38	28	
383	6279	Brugia malayi	10	5	10	5	
384	6280	Brugia pahangi	1		1		
385	6282	Onchocerca volvulus	3	39	3310	39	3307
386	6289	Haemonchus contortus	3		3		
387	6293	Wuchereria bancrofti	13	8	13	8	
388	6299	Litomosoides carinii	3		3		
389	6334	Trichinella spiralis	16	7	16	7	
390	6339	Heligmosomoides polygyrus	3		3		
391	6421	Hirudo medicinalis		3		3	
392	6454	Haliotis rufescens	1		1		
393	6491	Conus geographus	30		30		
394	6492	Conus magus	2		2		
395	6493	Conus striatus	11		11		
397	6536	Helix pomatia	1		1		
398	6594	Macrocallista nimbosa	1		1		
399	6661	Artemia franciscana	2		2		
400	6687	Penaeus monodon	10	23	10	23	
401	6689	Penaeus vannamei		140		140	
402	6690	Penaeus aztecus	51	31	51	31	
403	6728	Procambarus clarkii	3		3		
404	X 6761	Scylla serrata			13		13
405	6850	Limulus polyphemus		1		1	
406	6853	Tachylepus tridentatus	1		1		
407	6858	Androctonus australis	9		9		
408	6860	Androctonus mauritanicus mauritanicus	1		1		
409	6878	Centruroides noxioides	10		10		
410	6887	Tityus serrulatus	92		92		
411	6925	Latrodectus tredecimguttatus		1		1	
412	6938	Ornithodoros moubata	20		20		
413	6941	Rhipicephalus microplus	1		1		
414	6945	Ixodes scapularis	11		11		
415	6953	Dermatophagoides		578		578	

416	6954	Dermatophagooides farinae	33	111	35	111	2
417	6956	Dermatophagooides pteronyssinus	83	300	109	300	26
418	6958	Euroglyphus maynei		10		10	
419	6973	Blattella germanica	23	501	23	501	
420	6978	Periplaneta americana	16	6	22	6	6
421 X	7088	Lepidoptera				1	1
422	7108	Spodoptera frugiperda		4		4	
423	7130	Manduca sexta		3		3	
424	7137	Galleria mellonella	1		2		1
425	7154	Chironomus thummi	2	3	2	3	
426	7155	Chironomus thummi thummi	58	27	58	27	
427	7160	Aedes albopictus	7		7		
428	7165	Anopheles gambiae	8	2	8	2	
429	7227	Drosophila melanogaster	9	17	10	17	1
430	7234	Drosophila persimilis	1		1		
431	7386	Sarcophaga peregrina		1		1	
432	7441	Dolichovespula maculata	11	20	11	20	
433	7444	Vespa basalis	1		1		
434	7453	Vespula maculifrons	1		1		
435	7454	Vespula vulgaris	2	95	2	95	
436	7460	Apis mellifera	15	106	15	106	
437	7469	Apis mellifera ligustica		1		1	
438	7515	Ctenocephalides felis		2		2	
439	7719	Ciona intestinalis	2		2		
440	7726	Styela plicata	6		6		
441	7742	Vertebrata	4		4		
442	7777	Chondrichthyes	1		1		
443	7787	Tetronarce californica	149	75	149	75	
444	7788	Torpedo marmorata	3	3	3	3	
445	7955	Danio rerio	1	3	2	3	1
446	7957	Carassius auratus	3	1	3	1	
447	7962	Cyprinus carpio	4	1	4	1	
448	8005	Electrophorus electricus	3		4		1
449	8018	Oncorhynchus keta		6		6	
450	8022	Oncorhynchus mykiss	1		1		
451	8030	Salmo salar	31		31		
452	8049	Gadus morhua	43		43		
453	8053	Gadus morhua callarias	10		10		
454	8090	Oryzias latipes	2	1	2	1	
455	8255	Paralichthys olivaceus	1		1		
456	8355	Xenopus laevis	4	3	4	3	
457	8364	Xenopus tropicalis	2	2	2	2	
458 X	8554	Heloderma suspectum				1	1
459	8613	Bungarus fasciatus	1		1		
460	8616	Bungarus multicinctus	17	3	17	3	
461 X	8620	Dendroaspis polylepis polylepis			22	22	
462	8654	Naja nigricollis	3	2	3	2	
464	8656	Naja atra	8		14		6
465	8657	Naja oxiana	4		4		
466	8658	Naja pallida	1	1	1	1	
467	8663	Notechis scutatus	2		2		
468	8667	Oxyuranus scutellatus scutellatus	4		4		
469	8671	Pseudechis porphyriacus	3		3		
470	8704	Vipera ammodytes	1		1		
471	8722	Bothrops asper	1		1		
473	8725	Bothrops atrox	5		13		8
474	8726	Bothrops jararacussu	13		13		
475	8732	Crotalus durissus terrificus	4		4		
476	8753	Lachesis muta muta	45		45		
477	8801	Struthio camelus	2		2		
478 X	8839	Anas platyrhynchos			2		2
479	8845	Anser cygnoides	2		2		
480	8855	Cairina moschata	2	1	2	1	
481	8932	Columba livia		10		10	
482	8996	Numida meleagris	1		1		
483	9014	Colinus virginianus	1	3	1	3	

484	9031	Gallus gallus	331	337	338	346	7	9
485	9057	Phasianus colchicus colchicus	1		1			
487	9103	Meleagris gallopavo	5		6		1	
488	9258	Omnithorhynchus anatinus		1		1		
489	9322	Macropus sp.	1		1			
490	9337	Trichosurus vulpecula	45		45			
491	9397	Chiroptera	1		1			
492	9447	Lemur catta	1		1			
493	9479	Platyrhini	1		1			
494	9483	Callithrix jacchus		4	1	4	1	
495	9488	Saguinus mystax	1		1			
496	9491	Saguinus imperator	1		1			
497	9502	Alouatta caraya	1		1			
498	9505	Aotus trivirgatus	1		1			
499	9509	Ateles geoffroyi		1		1		
500	9510	Ateles paniscus	1		1			
501	9511	Ateles sp.	1		1			
502	9515	Sapajus apella	1		1			
503	9519	Lagothrix lagotricha	1		1			
504	9521	Saimiri sciureus	1		1			
505	9534	Chlorocebus aethiops		5		5		
506	9538	Erythrocebus patas		1		1		
507	9541	Macaca fascicularis	3	3	3	3		
508	9544	Macaca mulatta	2	5	3	5	1	
509	9548	Macaca radiata	14	1	14	1		
510	9555	Papio anubis	1		1			
511	9556	Papio cynocephalus	1		1			
512	9580	Hylobates lar		1		1		
513	9593	Gorilla gorilla		2		2		
514	9595	Gorilla gorilla gorilla		6		6		
515	9597	Pan paniscus		1		1		
516	9598	Pan troglodytes	7	25	7	25		
517	9600	Pongo pygmaeus		2		2		
518	9601	Pongo abelii		2		2		
519	9606	Homo sapiens	8503	246334	9022	298230	519	51896
520	9615	Canis lupus familiaris	12	1539	17	1575	5	36
521	9627	Vulpes vulpes	1		1			
522	9666	Mustela lutreola	1		1			
523	9685	Felis catus	40	99	40	99		
524	9721	Cetacea	1		1			
525	9755	Physeter catodon	1	34	1	34		
526	9796	Equus caballus	48	45	54	55	6	10
527	9798	Equus przewalskii		1		1		
528	9823	Sus scrofa	113	53	115	53	2	
529	9825	Sus scrofa domesticus		5		5		
530	9844	Lama glama	1		1			
531	9860	Cervus elaphus	2		6		4	
532	9864	Cervus canadensis nelsoni	5		5			
533	9874	Odocoileus virginianus	2		2			
534	9913	Bos taurus	1300	831	1320	844	20	13
535	9925	Capra hircus	11		11			
536	9940	Ovis aries	92	17	95	17	3	
537	9978	Ochotona princeps		1		1		
538	9986	Oryctolagus cuniculus	59	10	66	10	7	
539	10029	Cricetulus griseus	1		9		8	
540	10036	Mesocricetus auratus	56		58		2	
541	10090	Mus musculus	670	16890	697	20365	27	3475
542	10092	Mus musculus domesticus		12		12		
543	X 10095	Mus sp.			1		1	
544	10114	Rattus	11		11			
545	10116	Rattus norvegicus	242	30447	267	33167	25	2720
547	10118	Rattus sp.		1		1		
548	10141	Cavia porcellus	37	75	37	79		4
549	10243	Cowpox virus		25		25		
550	10244	Monkeypox virus	5	2	5	2		
551	10245	Vaccinia virus	11	495	11	547		52

552	10247	Vaccinia virus WR 65-16		4	4		
553	10248	Vaccinia virus LC16M8		5	5		
554	10249	Vaccinia virus Copenhagen	31	829	31	846	17
555	10251	Vaccinia virus IHD-J	1		1		
556	10253	Vaccinia virus Tian Tan		21	21		
557	10254	Vaccinia virus WR	31	6689	31	6689	
558	10255	Variola virus		248	248		
559	10261	Fowlpox virus		7	7		
560	10263	Fowlpox virus isolate HP-438/Munich		1	1		
561	10273	Myxoma virus		4	4		
562	10276	Swinepox virus		2	2		
563	10292	Herpesviridae		1	1		
564	10298	Human alphaherpesvirus 1	154	178	181	181	27 3
565	10299	Human alphaherpesvirus 1 strain 17	44	46	44	46	
566	10301	Human alphaherpesvirus 1 strain Angelotti		4	4		
567	10303	Human alphaherpesvirus 1 strain HFEM	2		2		
568	10304	Human alphaherpesvirus 1 strain F	17	5	17	5	
569	10306	Human alphaherpesvirus 1 strain KOS	17	4	17	4	
570	10308	Human alphaherpesvirus 1 strain Patton	3		3		
571	10309	Human alphaherpesvirus 1 strain SC16	5	2	5	2	
572	10310	Human alphaherpesvirus 2	224	226	295	226	71
573	10312	Human herpesvirus 2 strain 186	1	1	1	1	
574	10313	Human herpesvirus 2 strain 333	2	5	2	5	
575	10315	Human herpesvirus 2 strain HG52		31	31		
576	10317	Cercopithecine alphaherpesvirus 2		1	1		
577	10320	Bovine alphaherpesvirus 1	5	40	5	40	
578	10323	Bovine herpesvirus type 1.1 (strain Cooper)	9	17	9	17	
579	10324	Bovine herpesvirus type 1.1 (strain P8-2)	1		1		
580	10325	Macacine alphaherpesvirus 1	1		1		
581	10326	Equid alphaherpesvirus 1	7	218	7	218	
582	10331	Equid alphaherpesvirus 4	6		6		
583	10335	Human alphaherpesvirus 3	10	127	10	127	
584	10338	Human herpesvirus 3 strain Dumas		29	29		
585	10345	Suid alphaherpesvirus 1	6	2	7	2	1
586	10349	Suid herpesvirus 1 (strain NIA-3)	4		4		
587	10359	Human betaherpesvirus 5	118	538	119	613	1 75
588	10360	Human herpesvirus 5 strain AD169	233	417	233	432	15
589	10363	Human herpesvirus 5 strain Towne	5	26	94	26	89
590	10366	Murid betaherpesvirus 1	2	64	2	64	
591	10367	Murine cytomegalovirus (strain Smith)		32	32		
593	10369	Human herpesvirus 6 (strain GS)	2		2		
594	10370	Human herpesvirus 6 (strain Uganda-1102)	1	2	2	4	1 2
595	10372	Human betaherpesvirus 7	2	4	2	4	
596	10373	Macaca mulatta cytomegalovirus		76	76		
597	10376	Human gammaherpesvirus 4	2316	612	2324	632	8 20
598	10377	Human herpesvirus 4 strain B95-8	171	354	181	355	10 1
599	10378	Human herpesvirus 4 strain RAJI	1		1		
600	10381	Saimiriine gammaherpesvirus 2		3	3		
601	10390	Gallid alphaherpesvirus 2		1	1		
602	10407	Hepatitis B virus	265	643	267	645	2 2
603	10408	Hepatitis B virus subtype adw2	82	61	82	61	
604	10409	Hepatitis B virus adr4		13		13	
605	10410	Hepatitis B virus adw/991	2	2	2	2	
606	10411	Hepatitis B virus alpha1		24		24	
607	10412	Hepatitis B virus adw/Indonesia/PIDW420		3	3		
608	10414	Hepatitis B virus LSH/chimpanzee		2		2	
609	10415	Hepatitis B virus adw/Okinawa/PODW282		5	5		
610	10418	Hepatitis B virus subtype ayw	57	185	57	185	
611	10419	Hepatitis B virus subtype adyw	2	45	4	45	2
612	10430	Woodchuck hepatitis virus 1	3		3		
613	10433	Woodchuck hepatitis virus 8		34		34	
614	10479	Thermoproteus tenax virus 1	1		1		
615	10497	African swine fever virus	1		5		4
616	10498	African swine fever virus BA71V		46	46		
617	10515	Human adenovirus 2	28	8	28	16	
618	10519	Human adenovirus 7	4		4		8

619	10521	Human adenovirus 14	4	4		
620	10524	Human adenovirus 41	1	1		
621	10529	Human adenovirus 31	7		7	
622	10530	Murine adenovirus 1	1	2	1	2
623	10533	Human adenovirus 1	1		1	
624	10541	Human adenovirus 11	12		12	
625	10560	Bovine papillomavirus type 2	15		15	
626	10562	Bovine papillomavirus type 4	10	3	10	3
627	10566	Human papillomavirus	3	1	3	1
628	10573	Human papillomavirus type 13	1	1	1	1
630	10580	Human papillomavirus type 11	9	43	9	43
631	10583	Human papillomavirus type 1a	8	15	8	15
632	10585	Human papillomavirus type 31	13	7	13	7
633	10586	Human papillomavirus type 33	6	9	6	9
634	10587	Human papillomavirus type 35	1	1	1	1
635	10588	Human papillomavirus type 39	1	1	1	1
636	10589	Human papillomavirus type 41		1		1
637	10592	Human papillomavirus type 44		1		1
638	10593	Human papillomavirus type 45	2	9	2	9
639	10595	Human papillomavirus type 51	1	1	1	1
640	10596	Human papillomavirus type 56	1	5	1	5
641	10598	Human papillomavirus type 58	49	32	49	34
642	10600	Human papillomavirus type 6b	11	29	11	29
643	10611	Human papillomavirus type 30	1		1	
644	10614	Human papillomavirus 3		3		3
645	10615	Human papillomavirus type 40	1	1	1	1
646	10617	Human papillomavirus 4		4		4
647	10618	Human papillomavirus type 52	1	36	1	36
648	10620	Human papillomavirus type 7	1	3	1	3
649	10623	Kappapapillomavirus 2	5	7	5	7
650	10631	BK virus strain AS		1		1
651	10632	JC polyomavirus	7	78	9	78
652	10636	Murine polyomavirus strain A2		3		3
653	10638	Kilham polyomavirus		1		1
654	10658	Salmonella virus PRD1	2		2	
655	10665	Escherichia virus T4	10	20	10	20
656	10710	Escherichia virus Lambda		6		6
657	10754	Salmonella virus P22	5		5	
658	10760	Enterobacteria phage T7	1		1	
659	10783	Aleutian mink disease parvovirus (STRAIN G)	3		3	
660	10786	Feline panleukopenia virus		4		4
661	10788	Canine parvovirus	23	20	23	20
662	10790	Canine parvovirus strain CPV-D CORNELL 320	1		1	
663	10791	Canine parvovirus strain N	47		47	
664	10793	Mink enteritis virus strain Abashiri	1		1	
665	10796	Porcine parvovirus	40		40	
666	10798	Human parvovirus B19	93	44	93	44
667	10804	Adeno-associated virus - 2	42	153	42	153
668	10847	Escherichia virus phiX174	1		1	
669	10863	Enterobacteria phage f1	1	1	1	1
670	10864	Enterobacteria phage fd	7	1	7	1
671	10879	Pseudomonas virus phi6	7		7	
672	10884	Mammalian orthoreovirus 1 Lang	1		3	
673	10886	Mammalian orthoreovirus 3 Dearing	1		1	
674	10891	Reovirus sp.		2		2
675	10900	Bluetongue virus (serotype 10 / American isolate)	3		3	
676	10903	Bluetongue virus 17	4		4	
677	10904	Bluetongue virus (serotype 1 / isolate Australia)	7		7	
678	10906	Bluetongue virus 10	3		3	
679	10915	Porcine rotavirus serotype 5/strain OSU	1		1	
680	10917	Porcine rotavirus strain Gottfried	2		2	
681	10919	Porcine rotavirus strain YM	2	1	2	1
682	10923	Simian rotavirus A/SA11	8	5	8	5
683	10927	Bovine rotavirus	9	1	9	1
684	10933	Bovine rotavirus strain RF	12	7	12	7
685	10934	Bovine rotavirus strain UK/G6		1		1

686	10941	Human rotavirus A	14	84	14	84	
687	10950	Human rotavirus (SEROTYPE 2 / STRAIN DS1)	1		1		
688	10952	Human rotavirus strain KU	9		9		
689	10957	Human rotavirus strain P	1	4	1	4	
690	10958	Human rotavirus strain RRV	1		1		
691	10960	Human rotavirus G4 strain St. Thomas 3	6		6		
692	10962	Human rotavirus strain WA	10	7	10	7	
693	10995	Infectious bursal disease virus	12		12		
694	10996	Infectious bursal disease virus 52/70		10		10	
695	10997	Infectious bursal disease virus 002-73/AUS	1		1		
696	11002	Infectious pancreatic necrosis virus	1		1		
697	11021	Eastern equine encephalitis virus	42	2	42	2	
		Eastern equine encephalitis virus (STRAIN VA33[TEN BROECK])			1	1	
698	11022	Ross River virus			1		
699	11029	Ross river virus (STRAIN T48)	3		3		
700	11032	Semliki Forest virus	36	5	36	5	
701	11033	Sindbis virus	26		26		
702	11034	Venezuelan equine encephalitis virus	2	1	2	5	4
703	11036	Venezuelan equine encephalitis virus (strain TC-83)	24		24		
704	11037	Venezuelan equine encephalitis virus (strain Trinidad donkey)	15		15		
705	11038	Western equine encephalitis virus		1		1	
706	11041	Rubella virus	81	100	81	100	
708	11043	Rubella virus strain M33	3	11	3	11	
709	11044	Rubella virus vaccine strain RA27/3	2	6	2	6	
710	11045	Rubella virus strain Therien	20	35	20	35	
711	11047	Equine arteritis virus	3		3		
712	11048	Lactate dehydrogenase-elevating virus	14		14		
713	11049	Lelystad virus	66	12	66	12	
714	11053	Dengue virus 1	40	507	51	559	11 52
715	11057	Dengue virus 1 Thailand/AHF 82-80/1980		1		1	
716	11059	Dengue virus 1 Nauru/West Pac/1974	4	50	4	50	
717	11060	Dengue virus 2	178	641	184	713	6 72
718	11062	Dengue virus 2 Malaysia M2	1		1		
719	11064	Dengue virus 2 Jamaica/1409/1983	264	1254	264	1254	
720	11065	Dengue virus 2 Thailand/NGS-C/1944	18	37	20	37	2
721	11066	Dengue virus 2 Puerto Rico/PR159-S1/1969	32	21	32	21	
722	11067	Dengue virus 2 Tonga/EKB194/1974		3		3	
723	11069	Dengue virus 3	58	578	76	621	18 43
724	11070	Dengue virus 4	50	374	80	429	30 55
725	11072	Japanese encephalitis virus	40	143	49	143	9
726	11073	Japanese encephalitis virus strain SA-14	6	1	6	1	
727	11075	Japanese encephalitis virus strain JAOARS982	4	4	4	4	
728	11076	Japanese encephalitis virus strain Nakayama	2	2	2	2	
729	11077	Kunjin virus	12	1	12	1	
730	11078	Kunjin virus (STRAIN MRM61C)		4		4	
731	11079	Murray Valley encephalitis virus	21	9	21	9	
732	11080	Saint Louis encephalitis virus	9	1	9	1	
733	11081	St. Louis encephalitis virus (strain MS1-7)	7		7		
734	11082	West Nile virus	51	440	51	442	2
735	11083	Powassan virus		3	1	3	1
736	11084	Tick-borne encephalitis virus	14	137	14	137	
737	11085	Langat virus		1		1	
738	11087	Tick-borne encephalitis virus (STRAIN SOFJIN)	6		6		
739	11089	Yellow fever virus		1333		1352	19
740	11090	Yellow fever virus 17D		288		288	
741	11092	Kumlinge virus	26		26		
742	11096	Classical swine fever virus	14	4	15	4	1
743	11098	Classical swine fever virus - Brescia	4		4		
744	11099	Bovine viral diarrhea virus 1	1	12	1	12	
745	11100	Bovine viral diarrhea virus 1-NADL	4	3	4	3	
746	11103	Hepacivirus C	683	1127	696	1129	13 2
747	11104	Hepatitis C virus (isolate 1)	37	256	37	256	
748	11105	Hepatitis C virus (isolate BK)	3	90	3	90	
749	11108	Hepatitis C virus (isolate H)	145	84	145	84	

750	11110	Hepatitis C virus HCT18	1		1		
751	11113	Hepatitis C virus isolate HC-J6	8	3	8	3	
752	11115	Hepatitis C virus isolate HC-J8	1	1	1	1	
753	11116	Hepatitis C virus (isolate Japanese)	6	19	6	19	
754	11120	Infectious bronchitis virus	7	4	10	5	3 1
755	11127	Avian infectious bronchitis virus (strain M41)	4	3	4	3	
756	11128	Bovine coronavirus	7		7		
757	11137	Human coronavirus 229E		2		2	
758	11138	Murine hepatitis virus	3	31	3	31	
759	11142	Murine hepatitis virus strain A59	26	4	26	4	
760	11144	Murine hepatitis virus strain JHM	25	21	25	21	
761	11149	Transmissible gastroenteritis virus	15	1	15	1	
	11150	Porcine transmissible gastroenteritis coronavirus strain FS772/70		2		2	
762	11151	Porcine transmissible gastroenteritis coronavirus strain Purdue	14		14		
763	11152	Turkey coronavirus	1		1		
764	11169	Mumps virus strain Kilham	1		1		
765	11173	Mumps virus strain SBL-1	6		6		
766	11176	Avian avulavirus 1	14	5	15	5	1
767	11177	Newcastle disease virus (STRAIN AUSTRALIA-VICTORIA/32)		4		4	
768	11178	Newcastle disease virus strain Beaudette C/45	12		12		
769	11180	Newcastle disease virus strain D26/76	4		4		
770	11186	Newcastle disease virus strain Queensland/66	4		4		
771	11191	Murine respirovirus	63	10	63	10	
772	11194	Sendai virus (strain Enders)	7	11	7	11	
773	11195	Sendai virus (strain Fushimi)		1		1	
774	11196	Sendai virus (strain Harris)	2		2		
775	11198	Sendai virus (Z)		1		1	
776	11214	Human parainfluenza virus 2 (strain Toshiba)	3		3		
777	11215	Bovine respirovirus 3	3	1	3	1	
778	11216	Human respirovirus 3	2		2		
779	11217	Human parainfluenza 3 virus (strain NIH 47885)	8		8		
780	11232	Canine morbillivirus	10	9	14	9	4
781	11233	Canine distemper virus strain Onderstepoort	6	19	6	34	15
782	11234	Measles morbillivirus	64	39	64	39	
783	11235	Measles virus strain Edmonston	167	210	167	210	
784	11236	Measles virus strain Halle		34		34	
785	11241	Rinderpest morbillivirus	2	3	2	3	
786	11243	Rinderpest virus (strain L)	6		6		
787	11246	Bovine orthopneumovirus	3	2	3	2	
788	11249	Bovine respiratory syncytial virus (strain RB94)	4		4		
789	11250	Human orthopneumovirus	28	206	34	206	6
	11251	Human respiratory syncytial virus (subgroup B / strain 18537)	2	1	2	1	
790	11252	Human respiratory syncytial virus (strain RSB642)	2		2		
791	11255	Human respiratory syncytial virus (strain RSB6190)	6		6		
792	11256	Human respiratory syncytial virus (strain RSB6256)	10		11		1
793	11259	Human respiratory syncytial virus A2	81	136	91	136	10
794	11260	Human respiratory syncytial virus A strain Long	128	31	128	31	
795	11263	Murine orthopneumovirus		14		14	
796	11269	Marburg marburgvirus	4	95	5	95	1
800	11276	Vesicular stomatitis virus		10		10	
801	11277	Vesicular stomatitis Indiana virus	9	7	9	7	
802	11278	Vesicular stomatitis Indiana virus strain Glasgow		1		1	
803	11279	Vesicular stomatitis Indiana virus strain Mudd-Summers	1		1		
805	11285	Vesicular stomatitis Indiana virus strain San Juan		1		1	
806	11288	Viral hemorrhagic septicemia virus 07-71	12	1	12	1	
807	11290	Infectious hematopoietic necrosis virus	8		8		
808	11292	Rabies lyssavirus	13	26	13	26	
809	11293	Rabies virus AVO1		3		3	
810	11294	Rabies virus CVS-11	2		2		
811	11295	Rabies virus ERA	10	27	10	27	
812	11296	Rabies virus HEP-FLURY	7	1	7	1	
813	11298	Rabies virus Nishigahara RCEH	1		1		
814	11307	Sonchus yellow net nucleorhabdovirus		1		1	

815	11318	Dhori thogotovirus	1		1			
816	11320	Influenza A virus	70	529	74	533	4	4
818	11384	Influenza A virus (A/chicken/FPV/Weybridge(H7N7))		2		2		
819	11408	Influenza A virus (STRAIN A/EQUINE/NEW MARKET/76)		1		1		
820	11448	Influenza A virus (A/parrot/Ulster/73(H7N1))		1		1		
821	11484	Influenza A virus (A/whale/Maine/1/84(H13N9))	3		3			
822	11520	Influenza B virus	3	6	4	6	1	
823	11521	Influenza B virus (B/Ann Arbor/1/1986)		3		3		
824	11532	Influenza B virus (STRAIN B/HT/84)		1		1		
825	11541	Influenza B virus (B/Oregon/5/80)	16		16			
826	X 11550	Influenza B virus (B/Yamagata/1/73)				3		3
827	11552	Influenza C virus		1		1		
828	11553	Influenza C virus (C/Ann Arbor/1/50)	9		16		7	
829	11577	La Crosse virus	2	1	2	1		
830	11578	La Crosse virus L74		2		2		
831	11583	HoJo virus		1		1		
832	11588	Rift Valley fever virus	5	27	5	27		
833	11589	Rift valley fever virus (STRAIN ZH-548 M12)		2		2		
834	11602	Hantaan virus 76-118	14	68	14	132		64
835	11605	Puumala virus Hallnas B1		1		1		
836	11607	Sapporo rat virus	1	4	1	4		
837	11610	Seoul virus SR11		1		1		
838	11618	Arenavirus		2		2		
839	11620	Lassa mammarenavirus	13	670	13	670		
840	11621	Lassa virus GA391		54		54		
841	11622	Lassa virus Josiah	10	409	10	409		
842	11623	Lymphocytic choriomeningitis mammarenavirus	5	654	5	654		
843	11624	Lymphocytic choriomeningitis virus (strain Armstrong)		1158		1158		
844	11625	Lymphocytic choriomeningitis virus (strain Pasteur)		5		5		
845	11626	Lymphocytic choriomeningitis virus (strain Traub)		3		3		
846	11627	Lymphocytic choriomeningitis virus (strain WE)		69		69		
847	11628	Machupo mammarenavirus		800	1	800	1	
848	11629	Mopeia mammarenavirus		14		14		
849	11631	Tacaribe mammarenavirus		106		106		
850	11636	Reticuloendotheliosis virus	2	5	2	5		
851	11660	Caprine arthritis encephalitis virus	14	1	14	1		
852	11661	Caprine arthritis encephalitis virus strain Cork	9		9			
853	11662	Caprine arthritis encephalitis virus G63	6		6			
854	11665	Equine infectious anemia virus	93	112	93	112		
855	11670	Equine infectious anemia virus (CLONE 1369)		1		1		
856	11671	Equine infectious anemia virus (STRAIN WSU5)		19		19		
857	11673	Feline immunodeficiency virus		28		30	2	
858	11674	Feline immunodeficiency virus (isolate Petaluma)	2	3	2	4	1	1
859	X 11675	Feline immunodeficiency virus (isolate San Diego)				1		1
860	11676	Human immunodeficiency virus 1	196	481	236	499	40	18
861	11678	Human immunodeficiency virus type 1 BH10	2	26	2	27	1	
862	11679	Human immunodeficiency virus type 1 (CLONE 12)		7		7		
864	11682	Human immunodeficiency virus type 1 (BH5 ISOLATE)		1		1		
865	11683	Human immunodeficiency virus type 1 (Z2/CDC-Z34 ISOLATE)		1		1		
867	11685	HIV-1 M:B_ARV2/SF2	1	44	1	44		
868	11686	Human immunodeficiency virus type 1 (BRU ISOLATE)	1	4	1	4		
869	11687	Human immunodeficiency virus type 1 (CDC-451 ISOLATE)		3		3		
870	11688	Human immunodeficiency virus type 1 (JRCSF ISOLATE)	3	37	4	37	1	
871	11689	Human immunodeficiency virus type 1 (ELI ISOLATE)		7		7		
872	11690	Human immunodeficiency virus type 1 (SF33 ISOLATE)		3		3		
873	11691	Human immunodeficiency virus type 1 (SF162 ISOLATE)		2	1	2	1	
874	11694	Human immunodeficiency virus type 1 (JH3 ISOLATE)		4		4		
875	11695	Human immunodeficiency virus type 1 (NDK ISOLATE)		8		8		
876	11696	HIV-1 M:B_MN	10	23	11	27	1	4
877	11697	Human immunodeficiency virus type 1 (MAL ISOLATE)		8		8		
878	11698	Human immunodeficiency virus type 1 (NEW YORK-5 ISOLATE)		1	2	2	2	1

879		11699	Human immunodeficiency virus type 1 (OYI ISOLATE)		3		3	
880		11701	Human immunodeficiency virus type 1 (RF/HAT ISOLATE)	1	19	1	19	
881		11703	Human immunodeficiency virus type 1 (STRAIN UGANDAN / ISOLATE U455)		15		15	
882		11704	Human immunodeficiency virus type 1 (MFA ISOLATE)	2			2	
883		11705	Human immunodeficiency virus type 1 (WMJ2 ISOLATE)		1		1	
884		11706	HIV-1 M:B_HXB2R	13	14	13	17	3
885		11708	Human immunodeficiency virus type 1 (ZAIRE 6 ISOLATE)		1		1	
886		11709	Human immunodeficiency virus 2	1	7	1	8	1
887		11711	Simian immunodeficiency virus - mac		1		1	
888		11713	Human immunodeficiency virus type 2 (ISOLATE D194)		1		1	
889		11714	Human immunodeficiency virus type 2 (ISOLATE BEN)	12			12	
890		11715	Human immunodeficiency virus type 2 (ISOLATE CAM2)		2		2	
891		11716	Human immunodeficiency virus type 2 (ISOLATE D205,7)		2		2	
892		11717	Human immunodeficiency virus type 2 (ISOLATE GHANA-1)		7		7	
893		11718	Human immunodeficiency virus type 2 (ISOLATE SBLISY)		2		2	
894		11720	Human immunodeficiency virus type 2 (ISOLATE ROD)	2			2	
895		11723	Simian immunodeficiency virus		221		238	17
896		11730	Simian immunodeficiency virus (AGM3 ISOLATE)	1			1	
899		11733	Simian immunodeficiency virus (MM142-83 ISOLATE)	102			102	
900		11734	Simian immunodeficiency virus (MM251 ISOLATE)	1			1	
901		11735	Simian immunodeficiency virus - mac K6W	125			125	
902		11736	Simian immunodeficiency virus (K78 ISOLATE)	29			29	
903		11737	Simian immunodeficiency virus (F236/SMH4 ISOLATE) (SOOTY MANGABEY)		17		17	
904		11738	Simian immunodeficiency virus (PBJ/BC13 ISOLATE) (SOOTY MANGABEY)		2		2	
905		11742	Visna lentivirus (strain 1514)	1		1		
906		11743	Visna lentivirus (strain 1514 / clone LV1-1KS1)	4		4		
907		11746	Jaagsiekte sheep retrovirus	1		1		
908		11757	Mouse mammary tumor virus		12		12	
909		11764	Baboon endogenous virus strain M7	1		1		
910		11769	Feline leukemia virus strain A/Glasgow-1	6		6		
911		11780	Snyder-Theilen feline sarcoma virus	1		1		
912		11786	Murine leukemia virus	1	23	1	23	
913		11790	AKT8 murine leukemia virus	1		1		
914		11791	AKR (endogenous) murine leukemia virus		12		12	
915		11795	Friend murine leukemia virus	6	53	6	53	
916		11801	Moloney murine leukemia virus		5		5	
917		11812	Murine sarcoma virus 3611	4		4		
918		11824	Gardner-Arnstein feline leukemia oncovirus B	13		13		
919		11827	Human endogenous retrovirus	1	1	1	1	
920		11861	Avian erythroblastosis virus	1		1		
921		11864	Avian leukosis virus	2		4		2
922		11886	Rous sarcoma virus	4	4	4	4	
923		11901	Bovine leukemia virus	108	40	108	40	
925		11908	Human T-cell leukemia virus type I	234	280	236	280	2
926		11909	Human T-lymphotropic virus 2	63	2	63	2	
927		11926	Human T-cell lymphotrophic virus type 1 (strain ATK)	30	118	30	118	
928		11927	Human T-cell lymphotrophic virus type 1 (Caribbean isolate)		6		6	
929		11928	Human T-cell lymphotrophic virus type 1 (isolate MT-2)	1		1		
930		11942	Simian retrovirus 1	1		1		
931		11966	Aids-associated retrovirus		2		2	
932		11976	Rabbit hemorrhagic disease virus	4		4		
933		11978	Feline calicivirus	4		4	1	1
934		11980	Feline calicivirus strain Japanese F4	6		6		
935		11981	Feline calicivirus strain F9	2		2		
936		11983	Norwalk virus	4	1	4	1	
937		11984	Southampton virus	1		1		

938	12022	Enterobacteria phage MS2	1	1			
939	12060	Echovirus E9	1	1			
940	12063	Human parechovirus 1	7	7			
941	12064	Enterovirus E	13	13			
942	12065	Bovine enterovirus strain VG-5-27	6	6			
943	12066	Coxsackievirus	1	1			
944	12067	Coxsackievirus A9	30	30			
945	12071	Coxsackievirus B1	12	12			
946	12072	Coxsackievirus B3	7	15	7	15	
947	12073	Coxsackievirus B4	17	51	17	51	
948	12075	Swine vesicular disease virus	1	1			
949	12076	Swine vesicular disease virus (STRAIN H/3 '76)	5	5			
950	12077	Swine vesicular disease virus (STRAIN UKG/27/72)	3	3			
951	12078	Echovirus E11	1	1			
952	12080	Human poliovirus 1	6	1	6	1	
953	12081	Human poliovirus 1 Mahoney	62	31	62	31	
954	12082	Human poliovirus 1 strain Sabin	7	7			
955	12086	Human poliovirus 3	5	2	5	2	
956	12088	Poliovirus type 3 (strains P3/LEON/37 AND P3/LEON 12A[1]B)	4	15	4	15	
957	12092	Hepatovirus A	26	22	26	22	
958	12098	Human hepatitis A virus Hu/Australia/HM175/1976	86	83	86	83	
959	12104	Encephalomyocarditis virus		1		1	
960	12107	Mengo virus	5	13	5	13	
961	12110	Foot-and-mouth disease virus	24	5	25	5	1
962	12111	Foot-and-mouth disease virus - type A	3	5	3	6	1
963	12112	Foot-and-mouth disease virus (strain A10-61)	8		8		
964	12113	Foot-and-mouth disease virus (strain A5)	3		3		
965	12114	Foot-and-mouth disease virus (strain A12)	21	1	21	1	
966	12115	Foot-and-mouth disease virus (strain A24 Cruzeiro)	17	32	17	32	
967	12116	Foot-and-mouth disease virus - type C	6	26	6	26	
968	12117	Foot-and-mouth disease virus (strain C3 Indaial)	2		2		
969	12118	Foot-and-mouth disease virus - type O	43	5	44	8	1
970	12120	Foot-and-mouth disease virus (strain C1-Santa Pau)	1		1		
971	12121	Foot-and-mouth disease virus C1	1	4	1	4	
972	12123	Foot-and-mouth disease virus - type SAT 3		1		1	
973	12124	Theiler's encephalomyelitis virus		18	1	18	1
974	12125	Theiler's encephalomyelitis virus (STRAIN BEAN 8386)	16	52	16	52	
975	12126	Theiler's encephalomyelitis virus (STRAIN DA)	3	2	3	2	
976	12130	Human rhinovirus A2		11		11	
977	12131	Rhinovirus B14	15	1	15	1	
978	12132	Human rhinovirus A89	3		3		
979	12134	Human rhinovirus 1A		19		19	
980	12146	Tomato bushy stunt virus (STRAIN BS-3)	3		3		
981	12161	Beet yellows virus	5		5		
982	12162	Citrus tristeza virus	8		8		
983	12211	Plum pox virus	1		1		
984	12213	Plum pox virus isolate NAT		1		1	
985	12216	Potato virus Y	2		2		
986	12219	Potato virus Y strain N	1		1		
987	12220	Potato virus Y strain O	7		7		
988	12232	Zucchini yellow mosaic virus	1		1		
989	12242	Tobacco mosaic virus	36	13	36	13	
990	12243	Tobacco mosaic virus (<i>vulgare</i>)	1		1		
991	12246	Tobacco mosaic virus strain Dahlemense	2		2		
992	12260	Bean pod mottle virus	2		2		
993	12264	Cowpea mosaic virus		1		1	
994	12305	Cucumber mosaic virus	1		1		
995	12455	Borna disease virus	8	4	8	4	
996	12461	Hepatitis E virus	151	76	153	76	2
997	12475	Hepatitis delta virus	56	7	56	19	12
998	12509	Human herpesvirus 4 type 2	2	10	2	10	
999	12557	Seoul virus 80-39		3		3	
1000	12618	Chicken anemia virus	3		3		
1001	12637	Dengue virus	39	553	51	553	12
1002	12639	Duck hepatitis B virus	262	20	262	20	

1003	12643	Ectromelia virus		6	6		
1004	12663	Feline coronavirus		1	1		
1005	12701	Human astrovirus 2	1	2		1	
1006	12750	Visna/maedi virus EV1	1	1			
1007	12760	Murine hepatitis virus strain 4		5	5		
1008	12814	Respiratory syncytial virus			2		2
1009	12870	Variola major virus		17	17		
1010	13101	Juniperus ashei	13	13			
1011	13187	Parietaria officinalis	2	2			
1012	13286	Theromyzon tessulatum	1	1			
1013	13373	Burkholderia mallei	1	49	1	49	
1014	13415	Chamaecyparis obtusa	5	68	5	68	
1015	13451	Corylus avellana	27	57	27	57	
1016	13469	Cupressus sempervirens		8	8		
1017	13557	Hapalemur griseus		1	1		
1018	13616	Monodelphis domestica	1	4	1	4	
1019	13618	Myrmecia pilosula	2		2		
1020	13687	Sphingomonas	1	4	1	4	
1022	15368	Brachypodium distachyon	1		1		
1023	15957	Phleum pratense	63	1129	64	1143	1 14
1024	16719	Juglans nigra	1		1		
1025	27990	Plasmodium vivax-like sp.	3	1	3	1	
1026	28038	Lactobacillus curvatus		1		1	
1027	28080	Campylobacter upsaliensis	3		3		
1028	28108	Alteromonas macleodii		1		1	
1029	28130	Prevotella disiens		1		1	
1031	28227	Mycoplasma penetrans	40		40		
1032	28276	Human adenovirus 15	1		1		
1033 X	28280	Human adenovirus E4			1		1
1034	28282	Human adenovirus 12	11	3	11	3	
1035	28284	Human adenovirus 40	2	1	2	1	
1036	28285	Human adenovirus 5	25	184	26	185	1 1
1037	28295	Porcine epidemic diarrhea virus	2		5		3
1038	28300	Heron hepatitis B virus		1		1	
1039	28314	Aleutian mink disease virus	9		10		1
1040	28327	Murine rotavirus		3		3	
1041	28344	Porcine reproductive and respiratory syndrome virus	87	53	87	95	42
1042	28375	Soil-borne wheat mosaic virus	1		1		
1043	28448	Komagataeibacter xylinus		1		1	
1044	28450	Burkholderia pseudomallei	14	9	14	9	
1045	28479	Phalaris aquatica		12		12	
1046	28869	Ovine respiratory syncytial virus	1		1		
1047	28871	Taterapox virus		4		4	
1048	28873	Camelpox virus		2		2	
1049 X	28875	Rotavirus A			1		1
1050	28901	Salmonella enterica		57		141	84
1051	28903	Mycoplasma bovis	21		21		
1052	28909	Cynodon dactylon	27	48	27	48	
1053	29176	Neospora caninum	2	17	2	17	
1054	29271	Dasheen mosaic virus	1		1		
1055	29292	Pyrococcus abyssi		1		1	
1056	29320	Paenarthrobacter nicotinovorans	1		1		
1057	29339	Bacillus thuringiensis serovar kurstaki	3		3		
1058	29362	Ruminiclostridium papyrusolvens		1		1	
1059	29371	Ruminiclostridium cellobioparum subsp. termitidis	1		1		
1060	29388	Staphylococcus capitis	1		1		
1061	29430	Acinetobacter haemolyticus	1		1		
1062	29442	Pseudomonas tolaasii		1		1	
1063	29447	Xanthomonas albilineans		1		1	
1064	29459	Brucella melitensis	17	94	17	94	
1065	29461	Brucella suis	1	8	1	8	
1066	29477	Salmonella enterica subsp. enterica serovar Essen	1		1		
1067	29491	Aeromonas salmonicida subsp. salmonicida		1		1	
1068	29507	Leptospira kirschneri	1		1		
1069	29518	Borrelia afzelii	5	1	5	1	
1070	29519	Borrelia garinii	6	29	6	29	

1071	29661	Anthoxanthum odoratum		3	3	3	
1072	29679	Holcus lanatus	14	3	14	3	
1073	29715	Ambrosia psilostachya		10		10	
1074	29760	Vitis vinifera	1		1		
1075	29780	Mangifera indica	1		1		
1076	29918	Cladosporium herbarum		18		18	
1077	29960	Penaeus indicus	2		2		
1078	30069	Anopheles stephensi	1		1		
1080	X 30538	Vicugna pacos			1		1
1081	31271	Plasmodium chabaudi chabaudi		3		3	
1082	31273	Plasmodium vivax strain Belem	6	31	6	31	
1083	31276	Perkinsus marinus		1		1	
1084	31285	Trypanosoma brucei gambiense	2		2		
1085	31286	Trypanosoma brucei rhodesiense		9	1	9	1
1086	31330	Ephydatia fluviatilis		1		1	
1087	31512	Hepatitis B virus adr/mutant		1		1	
1088	31525	Human herpesvirus 4 strain CAO		1		1	
1089	31531	Vaccinia virus L-IPV		8		8	
1090	31545	Human adenovirus D8	1	1	1	1	
1091	31552	Human papillomavirus type 6	12	4	12	4	
1092	31560	Infectious bursal disease virus E	1		1		
1093	31569	Human rotavirus (serotype 2 / strain RV-5)	1		1		
1094	31604	Small ruminant morbillivirus	13	31	13	31	
1095	31608	Simian virus 5 (isolate canine/CPI+)	1		1		
1096	31611	Bovine respiratory syncytial virus (strain 391-2)	3		3		
1097	31615	Tacaribe virus strain V5		1		1	
1098	31616	Tacaribe virus strain V7		1		1	
1099	31621	Four Corners hantavirus	2	8	2	8	
1100	31631	Human coronavirus OC43		1		1	
1101	31634	Dengue virus 2 Thailand/16681/84	32	62	32	62	
1102	31635	Dengue virus 2 16681-PDK53	4	32	4	32	
1103	31641	Yellow fever virus 1899/81		36		36	
1104	31644	Hepatitis C virus HCV-KF	1	1	1	1	
1105	31645	Hepatitis C virus (isolate Taiwan)	3	15	3	15	
1106	31646	Hepatitis C virus subtype 1a	201	399	202	399	1
1107	31647	Hepatitis C virus subtype 1b	608	293	608	293	
1108	31649	Hepatitis C virus subtype 2a	80	22	80	22	
1109	31650	Hepatitis C virus subtype 2b	103	4	103	4	
1110	31653	Hepatitis C virus subtype 4a	1	1	1	1	
1111	31654	Hepatitis C virus subtype 5a	1	1	1	1	
1112	31655	Hepatitis C virus subtype 6a		1		1	
1113	31678	Human immunodeficiency virus type 1 (WMJ1 isolate)		16		16	
1115	31682	Simian immunodeficiency virus - mac1A11		18		18	
1116	31683	Simian immunodeficiency virus - stm		7		7	
1117	31684	Simian immunodeficiency virus (isolate AGM / clone GRI-1)		2		2	
1119	31704	Coxsackievirus A16	4		4		
1120	31708	Human rhinovirus A16		30		30	
1121	31715	Bean-pod mottle virus (strain Kentucky G7)	9	1	9	1	
1122	31721	Beet necrotic yellow vein virus	10		10		
1123	31767	Hepatitis E virus (strain Burma)		160		160	
1124	31768	Hepatitis E virus (strain Mexico)		31		31	
1125	32008	Burkholderia	1		1		
1126	32019	Campylobacter fetus subsp. fetus	3		3		
1127	32022	Campylobacter jejuni subsp. jejuni	2		2		
1128	32025	Helicobacter hepaticus		1		1	
1129	32049	Synechococcus sp. PCC 7002		1		1	
1130	32201	Carya illinoinensis	19		19		
1131	32278	Metapenaeus ensis	1	6	1	6	
1132	32603	Human betaherpesvirus 6A	2	7	2	7	
1133	32604	Human betaherpesvirus 6B	2	42	2	1394	1352
1134	32605	Buffalopox virus		1		1	
1135	32606	Rabbitpox virus		2		2	
1136	32614	Convict Creek 107 virus	1	3	1	3	
1137	32644	unidentified		16381		22056	5675
1138	33127	Parietaria judaica	65	2	65	2	

1139	33178	Aspergillus terreus	2	2			
1140	33703	Suid herpesvirus 1 strain Kaplan	4	4			
1141	33706	Caviid betaherpesvirus 2	3	3	3	3	
1142	33708	Murid gammaherpesvirus 4	1	53	1	53	
1143	33717	Bluetongue virus (serotype 13 / isolate USA)	2	2			
1144	33718	Bluetongue virus (serotype 17 / isolate USA)	4	4			
1145	33727	Marburg virus - Musoke, Kenya, 1980	3	84	3	84	
1146	33728	Lake Victoria marburgvirus - Popp	2	15	2	15	
1147	33734	Feline infectious peritonitis virus (strain 79-1146)	15	14	15	14	
1148	33741	Dengue virus 1 Singapore/S275/1990		245		245	
1149	33745	Hepatitis C virus genotype 4		2	1	10	1 8
1150	33746	Hepatitis C virus genotype 5		2		2	
1151	33747	Simian T-lymphotropic virus 1		14		14	
1152	33758	Echovirus		1		1	
1153	33892	Mycobacterium tuberculosis variant bovis BCG	12	146	12	146	
1154	33934	Anoxybacillus flavigermans		1		1	
1155	33990	Rickettsia bellii	1		1		
1156	34054	Yersinia enterocolitica (type O:8)		1		1	
1157	34245	Zinnia violacea		1		1	
1158	34631	Rhipicephalus appendiculatus	1		1		
1159	34632	Rhipicephalus sanguineus	1		1		
1160	34828	Eulemur mongoz	1		1		
1161	34862	Otospermophilus beecheyi		1		1	
1162	35241	Lactococcus phage Tuc2009	1		1		
1163	35258	Lambdapapillomavirus 2		25		25	
1164	35269	Woodchuck hepatitis virus	4	6	4	6	
1165	35275	Murine endogenous retrovirus		13		13	
1166	35288	Grapevine virus A	12		12		
1167	35292	Foot-and-mouth disease virus - type SAT 2	1	1	1	1	
1168	35297	Striped jack nervous necrosis virus	1		1		
1169	35305	California encephalitis virus		1		1	
1170	35327	Bluetongue virus 1	4		4		
1171	35329	Bluetongue virus 11	6		6		
1172	35330	Bluetongue virus 13	1		1		
1173	35331	Bluetongue virus 15	7		7		
1174	35336	Rotavirus G4		1		1	
1175	35345	Lactococcus phage TP901-1	3		3		
1176	35670	Naja naja	3		3		
1177	35725	Macrophomina phaseolina		1		1	
1178	35788	Rickettsia africae		1		1	
1179	35791	Rickettsia massiliae		1		1	
1180	35793	Rickettsia sibirica		4		4	
1181	35795	Ehrlichia muris	2	3	2	3	
1182	36329	Plasmodium falciparum 3D7	181	270	182	270	1 50
1183	36351	Human herpesvirus 6 strain Z29	1	96	1	146	
1184	36352	Human herpesvirus 4 type 1	4	14	4	14	
1185	36372	Feline immunodeficiency virus (strain UK8)		1		1	
1186	36374	Visna/maedi virus EV1 KV1772	2		2		
1187	36375	Human immunodeficiency virus type 1 (KB-1 isolate)		2		2	
1188	36382	Venezuelan equine encephalitis virus (strain 3880)		1		1	
1189	36386	Louping ill virus (strain 31)	1		1		
1190	36409	Rinderpest virus (strain RBOK)	33	5	33	5	
1191	36412	Human parainfluenza 1 virus (strains A1426 / 86-315 / 62M-753)		1		1	
1192	36418	Influenza A virus (A/chicken/Brescia/1902(H7N7))		1		1	
1193	36420	H1N1 swine influenza virus		13		13	
1194	36421	African horse sickness virus 4	42	4	42	4	
1195	36439	Bovine rotavirus strain NCDV/G6	1		1		
1196	36470	Streptococcus sp. 'group A'	21		21		
1197	36596	Prunus armeniaca	4		4		
1198	36809	Mycobacteroides abscessus		19		19	
1199	36826	Clostridium botulinum A	46		46		
1200	36827	Clostridium botulinum B	29		29		
1201	36829	Clostridium botulinum D	2		2		
1202	36830	Clostridium botulinum E	3	3	3	3	
1203	36831	Clostridium botulinum F	3		3		

1204	36855	Brucella canis		4		4	
1205	36911	Clavispora lusitaniae	1		1		
1206	36936	Lepidoglyphus destructor	5	10	5	10	
1208	37111	Human papillomavirus 28		1		1	
1209	37112	Human papillomavirus 29		1		1	
1210	37115	Human papillomavirus type 59	2	1	2	1	
1211	37120	Human papillomavirus type 67	2		2		
1212	37121	Human papillomavirus type 69		1		1	
1213	37124	Chikungunya virus	53	3	78	10	25
1214	37128	Potato mop-top virus	8		8		
1215	37132	Rabies virus Ontario fox	3		3		
1216	37137	Simian rotavirus A/SA11-both	20	2	20	2	
1217	37207	Rio Segundo hantavirus	1		1		
1218	37296	Human gammaherpesvirus 8	26	488	26	488	
1219	37325	Muscovy duck parvovirus	11		11		
1220	X 37326	Nocardia brasiliensis			6		6
1221	37329	Nocardia farcinica		1		1	
1222	37347	Tupaia belangeri		1		1	
1223	37546	Glossina morsitans morsitans	2		2		
1225	37762	Escherichia coli B	1	1	1	1	
1226	38020	marmosets	3		3		
1227	38033	Chaetomium globosum	1		1		
1228	38171	Avian reovirus strain S1133	5		5		
1229	38251	Goose parvovirus	9		9		
1230	38323	Bartonella henselae	1		1		
1231	38832	Micromonas		1		1	
1232	38873	Fraxinus excelsior		3		3	
1233	38973	Influenza A virus (A/Memphis/4/1973(H3N2))		1		1	
1234	39002	Puumala virus sotkamo/v-2969/81	196		196		
1235	39015	Human T-cell lymphotropic virus type 1 (african isolate)		2		2	
1236	39054	Enterovirus A71	91	1	111	1	20
1238	39113	Hepatitis GB virus B		4		4	
1239	39152	Methanococcus maripaludis	1		1		
1240	39414	Plantago lanceolata		2		2	
1241	39442	Mus musculus musculus		1		1	
1242	39457	Human papillomavirus type 70		1		1	
1244	39803	Escherichia virus Qbeta		2		2	
1245	39947	Oryza sativa Japonica Group	5	1	5	1	
1246	40051	Bluetongue virus	9		12	1	3
1247	40214	Acinetobacter johnsonii		1		1	
1248	40271	Hepatitis C virus genotype 2	41	6	41	6	
1249	40674	Mammalia	6		6		
1250	40697	Blomia tropicalis	19	6	19	6	
1251	41514	Salmonella enterica subsp. arizona serovar 62:z4,z23:-		4		4	
1252	41856	Hepatitis C virus genotype 1	2	163	2	177	14
1253	41857	Influenza A virus H3N2	2	49	2	49	
1254	41953	Pseudo-nitzschia	1		1		
1255	42097	Isla Vista hantavirus	1	2	1	2	
1256	42182	Hepatitis C virus genotype 6		7		7	
1257	42229	Prunus avium	3	1	3	1	
1258	42345	Phoenix dactylifera		3		3	
1259	42358	Hantavirus Monongahela-3		5		5	
1260	42764	Oliveros mammarenavirus		2		2	
1262	42782	Coxsackievirus A20	1		1		
1263	X 42789	Enterovirus D68			1		1
1264	42792	Hepatitis C virus subtype 3g	1		1		
1265	42862	Rickettsia felis		1		1	
1266	42897	Shigella flexneri 2a	35		35		
1267	43304	Mycobacterium peregrinum	2		2		
1268	43765	Corynebacterium amycolatum		1		1	
1269	43767	Rhodococcus hoagii	18	2	18	3	1
1270	X 43852	Toxicodendron			1	1	1
1271	44026	Sepik virus		1		1	
1272	44088	Canarypox virus		8		8	
1273	44104	Vibrio cholerae 569B	37		37		
1274	44271	Leishmania chagasi	3		3		

1275	44275	Leptospira interrogans serovar Copenhagen	2		2		
1276	44276	Leptospira interrogans serovar Pomona	2	3	2	3	
1277	44561	Murine type C retrovirus		1		1	
1278	44689	Dictyostelium discoideum	1	1	1	1	
1279	44755	New York hantavirus		2		2	
1280	45029	Bluetongue virus 16	3		3		
1281	45201	Mannheimia haemolytica serotype 1	82		82		
1282	45219	Guanarito mammarenavirus		842		842	
1283	45240	Human papillomavirus type 68		1		1	
1284	45409	Feline immunodeficiency virus (isolate wo)	3		3		
1285	45410	Hepatitis B virus adw4/Brazil/isolate w4b		12		12	
1286	45455	Macacine gammaherpesvirus 4		27		27	
1287	45582	[Candida] saitoana	1		1		
1288	45617	Human endogenous retrovirus K	14		14		
1289	45659	Human adenovirus B3	29	2	29	2	
1291	46015	Autographa californica nucleopolyhedrovirus		1		1	
1292	46221	Porcine circovirus	1	49	1	49	
1293	46242	Spodoptera litura nucleopolyhedrovirus		2		2	
1294	46245	Drosophila pseudoobscura pseudoobscura	1		1		
1295	46290	Foot-and-mouth disease virus C3	4	1	4	1	
1296	46457	Cycloclasticus oligotrophus		1		1	
1297	X 46506	Bacteroides stercoris				1	1
1298	46771	Simian virus 12	1		1		
1299	46835	Fasciola gigantica	2		3		1
1300	46919	Whitewater Arroyo mammarenavirus		349		349	
1301	46920	Rio Mamore hantavirus	1	1	1	1	
1302	46921	Human adenovirus D13	1		1		
1303	46941	Human adenovirus 46	1		1		
1305	47929	Macacine betaherpesvirus 3		99		99	
1306	48409	Salmonella enterica subsp. enterica serovar Virchow		1		1	
1307	48483	Reclinomonas americana		1		1	
1308	48935	Novosphingobium aromaticivorans		1		1	
1309	49011	Hesperocyparis arizonica	2	6	2	6	
1311	50557	Insecta	7		7		
1312	51031	Necator americanus	17		17		
1313	51033	Human papillomavirus type 73		1		1	
1314	51240	Juglans regia	34	19	34	19	
1315	53179	Porcine rubulavirus	3		3		
1316	53182	Feline foamy virus	7		7		
1317	53258	Variola minor virus		93		93	
1318	53751	Echinacea purpurea	1		1		
1319	54290	GB virus C	16		16		
1320	54315	Bovine viral diarrhea virus 2	1		1		
1321	54388	Salmonella enterica subsp. enterica serovar Paratyphi A		1		1	
1322	54390	Micrurus corallinus	123		123		
1323	55097	Mobala mammarenavirus	1		1		
1325	55429	Megathura crenulata	1		1		
1326	55513	Pistacia vera		6		6	
1327	55532	Influenza A virus (A/swine/Quebec/1192/1986(H1))		1		1	
1328	55601	Vibrio anguillarum	1		1		
1329	55635	Inula helenium		1		1	
1330	55951	Grapevine leafroll-associated virus 3	1		1		
1331	56636	Aeropyrum pernix	3	2	3	2	
1332	57068	Acanthisitta chloris		1		1	
1333	57266	Plasmodium falciparum 7G8	42	52	42	52	
1334	57270	Plasmodium falciparum Palo Alto/Uganda	38		38		
1335	57278	Human herpesvirus 7 strain JI		1		1	
1337	57372	Mycoplasma suis	3		3		
1338	57482	European bat 1 lyssavirus		1		1	
1339	57486	Mus musculus molossinus		1		1	
1340	57667	Simian-Human immunodeficiency virus	1		1		
1341	57678	Leptospira interrogans serovar Lai	10	10	10	10	
1342	58024	Spermatophyta	3	1	4	1	1
1343	58216	Loxosceles gaucho	1		1		
1344	58217	Loxosceles laeta	2		2		
1345	58218	Loxosceles intermedia	83		83		

1346	59201	Salmonella enterica subsp. enterica		18		18
1347	59202	Salmonella enterica subsp. salamae		1		1
1348	59203	Salmonella enterica subsp. arizonae		1		1
1349	59205	Salmonella enterica subsp. houtenae		1		1
1350	59375	Influenza A virus (A/South Carolina/1/1918(H1N1))	8	1	8	1
1351	59538	Pantholops hodgsonii		1		1
1352	59729	Taeniopygia guttata		1		1
1353	59799	Angomonas deanei		2		2
1354	60189	Rhipicephalus decoloratus	5		5	
1356	60552	Burkholderia vietnamiensis		2		2
1357	60876	Pixuna virus		1		1
1358	60879	Cabassou virus		1		1
1359	60893	Desulfovobacca acetoxidans		1		1
1360	61466	Gnathostoma binucleatum	10		10	
1361	61673	Porcine endogenous retrovirus	2	11	2	11
1362	62319	Halococcus saccharolyticus		1		1
1363	62330	Fagopyrum tataricum	5		5	
1364	62446	Influenza A virus (A/Argentina/3779/94(H3N2))		1		1
1365	62478	Influenza A virus (A/Kitakyushu/93(H3N2))		1		1
1366	62488	Influenza A virus (A/Nanchang/58/1993(H3N2))		1		1
1367	62496	Influenza A virus (A/New_York/17/94(H3N2))		1		1
1368	62503	Influenza A virus (A/Ohio/3/95(H3N2))		1		1
1369	62512	Influenza A virus (A/Shangdong/5/94(H3N2))		1		1
1370	62541	Influenza A virus (A/Christchurch/2/1988(H3N2))		1		1
1371	62549	Influenza A virus (A/Fukuoka/C29/1985(H3N2))	5		5	
1372	62559	Influenza A virus (A/Los Angeles/1987(H3N2))	5		5	
1373	62564	Influenza A virus (A/New_York/15/94(H3N2))		1		1
1374	62575	Influenza A virus (A/Sichuan/2/1987(H3N2))		5		5
1375	62596	Influenza A virus (A/USSR/26/1985(H3N2))		1		1
1377	62977	Acinetobacter sp. ADP1		2		2
1378	63106	Influenza A virus (A/Wuhan/359/1995(H3N2))	5		5	
1379	63221	Homo sapiens neanderthalensis		1		1
1380	63330	Hendra henipavirus	9	2	9	2
1381	63363	Aquifex aeolicus	2	3	2	3
1382	63421	Swine hepatitis E virus	7		10	3
1383	63673	Turbo cornutus	2		2	
1384	63737	Nostoc punctiforme PCC 73102		2		2
1385	63746	Hepatitis C virus (isolate H77)	137	208	152	208
1386	64284	Saboya virus		1		1
1387	64289	Carey Island virus		2		2
1388	64293	Tembusu virus	2		2	10
1389	64320	Zika virus	15	131	53	193
1390	64382	Human Endogenous Retrovirus IDDMK1,2-22	3		3	
1391	64495	Rhizopus oryzae	4	1	4	1
1392	65690	AK7 murine leukemia virus		1		1
1393	65699	Neisseria meningitidis serogroup A	5		5	
1394	65743	Blackcurrant reversion virus	2		2	
1395	66692	Bacillus clausii KSM-K16		1		1
1396	68621	Classical swine fever virus strain Riems		5		5
1397	68887	Torque teno virus	5	94	5	94
1398	68909	Deinococcus geothermalis	1		1	
1399	69008	Juniperus oxycedrus		3		3
1400	69153	Human enterovirus 71 (strain BRCR)	1		1	
1401	69156	Murine cytomegalovirus (strain K181)	2	14	2	14
1402	69245	Lechiguanas virus		9		9
1404	69247	Oran virus		2		2
1405	69248	Pergamino virus		1		1
1406	70146	Measles virus strain Edmonston-B	2	78	2	78
1407	70149	Measles virus strain Edmonston-Zagreb	1		1	
1408	70175	Androctonus australis hector	24		24	
1409	70203	Vibrio virus fs1		1		1
1410	70865	Murine rotavirus EDIM		27		27
1411	71238	Pseudomonas sp. G-179		1		1
1412	71421	Haemophilus influenzae Rd KW20		3		3
1415	72132	Rotavirus G1	1	1	1	1
1416	72539	Physalis mottle virus	2		2	

1417	72556	Achromobacter piechautii	1	1		
1418	72590	Salmonella sp. 'group B'	6	6		
1419 X	72664	Eutrema salsugineum		2		2
1420	73036	Rotavirus G3	1		1	
1421	73239	Plasmodium yoelii yoelii	22	42	22	42
1422	73482	Foot-and-mouth disease virus (strain O1)	18	1	18	1
1423	73484	Human immunodeficiency virus type 2 (isolate KR)		3		3
1424	74138	Pseudomonas sp. DJ-12		1		1
1425	74368	Sinonatrix annularis	1		1	
1426	74537	Vladivostok virus	1		1	
1428	74722	Stachybotrys chartarum	11		11	
1429	74942	Hantavirus CRF355		1		1
1431	75922	Mycolicibacterium tusciae		2		2
1433	76777	Malassezia sympodialis	1		1	
1434	76832	Myroides odoratimimus		1		1
1435	76869	Pseudomonas putida GB-1		1		1
1437	77009	Hordeum vulgare subsp. spontaneum	2		2	
1438	78245	Xanthobacter autotrophicus Py2		1		1
1439	79692	Human respiratory syncytial virus B1	1	25	1	25
1440	79695	Influenza A virus (A/Memphis/1/71H-A/Bellamy/42N)		1		1
1441	79889	Bovine herpesvirus type 1.1	2		2	
1442	79923	Clonorchis sinensis	2	1	2	1
1443	80365	Laminaria digitata	2		2	
1444	80859	Streptomyces ribosidificus		1		1
1445	80956	Pomacentrus moluccensis		1		1
1446	81475	Frateuria aurantia	1		1	
1447	81847	Trichophyton quinckeanum	1		1	
1448 X	81985	Capsella rubella		1		1
1449	82300	Adeno-associated virus - 5	9		9	
1450	82372	Influenza A virus (A/Sydney/05/97-like(H3N2))		1		1
1451	82470	Bovine viral diarrhea virus strain Oregon C24V	5	3	5	3
1452	82639	Coxsackievirus B2	2		2	
1453	82659	Sapporo virus-Manchester		1		1
1454	82823	Bovine respiratory syncytial virus strain leylstad	1		1	
1455	82824	Bovine respiratory syncytial virus strain snook	1	75	1	75
1456	82830	Epstein-barr virus strain ag876	1	1	14	1
1457	82831	Equid herpesvirus type 2 strain 86/87	1		1	
1459	83192	Topografov hantavirus	1		1	
1460	83206	Influenza A virus (A/swine/Scotland/410440/94(H1N2))		5		5
1461	83262	Mycobacteroides immunogenum		5		5
1462	83331	Mycobacterium tuberculosis CDC1551		42		42
1463	83332	Mycobacterium tuberculosis H37Rv	61	876	62	964
1464	83333	Escherichia coli K-12	23	19	28	19
1465	83334	Escherichia coli O157:H7		123		123
1466	83455	Myxococcus stipitatus		1		1
1467	83554	Chlamydia psittaci	78	2	86	2
1468	83555	Chlamydia abortus	3		12	9
1469 X	83556	Chlamydia felis		3		3
1470 X	83557	Chlamydia caviae		6		6
1471	83558	Chlamydia pneumoniae	67	24	84	24
1472 X	83559	Chlamydia suis		4		4
1473	83560	Chlamydia muridarum		3	12	3
1474	83810	Thosea asigna virus		1		1
1475	85106	Adeno-associated virus - 1		11		11
1476	85223	Laurus nobilis		1		1
1477	85552	Scylla paramamosain	7		7	
		Salmonella enterica subsp. enterica serovar				
1478	85569	Typhimurium str. DT104	1		1	
1479	85698	Achromobacter xylosoxidans	1		1	
1480	85708	Porcine circovirus 2	31		33	1
1481	85709	Porcine circovirus type 2-B	2		6	4
1482	85777	Agelas mauritiana		1		1
1483	85962	Helicobacter pylori 26695	13	10	40	10
1484	85963	Helicobacter pylori J99		53		53
1485 X	85991	Chlamydia pecorum		116		116
1486	86107	Coxsackievirus A6	1		1	

1487	86600	Discosoma sp.		1	1	
1488	86782	Amur virus		35	35	
1490	87883	Burkholderia multivorans	1	2	2	
1491	88036	Selaginella moellendorffii		1	1	
1492	X 88085	<i>Lachesis stenophrys</i>			13	13
1493	88086	Protobothrops elegans	7	7		
1494	88087	Protobothrops flavoviridis	3	3		
1495	88103	Influenza A virus (A/Hong Kong/532/1997(H5N1))		1	1	
1496	88104	Influenza A virus (A/Hong Kong/483/1997(H5N1))	3	10	3	10
1497	88776	Influenza A virus (A/Brevig Mission/1/1918(H1N1))		1	1	
1498	89169	Influenza A virus (A/Chicken/Pennsylvania/13552-1/98 (H7N2NSB))	1	1		
1499	89172	Influenza A virus (A/quail/Arkansas/16309-7/94 (H7N3NSA))	1	1		
1501	89462	Bubalus bubalis	7	1	7	1
1503	90370	Salmonella enterica subsp. enterica serovar Typhi	15	111	15	111
1504	90371	Salmonella enterica subsp. enterica serovar Typhimurium	15	76	16	76
1505	91465	Pseudomonas sp. MIS38		1	1	
1506	92652	Shrimp white spot syndrome virus	3	3		
1507	93061	Staphylococcus aureus subsp. aureus NCTC 8325	5	1	5	1
1508	93062	Staphylococcus aureus subsp. aureus COL	17	1	17	1
1509	93621	Heteropneustes fossilis		1	1	
1510	93678	TTV-like mini virus		1	1	
1511	93838	Influenza A virus (A/goose/Guangdong/1/1996(H5N1))	1	9	1	9
1512	94432	Human rotavirus MP409	1	1	1	1
1513	94966	Bluetongue virus 12	15		15	
1514	94967	Bluetongue virus 4	7		7	
1516	95486	Burkholderia cenocepacia	1	1	1	1
1517	95602	Eriocheir sinensis	10		10	
1518	95888	Influenza A virus (A/mallard duck/PA/10218/84(H5N2))	8		8	
1520	97348	Influenza A virus (A/Chicken/Hong Kong/G23/97(H9N2))		1	1	
1521	97353	Influenza A virus (A/Chicken/Hong Kong/739/94(H9N2))	1		1	
1522	97477	Acetomicrobium mobile		1	1	
1523	98360	Salmonella enterica subsp. enterica serovar Dublin		2	2	
1524	99287	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2		77	77	
1525	99586	Echis ocellatus	5		5	
1526	99875	Leishmania donovani donovani	1		1	
1527	99883	Tetraodon nigroviridis		2	2	
1528	100226	Streptomyces coelicolor A3(2)		1	1	1
1529	100835	Influenza A virus (A/Chicken/Hong Kong/258/97 (H5N1))	1		1	
1530	101350	Porcine rotavirus strain A253	2		2	
1531	102617	Helicobacter pylori SS1	3	3	3	3
1532	102793	H5N1 subtype	21	36	27	36
1533	102796	H9N2 subtype	1		1	
1534	102862	Proteus penneri	1		1	
1535	103448	Pleistophora sp. LS		1	1	
1536	103903	Coxsackievirus B3 (strain Nancy)	13	30	13	30
1537	103905	Coxsackievirus B4 (strain E2)	7	41	7	41
1538	103906	Coxsackievirus B4 (strain JVB / Benschoten / New York/51)		76		76
1539	103920	Guinea pig cytomegalovirus (strain 22122 / ATCC VR682) (GPCMV)	1		1	
1540	103929	Rabies virus strain Pasteur vaccin	2	1	2	1
1541	103930	Rhesus cytomegalovirus strain 68-1		18		18
1542	104102	Acetobacter tropicalis		1	1	
1543	105751	Aeromonas bestiarum		1	1	
1544	106820	Hepatitis B virus subtype adr	23	25	23	25
1545	106821	Hepatitis B virus subtype adw	17	75	17	75
1546	107404	Influenza B virus (B/Beijing/184/93)		1	1	
1547	107406	Influenza B virus (B/Chiba/447/98)		1	1	
1548	107493	Influenza A virus (A/Cordoba/3278/96(H3N2))		1	1	
1549	107558	Influenza A virus (A/France/75/97(H3N2))		1	1	
1550	107819	Clostridium perfringens D	44		44	
1551	108098	Human mastadenovirus B	1		1	
1552	110195	Foot-and-mouth disease virus - type Asia 1	10	3	10	3

1553	112509	Hordeum vulgare subsp. vulgare		18	18		
1554	114727	H1N1 subtype	12	44	15	44	3
1555	114729	H2N2 subtype		1		1	
1556	114742	Pythium insidiosum	2		2		
1557	X 115711	Chlamydia pneumoniae AR39			1		1
1558	115713	Chlamydia pneumoniae CWL029		48		48	
1559	117125	Cucumber mosaic virus (strain Pepo)	1		1		
1560	117204	African horse sickness virus 3	21		21		
1561	119210	H3N2 subtype	4	23	5	23	1
1562	119211	H3N8 subtype	1		1		
1563	119218	H7N7 subtype		1		1	
1564	119602	Streptococcus dysgalactiae subsp. equisimilis	21		21		
1565	119856	Francisella tularensis subsp. tularensis		5		5	
		Salmonella enterica subsp. enterica serovar					
1566	119912	Choleraesuis		3		3	
1567	120505	Baboon cytomegalovirus		1		1	
1568	121224	Pediculus humanus corporis	1		2		1
1569	121723	Photobacterium sp. SKA34		1		1	
1570	121759	Paracoccidioides brasiliensis	4	16	4	16	
1571	121791	Nipah henipavirus	5		5		
1572	122291	Kappapapillomavirus 1	2		2		
1573	122355	Pseudomonas psychrophila	1		1		
1574	122586	Neisseria meningitidis MC58	17		17		
1575	122928	Norovirus GI	2		2		
1576	122929	Norovirus GII	2		2		
1577	126283	Herpes simplex virus unknown type		1		1	
1578	126793	Plasmodium vivax Sal-1	17		17		
1579	126794	Vaccinia virus Ankara		127		127	
1580	127906	Vibrio cholerae O1	9		9		
1581	127999	Tanacetum parthenium		1		1	
1582	128947	Ebola virus - Gabon (1994-1997)		18		18	
1583	128948	Sudan virus - Boniface, Sudan,1976	2	1	2	1	
1584	128949	Sudan ebolavirus - Maleo (1979)		30		30	
1585	128951	Ebola virus - Zaire (1995)		1		1	
1586	128952	Ebola virus - Mayinga, Zaire, 1976	36	13	36	13	
1587	128982	Influenza A virus (A/Swine/Indiana/9K035/99 (H1N2))		2		2	
1588	128987	Grass carp reovirus		1		1	
1589	128999	Tai Forest virus - Cote d'Ivoire, Cote d'Ivoire, 1994	1	3	1	3	
1590	129000	Ebola virus - Eckron (Zaire, 1976)		12		12	
1591	129003	Reston ebolavirus - Reston	2	27	2	27	
1592	129052	Catelliglobospora koreensis		1		1	
1593	129138	Pseudomonas amygdali pv. morsprunorum	2		2		
1594	129727	Bovine papular stomatitis virus		2		2	
1595	129875	Human mastadenovirus A		1		1	
1596	129951	Human mastadenovirus C	1	3	1	3	
1597	X 130663	Fowl adenovirus 4			3		3
1598	130760	Influenza A virus (A/Hong Kong/1073/99(H9N2))	1	25	1	25	
1599	130763	Influenza A virus (A/Hong Kong/156/97(H5N1))	2	26	2	26	
1600	132475	Yaba-like disease virus		3		3	
1601	132487	Measles virus strain Schwarz	1	1	1	1	
1602	132504	Influenza A virus (A/X-31(H3N2))	77	189	77	189	
1604	132783	Influenza A virus (A/Netherlands/626/89 (H3N2))		1		1	
1605	132841	Influenza A virus (A/Netherlands/785e/90 (H3N2))		1		1	
1606	132884	Influenza A virus (A/Netherlands/458/98 (H3N2))		1		1	
1607	133704	Porcine circovirus 1	5		5		
1608	134537	Paraburkholderia fungorum	1		1		
		Influenza A virus (A/environment/Hong Kong/437-10/99 (H5N1))		1		1	
1610	135661						
1611	135720	Neisseria meningitidis serogroup C	3		3		
1612	136371	Umbilicaria papulosa	1		1		
1613	136474	Influenza A virus (A/Swine/Colorado/23619/99(H3N2))		1		1	
1614	136966	SEN virus		7		7	
1615	137578	Influenza A virus (A/England/939/69 x A/PR/8/34)		2		2	
1616	137885	Influenza A virus (A/parakeet/Chiba/1/97(H9N2))		4		4	
1617	137886	Influenza A virus (A/parakeet/Narita/92A/98(H9N2))		2		2	
1618	138948	Enterovirus A	1		1		

1619	138950	Enterovirus C	6	3	6	3	
1623	142948	Influenza A virus (A/ruddy turnstone/Delaware/67/1998(H12N4))	1		1		
1624	144549	Mycobacterium fortuitum subsp. fortuitum	1		1		
1625	145262	Methanothermobacter thermautotrophicus	1		1		
1626	145306	Influenza A virus (A/swine/Hong Kong/10/98(H9N2))	5		5		
1627	145307	Influenza A virus (A/swine/Hong Kong/9/98(H9N2))	2		2		
1628	147095	Influenza A virus (A/Swine/Italy/25823/94(H3N2))	2		2		
1629	147272	Paspalum notatum	16		16		
1630	148360	Watermelon mosaic virus 2 (isolate USA)	2		2		
1631	148363	Helicoverpa armigera nucleopolyhedrovirus G4	2		2		
1632	149539	Salmonella enterica subsp. enterica serovar Enteritidis	2	1	2	1	
1633	150080	Norovirus isolates	1		1		
1634	150127	Influenza B virus (B/Osaka/983/97-V3)	1		1		
1635	150340	Vibrio antiquarius	15		15		
1636	150396	Pseudomonas sp. MT-1	1		1		
1637	150846	Enterovirus 5865/sin/000009	2		2		
1638	151250	Kali turgidum	22		22		
1639	152219	Menangle virus	2		2		
1640	152794	Corynebacterium efficiens	5		5		
1641	153969	Influenza A virus (A/Hong Kong/497/97(H3N2))	1		1		
1642	154540	Influenza A virus (A/Kayano/57(H2N2))	1		1		
1643	155017	Anogeissus	1		1		
1644	155091	Secale cereale subsp. afghanicum	2		2		
1645	155218	Influenza A virus (A/Hong Kong/482/97(H5N1))	7	1	7	1	
1646	155220	Influenza A virus (A/Hong Kong/542/97(H5N1))	1		1		
1647	155222	Influenza A virus (A/Hong Kong/488/97(H5N1))	1		1		
1648	155225	Influenza A virus (A/Hong Kong/507/97(H5N1))	5		5		
1649	155226	Influenza A virus (A/Hong Kong/514/97(H5N1))	1		1		
1650	155227	Influenza A virus (A/Hong Kong/516/97(H5N1))	2		2		
1651	155864	Escherichia coli O157:H7 str. EDL933	3	32	4	32	1
		Influenza A virus (A/NWS/33HA-					
1652	155917	A/tern/Australia/G70C/75NA(H1N9))	1		1		
1653	156230	Karenia brevis	1		1		
1654	156586	Flavobacteria bacterium BBFL7	1		1		
1656 X	157703	Murine polyomavirus strain A3	4		4	4	4
1657	157914	Ziziphus mauritiana	4		4		
1658	158306	Influenza A virus (A/swine/Cotes d'Armor/800/00(H1N2))	1		1		
1659	158465	Human calicivirus Hu/NLV/GII/MD145-12/1987/US	1		1		
1660	158474	Bovine viral diarrhea virus strain Trangie Y546	1		1		
1661	158879	Staphylococcus aureus subsp. aureus N315	5		5		
1662	159091	Pseudomonas sp. KIE171	1		1		
1663 X	159449	Streptomyces scabrisporus			1	1	
1664	159471	Influenza A virus (A/eq/Sussex/89/(H3N8))	4		4		
1665	159479	Saaremaa hantavirus	21		21		
1666	160490	Streptococcus pyogenes M1 GAS	13	2	13	2	
1667	160491	Streptococcus pyogenes str. Manfredo	3	35	3	35	
1668	160753	Simian immunodeficiency virus 17E-Fr	2		2		
1669	161502	Influenza A virus (A/swine/Italy/1509-6/97(H1N1))	15		15		
1670	161600	Yellow grouper nervous necrosis virus	1		1		
1671	161727	Foot-and-mouth disease virus A10/Holland	11	14	11	14	
1672	161934	Beta vulgaris	5		5		
1673	162145	Human metapneumovirus	8	130	8	130	
1674	162326	Influenza A virus (A/Hong Kong/1143/99(H3N2))	1		1		
1675	163164	Wolbachia endosymbiont of Drosophila melanogaster	1		1		
1676	164326	Influenza A virus (A/Hong Kong/1131/1998(H1N1))	1	1	1	1	
1677	164756	Mycobacterium sp. MCS	73		73		
1678	164757	Mycobacterium sp. JLS	77		77		
1679	165420	Influenza A virus (A/Turkey/MO/24093/99(H1N2))	4		4		
1680	165512	Influenza A virus (A/goose/Guangdong/3/1997(H5N1))	3	1	3	1	
1682	167758	TTV-like virus DXL1	10		10		
1683	168278	Influenza A virus (A/swine/Finistere/127/99(H3N2))	4		4		
1684	168807	Escherichia coli O127:H6	1		1		
1685	169166	Influenza A virus (A/swine/Italy/1521/98(H1N2))	4		4		
1686	169169	Influenza A virus (A/swine/Cotes d'Armor/1482/1999(H1N1))	1		1		

1687	169173	Choclo virus		3	3		
1689	169963	Listeria monocytogenes EGD-e	5	64	5	64	
1691	170187	Streptococcus pneumoniae TIGR4		2		2	
1692	170325	Canid alphaherpesvirus 1		1		1	
1693	170342	Influenza A virus (A/swine/Italy/1654-1/99(H1N2))		1		1	
1694	170500	H1N9 subtype	1		1		
1695	170525	Measles virus genotype D4	1		1		
1696	170529	Measles virus genotype D7	1		1		
1697	170955	Amur virus Solovey/AP63/1999		2		2	
1698	171101	Streptococcus pneumoniae R6		12	1	12	1
1699	171264	Measles virus genotype D3	1		1		
1700	171425	Influenza B virus (B/Kobe/87/2001)	1		1		
1701	171929	Anacardium occidentale	64	10	64	10	
1702	172148	Alkhumra hemorrhagic fever virus		4		4	
1703	172149	Influenza A virus (A/swine/Quebec/192/81(H1N1))	1		1		
1704	172851	Avian hepatitis E virus	20		20		
1705	173473	Influenza A virus (A/swine/Hong Kong/2106/98(H9N2))		2		2	
1706	173477	Influenza A virus (A/swine/Hong Kong/3297/98(H9N2))		3		3	
		Influenza A virus (A/Duck/Hong Kong/ww461/2000(H5N1))		1		1	
1709	177128	Influenza A virus (A/SW/MN/12883/00(H1N2))		2		2	
1710	177131	Influenza A virus (A/SW/KS/13481-T/00(H1N2))	1		1		
1711	177188	Influenza A virus (A/SW/MN/3227/00(H1N2))		1		1	
1712	177416	Francisella tularensis subsp. tularensis SCHU S4		92		92	
1713	178876	Cryptococcus neoformans var. grubii	1		1		
1714	180454	Anopheles gambiae str. PEST	6	2	6	2	
1715	180498	Jatropha curcas	6		6		
1716	182082	Chlamydia pneumoniae TW-183	7		7		
		Influenza A virus (A/Goose/Hong Kong/385.3/2000(H5N1))		1		1	
1717	182781	Mycobacterium tuberculosis subsp. tuberculosis		1		1	
1718	182785	Influenza A virus (A/Chicken/Shanghai/F/98(H9N2))	5		5		
1719	183741	Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))	7	100	7	100	
1720	183764	Influenza A virus (A/quail/Hong Kong/SF550/00(H6N1))		2		2	
1721	183778	Influenza A virus (A/duck/Hong Kong/3096/99(H6N2))		2		2	
1722	183783	Influenza B virus (B/Kadoma/122/99)	2		2		
1723	184816	Giardia lamblia ATCC 50803	249		249		
1724	184922	Trypanosoma brucei brucei TREU927		1		1	
1725	185431	Hepatitis E virus type 1	3		3		
1726	185579	Hepatitis E virus type 4	1		1		
1727	185580	Influenza A virus (A/mallard/NZ/1/97(H5N2))		1		1	
1728	185794	Human rhinovirus A34		54		54	
1729	185905	Human rhinovirus A39		1		1	
1730	185907	Influenza A virus (A/Sphingomonas aurantiaca)		1		1	
1731	185949	Influenza A virus (A/swine/New Jersey/11/1976(H1N1))	1		1		
1732	186460	Ebolavirus	60		61	1	1
1733	186536	Zaire ebolavirus	20	870	99	886	79
1734	186538	Reston ebolavirus	1	11	1	11	16
1735	186539	Sudan ebolavirus	2	280	4	292	2
1736	186540	Tai Forest ebolavirus		1		1	12
1737	186541	Influenza A virus (A/Swine/Minnesota/55551/2000(H1N2))		1		1	
1738	187164	Yersinia pestis KIM10+		11		11	
1739	187410	Methanothermobacter thermautotrophicus str. Delta H	1		1		
1740	187420	Panine betaherpesvirus 2		4		4	
1741	188763	Leptospira interrogans serovar Lai str. 56601	1		1		
1742	189518	Mycobacterium sp. KMS		69		69	
1743	190918	Influenza A virus (A/Weiss/1943(H1N1))		1		1	
1744	191090	Bacillus anthracis str. A2012		29		29	
1745	191218	Pseudomonas syringae pv. atrofaciens	4		4		
1746	192087	Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819	10	22	10	22	
1747	192222	Influenza A virus (A/Saudi Arabia/7971/2000(H1N1))		1		1	
1748	192535	Influenza A virus (A/Egypt/96/2002(H1N2))		1		1	
1749	192549	Influenza A virus (A/Saudi Arabia/2581/2001(H1N2))		1		1	
1750	192720	Vipera aspis aspis	3		3		
1751	194601						

1752	194958	Porcine endogenous retrovirus A	2	2		
1753	194959	Porcine endogenous retrovirus B	1	1		
1755	195099	Campylobacter jejuni RM1221	13	13		
1756	195102	Clostridium perfringens str. 13	1	1		
1757	195700	Avian rotavirus PO-13	6	6		
1758	196164	Corynebacterium efficiens YS-314	4	4		
1759	196403	Baboon endogenous virus	1	1	1	1
1760	196462	Influenza A virus (A/chicken/California/1002a/00(H6N2))	1	1	1	1
1761	196600	Vibrio vulnificus YJ016	75	75		
1762	196620	Staphylococcus aureus subsp. aureus MW2	7	7		
1763	196627	Corynebacterium glutamicum ATCC 13032	14	14		
1764	197575	Haemophilus aegyptius	1	1		
1765	197579	Influenza A virus (A/Chicken/Guangdong/11/97(H9N2))	1	1		
1766	197585	Influenza A virus (A/chicken/Shandong/6/96(H9N2))	1	1		
1767	197589	Influenza A virus (A/Quail/Shanghai/8/96(H9N2))	1	1		
1768	197780	Bluetongue virus 8	2	21	2	21
1769	198059	Influenza A virus (A/England/627/01(H1N2))	2	2		
1770	198094	Bacillus anthracis str. Ames	2	2		
1771	198214	Shigella flexneri 2a str. 301	4	4		
1772	198215	Shigella flexneri 2a str. 2457T	2	2		
1773	199306	Coccidioides posadasii	9	9		
1774	199310	Escherichia coli CFT073	1	2	1	2
1775	X 199738	uncultured Chlamydia sp.		2		2
1776	201444	Aracatuba virus	5	5		
1777	202812	Adeno-associated virus - 7	2	2		
1778	202813	Adeno-associated virus - 8	17	14	17	14
1779	203119	Hungateiclostridium thermocellum ATCC 27405	1	1		
1780	203124	Trichodesmium erythraeum IMS101	2	2		
1781	203126	Influenza A virus (A/Kamata/14/91(H3N2))	1	1		
1782	203129	Influenza A virus (A/Aichi/2/1994(H3N2))	1	1		
1783	203172	Camelpox virus CMS	28	28		
1784	203173	Camelpox virus M-96	133	133		
1785	203174	Camelpox virus CP1	1	1		
1787	204428	Chlamydiae	16	16		
1788	204711	Theilovirus	10	10		
1789	204722	Brucella suis 1330	1	29	1	29
1791	205488	Ebola virus sp.	2	2		
1792	205913	Bifidobacterium longum DJO10A	2	2		
1793	205914	Histophilus somni 129PT	2	2		
1794	205920	Ehrlichia chaffeensis str. Arkansas	23	23		
1795	205946	Influenza A virus (A/Chicken/Beijing/1/95(H9N2))	1	1		
1797	206203	Influenza B virus (B/Hong Kong/330/2001)	23	23		
1798	207401	Influenza A virus (A/finch/Canada/NS1301/2001(H3N8))	1	1		
1799	208435	Streptococcus agalactiae 2603V/R	1	2	1	2
1800	208726	Human hepatitis A virus	4	1	4	1
1801	208893	Human respiratory syncytial virus A	6	4	8	4
1803	208899	Cupixi mammarenavirus		1		1
1804	208963	Pseudomonas aeruginosa UCBPP-PA14		23		23
1805	208964	Pseudomonas aeruginosa PAO1	1	5	2	39
		Salmonella enterica subsp. enterica serovar Typhi str.				
1806	209261	Ty2		5		16
1807	209841	Actinobacillus pleuropneumoniae serovar 7	1	1		
1808	209882	Fusobacterium nucleatum subsp. vincentii ATCC 49256	2	2		
1809	210655	Influenza A virus (A/Duck/Shantou/2144/00(H9N2))	1	1		
1810	210656	Influenza A virus (A/Duck/Shantou/1881/00(H9N2))	1	1		
1811	210659	Influenza A virus (A/Duck/Shantou/2088/01(H9N2))	1	1		
1812	210663	Influenza A virus (A/Duck/Shantou/2134/00(H9N2))	1	1		
1813	211044	Influenza A virus (A/Puerto Rico/8/1934(H1N1))	31	478	33	504
1814	211110	Streptococcus agalactiae NEM316		1		1
1815	211882	Leptospira interrogans serovar Australis	2	2		
1816	212042	Anaplasma phagocytophilum str. HZ	21	21		
1817	212045	Bacillus anthracis str. Western North America USA6153	1	1		
1818	212717	Clostridium tetani E88		16		16
1819	214092	Yersinia pestis CO92	4	22	39	22
1821	214697	Musa acuminata AAA Group	1	1		
1823	214856	Alistipes finegoldii		1		1

1824	215862	Influenza A virus (A/Chicken/Nanchang/2-220/2001(H3N6))		1		1	
1826	216466	Streptococcus agalactiae serogroup V	1		1		
1827	216495	Streptococcus agalactiae serogroup III	12		12		
1828	216592	Escherichia coli 042	2		2		
1829	216594	Mycobacterium marinum M		29		29	
		Salmonella enterica subsp. enterica serovar					
1830	216597	Typhimurium str. SL1344		2		2	
1831	216600	Streptococcus pneumoniae 23F	6		6		
1832	216877	Influenza A virus (A/quail/Hong Kong/FY298/00(H9N2))		4		4	
1833	216895	Vibrio vulnificus CMCP6		53		53	
1834	217686	Little cherry virus 1		1		1	
1835	217992	Escherichia coli O6		7		7	
1836	219334	Lactobacillus casei subsp. casei ATCC 393	2		2		
		Salmonella enterica subsp. enterica serovar Typhi str.					
1837	220341	CT18		92		92	
1838	220837	Cryptosporidium sp. MNJ-1		1		1	
1839	220977	Influenza A virus (A/England/10/67(H2N2))		1		1	
1840	221012	Influenza A virus (A/Rio/6/69(H3N2))		1		1	
1841	221918	Bovine viral diarrhea virus VEDEVAC	6		6		
1842	221988	[Mannheimia] succiniciproducens MBEL55E		2		2	
1843	222523	Bacillus cereus ATCC 10987		1		1	
1844	223337	Tobacco leaf curl Zimbabwe virus		1		1	
1845	223926	Vibrio parahaemolyticus RIMD 2210633	2	17	2	17	
1846	223931	Influenza A virus (A/Bangkok/10/1983(H1N1))		1		1	
1848	223935	Influenza A virus (A/Okuda/1957(H2N2))	1	9	1	9	
1849	223947	Influenza A virus (A/Hokkaido/20/89(H3N2))		3		3	
1850	223997	Murine norovirus 1	4	1	4	1	
1851	224197	Influenza C virus (C/Nara/1/85)		1		1	
1852	224206	Simian immunodeficiency virus - mon		1		1	
1853	224308	Bacillus subtilis subsp. subtilis str. 168		1		1	
1854	224324	Aquifex aeolicus VF5	1	1	1	1	
1855	224326	Borrelia burgdorferi B31	104	10	107	10	3
1856	224819	Influenza A virus (A/Nagasaki/76/98(H3N2))		1		1	
1857	224914	Brucella melitensis bv. 1 str. 16M	6	14	6	14	
1858	224964	Influenza B virus (B/Johannesburg/5/99)	1		1		
1859	225071	Influenza A virus (A/Tokyo/1566/98(H3N2))		1		1	
1860	225088	Influenza A virus (A/Kitakyushu/159/93(H3N2))		1		1	
1861	225089	Influenza A virus (A/equine/NewMarket/D64/79(H3N8))		1		1	
1862	226186	Bacteroides thetaiotaomicron VPI-5482		1		1	
1863	226900	Bacillus cereus ATCC 14579		2		2	
1864	227377	Coxiella burnetii RSA 493		13		13	
1865	227859	SARS coronavirus	170	501	170	501	
1866	227984	SARS coronavirus Tor2	171	2205	171	2205	
1867	228330	SARS coronavirus Urbani	24	52	24	52	
1868	228399	Actinobacillus pleuropneumoniae serovar 1 str. 4074	2	1	2	1	
1869	228400	Histophilus somni 2336	1		1		
1871	228407	SARS coronavirus BJ01	64	28	64	28	
1872	228928	Influenza A virus (A/Memphis/31/98(H3N2))	6		6		
1873	229032	Porcine epidemic diarrhea virus CV777	5		5		
1874	229051	Influenza A virus (A/81/HO)		6		6	
1875	229992	SARS coronavirus Frankfurt 1	5	26	5	26	
1876	231428	Avian infectious bronchitis virus (strain Vic S)	11	8	11	8	
1877	231455	Dyella japonica	1		1		
1878	231851	Influenza A virus (A/Hong Kong/1774/99(H3N2))		1		1	
1879	233262	Bovine enteric coronavirus (strain 98TXSF-110-ENT)		1		1	
1880	233412	[Haemophilus] ducreyi 35000HP	1		1		
1881	233413	Mycobacterium tuberculosis variant bovis AF2122/97		50		54	4
1882	234267	Candidatus Solibacter usitatus Ellin6076		2		2	
1883	234603	Sapovirus Mc114		1		1	
1884	234826	Anaplasma marginale str. St. Maries	16	28	16	28	
1885	235279	Helicobacter hepaticus ATCC 51449	2		2		
1886	235455	Adeno-associated virus 9	9		10		1
1888	237561	Candida albicans SC5314		3		3	
1889	237609	Pseudomonas alkylphenolica		1		1	
1890	237631	Ustilago maydis 521		2		2	

1891	237895	Cryptosporidium hominis		3	3	
1893	240426	Squirrelpox virus		1	1	
1895	242619	Porphyromonas gingivalis W83	4	4		
1896	243160	Burkholderia mallei ATCC 23344		40	40	
1897	243161	Chlamydia muridarum str. Nigg		42	42	
1898	243164	Dehalococcoides mccartyi 195		1	1	
1899	243230	Deinococcus radiodurans R1	1	1		
1900	243232	Methanocaldococcus jannaschii DSM 2661	3	1	3	1
1901	243243	Mycobacterium avium 104		43	43	
1902	243273	Mycoplasma genitalium G37	8	1	8	1
1903	243276	Treponema pallidum subsp. pallidum str. Nichols	277	9	277	9
1904	243277	Vibrio cholerae O1 biovar El Tor str. N16961	4	3	4	3
1905	244320	Escherichia coli O55:H7		1	1	
1906	244367	Foot-and-mouth disease virus C-S8c1	15	17	15	17
1907	246196	Mycobacterium smegmatis MC2 155		61	61	
1908	246202	Streptococcus sobrinus 6715	4	4	4	4
1909	246437	Tupaia chinensis	1		1	
1910	246618	Bifidobacterium thermacidophilum	1		1	
1911	246878	Canine parvovirus 2	3		3	
1912	249372	Influenza A virus (A/duck/Hokkaido/13/00(H9N2))	2		2	
1913	251297	Influenza A virus (A/Netherlands/127/03(H7N7))		1	1	
1914	253182	Human Respiratory syncytial virus 9320	1		1	
1915	253682	Influenza A virus (A/swine/Hong Kong/5190/99(H3N2))		3	3	
1916	253686	Influenza A virus (A/swine/Hong Kong/74/02(H3N2))		1	1	
1917	254252	Lactococcus virus P2	2		2	
1918	254355	Small ruminant lentivirus	1		1	
1919	255681	Influenza A virus (A/Yokohama/22/2002(H1N2))		2	2	
1920	255682	Influenza A virus (A/Yokohama/47/2002(H1N2))		1	1	
1921	256045	Influenza A virus (A/swine/Chiai/77-10/2001(H3N1))		1	1	
1922	256080	Influenza B virus (B/Kobe/1/2003)	1		1	
1923	257313	Bordetella pertussis Tohama I		11	11	
1924	257363	Rickettsia typhi str. Wilmington		6	6	
1925	260799	Bacillus anthracis str. Sterne	5	4	5	4
1926	260806	Influenza A virus (A/FPV/Dutch/1927(H7N7))	1		1	
1927	260965	Cercopithecine herpesvirus 1 (strain E2490)	18		18	
1928	261202	Alto Paraguay hantavirus		3	3	
1929	261204	Itapua hantavirus		10	10	
1930	261594	Bacillus anthracis str. 'Ames Ancestor'		1	1	
1931	261658	Cavenderia fasciculata		1	1	
1932	262307	Measles virus genotype A	4		4	
1933	262316	Mycobacterium avium subsp. paratuberculosis K-10	4	58	4	58
1934	262698	Brucella abortus bv. 1 str. 9-941		1	1	
1935	262722	Mycoplasma hyopneumoniae 7448	1		1	
1936	262727	Haemophilus influenzae R2846		6	6	
1937	262728	Haemophilus influenzae R2866		2	2	
1938	263683	Bovine herpesvirus 5 strain TX89	2		2	
1939	263815	Pneumocystis murina	3		3	
		Influenza A virus				
1940	264510	(A/chicken/Thailand/LV1NF/2004(H5N1))		1	1	
1942	264635	Acholeplasma granularum	1		1	
1943	264730	Pseudomonas savastanoi pv. phaseolicola 1448A		1	1	
1944	264732	Moorella thermoacetica ATCC 39073		1	1	
1945	265120	Influenza A virus (A/turkey/Italy/214845/2002(H7N3))	1		1	
1946	265619	Ornithodoros erraticus	22		22	
1947	265669	Listeria monocytogenes serotype 4b str. F2365		7	7	
1948	265872	Cowpox virus (Brighton Red)		1	1	
1949	266093	Influenza A virus (A/chicken/Yamaguchi/7/2004(H5N1))	3		3	
1950	266264	Cupriavidus metallidurans CH34		3	3	
1951	266779	Chelativorans sp. BNC1		4	4	
1952	266827	Influenza A virus (A/Thailand/1(KAN-1)/2004(H5N1))	3		4	1
1953	266834	Sinorhizobium meliloti 1021		3	3	
1954	266940	Kineococcus radiotolerans SRS30216 = ATCC BAA-149		2	2	
1955	267409	Listeria monocytogenes serotype 1/2a str. F6854		3	3	
1956	267410	Listeria monocytogenes serotype 4b str. H7858		25	25	
1957	267671	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	11		11	

1958	269482	Burkholderia vietnamiensis G4		9		9	
1959	269484	Ehrlichia canis str. Jake	16	16			
1960	269798	Cytophaga hutchinsonii ATCC 33406		1		1	
1962	269801	Bacillus cereus G9241		41		41	
1963	270338	Human poliovirus 3 strain Sabin	80	1	80	1	
1964	270473	Pneumonia virus of mice J3666		10		10	
1965	270478	Zantedeschia mild mosaic virus		1		1	
1966	270484	Influenza A virus (A/tiger/Thailand/CU-LV/2004(H5N1))		2		2	
1967	270490	Influenza A virus (A/chicken/Nakorn-Patom/Thailand/CU-K3/2004(H5N1))		1		1	
1968	270510	Influenza A virus (A/chicken/Vietnam/HD1/2004(H5N1))		3		3	
1969	270945	Influenza A virus (A/Thailand/4(SP-528)/2004(H5N1))		21		21	
1970	271108	Bombyx mori nucleopolyhedrovirus	2		2		
1971	271848	Burkholderia thailandensis E264		2		2	
1972	272560	Burkholderia pseudomallei K96243	3	735	3	735	
1973	272561	Chlamydia trachomatis D/UW-3/CX		26	1	26	1
1974	272562	Clostridium acetobutylicum ATCC 824		1		1	
1975	272564	Desulfitobacterium hafniense DCB-2		3		3	
1976	272620	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	28		28		
		Legionella pneumophila subsp. pneumophila str.					
1978	272624	Philadelphia 1	1		1		
1979	272627	Magnetospirillum magnetotacticum MS-1		5		5	
1980	272631	Mycobacterium leprae TN		30		30	
1981	272634	Mycoplasma pneumoniae M129	9		9		
1982	272636	Adeno-associated virus		18		18	
1983	272831	Neisseria meningitidis FAM18	1		1		
1984	272843	Pasteurella multocida subsp. multocida str. Pm70		5		5	
1985	272943	Rhodobacter sphaerooides 2.4.1		1		1	
1986	272944	Rickettsia conorii str. Malish 7		5		5	
1987	272947	Rickettsia prowazekii str. Madrid E		8		8	
1988	272951	Rickettsia sibirica 246		27		27	
1989	273123	Yersinia pseudotuberculosis IP 32953		1		1	
1991	274828	Influenza A virus (A/duck/Fujian/13/2002(H5N1))		1		1	
1992	274829	Influenza A virus (A/duck/Fujian/17/2001(H5N1))		1		1	
1993	278137	Mycobacterium gilvum Spry1		53		53	
1994	279150	Classical swine fever virus 96TD	2		2		
		Influenza A virus (A/egret/Hong Kong/757.3/2002(H5N1))					
1995	279797			3		3	
1997	279889	Triticum spelta var. arduini		3		3	
1998	280240	Nocardiopsis baichengensis	1		1		
1999	280463	Emiliania huxleyi CCMP1516		1		1	
2000	281310	Haemophilus influenzae 86-028NP	13		13		
2001	281689	Desulfovomonas acetoxidans DSM 684		1		1	
2002	282124	Influenza A virus (A/mallard/Alberta/127/00(H3N8))		1		1	
2003	282458	Staphylococcus aureus subsp. aureus MRSA252	86		86		
2004	283166	Bartonella henselae str. Houston-1		1		1	
2005	283643	Cryptococcus neoformans var. neoformans B-3501A	1	3	1	3	
2006	284168	Influenza A virus (A/Ck/HK/2133.1/2003(H5N1))		1		1	
2007	284177	Influenza A virus (A/Ck/HK/YU22/2002(H5N1))		1		1	
2008	284190	Influenza A virus (A/Ck/Viet Nam/36/2004(H5N1))		1		1	
2009	284195	Influenza A virus (A/Ck/YN/115/2004(H5N1))		1		1	
2010	284202	Influenza A virus (A/Dk/ST/5048/2001(H3N8))	1		1		
2011	284218	Influenza A virus (A/Viet Nam/1203/2004(H5N1))	71	133	73	134	2 1
2012	284672	SARS coronavirus TJF		14		14	
2013	284813	Encephalitozoon cuniculi GB-M1		28		28	
2014	285006	Saccharomyces cerevisiae RM11-1a		2		2	
		Influenza A virus (A/red knot/Delaware/2561/1987(H10N5))					
2015	286239			1		1	
2016	286542	Soochong virus-2		1		1	
2017	286636	Streptococcus pyogenes MGAS10394		1		1	
2018	286783	Salmonella enterica subsp. enterica serovar Indiana		1		1	
2019	287752	Aurantimonas manganoxydans SI85-9A1		1		1	
2021	289338	Influenza B virus (B/Nanchang/12/98)		1		1	
2022	289365	Human parvovirus 4		3		3	
2024	290512	Prosthecochloris aestuarii DSM 271		1		1	
2025	291592	Influenza A virus (A/crow/Kyoto/53/2004(H5N1))	1		1		
2026	292039	Influenza A virus (A/chicken/HongKong/SF1/03(H9N2))	1		1		

		Influenza A virus					
2027	292045	(A/chicken/HongKong/YU427/03(H9N2))	1	1			
2028	292348	Canine calicivirus (strain 48)	2	2			
2029	292349	Feline calicivirus (strain Urbana)	1	1			
2030	292590	Influenza A virus (A/swine/Ontario/42729A/01(H3N3))	1	1			
2031	292633	Dragon grouper nervous necrosis virus	20	20			
2032	293054	Influenza A virus (A/turkey/Ontario/6213/66(H5N?))	1	1			
2033	293055	Influenza A virus (A/mallard/Ohio/556/1987(H5N9))	1	1			
2034	293090	Influenza A virus (A/Fujian/411/2002(H3N2))	1	1			
2035	293614	Rickettsia akari str. Hartford	1	1			
2036	294381	Entamoeba histolytica HM-1:IMSS	103	103			
2037	295027	Human herpesvirus 5 strain Merlin	2	3	2	3	
		Salmonella enterica subsp. enterica serovar Paratyphi A					
2038	295319	str. ATCC 9150		3		3	
2039	295358	Mycoplasma hyopneumoniae 232	21	21			
2040	298653	Frankia sp. EAN1pec	2	2			
2041	298713	Influenza A virus (A/chicken/Korea/SNU0091/00(H9N2))	1	1			
		Influenza A virus					
2042	298716	(A/chicken/Korea/SNU1035C/00(H9N2))	1	1			
2043	299386	Equine arteritis virus Bucyrus	2	2			
2044	299390	Influenza A virus (A/Viet Nam/HN/2004(H5N1))	6	6			
		Influenza A virus (A/chicken/Viet Nam/AG-					
2045	299730	010/2004(H5N1))	1	1			
2047	300015	Lactate dehydrogenase elevating virus C	1	1			
2048	300016	Lactate dehydrogenase elevating virus Plagemann	1	1			
2049	300021	Candida albicans var. stellatoidea	2	2			
2050	300180	Mopeia Lassa virus reassortant 29	4	4			
2051	300267	Shigella dysenteriae Sd197	5	5			
2052	300268	Shigella boydii Sb227	5	5			
2053	300269	Shigella sonnei Ss046	9	9			
2054	300559	PRRSV VR2332	21	21	7		7
2055	X 300563	PRRSV HB-1(sh)/2002		1		1	
2056	300748	Influenza A virus (A/swine/Korea/S190/2004(H9N2))	3	3			
2057	300749	Influenza A virus (A/swine/Korea/S452/2004(H9N2))	1	1			
2058	300750	Influenza A virus (A/chicken/Korea/S1/2003(H9N2))	1	1			
2059	300852	Thermus thermophilus HB8	1	1			
2060	301448	Streptococcus pyogenes serotype M3	1	1			
2061	301449	Streptococcus pyogenes serotype M5	56	57	56	57	
2062	301450	Streptococcus pyogenes serotype M6	9	7	9	7	
2063	301451	Streptococcus pyogenes serotype M18	1	1			
2064	301452	Streptococcus pyogenes serotype M49	1	1			
2065	301478	Murray valley encephalitis virus (strain MVE-1-51)	11	14	11	14	
2066	301964	CY1014 virus		1		1	
2067	302272	Sendai virus (strain Ohita)	1	1			
2068	303316	Influenza A virus (A/Hatay/2004/(H5N1))	3	3			
2069	304883	Influenza A virus (A/Belfast/53582/2004(H3N?))	2	2			
2070	304895	Catenulispora acidiphila	1	1			
2071	305674	Deerpox virus W-848-83	2	2			
2072	306061	Influenza A virus (A/swine/IDT/Bakum1832/2000(H1N2))	1	1			
2073	306254	Campylobacter coli RM2228	3	3			
2074	306263	Campylobacter lari RM2100	1	1			
2075	306264	Campylobacter upsaliensis RM3195	1	1			
2076	306537	Corynebacterium jeikeium K411	1	1			
2077	307044	West Nile virus strain 385-99	22	12	22	12	
2078	307819	Influenza A virus (A/Jiangsu/38/2004(H3N2))	1	1			
2079	308061	Hantavirus HPR/02-73	1	1			
2080	308159	Araucaria virus	6	6			
2081	310542	Chimpanzee adenovirus	2	2			
2082	311169	Influenza A virus (A/duck/Korea/S10/03(H3N2))	1	1			
2083	311339	Human herpesvirus 5 strain Toledo	9	9			
2084	311695	Influenza A virus (A/New York/124/2001(H3N2))	1	1			
2086	311775	Influenza A virus (A/New York/205/2001(H1N1))	12	12			
2087	313589	Janibacter sp. HTCC2649	1	1			
2088	313596	Robiginitalea biformata HTCC2501	1	1			
2089	313606	Microscilla marina ATCC 23134	1	1			
2090	313627	Bacillus sp. NRRL B-14911	2	2			
2091	314262	Roseobacter sp. MED193	1	1			

2092	314275	Alteromonas mediterranea		1	1	
2093	314278	Nitrococcus mobilis Nb-231		1	1	
2094	314283	Reinekea blandensis MED297		1	1	
2095	314285	Congregibacter litoralis KT71		1	1	
2096	314288	Vibrio alginolyticus 12G01		3	3	
2097	314291	Vibrio splendidus 12B01		2	2	
2098	314292	Photobacterium angustum S14		1	1	
2099	315277	Chlamydia trachomatis A/HAR-13	6	1	6	1
2100	315456	Rickettsia felis URRWXCal2		7	7	
2101	315730	Bacillus mycoides KBAB4		5	5	
2102	315749	Bacillus cytotoxicus NVH 391-98		3	3	
2103	316056	Rhodopseudomonas palustris BisB18		1	1	
2104	316068	Leadbetterella byssophila		1	1	
2105	316287	Ceratogyrus marshalli		1	1	
2106	316385	Escherichia coli str. K-12 substr. DH10B		3	3	
2107	316401	Escherichia coli ETEC H10407	64	31	64	31
2108	316407	Escherichia coli str. K-12 substr. W3110		1	1	
2109	317652	Influenza A virus (A/Hong Kong/2/68(H3N2))		4	4	
2110	317655	Sphingopyxis alaskensis RB2256		1	1	
2111	318586	Paracoccus denitrificans PD1222		2	2	
2112	319224	Shewanella putrefaciens CN-32		1	1	
2113	320306	Influenza A virus (A/crested eagle/Belgium/01/2004(H5N1))		2	2	
2114	320372	Burkholderia pseudomallei 1710b		4	4	
2115	320373	Burkholderia pseudomallei 668		10	10	
2116	320374	Burkholderia pseudomallei S13		2	2	
2117	320388	Burkholderia mallei SAVP1		29	29	
2118	320390	Burkholderia mallei GB8 horse 4		1	1	
2119	320483	Anaplasma marginale str. Florida	19	61	19	61
2120	X 320667	Trichosanthes dioica			1	1
2121	321314	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67		5	5	
2122	322053	Konjac mosaic virus	1	1		
2123	322564	Influenza A virus (A/tiger/Thailand/CU-T4/04(H5N1))		5	5	
2124	322566	Influenza A virus (A/tiger/Thailand/CU-T6/04(H5N1))		1	1	
2125	322710	Azotobacter vinelandii DJ		2	2	
2127	325240	Shewanella baltica OS155		2	2	
2128	327105	HIV-1 O_ANT70	1	1		
2129	327205	Influenza A virus (A/New York/348/2003(H1N1))		146	149	3
2130	327310	Influenza A virus (A/Kinmen/645/04(H3N2))		1	1	
2131	327311	Influenza A virus (A/Yilan/515/03(H3N2))		1	1	
2132	328670	Banana streak GF virus		4	4	
2133	328671	Banana streak OL virus		4	4	
2135	329389	Hepatitis C virus (isolate Glasgow)	3	4	3	4
2136	329593	Influenza A virus (A/chicken/Fujian/25/00(H9N2))		6	6	
2137	329854	Bacteroides intestinalis		1	1	
2138	330879	Aspergillus fumigatus Af293		18	18	
2139	331111	Escherichia coli O139:H28 str. E24377A		36	36	
2140	331112	Escherichia coli HS		14	14	
2141	331271	Burkholderia cenocepacia AU 1054		7	7	
2142	331272	Burkholderia cenocepacia HI2424		1	1	
2143	X 331635	Chlamydia pecorum E58			1	1
2144	331636	Chlamydia psittaci 6BC	1	1		
2145	331978	Burkholderia pseudomallei Pasteur 52237		1	1	
2146	332193	Vaccinia Virus Acambis 3000 MVA		20	20	
2148	332747	Influenza A virus (A/swine/Tennessee/25/1977(H1N1))	1	1		
2149	333278	H7N9 subtype	1	26	3	26
2150	333284	Hepatitis C virus (isolate Con1)	4	3	4	3
2151	333367	[Clostridium] asparagiforme		1	1	
2152	333668	Theileria parva strain Muguga	14	18	14	19
2153	333751	Human papillomavirus type 2		7		7
2154	333754	Alphapapillomavirus 10		4	4	
2155	333760	Human papillomavirus type 16	335	429	349	463
2156	333761	Human papillomavirus type 18	26	85	26	104
2157	333762	Human papillomavirus type 26		1		1
2158	333763	Human papillomavirus type 32	1	1	1	1

2159	333765	Human papillomavirus type 53		1	1	
2160	333849	Enterococcus faecium DO		1	1	
2161	333923	Human papillomavirus 5	1	1	1	
2162	334203	Mupapillomavirus 1	1	38	1	38
2163	334380	Orientia tsutsugamushi str. Ikeda		1	1	
2164	334426	Angiostrongylus costaricensis	1	1	1	1
2166	334590	Influenza A virus (A/Moscow/343/2003(H3N2))		1	1	
2167	334802	Burkholderia mallei FMH		1	1	
2168	334803	Burkholderia mallei JHU		2	2	
2169	335333	Influenza A virus (A/New York/384/2005(H3N2))		64	64	
2170	335337	Influenza A virus (A/New York/388/2005(H3N2))		14	14	
2171	335358	Influenza A virus (A/New York/232/2004(H3N2))		110	110	
2172	335812	Influenza B virus (B/Shanghai/361/2002)	1	1		
		Influenza A virus (A/black-headed				
2173	336092	goose/Qinghai/1/2005(H5N1))	2	2		
2174	336205	Influenza A virus (A/swine/Bakum/5/95(H1N1))		2	2	
2175	336207	Influenza A virus (A/swine/Bakum/1832/2000(H1N2))		3	3	
		Influenza A virus (A/Bar-headed				
2176	336238	Goose/Qinghai/61/05(H5N1))		8	8	
2177	336407	Rickettsia bellii RML369-C		7	7	
		Influenza A virus				
2178	336794	(A/equine/Massachusetts/213/2003(H3N8))		1	1	
2179	336800	Influenza A virus (A/equine/New York/1/1999(H3N8))		3	3	
2180	336982	Mycobacterium tuberculosis F11		24	24	
2181	337042	Alphapapillomavirus 7	9	11		2
2182	337043	Alphapapillomavirus 4		1	1	
2183	337052	Deltapapillomavirus 4	24	24		
2184	337090	Chlorobium chlorochromatii		1	1	
2185	338188	Bacteroides finegoldii		1	1	
2186	338966	Pelobacter propionicus DSM 2379		3	3	
2187	339670	Burkholderia ambifaria AMMD		4	4	
2188	339854	Bacillus thuringiensis serovar israelensis ATCC 35646		6	6	
2189	340177	Chlorobium chlorochromatii CaD3		1	1	
2190	340184	Escherichia coli B7A		5	5	
2191	340185	Escherichia coli E22		13	13	
2192	340186	Escherichia coli E110019		2	2	
2193	340197	Escherichia coli F11		12	12	
2195	341663	Aspergillus terreus NIH2624	2	2		
2196	341946	Woodchuck hepatitis virus 2	4	4		
2197	341980	Human herpesvirus 3 strain Oka vaccine	3	34	3	62
2198	342023	Streptococcus pyogenes serotype M12	3	1	3	1
2199	342137	Influenza A virus (A/chicken/CA/375TR/2002(H6N2))		1	1	
2200	342145	Influenza A virus (A/turkey/MN/735/79(H6N2))		2	2	
		Influenza A virus				
2201	342207	(A/shorebird/Delaware/141/2002(H9N9))		1	1	
		Influenza A virus				
2202	342210	(A/shorebird/Delaware/275/2001(H9N7))		1	1	
2203	342221	Influenza A virus (A/chicken/Korea/S4/2003(H9N2))		1	1	
		Influenza A virus (A/turkey/Canada-Ontario/NS-01839-				
2204	342396	1/05(H3))		1	1	
2205	342508	Influenza A virus (A/New York/444/2001(H1N1))		24	25	1
2207	342610	Pseudoalteromonas atlantica T6c		1	1	
2208	342613	Streptococcus agalactiae 18RS21	2	2		
2209	342614	Streptococcus agalactiae 515	1	1		
2210	342615	Streptococcus agalactiae H36B	1	1		
2211	342617	Streptococcus agalactiae CJB111	2	2		
2212	343462	Human adenovirus 11p	7	7		
2213	343463	Human adenovirus 11a	1	1		
		Influenza A virus (A/whooper				
2214	344598	swan/Mongolia/6/05(H5N1))		1	1	
2215	344601	Escherichia coli B171		25	25	
2216	344609	Shigella boydii CDC 3083-94		20	20	
2217	344610	Escherichia coli 53638		1	1	
2218	345072	Vibrio cholerae MO10		1	1	
2219	345073	Vibrio cholerae O395		4	4	
2220	345074	Vibrio cholerae RC385		2	2	
2221	345075	Vibrio cholerae V51		3	3	

2222	345076	Vibrio cholerae V52		32	32	
2223	347257	Mycoplasma agalactiae PG2	3	3		
2224	347495	Bacillus cereus F837/76		1	1	
2225	347515	Leishmania major strain Friedlin	29	38	29	38
2226	348776	Mycobacterium tuberculosis C		177	177	
2227	349101	Rhodobacter sphaeroides ATCC 17029		1	1	
2228	349163	Acidiphilum cryptum JF-5		1	1	
2229	349344	Bat SARS CoV Rp3/2004		1	1	
2230	349746	Yersinia pestis Angola		3	3	
2231	349747	Yersinia pseudotuberculosis IP 31758		9	9	
2232	349966	Yersinia frederiksenii ATCC 33641		2	2	
2233	349967	Yersinia molaris ATCC 43969		3	3	
2234	349968	Yersinia bercovieri ATCC 43970		5	5	
2235	350054	Mycobacterium gilvum PYR-GCK		64	64	
2236	350058	Mycobacterium vanbaalenii PYR-1		55	55	
2237	350702	Burkholderia cenocepacia PC184		1	1	
2238	350703	Pseudomonas aeruginosa 2192		2	2	
2239	350704	Pseudomonas aeruginosa C3719		2	2	
2240	351071	Newcastle disease virus AF2240	1		1	
2241	351073	Mammalian orthoreovirus		1	1	
2242	351277	Influenza A virus (A/Nanchang/0058/1994(H3N2))		1	1	
2243	351581	Francisella tularensis subsp. holarktica FSC200		1	1	
2244	351607	Acidothermus cellulolyticus 11B		2	2	
2245	351627	Caldicellulosiruptor saccharolyticus DSM 8903		1	1	
2246	351745	Shewanella sp. W3-18-1		1	1	
2247	351746	Pseudomonas putida F1		6	6	
2248	352034	Influenza A virus (A/duck/Potsdam/1402-6/1986(H5N2))	1		1	
2249	352348	Influenza A virus (A/chicken/Hong Kong/17/1977(H6N1))		1	1	
2250	352520	Influenza A virus (A/mallard/Alberta/35/1976(H1N1))		6	1	6
2251	352561	Influenza A virus (A/duck/Australia/341/1983(H15N8))		1		1
2252	352564	Influenza A virus (A/mallard/Astrakhan/263/1982(H14N5))		1	1	
2253	352764	Influenza A virus (A/mallard/Alberta/202/1996(H2N5))	1		1	
2254	352914	Plasmodium yoelii yoelii 17XNL	6	3	6	3
2255	352963	Influenza A virus (A/California/7/2004(H3N2))		1		1
2256	353152	Cryptosporidium parvum Iowa II		84		84
2257	353153	Trypanosoma cruzi strain CL Brener	2058	10	2058	10
2258	353154	Theileria annulata strain Ankara		4		4
2259	353253	Influenza A virus (A/duck/Novosibirsk/56/2005(H5N1))	6	2	6	2
2260	353466	Influenza A virus (A/Canterbury/236/2005(H3N2))		1		1
2261	354228	Influenza A virus (A/Gf/HK/SSP607/2003(H9N2))		1		1
2262	354235	Influenza A virus (A/Ck/HK/CSW161/2003(H9N2))		1		1
2263	354242	Campylobacter jejuni subsp. jejuni 81-176		4		4
2264	355315	Streptococcus agalactiae serogroup la		1	1	
2266	356114	Hepatitis C virus genotype 3	121	17	121	17
2267	356386	Hepatitis C virus (isolate India)		1		1
2268	356391	Hepatitis C virus (isolate 6a33)		11		11
2269	356410	Hepatitis C virus (isolate HC-G9)		2	1	2
2270	356411	Hepatitis C virus JFH-1		8	1	8
2271	356413	Hepatitis C virus (isolate BEBE1)			14	
2272	356415	Hepatitis C virus (isolate NZL1)	1	3	1	3
2273	356416	Hepatitis C virus (isolate HCV-K3a/650)			21	
2274	356417	Hepatitis C virus (isolate JK049)			6	
2275	356418	Hepatitis C virus ED43			1	
2276	356419	Hepatitis C virus (isolate EUH1480)			5	
2277	356421	Hepatitis C virus (isolate Th580)			7	
2278	356424	Hepatitis C virus (isolate VN004)			1	
2279	356426	Hepatitis C virus subtype 3a	12	105	12	105
2280	357205	Influenza A virus (A/chicken/Hong Kong/3123.1/2002(H5N1))			1	
2281	357208	Influenza A virus (A/Vietnam/CL26/2004(H5N1))			79	
2282	357210	Influenza A virus (A/Vietnam/CL100/2004(H5N1))	1		1	
2283	357244	Orientia tsutsugamushi str. Boryong		2	2	2
2284	357348	Burkholderia pseudomallei 1106a			2	
2285	357355	Hepatitis C virus (isolate Tr Kj)			3	
2286	358708	Shigella dysenteriae 1012			1	

2287	358709	Escherichia coli 101-1		5	5	
2288	358769	Classical swine fever virus - Alfort/187	70	70		
2289	358805	Classical swine fever virus - Alfort/Tuebingen	5	5		
2290	358812	Classical swine fever virus - C	2	2		
2291	359391	Brucella abortus 2308		31	31	
2292	359921	Influenza A virus (A/Australian shelduck/Western Australia/1756/1983(H1N2))	1	1		
2293	360095	Bartonella bacilliformis KC583		1	1	
2294	360102	Yersinia pestis Antiqua		36	36	
2295	360112	Campylobacter jejuni subsp. jejuni HB93-13		2	2	
2296	360115	Coxiella burnetii RSA 331		8	8	
2297	360116	Coxiella burnetii 'MSU Goat Q177'		7	7	
2298	360117	Coxiella burnetii Q321		14	14	
2299	360118	Burkholderia pseudomallei 406e		2	2	
2300	360549	Themiste hennahi	1	1		
2301	360910	Bordetella avium 197N		1	1	
2302	362242	Mycobacterium ulcerans Agy99		16	16	
2303	362651	Human immunodeficiency virus type 1 (isolate YU2)	15	21	16	21
2304	362663	Escherichia coli 536		65	65	
2305	363020	Avian leukosis virus HPRS103	1	1		
2306	364106	Escherichia coli UTI89		2	2	
2307	364132	Influenza A virus (A/New York/504/1998(H3N2))		1	1	
2308	365044	Polaromonas naphthalenivorans CJ2		2	2	
2310	365078	Influenza A virus (A/duck/Guangxi/1586/2004(H5N1))		1	1	
2311	365080	Influenza A virus (A/duck/Guangxi/1793/2004(H5N1))		1	1	
2312	365129	Influenza A virus (A/chicken/Vietnam/DT171/2004(H5N1))		1	1	
2314	366394	Sinorhizobium medicae WSM419		1	1	
2316	367120	Influenza A virus (A/Fort Monmouth/1/1947(H1N1))	1	1		
2317	367400	Neembucu hantavirus		5	5	
2318	367830	Staphylococcus aureus subsp. aureus USA300	1	1		
2319	368445	Crocodilepox virus		2	2	
2320	370127	Influenza A virus (A/Victoria/1968(H3N2))		1	1	
2321	370128	Influenza A virus (A/Northern Territory/60/1968(H3N2))		3	3	
2322	370354	Entamoeba dispar SAW760		19	19	
2323	370810	Influenza A virus (A/Anhui/1/2005(H5N1))	6	6		
2324	370811	Influenza A virus (A/Anhui/2/2005(H5N1))	1	1		
2325	370813	Influenza A virus (A/duck/IT/701/2005(H10N7))		1	1	
2326	370830	Hantaan virus Q32		4	4	
2327	371082	Influenza A virus (A/Taiwan/2/2006(H1N1))		7	7	
2328	371094	Chikungunya virus strain S27-African prototype	24	24		
2329	371214	Influenza A virus (A/chicken/Taiwan/0329/01(H6N1))	5	5		
2330	373098	Gambierdiscus toxicus	6	6		
2332	373153	Streptococcus pneumoniae D39		52	61	9
2333	373384	Shigella flexneri 5 str. 8401		23	23	
2334	373665	Yersinia pestis biovar Orientalis str. IP275		1	1	
2335	X 374405	Influenza C virus (C/Yamagata/15/2004)		2	2	
2336	374507	Human rotavirus G9 isolate F45	7	7		
2337	374927	Haemophilus influenzae 22.1-21		3	3	
2338	374928	Haemophilus influenzae PittAA		2	2	
2339	374931	Haemophilus influenzae PittGG		1	1	
2340	374932	Haemophilus influenzae PittHH	1	1		
2341	374933	Haemophilus influenzae PittII		3	3	
2342	375177	Haemophilus influenzae 3655		1	1	
2343	375432	Haemophilus influenzae R3021		2	2	
2344	375450	Yersinia pestis FV-1		2	2	
2345	376619	Francisella tularensis subsp. holarktica LVS	10	291	10	291
2346	376721	Influenza A virus (A/chicken/Kurgan/05/2005(H5N1))	1	1		
2347	377628	Yersinia pestis Nepal516		135	135	
2348	378131	Influenza A virus (A/Memphis/13/1978(H1N1))		1	1	
2349	378139	Influenza A virus (A/Memphis/1/1978(H1N1))		7	7	
2350	378809	Ravn virus - Ravn, Kenya, 1987	1	32	2	32
2351	378830	Lake Victoria marburgvirus - Angola2005	6	18	6	18
2353	380210	Influenza A virus (A/England/333/1980(H1N1))	1	1	1	1
2354	380213	Influenza A virus (A/Taiwan/1/1986(H1N1))		1	1	
2355	380217	Influenza A virus (A/swine/Hong Kong/4/1976(H3N2))		1	1	

2356	380282	Influenza A virus (A/Fort Monmouth/1/1947-mouse adapted(H1N1))		47		47	
2357	380284	Influenza A virus (A/England/268/1996(H7N7))	1	1	1	1	
2358	380285	Influenza A virus (A/turkey/Ireland/1378/1983(H5N8))		1		1	
2359	380299	Influenza A virus (A/turkey/Wisconsin/1968(H5N9))		1		1	
2360	380301	Influenza A virus (A/turkey/Ontario/7732/1966(H5N9))	5	8	5	8	
2361	380330	Influenza A virus (A/goose/Hong Kong/8/1976(H1N1))		2		2	
2362	380332	Influenza A virus (A/swine/Hong Kong/273/1994(H1N1))		1		1	
2363	380337	Influenza A virus (A/equine/Prague/1/1956(H7N7))		1		1	
2364	380339	Influenza A virus (A/equine/Tennessee/5/1986(H3N8))		1		1	
2365	380340	Influenza A virus (A/equine/London/1416/1973(H7N7))	1	1	1	1	
2366	380342	Influenza A virus (A/swine/Iowa/15/1930(H1N1))		1		1	
		Influenza A virus (A/ruddy turnstone/New Jersey/47/1985(H4N6))			2	2	
2367	380343						
2368	380346	Influenza A virus (A/Wisconsin/3523/1988(H1N1))	2		2		
2370	380836	Influenza A virus (A/chicken/Vietnam/5/2003(H5N1))		1		1	
2371	380842	Influenza A virus (A/duck/Vietnam/15/2003(H5N1))		3		3	
2372	380905	Influenza A virus (A/X-47(H3N2))		3	2	3	2
2373	380950	Influenza A virus (A/Beijing/32/1992(H3N2))			54		54
2374	380951	Influenza A virus (A/Hebei/19/1995(H3N2))	1		1		
2375	380960	Influenza A virus (A/Tokyo/3/1967(H2N2))	2		2		
2376	380964	Influenza A virus (A/Texas/36/1991(H1N1))			1		1
2377	380978	Influenza A virus (A/Wisconsin/4755/1994(H1N1))			5		5
2378	380979	Influenza A virus (A/Wisconsin/4754/1994(H1N1))			1		1
2379	X 380982	Influenza A virus (A/WSN(H1N1))				1	1
2380	X 380984	Influenza A virus (A/Leningrad/134/17/1957(H2N2))				2	2
2381	380985	Influenza A virus (A/Chile/1/1983(H1N1))			4		4
2382	381512	Influenza A virus (A/New Caledonia/20/1999(H1N1))	39	228	39	236	8
2383	381513	Influenza A virus (A/Panama/2007/1999(H3N2))	10	14	10	14	
2384	381516	Influenza A virus (A/USSR/90/1977(H1N1))	11		12		1
2385	381517	Influenza A virus (A/Udorn/307/1972(H3N2))			5		5
2386	381518	Influenza A virus (A/Wilson-Smith/1933(H1N1))	1	148	1	149	1
2387	381666	Cupriavidus necator H16			1		1
2388	382781	Influenza A virus (A/Singapore/1/1957(H2N2))	1	31	1	32	1
2389	382813	Influenza A virus (A/Japan/305+/1957(H2N2))	2		2		
2390	382825	Influenza A virus (A/Philippines/2/1982(H3N2))	1	1	1	1	
2391	382828	Influenza A virus (A/R/1/5-/1957(H2N2))			1		1
2392	382832	Influenza A virus (A/VM113-V1(H1N1))	1		1		
2393	382835	Influenza A virus (A/WSN/1933(H1N1))	6	3	7	3	1
2394	382842	Influenza A virus (A/swine/29/1937(H1N1))			2		2
2395	382848	Influenza A virus (A/swine/Hong Kong/126/1982(H3N2))			1		1
2396	383028	Influenza A virus (A/New York/687/1995(H3N2))	1		1		
2397	383121	Influenza A virus (A/Waikato/7/2000(H3N2))			2		2
2398	383152	Influenza A virus (A/Wellington/22/2001(H3N2))			1		1
2399	383231	Influenza A virus (A/Wellington/8/2004(H3N2))			2		2
2400	383281	Influenza A virus (A/Otago/5/2005(H1N1))			1		1
2401	383379	Toxoplasma gondii RH		27	23	27	23
2402	383531	Influenza A virus (A/swine/Italy/2/1979(H1N1))			4		4
2403	383537	Influenza A virus (A/swine/Iowa/1946(H1N1))			1		1
2404	383550	Influenza A virus (A/duck/England/1/1956(H1N6))			2		2
2406	383561	Influenza A virus (A/swine/Italy/1850/1977(H3N2))			1		1
2407	383566	Influenza A virus (A/swine/Italy/425/1976(H1N1))			1		1
2408	383568	Influenza A virus (A/Shanghai/11/1987(H3N2))			1		1
2409	383571	Influenza A virus (A/Memphis/6/1986(H3N2))	4		4	1	1
2410	383574	Influenza A virus (A/Memphis/2/1985(H3N2))	1		1		
2411	383577	Influenza A virus (A/Memphis/1/1990(H3N2))			1		1
2412	383578	Influenza A virus (A/Memphis/4/1980(H3N2))			1		1
2413	383586	Influenza A virus (A/Memphis/1/1971(H3N2))	19	11	19	11	
		Influenza A virus (A/Anas acuta/Primorje/695/1976(H2N3))			17		17
2415	383603	Influenza A virus (A/turkey/Minnesota/833/1980(H4N2))			1		1
2417	384483	Influenza A virus (A/swine/Hong Kong/127/1982(H3N2))			1		1
2418	384484	Influenza A virus (A/swine/Hong Kong/81/1978(H3N2))			12		12
2419	384487	Influenza A virus (A/Swine/Indiana/1726/1988(H1N1))			2		2
2420	384493	Influenza A virus (A/seal/Mass/1/1980(H7N7))	1	1	1	1	
2421	384495	Influenza A virus (A/Kiev/59/1979(H1N1))			5		5

2422	384498	Influenza A virus (A/Ann Arbor/6/1960(H2N2))		270		270	
2423	384499	Influenza A virus (A/gull/Maryland/704/1977(H13N6))		1		1	
2424	384500	Influenza A virus (A/Beijing/11/1956(H1N1))		30		30	
2426	384505	Influenza A virus (A/nt/60/1968(H3N2))		69		69	
2427	384509	Influenza A virus (A/tern/Australia/G70C/1975(H11N9))	9		9		
2428	384510	Influenza A virus (A/tern/South Africa/1961(H5N3))	1		1		
2429	384527	Influenza A virus (A/Cameron/1946(H1N1))		1		1	
2430	384676	Pseudomonas entomophila L48		1		1	
2431	384946	Influenza A virus (A/duck/Hungary/1/1970(H6N2))		1		1	
2432	385576	Influenza A virus (A/Alaska/6/1977(H3N2))		2		2	
2433	385580	Influenza A virus (A/duck/Ukraine/1/1963(H3N8))	3		3		
2434	385583	Influenza A virus (A/Denver/1957(H1N1))		2		2	
2435	385585	Influenza A virus (A/equine/Jilin/1/1989(H3N8))	1		1		
		Influenza A virus					
2436	385586	(A/chicken/Pennsylvania/1/1983(H5N2))		1		1	
2437	385587	Influenza A virus (A/budgerigar/Hokkaido/1/1977(H4N6))		10		10	
2438	385599	Influenza A virus (A/udorn/1972(H3N2))		1		1	
		Influenza A virus (A/Puerto					
2439	385600	Rico/8/1934(Cambridge)(H1N1))	1		1		
2440	385605	Influenza A virus (A/equine/Kentucky/2/1986(H3N8))		3		3	
2441	385616	Influenza A virus (A/ruddy turnstone/NJ/60/1985(N9))		1		1	
		Influenza A virus					
2442	385617	(A/chicken/Pennsylvania/1370/1983(H5N2))	1		1		
2443	385624	Influenza A virus (A/Port Chalmers/1/1973(H3N2))	7	1	7	1	
2444	385630	Influenza A virus (A/Bangkok/1/1979(H3N2))	1	7	1	7	
2445	385640	Influenza A virus (A/Memphis/102/1972(H3N2))		8		8	
2446	385644	Influenza A virus (A/swine/Ukkel/1/1984(H3N2))		1		1	
2447	386032	Reston ebolavirus - Reston (1989)		4		4	
2448	386033	Sudan ebolavirus - Uganda (2000)	1	6	1	6	
2449	386043	Listeria welshimeri serovar 6b str. SLCC5334		3		3	
2450	386056	Paraburkholderia ferrariae		1		1	
2451	386415	Clostridium novyi NT		2		2	
2452	386585	Escherichia coli O157:H7 str. Sakai		17		17	
2453	386656	Yersinia pestis Pestoides F		2		2	
2454	387093	Sulfurovum sp. NBC37-1		1		1	
2455	387139	Influenza A virus (A/Aichi/2/1968(H3N2))	10	11	10	11	
2456	387147	Influenza A virus (A/England/878/1969(H3N2))	1	2	1	2	
2457	387156	Influenza A virus (A/Harbin/1/1988(H1N2))		17		17	
2458	387161	Influenza A virus (A/Japan/305/1957(H2N2))	4	29	4	29	
2459	387191	Influenza A virus (A/camel/Mongolia/1982(H1N1))		8		8	
2460	387203	Influenza A virus (A/duck/Bavaria/2/1977(H1N1))		1		1	
2461	387207	Influenza A virus (A/duck/Hokkaido/8/1980(H3N8))		6		6	
2463	387213	Influenza A virus (A/equine/Alaska/1/1991(H3N8))		1		1	
2464	387223	Influenza A virus (A/equine/Miami/1963(H3N8))	5		5		
2465	387239	Influenza A virus (A/gull/Delaware/475/1986(H2N2))		1		1	
2466	387243	Influenza A virus (A/herring gull/DE/677/1988(H2N8))		1		1	
		Influenza A virus (A/bar-headed					
2467	388041	goose/Qinghai/1A/2005(H5N1))	1		1		
2468	388272	Pseudomonas aeruginosa PACS2		12		12	
2469	388634	Bombyx mandarina nuclear polyhedrosis virus		1		1	
2470	388799	HIV-1 group O	1		1		
2471	389259	Influenza A virus (A/Nagasaki/N03/2005(H3N2))		1		1	
2472	390236	Borrelia afzelii PKo	2		2		
2473	391646	Hepatitis B virus ayw3	1		1		
2474	391647	Hepatitis B virus ayw2		8		8	
2475	391650	Hepatitis B virus ayw4	1		1		
2476	391896	Rickettsia bellii OSU 85-389		3		3	
2477	392021	Rickettsia rickettsii str. 'Sheila Smith'		3	1	9	1 6
2478	392734	Terriglobus roseus		1		1	
2479	392809	Influenza A virus (A/Victoria/3/1975(H3N2))	45	9	45	9	
2480	392810	Influenza A virus (A/chicken/Rostock/8/1934(H7N1))	2	4	2	4	
2481	392811	Influenza A virus (A/Udorn/8/1972(H3N2))	1		1		
2482	393011	Francisella tularensis subsp. holarktica OSU18		6		6	
2483	393115	Francisella tularensis subsp. tularensis FSC198		85		85	
2484	393117	Listeria monocytogenes FSL J1-194		2		2	
2485	393124	Listeria monocytogenes FSL N3-165		2		2	
2486	393125	Listeria monocytogenes FSL R2-503		1		1	

2487	393126	Listeria monocytogenes FSL R2-561		1	1	
2488	393128	Listeria monocytogenes F6900		1	1	
2489	393130	Listeria monocytogenes J0161		6	6	
2490	393133	Listeria monocytogenes 10403S		4	4	
2491	393305	Yersinia enterocolitica subsp. enterocolitica 8081		16	16	
2493	393548	Influenza A virus (A/chicken/Tula/Russia/Oct-5/2005(H5N1))		1	1	
2494	393557	Influenza A virus (A/Leningrad/1954/1(H1N1))		8	8	
2495	393697	Influenza A virus (A/Liaoning/25/2000(H1N1))		1	1	
2496	393902	Influenza A virus (A/Wisconsin/67/2005(H3N2))	1	5	1	5
2497	395095	Mycobacterium tuberculosis str. Haarlem		127	127	
2498	395494	Gallionella capsiferriformans ES-2		1	1	
2499	395841	Influenza A virus (A/duck/Hokkaido/1130/01(H1N1))		1	1	
2500	395842	Influenza A virus (A/tern/Australia/1/04(H2N5))		1	1	
2501	397342	Horsepox virus		6	6	
2503	398031	Toxoplasma gondii type III		1	1	
2504	398812	TGEV virulent Purdue	4		4	
2506	399741	Serratia proteamaculans 568		1	1	
2507	400331	Influenza A virus (A/New South Wales/15/1999(H3N2))		1	1	
2508	400667	Acinetobacter baumannii ATCC 17978	10	13	10	13
2509	400788	Influenza A virus (A/Indonesia/5/2005(H5N1))	1	3	1	3
2510	400810	Influenza A virus (A/Indonesia/CDC594/2006(H5N1))	1		1	
2511	400828	Influenza A virus (A/Indonesia/CDC669/2006(H5N1))	4		5	1
2512	400830	Influenza A virus (A/Indonesia/CDC699/2006(H5N1))	2		2	
2514	401650	Listeria monocytogenes HPB2262		3	3	
2515	401671	HIV-1 M:B_89.6		1	1	
2516	402194	Influenza A virus (A/Istanbul/CTF/10/2004(H3N2))		1	1	
2517	402464	Influenza A virus (A/gray teal/Australia/2/1979(H4N4))		1	1	
2518	402489	Influenza A virus (A/turkey/Minnesota/1200/1980(H7N3))		1	1	
2519	402518	Influenza A virus (A/Canada/rv504/2004(H7N3))	1		1	
2520	402527	Influenza A virus (A/chicken/Scotland/1959(H5N1))		1	1	
2521	402938	Influenza A virus (A/Michigan/2/2003(H1N2))	1		1	
2522	404137	Influenza A virus (A/chicken/Beijing/nl/2002(H9N2))		1	1	
2524	404150	Influenza A virus (A/chicken/Hubei/wk/1997(H5N1))		2	2	
2526	404155	Influenza A virus (A/chicken/Hunan/fg/2004(H5N1))		2	2	
2527	404163	Influenza A virus (A/chicken/Jilin/hg/2002(H5N1))		1	1	
2528	404330	Streptococcus pyogenes serotype M2	2		2	
2529	404331	Streptococcus pyogenes serotype M4	2		2	
2530	404408	Influenza A virus (A/chicken/Shanxi/2/2006(H5N1))	1		1	
2531	404573	Influenza A virus (A/chicken/Netherlands/03010132/03(H7N7))	1		1	
2532	404974	Vibrio cholerae AM-19226		1	1	
2533	405050	Influenza A virus (A/tern/Australia/1402/2004(H2N5))		1	1	
2534	405531	Bacillus cereus G9842		3	3	
2535	405532	Bacillus cereus B4264		1	1	
2536	405533	Bacillus cereus AH1134		3	3	
2537	405536	Bacillus anthracis str. Tsiankovskii-I		1	1	
2538	405917	Bacillus cereus W		1	1	
2539	405955	Escherichia coli APEC O1		8	8	
2540	406269	West Nile virus strain PTRoxo		12	12	
2541	407134	Yellow fever virus strain Ghana/Asibi/1927		5	5	
2542	407141	Yellow fever virus isolate Ethiopia/Couma/1961		2	2	
2543	407148	Campylobacter jejuni subsp. jejuni 81116		14	14	
2544	407418	Influenza A virus (A/chicken/Guiyang/2147/2005(H5N1))		1	1	
2545	408599	Human rotavirus G9P[8]	1		1	
2546	408685	Dengue virus 1 Brazil/97-11/1997		1058	1058	
2547	408686	Dengue virus 4 Philippines/H241/1956	4	947	4	947
2548	408687	Dengue virus 4 Singapore/8976/1995		5	5	
2549	408688	Dengue virus 4 Thailand/0348/1991		15	15	
2550	408689	Dengue virus 4 Thailand/0476/1997		3	3	
2551	408690	Dengue virus 3 China/80-2/1980		84	84	
2552	408691	Dengue virus 3 Martinique/1243/1999		889	889	
2553	408692	Dengue virus 3 Sri Lanka/1266/2000		66	66	
2554	408693	Dengue virus 3 Singapore/8120/1995		69	69	
2555	408694	Dengue virus 2 Peru/IQT2913/1996		87	87	

2556	408870	Dengue virus 3 Philippines/H87/1956	8	13	8	13	
2557	408871	Dengue virus 4 Dominica/814669/1981	1	256	1	256	
2558	410069	Streptococcus pyogenes serotype M80	1		1		
2559	410072	Coprococcus comes	1		1		
2560	410078	Human respiratory syncytial virus S2	1		1		
		Mycobacterium tuberculosis variant bovis BCG str.					
2561	410289	Pasteur 1173P2	1	229	1	229	
2562	411157	Influenza A virus (A/Thailand/271/2005(H1N1))	1		1		
2563	411167	Influenza A virus (A/Queensland/11/2001(H3N2))		1		1	
2564	411662	Influenza A virus (A/Hanoi/TN405/2005(H3N2))		1		1	
2565	412022	Burkholderia mallei NCTC 10229		9		9	
2566	412419	Borrelia duttonii Ly	7		7		
2567	412420	Yersinia pestis CA88-4125		21		21	
2568	412614	Vibrio cholerae 2740-80		44		44	
2569	412694	Bacillus thuringiensis str. Al Hakam		8		8	
2570	412883	Vibrio cholerae MZO-3		1		1	
2571	412966	Vibrio cholerae 1587		3		3	
2572	412967	Vibrio cholerae MAK 757		9		9	
2573	413999	Clostridium botulinum A str. ATCC 3502		3		3	
2574	414044	Influenza A virus (A/Thailand/1(KAN-1A)/2004(H5N1))	1		1		
2575	415166	Influenza A virus(A/swine/Henan/2/2004(H9N2))		1		2	1
2576	415167	Influenza A virus(A/swine/Henan/3/2004(H9N2))		1		1	
2577	415169	Influenza A virus(A/swine/Henan/5/2004(H9N2))		1		1	
2578	415172	Influenza A virus(A/swine/Henan/8/2004(H9N2))		2		2	
2579	415176	Influenza A virus(A/swine/Shandong/fNY/2003(H9N2))		3		3	
2580	415177	Influenza A virus(A/swine/Shandong/fZC/2003(H9N2))		7		7	
2581	416035	Norovirus Hu/GII.4/DenHaag89/2006/NL	1		1		
2582	416276	Rickettsia massiliae MTU5		2		2	
2583	416674	Influenza B virus (B/Yamagata/16/1988)	4		4		
2584	416730	Influenza A virus (A/Memphis/10/1996(H1N1))		1		1	
2585	417398	Vibrio cholerae MZO-2		2		2	
2586	417399	Vibrio cholerae NCTC 8457		1		1	
2587	417400	Vibrio cholerae B33		5		5	
2588	417758	Influenza A virus (A/quail/Shantou/1475/2004(H9N2))	1		1		
2589	418136	Francisella tularensis subsp. tularensis WY96-3418		2		2	
		Influenza A virus (A/Egypt/14724-					
2590	418868	NAMRU3/2006(H5N1))		1		1	
2591	419109	Vibrio parahaemolyticus AQ3810		38		38	
2592	419947	Mycobacterium tuberculosis H37Ra		130		130	
2593	420174	Hepatitis C virus isolate HC-J4	1	143	1	160	17
2594	420245	Leishmania braziliensis MHOM/BR/75/M2904	14	8	14	8	
2595	420246	Geobacillus thermodenitrificans NG80-2	1		1		
2596	420521	Expression vector pNIC-NHT-CF	1		1		
2597	420662	Methylibium petroleiphilum PM1		1		1	
2598	421472	Influenza A virus (A/Indonesia/CDC1032N/2007(H5N1))	1		1		
2599	421877	Hepatitis C virus isolate HC-J1	3	26	3	26	
2600	421901	Influenza A virus (A/Egypt/0636-NAMRU3/2007(H5N1))	2	1	2	1	
		Salmonella enterica subsp. enterica serovar Newport					
2601	423368	str. SL254		1		1	
2602	424717	Shigella flexneri 3a	4		4		
2603	424718	Shigella flexneri 5a	2		2		
2604	424720	Shigella flexneri Y	8		8		
2605	425067	Burkholderia pseudomallei 305		2		2	
2606	425088	Tanganya virus		1		1	
2607	425551	Influenza A virus (A/AA/Huston/1945(H1N1))	1		1		
2608	425557	Influenza A virus (A/California/10/1978(H1N1))		1		1	
2609	426430	Staphylococcus aureus subsp. aureus str. Newman	2		7		5
2610	426738	Influenza A virus (A/swine/Miyagi/5/2003(H1N2))		2		2	
2611	427773	Influenza A virus (A/Thailand/SP83/2004(H5N1))	1		1		
2612	427826	Influenza B virus (B/Hong Kong/8/1973)		1		1	
2613	427890	Influenza A virus (A/Viet Nam/JP4207/2005(H5N1))	1		1		
2615	430066	Brucella abortus S19		15		15	
2616	430417	Influenza A virus (A/Wyoming/3e5/2003(H3))	1		1		
2617	430511	Juquitiba virus		2		2	
2618	430557	Francisella tularensis subsp. tularensis FSC033		27		27	
2619	431944	Magnetospirillum gryphiswaldense MSR-1		1		1	

2620	431947	Porphyromonas gingivalis ATCC 33277	1	4	20	4	19
2621	432070	Influenza A virus (A/Hong Kong/213/2003(H5N1))	1	4	1	4	
2622	432094	Influenza A virus (A/Wyoming/3/2003-X-147(H3N2))		1		1	
2623	432359	Toxoplasma gondii VEG	14		14		
2624	434922	Coxiella burnetii Dugway 5J108-111		8		8	
2625	434923	Coxiella burnetii CbuG_Q212		1		1	
2626	434924	Coxiella burnetii CbuK_Q154		1		1	
2627	435258	Leishmania infantum JPCM5	28	5	28	5	
2628	435359	Influenza A virus (A/chicken/Hebei/706/2005(H5N1))		2		2	
2629	436004	Influenza A virus (A/kunke/1/71(H3N2))		1		1	
2630	439235	Desulfatibacillum alkenivorans AK-01		1		1	
2631	439843	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633		1		1	
2632	439847	Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29		1		1	
2633	440534	Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701		1		1	
2634	441158	Burkholderia pseudomallei 9		1		1	
2635	441159	Burkholderia pseudomallei 91		2		2	
2636	441160	Burkholderia pseudomallei 14		1		1	
2637	441769	Bacillus coahuilensis m4-4		1		1	
2638	441771	Clostridium botulinum A str. Hall	44		44		
2639	441962	Influenza A virus (A/duck/Mongolia/47/2001(H7N1))		3		3	
2640	444178	Brucella ovis ATCC 25840		8		8	
2641	444185	Simian rotavirus A strain RRV	10	1	10	1	
2642	444186	Simian rotavirus A strain TUCH		5		5	
2643	444318	Influenza A virus (A/Texas/1/1977(H3N2))	1	15	1	15	
2644	444793	Influenza A virus (A/Auckland/590/2000(H1N1))		1		1	
2645	445335	Clostridium botulinum NCTC 2916		2		2	
2646	445338	Clostridium botulinum str. Iwanei E	6		6		
2647	X 445983	Borrelia burgdorferi 156a			1		1
2648	445985	Borrelia burgdorferi ZS7	2	45	3	45	1
2649	446023	Influenza A virus (A/Hong Kong/68(H3N2))	1		1		
2651	447095	Blastomyces dermatitidis ATCC 26199		1		1	
2652	447133	Influenza A virus (A/chicken/Japan/1925(H7N7))	1		1		
2653	447188	Influenza A virus (A/duck/Tasmania/277/2007(H7N2))	1		1		
2654	448058	Influenza A virus (A/swine/Guangdong/01/2005(H3N2))		1		1	
2655	449278	West Nile virus SPU116/89		1		1	
2656	449656	Influenza A virus (A/chicken/Taiwan/2838V/00(H6N1))	15		15		
2658	451707	Bacillus cereus NVH0597-99		7		7	
2659	451708	Bacillus cereus H3081.97		12		12	
2660	451709	Bacillus cereus 03BB108		8		8	
2661	451804	Aspergillus fumigatus A1163		13		13	
2662	452646	Neovison vison		1		1	
2663	452652	Kitasatospora setae KM-6054		1		1	
2664	452659	Rickettsia rickettsii str. Iowa		1		1	
2665	453057	Influenza A virus (A/Indonesia/CDC540/2006(H5N1))	1		1		
2666	453927	Juniperus formosana	1		1		
2668	458234	Francisella tularensis subsp. holarctica FTNF002-00		1		1	
2669	458678	Hantaanvirus CGRn93P8		2		2	
2670	461739	Influenza B virus (B/Florida/4/2006)	1		1		
2671	461772	Influenza A virus (A/Wisconsin/43/2006(H3N2))	1		1		
2672	462695	Influenza A virus (A/Hiroshima/52/2005(H3))	2		2		
2673	463722	Murine norovirus GV/CR6/2005/USA		1		1	
2674	464314	Influenza A virus (A/Anhui/T2/2006(H5N1))	1		1		
2675	464417	Influenza B virus (B/Malaysia/2506/2004)	1		1		
2676	464622	Influenza A virus (A/Solomon Islands/3/2006 (Egg passage)(H1N1))	1		1		
2677	464623	Influenza A virus (A/Solomon Islands/3/2006(H1N1))	9		12		3
2678	465541	Streptomyces sp. Mg1		1		1	
2679	467144	Modified Vaccinia Ankara virus		22		22	
2680	468968	Influenza A virus (A/Indonesia/560H/2006(H5N1))	1		1		
2681	470137	Brucella suis ATCC 23445	1	5	1	5	
2682	471223	Geobacillus sp. WCH70		2		2	
2683	471721	HIV-1 CRF01_AE	1		1		
2684	472511	Influenza A virus (A/Indonesia/TLL007/2006(H5N1))	1		1		
2685	475478	Influenza A virus (A/equine/New Market/1/1979(H3N8))	1		1		

2686	475493	Influenza A virus (A/equine/California/8560/2002(H3N8))		2		2	
2687	476294	Influenza A virus (A/Brisbane/10/2007(H3N2))	5	5			
2688	476303	Influenza A virus (A/California/04/2007(H1N1))		1		1	
2689	478005	Escherichia coli O157:H7 str. EC4486		1		1	
2690	478006	Escherichia coli O157:H7 str. EC4501		2		2	
2691	478008	Escherichia coli O157:H7 str. EC869		13		13	
2692	480019	Influenza A virus (A/Moscow/10/1999(H3N2))		2		2	
2693	480024	Influenza A virus (A/Wyoming/03/2003(H3N2))		8		8	
2694	481805	Escherichia coli ATCC 8739		1		1	
2695	482134	Hepatitis B virus adw/Japan/Nishioka/1983		1		1	
2696	482628	Campylobacter jejuni subsp. jejuni BH-01-0142		1		1	
2697	482957	Burkholderia lata		2		2	
2698	483179	Brucella canis ATCC 23365		9		9	
		Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044		1		1	
2699	484021	Torque teno virus VT416		3		3	
2700	486280	Bacillus anthracis str. A0193		3		3	
2701	486619	Bacillus anthracis str. A0465		5		5	
2702	486620	Bacillus anthracis str. A0442		1		1	
2703	486621	Bacillus anthracis str. A0389		5		5	
2704	486623	Bacillus anthracis str. A0488		91		91	
2705	486624	Torque teno virus Human/Ghana/GH1/1996		3		3	
2706	487067	Mycobacterium intracellulare ATCC 13950	1		1		
2707	487521	Influenza A virus (A/Iran/1/1957(H2N2))		1		1	
2708	488233	Influenza A virus (A/Korea/426/1968(H2N2))		2		2	
2709	488241	Norovirus GII.3		1		1	
2710	489455	Norovirus GII.4		1		1	
2711	489460	Hepatitis B virus ayw/China/Tibet127/2002		1		1	
2712	489466	Hepatitis B virus ayw/China/Tibet127/2002	10		10	11	11
2713	489469	Hepatitis B virus ayw/China/Tibet127/2002		1		1	
2714	489483	Hepatitis B virus ayw/China/Tibet127/2002		1	3	1	3
2715	489821	Norovirus GII.4	1	10	2	11	1
2716	489822	Norovirus Hu/Houston/TCH186/2002/US	2		2		
2717	490039	Norovirus GII.2		1		1	
2718	X 490041	Norovirus GII.3			1		1
2719	490133	Hepatitis B virus ayw/France/Tiollais/1979		4		4	
2720	493803	Merkel cell polyomavirus	2	2	2	2	
2721	496036	Influenza A virus (A/duck/Vietnam/37/2007(H5N1))		1		1	
2722	497976	Salmonella enterica subsp. enterica serovar Typhi str. E00-7866		1		1	
2723	497977	Salmonella enterica subsp. enterica serovar Typhi str. 404ty		1		1	
2724	499191	Influenza A virus (A/Hong Kong/CUHK13527/2003(H3N2))	1		1		
2725	499286	Vaccinia virus GLV-1h68		2		2	
2726	502057	Paracoccidioides brasiliensis Pb18		1	1	1	1
2727	502780	Aeromonas diversa		1		1	
2728	502790	Influenza B virus (B/Kobe/3/2004)		1		1	
2729	503386	Influenza B virus (B/Kobe/67/2005)		1		1	
2730	504660	Influenza B virus (B/Kobe/39/2005)		1		1	
2731	504662	Influenza B virus (B/Kobe/113/2005)		1		1	
2732	504664	Influenza B virus (B/Kobe/115/2005-T1)		1		1	
2733	504666	Influenza A virus (A/Cygnus olor/Czech Republic/10732/07(H5N1))		1		1	
2734	504697	Influenza A virus (A/Bras/59/2007(H1N1))		1		1	
2735	504904	Influenza A virus (A/Wellington/75/2006(H1N1))	26	13	26	13	
2736	504910	HIV-1 M:A		1		1	
2737	505184	HIV-1 M:B	9	1	9	1	
2738	505185	HIV-1 M:C	8	1	8	1	
2739	505186	HIV-1 M:D	10		10		
2740	505228	HIV-1 M:E	4		4		
2741	506282	Influenza A virus (A/unknown/New York/11646-5/2005(H7N2))		1		1	
2742	506350	Influenza A virus (A/Hong Kong/1/1968(H3N2))	18	2	18	3	1
2744	507601	Toxoplasma gondii GT1			205		205
2745	508767	Clostridium botulinum E3 str. Alaska E43		1		1	
2746	508771	Toxoplasma gondii ME49	21	88	21	89	1
2747	508775	Norovirus GII.9	1	1	1	1	

2748	509173	Acinetobacter baumannii AYE		1	1	1	
2750	510222	Influenza A virus (A/duck/Vietnam/NCVD-9/2007(H5N1))	1	31	1	31	
2751	511145	Escherichia coli str. K-12 substr. MG1655					
2752	511839	Influenza A virus (A/Turkey/England/N28/1973(H5N2))	1		1		
2753	514193	Influenza A virus (A/CHU/2-524/2005(H3N2))		2		2	
2754	515581	Influenza A virus (A/swine/Ohio/24366/2007(H1N1))		1		2	1
2756	515817	Amphioctopus fangtiao	1		1		
2757	518922	Influenza A virus (A/Beijing/262/1995(H1N1))	1		1		
2758	518968	Influenza A virus (A/X-31B(Puerto Rico/8/1934-Aichi/2/1968)(H3N2))	1		1		
2759	518987	Influenza B virus (B/Lee/1940)	5	3	5	3	
2761	520450	Brucella abortus bv. 2 str. 86/8/59		1		1	
2762	520464	Brucella melitensis bv. 1 str. Rev.1	1		1		
2763	520963	Norovirus GII.11	1		1		
2764	520964	Norovirus GII.18	1		1		
2765	521004	Haemophilus influenzae 6P18H1		1		1	
2766	521005	Haemophilus influenzae 7P49H1		1		1	
2767	521007	Borrelia burgdorferi N40	4	3	4	3	
2768	522740	Influenza A virus (A/swine/Hannover/1/1981(H1N1))		12		12	
2769	524364	Norovirus Hu/1968/US	3	1	3	1	
2770	525281	Escherichia coli 83972		3		3	
2771	525368	Mycobacterium parascrofulaceum ATCC BAA-614		35		35	
2772	525374	Staphylococcus epidermidis BCM-HMP0060		1		1	
2773	526974	Bacillus cereus BDRD-ST24		1		1	
2774	526977	Bacillus cereus ATCC 4342		1		1	
2776	527024	Bacillus thuringiensis serovar toochigiensis BGSC 4Y1		1		1	
2777	527026	Bacillus thuringiensis serovar sotto str. T04001		1		1	
2779	528354	Neisseria gonorrhoeae MS11	8		8		
2780	529058	Influenza A virus (A/Uruguay/716/2007(H3N2))	1		1		
2781	529507	Proteus mirabilis HI4320	1		1		
2782	533026	Influenza A virus (A/Turkey/Ohio/313053/2004(H3N2))	1	2	1	2	
2783	535026	Bacillus subtilis subsp. subtilis str. NCIB 3610		1		1	
2784	535852	Influenza A virus (A/California/06/2008(H1N1))		1		1	
2785	538555	Influenza A virus (A/swine/Korea/Hongsong2/2004(H1N2))		2		2	
2786	543153	Mycobacterium phage Predator		1		1	
2787	543824	Synechocystis aquatilis		2		2	
2788	546980	Norovirus Hu/GII-4/Saga1/2006/JP	1		1		
2789	548470	Staphylococcus aureus subsp. aureus MN8	11		11		
2790	549169	Pseudogulbenkiania ferrooxidans		1		1	
2791	552536	Listeria monocytogenes HCC23		2		2	
2792	553345	Influenza A virus (A/Aichi/72/2007(H3N2))	1		1		
2793	553583	Staphylococcus aureus A9635	1		1		
2794	554290	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601		3		3	
2795	557433	Lactobacillus reuteri JCM 1112	3		3		
2796	557599	Mycobacterium kansasii ATCC 12478	1		1		
2797	558177	Influenza A virus (A/mallard/Bavaria/10/2007(H5N1))		1		1	
2798	559292	Saccharomyces cerevisiae S288C	8		16	1	8 1
2799	560463	Influenza A virus (A/Taiwan/VGHYM0325-06/2002(H3N2))		1		1	
2802	562988	Influenza A virus (A/Egypt/2289-NAMRU3/2008(H5N1))	1		1		
2803	562992	Influenza A virus (A/Egypt/3300-NAMRU3/2008(H5N1))	1		1		
2804	563041	Helicobacter pylori G27	2		2		
2805	563773	Vibrio parahaemolyticus AN-5034		4		4	
2806	565995	Bundibugyo ebolavirus	7		14		7
2808	566466	gamma proteobacterium NOR5-3		1		1	
2809	567106	Campylobacter jejuni subsp. jejuni IA3902		1		1	
2810	568206	Bacillus anthracis str. CDC 684		3		3	
2811	568819	Listeria monocytogenes serotype 4b str. CLIP 80459		6		6	
2812	571800	Psychrobacter sp. G	1		1		
2813	572264	Bacillus cereus 03BB102		2		2	
2814	572307	Neospora caninum Liverpool		1		1	
2815	573797	Influenza A virus (A/England/654/2007(H1N1))		1		1	
2816	573977	Human bocavirus 2	4		4		
2817	574556	Anaplasma centrale str. Israel		2		2	
2818	575590	Bacteroidetes oral taxon 274 str. F0058	1		1		

2819	575591	Brucella abortus NCTC 8038		1	1	
2820	575788	Vibrio tasmaniensis LGP32		1	1	
2822	577543	Influenza A virus (A/Xinjiang/1/2006(H5N1))	4	4		
2823	578079	Influenza A virus (A/ferret/Maryland/P10-UMD/2008(H9N2))		1	1	
2824	X 580047	Chlamydia trachomatis A2497		1	1	
2825	585034	Escherichia coli IAI1	3	3		
2826	585544	Bacteroides sp. D22	1	1		
2827	587200	Variola virus human/India/Ind3/1967		4	4	
2828	587884	Influenza A virus (A/Sydney/5/1997(H3N2))	7	7		
2829	588533	Norovirus Hu/GII/GZ-1/2008/CHN	1	1		
2830	591020	Shigella flexneri 2002017		1	1	
2831	592021	Bacillus anthracis str. A0248		1	1	
2832	592313	Vibrio cholerae 12129(1)		1	1	
2833	598745	Giardia intestinalis ATCC 50581		7	7	
2834	604436	Influenza B virus (B/Brisbane/60/2008)	2	2		
2835	614035	Influenza A virus (A/swine/Belgium/1/1998(H1N1))	1	1		
2836	616922	Influenza A virus (A/chicken/Anhui/1/1998(H9N2))		1	1	
2837	617102	Yellow fever virus 17D/Tiantan	4	5	4	5
2838	619693	Prevotella sp. oral taxon 472 str. F0295	1	1		
2839	627442	SARS coronavirus P2	1	1		
2840	627611	Vibrio parahaemolyticus K5030		22	22	
2841	630277	Tarsius lariang		1	1	
2842	632134	Influenza A virus (A/chicken/Pakistan/UDL-01/2008(H9N2))	7	7		
2843	633557	Infectious bronchitis virus CK/CH/LHLJ/04V	1	1		
2844	X 634464	Chlamydia trachomatis Sweden2		1	1	
2845	637383	Helicobacter pylori NCTC 11639		2	8	6
2846	638313	Human bocavirus 3	6	6		
2847	641140	Brucella abortus str. 2308 A		1	1	
2848	641501	Influenza A virus (A/California/04/2009(H1N1))	65	103	74	127 9 24
2849	641809	Influenza A virus (A/California/07/2009(H1N1))	25	13	31	14 6 1
2850	641812	Influenza A virus (A/Texas/05/2009(H1N1))	1	1		
2851	642261	Influenza A virus (A/California/08/2009(H1N1))	8	8		
2852	642794	Influenza A virus (A/Auckland/1/2009(H1N1))		1	1	
2853	643212	Influenza A virus (A/Netherlands/602/2009(H1N1))	2	14	2	14
2854	643680	Saccharomyces cerevisiae EC1118		1	1	
2855	644289	Influenza A virus (A/Korea/01/2009(H1N1))	3	3		
2856	644788	Influenza A virus (A/Vietnam/1194/2004(H5N1))	13	4	14	9 1 5
2857	X 645463	Clostridioides difficile R20291		1	1	
2858	645724	Influenza A virus (A/Hong Kong/01/2009(H1N1))	3	3		
2859	X 645771	Influenza A virus (A/Catalonia/63/2009(H1N1))			1	1
2860	647096	Influenza A virus (A/Beijing/01/2009(H1N1))		24	27	3
2861	647514	Norovirus GI.1	1	1		
2862	647515	Norovirus GI.2	1	1		
2863	647516	Norovirus GI.3		1	1	
2864	647519	Norovirus GI.5	1	1		
2865	647521	Norovirus GI.7	1	1		
2866	647923	Influenza A virus (A/reassortant/NYMC X-179A(California/07/2009 x NYMC X-157)(H1N1))	7	16		9
2867	648194	Neisseria meningitidis serogroup Y	3	3		
2868	648856	Influenza A virus (A/Beijing/501/2009(H1N1))	1	1		
2869	650131	Equine rhinitis B virus 1 strain P1436/71	6	6		
2870	652616	Mycobacterium tuberculosis str. Erdman = ATCC 35801	15	19	15	19
2871	654811	Influenza A virus (A/Perth/16/2009(H3N2))	1	3		2
2872	655288	Influenza A virus (A/mallard/Quebec/10969/2006(H2N3))		1	1	
2873	X 655827	Metarhizium acridum CQMa 102			1	1
2874	655863	Grosmannia clavigera kw1407		1	1	
2875	657165	Influenza A virus (A/Hong Kong/213/03)	2	2	2	2
2876	658578	Influenza A virus (A/duck/Beijing/MG0617/2005(H9N2))		1	1	
2877	658655	Lachnospiraceae bacterium 1_4_56FAA		1	1	
2878	658858	Giardia lamblia P15		1	1	
2879	661367	Legionella longbeachae NSW150		1	1	
2881	667015	Bacteroides salanitronis DSM 18170		1	1	
2882	X 672161	Chlamydia trachomatis B/TZ1A828/OT		3	3	

2883	673446	Influenza A virus (A/reassortant/NYMC X-181(California/07/2009 x NYMC X-157)(H1N1))	1	1			
2884	679206	Escherichia coli MS 119-7	1	1			
2885	679716	Trypanosoma brucei gambiense DAL972	1	1			
2886	680689	Influenza A virus (A/England/AV877/1996(H7N7))	1	1			
2887	680690	Influenza A virus (A/Hong Kong/1074/1999(H9N2))	2	1	2	1	
2888	680692	Influenza A virus (A/Hong Kong/485/1997(H5N1))	1	1	1	1	
2889	680693	Influenza A virus (A/Netherlands/219/2003(H7N7))	1		1		
2890	680729	Influenza A virus (A/chicken/Italy/1067/1999(H7N1))	17		17		
		Influenza A virus (A/chicken/Mexico/37821-771/1996(H5N2))		1		1	
2891	680739	Influenza A virus (A/duck/Hong Kong/140/1998(H5N1))	1		1		
2892	680767	Influenza A virus (A/environment/Hong Kong/156/1997(H5N1))	1		1		
2893	680785	Influenza A virus (A/environment/Viet Nam/1203/2004(H5N1))	1		1		
2894	680789	Influenza A virus (A/goose/Hong Kong/437-6/1999(H5N1))	1		1		
2895	680799	Influenza A virus (A/goose/Hong Kong/739.2/2002(H5N1))	1		1		
2898	682728	Influenza A virus (A/Quebec/144147/2009(H1N1))	10		10		
2899	687340	Torque teno virus 1		3		3	
2900	687341	Torque teno virus 2		4		4	
2901	687342	Torque teno virus 3		4		4	
2902	687343	Torque teno virus 4		6		6	
2903	687345	Torque teno virus 6		2		2	
2904	687346	Torque teno virus 7		3		3	
2905	687347	Torque teno virus 8		6		6	
2906	687350	Torque teno virus 11		1		1	
2907	687353	Torque teno virus 14		5		5	
2908	687354	Torque teno virus 15		3		3	
2909	687355	Torque teno virus 16		4		4	
2910	687358	Torque teno virus 19		5		5	
2911	687359	Torque teno virus 20		2		2	
2912	687360	Torque teno virus 21		2		2	
2913	687362	Torque teno virus 23		2		2	
2914	687363	Torque teno virus 24		3		3	
2915	687364	Torque teno virus 25		3		3	
2916	687365	Torque teno virus 26		5		5	
2917	687366	Torque teno virus 27		5		5	
2918	687367	Torque teno virus 28		3		3	
2919	687368	Torque teno virus 29		4		4	
2920	687369	Torque teno mini virus 1		1		1	
2921	687371	Torque teno mini virus 3		2		2	
2922	687375	Torque teno mini virus 7		2		2	
2923	687376	Torque teno mini virus 8		2		2	
2924	687382	Torque teno tamarin virus		2		2	
2925	687383	Torque teno douroucouli virus		5		5	
2926	687384	Torque teno felis virus		1		1	
2927	687385	Torque teno canis virus		1		1	
2928	687386	Torque teno sus virus 1a	12	1	12	1	
2929	689403	Human bocavirus 1	8		8		
2932	694009	Severe acute respiratory syndrome-related coronavirus		1		1	
2933	696871	Vaccinia virus Western Reserve		4		4	
2934	697610	Influenza A virus (A/India/GWMH05/2009(H1N1))		1		1	
2935	703352	Brucella melitensis M5-90	5	26	5	26	
2936	714978	Human adenovirus 55	4		4		
2937	715091	Influenza A virus (A/Roma/ISS1941/2009(H1N1))		1		1	
2938	715494	Influenza A virus (A/Hong Kong/33982/2009(H9N2))		3		3	
2939	722438	Mycoplasma pneumoniae FH	3		3		
		Influenza A virus (A/slaty-backed gull/Japan/6KS0185/2006(H4N8))		1		1	
2940	742305	Tokudaia mueninki		1		1	
2941	742503	Sphingobacterium sp. 21		1		1	
2942	743722	Taylorella equigenitalis ATCC 35865	1		1		
2943	743973	Naegleria gruberi strain NEG-M	1		1		
2944	744533	Aspergillus fumigatus	126	86	126	86	

2946	747305	Norovirus GII.10	1	7	1	6
2947	754027	Treponema phagedenis F0421	1	1	1	
2948	754366	Influenza A virus (A/Ontario/309862/2009(H1N1))	1	1	1	
2949	754503	Mycoplasma hyopneumoniae 7422	1	1	1	
2950	759272	Chaetomium thermophilum var. thermophilum DSM 1495	1	1	1	
2951	761193	Runella slithyformis DSM 19594	1	1	1	
2952	761251	Influenza A virus (A/Mexico City/WR1704T/2009(H1N1))	1	1	1	
2953	762378	Influenza A virus (A/bar-headed goose/Qinghai/3/2005(H5N1))	1	1	1	
2955	763552	Mus musculus papillomavirus type 1	4	4	4	
2956	768646	Influenza A virus (A/chicken/Uchal/8293/2006(H9N2))	1	1	1	
2957	768647	Influenza A virus (A/chicken/Uchal/8286/2006(H9N2))	1	1	1	
2958	857099	Streptococcus mutans OMZ175	2	1	2	1
2959	857571	Moraxella catarrhalis O35E	3	27		24
2960	868597	Stenotrophomonas maltophilia JV3	1	1		
2961	870484	Nonlabens agnitus	1	1	1	
2962	871575	Ogataea parapolymorpha DL-1	1	1	1	
2963	875328	Mycolicibacter sinensis	10		10	
2965	885311	Entamoeba histolytica KU27	1	1	1	
2966	887118	Influenza A virus (A/Mexico/UASLP-012/2008(H3N2))	1	1	1	
2967	908203	Influenza A virus (A/Thailand/CU-H126/2009(H1N1))	1	1	1	
2968	909420	Neisseria meningitidis H44/76	1	2		1
2969	913028	Yersinia enterocolitica W22703	1	1	1	
2970	915014	Influenza A virus (A/swine/Heilongjiang/44/2009(H1N1))	1	1		
2971	928301	Fowlpox virus strain NVSL	3		3	
2972	928313	Tacaribe virus strain Franze-Fernandez	6		6	
2973	929439	Leishmania mexicana MHOM/GT/2001/U1103	1		1	
2974	932622	Influenza A virus (A/chicken/Huadong/4/2008(H5N1))	1	1		
2975	935198	Clostridium botulinum B str. Eklund 17B (NRP)	1	1	1	
2976	936115	Influenza A virus (A/Netherlands/18/1994(H3N2))	1	1	1	
2977	940614	Granulicella mallensis	1		1	
2978	947939	Influenza A virus (A/aquatic bird/Korea/w44/2005(H7N3))	1		1	
2979 X	981087	Leishmania donovani BPK282A1			9	9
2980	986174	Influenza A virus (A/swine/Korea/4382/2009(H1N2))	1	1	1	
2981	991335	Influenza A virus (A/swine/Hong Kong/71/2009(H1N1))	1		1	
2982	992121	Helicobacter pylori Hp M5	1	1		
2983	996581	Influenza A virus (A/chicken/Shanghai/Q0808-1/2008(H9N2))	1		1	
2984	1003835	Severe fever with thrombocytopenia virus	1	1	1	
2985	1004253	Cyberlindnera mrakii	1	1	1	1
2986	1005048	Collimonas fungivorans Ter331	2		2	
2987	1005962	Ogataea parapolymorpha	1		1	
2988	1006581	Mycoplasma gallisepticum S6	1	1		
2989	1009714	Pseudomonas aeruginosa PAK	7	3	7	3
2990	1016852	Banana streak CA virus	5		5	
2991	1016853	Banana streak IM virus	10		10	
2992	1016998	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7		11	11	
2993	1035514	Plasmodium vivax North Korean	1		1	
2994	1041522	Mycobacterium colombiense CECT 3035		20	20	
2995	1041990	Influenza A virus (A/Guangdong/15/2007(H3N2))	3		3	
2996	1045775	Paenibacillus catalpae	1		1	
2997 X	1050221	Chlamydia psittaci NJ1			10	10
2998	1053141	Recombinant Hepatitis C virus J6/JFH1-J6	2	2		
2999	1068705	Influenza A virus (A/swine/Guangdong/221/2009(H1N1))	1		1	
3000	1077587	Influenza B virus (B/Victoria/2/1987)	2	1	2	4
3001	1081253	Influenza A virus (A/Indiana/08/2011(H3N2))		6		6
3002	1082519	Influenza A virus (A/chicken/Taixing/10/2010(H9N2))	2		2	
3003	1086859	Influenza A virus (A/Bilthoven/4791/1981(H3N2))		3		3
3004	1091045	Cutibacterium acnes subsp. defendens ATCC 11828	5		5	
3005	1093545	Influenza A virus (A/shorebird/Delaware Bay/277/2000(H9N7))	1		1	
3006 X	1112253	Chlamydia psittaci 02DC14			1	1
3007 X	1112258	Chlamydia psittaci 02DC22			1	1
3008 X	1112262	Chlamydia psittaci 03DC29			1	1

3009	1117322	Glaesserella parasuis str. Nagasaki	1	1	1	
3010	1122279	Influenza A virus (A/equine/Guangxi/3/2011(H9N2))	1	1	1	
3011	1125722	Porphyromonas gingivalis W50	36	36		
3012	1126212	Macrophomina phaseolina MS6	1	1		
3013	1133363	Schmallenberg virus	6	6		
3014 X	1133968	Babesia microti strain RI		3	3	
3015	1144025	Influenza A virus (A/Shandong/9/1993(H3N2))	13	13		
3016	1146883	Blastococcus saxobsidens DD2	1	1		
3017	1156983	Norovirus Hu/GII.4/Minerva/CS1258/2006/USA	1	1		
3018	1163697	Influenza A virus (A/Oklahoma/309/2006(H3N2))	4	4	3	
3019	1169127	Clostridioides difficile genomovar ribotype_087	1	1		
		Influenza A virus				
3020	1171336	(A/swine/Nebraska/A01116984/2011(H3N2))		1	1	
3021	1172206	Neisseria meningitidis NMB	1	1		
3022	1176042	Influenza A virus (A/swine/Italy/1513-1/1998(H1N1))		1	1	
3023	1178016	Encephalitozoon romaleae SJ-2008		1	1	
3024	1182144	Norovirus Hu/GII.4/Minerva/2006/USA	2	2		
3025	1184252	Streptococcus suis S735	2	2		
3026	1186058	Trichosporon asahii var. asahii CBS 2479		1	1	
3027	1197131	Escherichia coli F576	1	1		
		Mycobacteroides abscessus subsp. massiliense str. GO				
3028	1198627	06		1	1	
3029	1198676	Streptococcus mutans GS-5		14	14	
3030	1207470	Streptococcus pyogenes M1 476	1	1		
3031	1209523	Toxoplasma gondii type II		2	2	
3032	1209525	Toxoplasma gondii type I		2	2	
3033	1214154	Streptococcus suis 2651	1	1		
3034	1214159	Streptococcus suis 13730	2	2		
3035	1214225	Acidocella sp. MX-AZ02	1	1		
3036	1218488	Torque teno sus virus k2	11	11		
3037	1219377	Human rhinovirus C3		52	52	
3038	1225860	Porcine torque teno virus 1	2	2		
3039 X	1229831	Chlamydia avium 10DC88		2	2	
3040	1235996	Human betacoronavirus 2c EMC/2012	7	7		
3041	1236978	Staphylococcus epidermidis JCM 2414	1	1		
3042	1239567	Mamastrovirus 3	2	2		
3043	1241973	Norovirus Hu/GII.4/Sydney/NSW0514/2012/AU	1	3	2	
3044	1263102	Prevotella copri CAG:164		1	1	
3045	1263720	Betacoronavirus England 1	5	9	4	
3046	1268303	Rhodococcus sp. AW25M09	1	1	1	
3047 X	1268360	Influenza A virus (A/Victoria/361/2011(H3N2))		4	4	
3048	1278073	Myxococcus stipitatus DSM 14675	1	1		
3049	1285600	Nile crocodilepox virus	2	2		
3050	1285902	Artificial vector pGEX-2T	1	1		
3051	1286616	Norovirus Hu/GII.3/693/425/2008/AU	6	6		
3052	1286635	Desulfotignum phosphitoxidans DSM 13687		1	1	
3053	1288825	Shigella flexneri 2b	2	2		
3054	1289562	Influenza A virus (A/swine/Spain/SF11131/2007(H1N1))		3	3	
		Influenza A virus (A/chicken/West Java/Sbg-29/2007(H5N1))				
3055	1310532		7	7		
3056	1318439	Influenza A virus (A/Washington/05/2011(H1N1))	1	1		
3057 X	1321009	Influenza A virus (A/Texas/50/2012(H3N2))		1	1	
3059	1331560	Influenza A virus (A/Singapore/H2011.447/2011(H3N2))	1	1		
3060	1332244	Influenza A virus (A/Shanghai/02/2013(H7N9))	7	9	2	
3061	1335626	Middle East respiratory syndrome-related coronavirus	4	12	6	12
3062	1337063	Puumala virus bank vole/CG1820/Russia/1984		1	1	
3063	1337393	Helicobacter pylori PZ5056	1	1		
		Influenza A virus (A/chicken/Hong Kong/TP38/2003(H9N2))				
3064	1342397		3	3		
3065	1342434	Influenza A virus (A/turkey/Minnesota/511/1978(H9N2))	1	1		
3066	1345266	HIV-1 M:CRF01_AE	1	1		
3067	1346336	Influenza A virus (A/Fort Monmouth/1-JY2/1947(H1N1))		1	1	
3068	1352357	Helicobacter pylori SouthAfrica50	1	1		
3069	1355477	Bradyrhizobium diazoeficiens		1	1	
3070	1380386	Mycobacterium sp. URHB0044		1	1	
3071	1389959	Mycobacterium tuberculosis variant bovis AN5	9	28	9	28
3072	1391655	Influenza A virus (A/Aichi/2-1/1968(H3N2))	1	1		

3074		1392869	Escherichia coli K1		1	1		
3075	X	1398154	<i>Sporothrix brasiliensis</i> 5110			4		4
3076		1399582	Duck Tembusu virus	3	7		4	
3077		1401444	Avian leukosis virus ev/J	5	5			
3078		1403335	Porphyromonas gingivalis 381	71	55	71	55	
3079		1403514	Influenza A virus (A/chicken/Jiangsu/x1/2004(H9N2))	7	7			
3080	X	1405296	<i>Chlamydia suis</i> MD56		1		1	
3081		1408475	Taylorella asinigenitalis ATCC 700933	1	1			
3082		1413188	Influenza A virus (A/Anhui/PA-1/2013(H7N9))	1	3	1	3	
3083		1416333	Trypanosoma cruzi Dm28c	2	2			
3084		1420840	Influenza A virus (A/Luxembourg/46/2009(H1N1))		1	1		
3085	X	1427371	<i>Chlamydia pecorum</i> VR629		5		5	
3086		1432555	Escherichia coli ISC7		1	1		
3087		1440122	Murid herpesvirus 68		2	2		
3088	X	1447813	Influenza A virus (A/Shanghai/5190T/2013(H7N9))			6		6
3089	X	1451093	Influenza A virus (A/chicken/Taiwan/67/2013(H6N1))			5		5
3090	X	1457141	<i>Chlamydia avium</i>		1	1		
3091	X	1457153	<i>Chlamydia gallinacea</i>		3	3		
3092		1458279	Staphylococcus aureus USA300-ISMMS1	1	1			
3093		1463841	Streptomyces sp. NRRL F-2580		1	1		
3094		1464048	<i>Micromonospora parva</i>		1	1		
3095		1470614	Influenza A virus (A/swine/Thailand/CU-S3673N/2012(H3N2))		1	1		
3096		1476909	Banana streak MY virus	39	39			
3097		1481964	Influenza A virus (A/Anhui/1-DEWH730/2013(H7N9))	1	35	1	35	
3098		1498499	<i>Legionella norlandica</i>		1	1		
3099		1507381	Influenza A virus (A/Minnesota/11/2010(H3N2))	10	11		1	
3102		1581419	Amblyomma sculptum	1	1			
3103	X	1634342	Norovirus Hu/GII/JP/2015/GII.P17_GII.17/Kawasaki308		1	1		
3104		1663864	Influenza A virus (A/Anhui/1-YK_RG134/2013(H7N9))		1	1		
3105		1663934	Influenza A virus (A/Anhui/1-YK_RG64/2013(H7N9))		2	2		
3106		1663996	Influenza A virus (A/Anhui/1-YK_RG01/2013(H7N9))	1	1			
3107		1665645	Norovirus GI/Hu/NL/2012/GI.6/Groningen		1	1		
3108		1671798	Human papillomavirus type 54		1	1		
3109		1727172	Influenza A virus (A/duck/Bavaria/1/1977(H1N1))		2	2		
3110		1835656	Rotavirus A RVA/Cow-tc/USA/B223/1983/G10P[11]	2	2			
3111	X	1891187	Zaire ebolavirus Makona			34	34	
3112		1891729	<i>Mesocricetus auratus</i> polyomavirus 1	11	11			
3113		1891730	<i>Mus musculus</i> polyomavirus 1	4	30	4	30	
3114		1891762	Human polyomavirus 1	3	52	3	52	
3115		1891767	<i>Macaca mulatta</i> polyomavirus 1	16	42	16	42	
3116		1898104	Bacteroidetes bacterium		1	1		
3117		1933300	Watermelon silver mottle tospovirus	3	3			
3118		1979160	Human rubulavirus 2	10		10		
3119		1979162	Mammalian rubulavirus 5	1	1	1	1	
3120		1979165	Mumps rubulavirus	3		3		
3121		1980442	Orthohantavirus		15		15	
3122		1980456	Andes orthohantavirus	2	77	2	77	
3123		1980459	Bayou orthohantavirus	1		1		
3124		1980463	Cano Delgadito orthohantavirus		1	1		
3125		1980467	Dobrava-Belgrade orthohantavirus		25		25	
3126		1980468	El Moro Canyon orthohantavirus		2	2		
3127		1980471	Hantaan orthohantavirus	2	52	2	60	8
3128		1980475	Khabarovsk orthohantavirus		1	1		
3129		1980476	Laguna Negra orthohantavirus		12		12	
3130		1980481	Montano orthohantavirus	3		3		
3131		1980485	Prospect Hill orthohantavirus	1	2	1	2	
3132		1980486	Puumala orthohantavirus		32	20	32	20
3133		1980489	Sangassou orthohantavirus		6		6	
3134		1980490	Seoul orthohantavirus		5		5	
3135		1980491	Sin Nombre orthohantavirus	1	35	1	35	
3136		1980494	Tula orthohantavirus	1	14	1	14	
3137		1980519	Crimean-Congo hemorrhagic fever orthonaïrovirus	20	2	82	18	62
3138			Zika virus ZIKV/H. sapiens/FrenchPolynesia/10087PF/2013			54		54
3139	X	2043570	Influenza A virus (A/chicken/Jiangsu/W1-8/2015(H7N9))		6		6	

3141	2116544	Synechococcus lacustris	1		1		
3142	2169971	Visna-maedi virus	5	7	5	7	
3143	2169986	Barley yellow dwarf virus PAV	1		1		
3144	2169991	Argentinian mammarenavirus	5	873	8	873	3
3145	2169992	Brazilian mammarenavirus		879		879	
3146	2169993	Cali mammarenavirus		11		11	
3147	2169994	Paraguayan mammarenavirus		1		1	
3148	2169996	Serra do Navio mammarenavirus		3		3	
3149	10000000	Mus musculus BALB/c		3		3	
3150	10000055	Mus musculus DBA/2	1		1		
3151	X	10000067 Mus musculus C57BL/6				6005	6005
3152	10000187	Sus scrofa Landrace X Large White	1		1		
3153	10000291	Bacillus anthracis str. Sterne 34F2	1		1		
3154	10000293	Clostridium botulinum A 1	1		1		
3155	10000294	Clostridium botulinum A 2	2		2		
3156	10000295	Clostridium botulinum B 111	2		2		
3157	10000296	Clostridium botulinum D 1873	2		2		
3158	10000297	Clostridium botulinum C 92-13	5		5		
3159	10000299	Clostridium botulinum E Beluga	2		2		
3160	10000301	Clostridium botulinum A str. Hall hyper	3		3		
3161	10000302	Clostridium botulinum A Kyoto-F	1		1		
3162	10000303	Clostridium botulinum B Lammann	1		1		
3163	10000304	Clostridium botulinum F NCTC 10281	1		1		
3164	10000305	Clostridium botulinum B Okra	3		3		
3165	10000306	Clostridium botulinum C Stockholm	2		2		
3166	10000307	Clostridium difficile BART'S W1	1		1		
3167	10000308	Listeria monocytogenes ATCC 35967		1		1	
3168	10000309	Listeria monocytogenes ATCC 43251		3		3	
3169	10000313	Mycobacterium avium serovar 1	1		1		
3170	10000314	Mycobacterium avium serovar 2	1		1		
3171	10000316	Mycobacterium avium serovar 25	1		1		
3172	10000317	Mycobacterium avium serovar 26	1		1		
3173	10000318	Mycobacterium avium serovar 4	2		2		
3174	10000319	Mycobacterium avium serovar 8	1	1	1	1	
3175	10000320	Mycobacterium avium serovar 9	1		1		
3176	10000323	Mycobacterium bovis T/91/1378		6		6	
3177	10000328	Mycobacterium avium subsp. paratuberculosis Strain Ben		1		1	
3178	10000329	Mycobacterium tuberculosis 103	1		1		
3179	10000331	Mycobacterium gastri W471	1		1		
3180	10000335	Candida albicans A-9 (serotype B)	1		1		
3181	10000337	Candida albicans KIT 1113	1		1		
3182	10000339	Candida albicans serotype A	1		1		
3183	10000341	Leishmania donovani donovani 1S2D	1		1		
3184	10000345	Leishmania infantum LEM 75	14		14		
3185	10000348	Trypanosoma cruzi G	1		1		
3186	10000351	Trypanosoma cruzi Y	1		1		
3187	10000352	Entamoeba histolytica YS-27	1		1		
3188	10000353	Toxoplasma gondii 76K	5	5	5	5	
3189	10000354	Toxoplasma gondii BK	1	1	1	1	
3190	10000355	Toxoplasma gondii Prugniaud		1		1	
3191	10000356	Plasmodium berghei NK65	2	2	2	2	
3192	10000357	Plasmodium chabaudi adami DS	2	37	2	37	
3193	10000358	Plasmodium falciparum 366		1		1	
3197	10000363	Plasmodium falciparum Brazil-608	1	1	1	1	
3198	10000366	Plasmodium falciparum FCB-2	1		1		
3199	10000369	Plasmodium falciparum FVO		5		5	
3200	10000370	Plasmodium falciparum GAM5		1		1	
3201	10000371	Plasmodium falciparum Indochina I/CDC	32		32		
3202	10000373	Plasmodium falciparum ItG2G1		1		1	
3203	10000375	Plasmodium falciparum RO71	1	1	1	1	
3204	10000376	Plasmodium falciparum UF-5	2		2		
3205	10000378	Plasmodium vivax NK		2		2	
3206	10000381	Plasmodium yoelii yoelii YM	1	5	1	5	
3207	10000382	Babesia bovis Mexico	1	4	1	4	
3208	10000383	Babesia bovis Mexico Mo7	1	33	1	33	

3209	10000385	Schistosoma mansoni Puerto Rico		20	7	20	7	
3210	10000386	Monkeypox virus USA_2003_039			1		1	
3211	10000388	Vaccinia virus NYCBH - Dryvax			29		29	
3212	10000390	Variola major virus India-1967			1		1	
3213	10000391	Equid herpesvirus 2 ER32		1		1		
3214	10000394	Human herpesvirus 1 103/65		1		1		
3215	10000396	Human herpesvirus 1 McIntyre			1		1	
3216	10000398	Human herpesvirus 1 NS		1		1		
3217	10000404	Bovine herpesvirus 1 Lam		1		1		
3218	10000405	Equid herpesvirus 4 TH20		2		2		
3219	10000406	Human herpesvirus 3 H-551		26	15	26	15	
3220	10000408	Human herpesvirus 5 TB40			1		1	
3221	10000411	Murid herpesvirus 1 deltaMS94.5			2		2	
3222	10000412	Murid herpesvirus 1 Isolate G4			1		1	
3223	10000413	Murid herpesvirus 1 Isolate K6			1		1	
3225	10000420	Human herpesvirus 4 BL74			1		1	
3226	10000421	Human herpesvirus 4 CKL			10		10	
3227	10000424	Human herpesvirus 4 GD1			1	4	1	4
3228	10000427	Human herpesvirus 4 type A			5		5	
3230	10000435	Hepatitis B virus genotype D			6		6	
3231	10000436	Hepatitis B virus subtype AY		7		7		
3232	10000437	Hepatitis B virus subtype AYR			1		1	
3233	10000438	Human parvovirus B19 genotype 1		1		1		
3234	10000439	Eastern equine encephalitis virus SV		8		8		
3235	10000440	Dengue virus type 1 Hawaii		29	22	29	22	
3236	10000442	Dengue virus type 3 CH53489			7		7	
3237	10000444	Japanese encephalitis virus CH2195LA		1		1		
3238	10000445	Japanese encephalitis virus JaOH0566		1		1		
3239	10000447	West Nile virus 3000.0259		2		2		
		Tick-borne encephalitis virus (WESTERN SUBTYPE) -						
3240	10000449	Neudoerfl		10		10		
3241	10000451	Classical swine fever virus Shimen		16		16		
3242	10000453	Hepatitis C virus subtype 1a (isolate Gla)		5		5		
3243	10000455	Hepatitis C virus subtype 1a 1/910			18		18	
3244	10000456	Hepatitis C virus subtype 1b AD78		71		71		
3245	10000457	Hepatitis C virus subtype 1a Chiron Corp.		1	1	1	1	
3247	10000460	Hepatitis C virus subtype 1b JK1		13		13		
3248	10000462	Measles virus CAM/RB			1		1	
3249	10000463	Phocine distemper virus 2558/Han 88		5		5		
3250	10000465	Rinderpest virus LATC		2		2		
3251	10000467	Rabies virus CVS		14		14		
3252	10000470	Rabies virus Flury LEP			1		1	
3253	10000471	Rabies virus RC-HL		4		4		
3254	10000472	Bovine ephemeral fever virus BB7721		2		2		
3255	10000474	Influenza A virus H3N2 (A/Resvir-9 (H3N2))			10		10	
3256	10000477	H1N1 subtype Influenza A virus (A/Netherlands/306/00 (H1N1))			1		1	
3257	10000482	Rift Valley fever virus ZH501		2		2		
3258	10000483	Puumala virus CG18-20		4		4		
3259	10000484	Puumala virus Kazan		26	7	26	7	
3260	10000485	Puumala virus (STRAIN HALLNAS B1) Vranica/Hallnas		4		4		
3261	10000487	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 4)		1		1		
3262	10000488	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 53b)			61		61	
3263	10000490	Lymphocytic choriomeningitis virus A22.2b		1		1		
3264	10000491	Lymphocytic choriomeningitis virus Docile		2		2		
3265	10000494	Lymphocytic choriomeningitis virus (strain WE) variant 8.7			1		1	
3266	10000495	Lymphocytic choriomeningitis virus (strain WE) CL1.2			1		1	
3267	10000496	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 3)			1		1	
3268	10000497	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 5)		1		1		
3269	10000499	Equine infectious anemia virus PV			2		2	
3270	10000500	Human immunodeficiency virus 1 IIIB		1	2	1	2	

3271	10000501	Simian immunodeficiency virus - mac - mac 239		474		474	
3272	10000502	Simian immunodeficiency virus - mac - mac 32H		9		9	
3273	10000503	Simian immunodeficiency virus - mac - mac BK28		4		4	
3274	10000504	Simian immunodeficiency virus - mac - mac F965		2		2	
3276	10000506	Simian immunodeficiency virus - sm - sm PT573		3		3	
3277	10000507	Rabbit hemorrhagic disease virus Olot/89 Foot-and-mouth disease virus (strain O1) (O1	1		1		
3278	10000513	Kaufbeuren)	43	8	43	8	
3279	10000514	Foot-and-mouth disease virus (strain O1) (O1BFS 1860)	9		9		
3280	10000515	Foot-and-mouth disease virus (strain O1) (O1BFS)	5		5		
3281	10000516	Foot-and-mouth disease virus (strain O1) (O1 Campos)	18	19	18	19	
3282	10000518	Borna disease virus Giessen strain He/80	6		6		
3283	10000519	Hepatitis E virus China Xinjiang	1		1		
3284	10000520	Hepatitis E virus SAR-55	2	6	2	6	
3285	10000523	Hepatitis delta virus TW2667		5		5	
3286	10000524	Equid herpesvirus 2 691	1		1		
3287	10000525	Equid herpesvirus 2 16V	1		1		
3288	10000526	Equid herpesvirus 2 5FN	1		1		
3289	10000527	Equid herpesvirus 2 FIN60	1		1		
3290	10000528	Porcine respiratory and reproductive syndrome virus BJ-4	1		1		
3291	10000529	Porcine respiratory and reproductive syndrome virus CH-1a	7	1	7	1	
3292	10000530	Borrelia garinii IP90	3		3		
3293	10000535	Human herpesvirus 6B HST	1		1		
3294	10000536	Murid herpesvirus 4 G2.4		3		3	
3295	10000537	Murid herpesvirus 4 WUMS		19		19	
3296	10000542	Streptococcus pyogenes serotype M3 D58	4		4		
3297	10000544	Sin Nombre virus NM H10	4		4		
3298	10000547	Human enterovirus 71 Subgenogroup B5	12		12		
3299	10000548	Human enterovirus 71 Subgenogroup C2	19		19		
3300	10000549	Human enterovirus 71 Subgenogroup C4	11		11		
3301	10000550	Influenza A virus H3N2 (A/Netherlands/9/03 (H3N2))		1		1	
3302	10000553	Andes virus CHI-7913	53		53		
3303	10000554	Salmonella enterica subsp. enterica serovar Minnesota R595	2		2		
3304	10000555	Plasmodium yoelii yoelii 265BY		1		1	
3305	10000556	Foot-and-mouth disease virus (strain O1) Kaufbeuren	43	12	44	12	1
3306	10000559	Chlamydophila abortus B-577	11		11		
3307	10000560	Norovirus genogroup 3 Bo/Jena/1980/DE	1		1		
3308	10000566	Paracoccidioides brasiliensis B339		8		8	
3309	10000567	Vibrio cholerae O1 serotype Inaba	1		1		
3310	10000568	Vibrio cholerae O1 serotype Ogawa	6		6		
3311	10000571	Cowpox virus (Brighton Red) White-pock		1		1	
3312	10000662	Rattus norvegicus Lewis		1		1	
3313	10000675	Borrelia burgdorferi CA12		6		6	
3314	10000679	Campylobacter jejuni subsp. jejuni 16971.94GSH (O:41)	2		2		
3315	10000718	Helicobacter pylori J223	2		2		
3316	10000720	Helicobacter pylori UA948	2		2		
3317	10000721	Helicobacter pylori UA955	1		1		
3318	10000723	Pseudomonas aeruginosa Immunotype 4	4		4		
3319	10000727	Escherichia coli 180/C3	1		1		
3320	10000728	Escherichia coli B/r CM6		1		1	
3321	10000733	Escherichia coli O5:K4:H4	1		1		
3322	10000734	Escherichia coli O65:K:-H-	1		1		
3323	10000738	Salmonella typhimurium PL5 (O9,12)	1		1		
3324	10000739	Salmonella typhi 620Ty	1		1		
3325	10000740	Salmonella typhi Ty21a		6		6	
3326	10000742	Salmonella typhimurium SH 4809	4		4		
3327	10000743	Salmonella typhimurium SL3261		4		4	
3328	10000748	Shigella dysenteriae serotype 1	3		3		
3329	10000749	Shigella dysenteriae serotype 1 114Sd	1		1		
3330	10000752	Shigella flexneri 5b	1		1		
3331	10000754	Shigella flexneri X	1		1		
3332	10000756	Yersinia pestis KIM 5	21		21		
3333	10000757	Yersinia pestis 195/P	5		5		
3334	10000759	Pasteurella multocida X-73	2		2		

3335	10000760	Anaplasma marginale South Idaho		2	2	
3336	10000761	Orientia tsutsugamushi Karp	1	1		
3337	10000763	Chlamydia trachomatis Serovar C	16	1	16	1
3338	10000764	Chlamydia trachomatis Serovar E	19	2	19	2
3339	10000765	Chlamydia trachomatis Serovar H	7		7	
3340	10000766	Chlamydia trachomatis Serovar I	10		10	
3341	10000767	Chlamydia trachomatis serovar K	14		14	
3342	10000768	Chlamydia trachomatis Serovar L2	15	12	15	12
3343	10000769	Chlamydia trachomatis Serovar L3	2		2	
3344	10000773	Streptococcus mutans MT 8148	40	12	40	12
3345	10000775	Streptococcus pyogenes 156	1		1	
3346	10000776	Streptococcus pyogenes 88/25	1		1	
3347	10000777	Streptococcus pyogenes 88/30	1		1	
3348	10000778	Streptococcus pyogenes 88/544	1		1	
3349	10000779	Streptococcus pyogenes 90/85	1		1	
3350	10000780	Streptococcus pyogenes serotype M12 A374	1		1	
3351	10000781	Streptococcus pyogenes BSA10	3		3	
3352	10000782	Streptococcus pyogenes NS1	1		1	
3353	10000783	Streptococcus pyogenes NS14	1		1	
3354	10000784	Streptococcus pyogenes NS27	1		1	
3355	10000785	Streptococcus pyogenes NS5	1		1	
3356	10000786	Streptococcus pyogenes serotype M11	2		2	
3357	10000787	Streptococcus pyogenes serotype M13	1		1	
3358	10000788	Streptococcus pyogenes serotype M22	1		1	
3359	10000789	Streptococcus pyogenes serotype M24	6	2	6	2
3360	10000790	Streptococcus pyogenes serotype M30	1		1	
3361	10000791	Streptococcus pyogenes serotype M41	1		1	
3362	10000792	Streptococcus pyogenes serotype M52	1		1	
3363	10000793	Streptococcus pyogenes serotype M54	1		1	
3364	10000794	Streptococcus pyogenes serotype M55	1		1	
3365	10000795	Streptococcus pyogenes serotype M57	1		1	
3366	10000796	Streptococcus pyogenes serotype M60	1		1	
3367	10000797	Streptococcus pyogenes serotype M75	1		1	
3368	10000798	Streptococcus pyogenes serotype M8	1		1	
3369	10000801	Foot-and-mouth disease virus - type O (O/SKR/2002)	1		1	
3370	10000802	Taenia crassiceps Strain ORF	3	3	3	3
3371	10000804	Chlamydia trachomatis Serovar B	47	5	47	5
3372	10000806	Foot-and-mouth disease virus (strain O1) (O1 Manisa)	5		5	
3373	10000807	Haemophilus influenzae NTHi UC19	2	2	2	2
3374	10000809	Swine vesicular disease virus ITL/1/66	1		1	
3375	10000814	Leptospira interrogans serovar Lai str. HY-1	1		1	
3376	10000815	Pseudomonas aeruginosa PAO	2	2	2	2
3377	10000816	Plasmodium falciparum T9/96	1	1	1	1
3378	10000817	Pseudomonas aeruginosa KB7	2		2	
3379	10000818	Pseudomonas aeruginosa P1	1		1	
		Foot-and-mouth disease virus (strain O1)				
3380	10000820	(O/Taiwan/1/97)	1		1	
3381	10000822	Pseudomonas aeruginosa Immunotype 3	1		1	
3382	10000824	Streptococcus pyogenes serotype M6 strain D471	4		4	
3383	10000825	Infectious bronchitis virus Avian strain D207	11		11	
3384	10000828	Ajellomyces dermatitidis ATCC 60636		2		2
3385	10000829	Norovirus genogroup 2 Mexico type strain 36	3		3	
3386	10000832	Norovirus genogroup 2 Camberwell 1890	1		1	
3387	10000833	Haemophilus influenzae NTHi 1128	6		6	
3388	10000835	Equine rhinitis A virus 393/76	4		4	
3389	10000836	Foot-and-mouth disease virus C1 CS8	22	24	22	24
3390	10000840	Foot-and-mouth disease virus C1 Brescia It/64	2		2	
3391	10000842	Swine vesicular disease virus NET/1/92	1		1	
3392	10000843	Neisseria meningitidis serogroup B H44/76	74	22	74	22
3393	10000845	Chlamydia trachomatis Serovar F	3		3	
3394	10000848	Theileria sergenti Type B1		1		1
3395	10000849	Theileria sergenti Type B2		2		2
3396	10000850	Theileria sergenti Type C		5		5
3397	10000851	Theileria sergenti Type I		1		1
3398	10000852	Chlamydophila pneumoniae Kajaani 6		7		7
3399	10000853	Chlamydia trachomatis Serovar L1	21	3	21	3

3400	10000855	Theiler's murine encephalomyelitis virus (strain BeAn 8386) (variant M2)		1		1	
3401	10000856	Foot-and-mouth disease virus - type O isolate O/UKG/35/2001		14		14	
3403	10000858	Chlamydia trachomatis B/Jali-20/OT	2		2		
3404	10000859	Porcine respiratory and reproductive syndrome virus JA142	1		1		
3405	10000860	Haemophilus influenzae Serotype B	18	9	18	9	
3406	10000861	Haemophilus influenzae Variant d1	18		18		
3407	10000862	Plasmodium vivax VK247	1		1		
3408	10000863	Neisseria gonorrhoeae 4505	1		1		
3409	10000864	Porcine respiratory and reproductive syndrome virus MD-001	2		2		
3410	10000865	Influenza A virus H3N2 (A/Kiev/301/94)	3		3		
3411	10000888	Porcine respiratory and reproductive syndrome virus Olot/91	3	5	3	5	
3412	10000890	Porcine respiratory and reproductive syndrome virus SD92-23983		33		33	
3413	10000960	Human respiratory syncytial virus A Mon/3/88	6		6		
3414	10000961	Dengue virus type 1 strain 16007	15		15		
3415	10000964	Foot-and-mouth disease virus (strain O1) (O1 Brugge)	2		2		
3416	10000965	Dengue virus type 1 FGA/89	4		4		
3417	10000968	Hepatitis C virus subtype 1b isolate BE-11	3		3		
3418	10000969	Porcine respiratory and reproductive syndrome virus 111/92	9		9		
3419	10000971	West Nile virus NY-99	15	21	15	21	
3420	10000972	Neisseria meningitidis serogroup B Strain B16.B6	1		1		
3421	10000979	Neisseria meningitidis serogroup B Strain 8047	4		4		
3422	10000980	Arcanobacterium pyogenes Strain 42	4		4		
3423	10000986	Foot-and-mouth disease virus C1 CS30	1		1		
3424	10000987	Human rhinovirus 2 Vienna	5		5		
3425	10000989	Foot-and-mouth disease virus - type A (strain A22)	8	6	8	6	
3426	10000991	Foot-and-mouth disease virus - type A (strain A22 Iraq)	5	1	5	1	
3427	10000992	Foot-and-mouth disease virus - type SAT 1 (Strain Bot 1/68)		1		1	
3428	10000993	Foot-and-mouth disease virus - type SAT 2 (Strain Ken 3/57)		1		1	
3429	10000994	Foot-and-mouth disease virus - type SAT 3 (Strain Bec 1/65)		1		1	
3430	10000995	Foot-and-mouth disease virus - type Asia 1 Pakistan		1		1	
3431	10001000	Foot-and-mouth disease virus - type SAT 2 (strain Rho 1/48)		4		4	
3432	10001002	Swine vesicular disease virus SPA/1/93	16		16		
3433	10001003	Neisseria meningitidis serogroup B CU385	2		2		
3434	10001004	Human T-cell lymphotropic virus type 1 (Caribbean isolate) (Strain HS35)		1		1	
3435	10001006	Proteus mirabilis CFT322		1		1	
3436	10001008	Chlamydia trachomatis Serovar J		6		6	
3437	10001019	Mus musculus B10.D2			1		1
3438	10001020	Peste-des-petits-ruminants virus (strain Nigeria 75/1)			1		1
3439	10001021	Treponema pallidum subsp. pallidum (strain Chicago)	19		19		
3440	10001025	Classical swine fever virus Glentorf		26		26	
3441	10001027	Vaccinia virus Connaught	1		1		
3442	10001028	Human poliovirus 2 (strain MEF-1)	1		1		
3443	10001032	Newcastle disease virus (strain La Sota)	1		1		
3444	10001039	Foot-and-mouth disease virus C3 (strain Resendne-Br/55)		1		1	
3445	10001040	Human poliovirus 2 (strain Sabin)	2	7	2	7	
3446	10001042	Haemophilus influenzae NTHi 1479	12	4	12	4	
3447	10001044	Neisseria meningitidis serogroup C MC51	1		1		
3448	10001047	West Nile virus strain 2741	32		32		
3449	10001049	Neisseria meningitidis serogroup B Strain S3446	1		1		
3450	10001050	Neisseria meningitidis serogroup B Strain 7967	1		1		
3451	10001051	Neisseria meningitidis serogroup A Strain 8659	1		1		
3452	10001053	Haemophilus influenzae MinnA	9		9		
3453	10001055	Haemophilus influenzae 6U	2		2		
3454	10001056	Haemophilus influenzae ATCC 9795		2		2	

3455	10001057	Pseudomonas aeruginosa CD4	1	1		
3456	10001058	Pseudomonas aeruginosa K122-4	1	1		
3457	10001077	Neisseria gonorrhoeae SU89	1	1		
3458	10001078	Neisseria gonorrhoeae SU96	3	3		
3459	10001081	Porphyromonas gingivalis HG66	2	2		
3460	10001085	Chlamydia trachomatis Serovar D	3	3		
3461	10001091	Borrelia burgdorferi BEP4	1	1		
3462	10001097	Sus scrofa Yorkshire	1	1		
3463	10001100	Plum pox virus (strain W)	6	6		
		Foot-and-mouth disease virus (strain O1)				
3464	10001102	O/UKG/11/2001	1	1	1	1
3465	10001116	Norovirus genogroup 1 isolates 96-908	4	4		
		Foot-and-mouth disease virus - type O (strain HKN/14/82)				
3466	10001118	HKN/14/82)	2	2		
3467	10001120	Cryptococcus neoformans var. neoformans Serotype D	1	1		
3468	10001121	Chlamydia trachomatis Serovar Da	1	1		
3469	10001130	Feline leukemia virus subtype A	2	2		
3470	10001132	Cryptococcus neoformans var. neoformans Serotype A	1	1		
3471	10001133	Rattus norvegicus DA		3	3	
3472	10001138	Newcastle disease virus (strain Eaves)	1	1		
3473	10001140	Newcastle disease virus (strain WA2116)	1	1		
3474	10001141	Chlamydia trachomatis Serovar A	22	8	22	8
3475	10001145	Escherichia coli 1471	2	2		
3476	10001149	Haemophilus influenzae Subtype 1H	23	23		
3477	10001150	Haemophilus influenzae Strain Eagan	58	58		
3478	10001154	Transmissible gastroenteritis virus MAD88	8	1	8	1
3479	10001155	Haemophilus influenzae strain 1479	2	2		
3480	10001156	Hepatitis B virus subtype AD	3	2	3	2
3481	10001157	H3N2 subtype Influenza A virus (A/Hong Kong(H3N2))		15	15	
3482	10001161	Neisseria meningitidis serogroup B Strain 2996	1	1		
3483	10001162	Neisseria meningitidis serogroup B Strain M1239	2	4		2
3484	10001207	Murine leukemia virus LP-BM5		1	1	
3485	10001209	Tobacco mosaic virus (strain PM5)	1	1		
3486	10001210	Tobacco mosaic virus (strain Ni568)	1	1		
3487	10001213	Human coxsackievirus B3 (strain RK)	1	1		
3488	10001215	Human rotavirus G9 WI61	1	1		
3489	10001216	Rotavirus G3 strain RV-3	1	1		
3490	10001223	Porphyromonas gingivalis OMZ 409		23	23	
3491	10001225	H1N1 subtype Influenza A/Oklahoma/7485/01		5	5	
3492	10001238	Puumala virus (strain Umea/hu)	1	1		
3493	10001239	Porcine circovirus strain ISU31	7	7		
3494	10001243	Theileria parva strain Marikebuni		1	1	
3495	10001307	Small ruminant lentivirus strain It-561	1	1		
3496	10001308	Small ruminant lentivirus strain It-Pi1	1	1		
		H1N1 swine influenza virus				
3497	10001315	(A/swine/Korea/S10/2004(H1N1))		3	3	
		H1N1 swine influenza virus				
3498	10001316	(A/swine/Korea/S175/2004(H1N1))		1	1	
		H9N2 subtype Influenza A virus				
3499	10001317	(A/swine/Korea/S81/2004(H9N2))		1	1	
		H9N2 subtype Influenza A virus				
3500	10001318	(A/swine/Korea/S83/2004(H9N2))		2	2	
3501	10001335	Japanese encephalitis virus Vellore P20778	1	1	1	1
3502	10001392	Human adenovirus B strain Harbin04B	5		5	
3503	10001396	Murine cytomegalovirus (strain Smith) MW97.01		5	5	
3504	10001412	Rattus norvegicus Wistar-Furth		11	11	
3505	10001424	Brucella abortus W99	1	1		
3506	10001431	Infectious bronchitis virus CK/CH/LDL/97I	1	1		
3507	10001439	Streptococcus sanguinis strain BD113-20		6	6	
3508	10001456	Human respiratory syncytial virus A strain RGH	1	1		
3509	10001459	Babesia bovis Argentina R1A	4	4		
3510	10001484	Norovirus genogroup 1 GI.12	1	1		
3511	10001485	Norovirus genogroup 3 GII.1	1	1		
3512	10001489	Proteus vulgaris Strain 5/43	1	1		
3513	10001490	Proteus mirabilis O24	1	1		
3514	10001491	Proteus mirabilis O29	1	1		

		Salmonella enterica subsp. enterica serovar Enteritidis					
3515	10001492	SH1262	3	3			
3517	10001498	Proteus mirabilis O23	1	1			
3518	10001499	Proteus mirabilis O6	1	1			
3519	10001500	Proteus mirabilis O43	1	1			
3520	10001501	Proteus penneri ATCC 33519	1	1			
3521	10001502	Escherichia coli J-5	1	1			
3522	10001503	Acinetobacter Iwoffii F78	1	1			
3523	10001504	Yokenella regensburgei PCM 2476	1	1			
3524	10001505	Yokenella regensburgei PCM 2477	1	1			
3525	10001511	Salmonella 'group A'	2	2			
3526	10001514	Providencia stuartii O33	1	1			
3527	10001519	Pseudomonas aeruginosa serotype O11	1	1			
3528	10001520	Haemophilus influenzae strain RM7004	1	1			
3529	10001523	Haemophilus influenzae strain I-69 Rd-/b+	4	4			
3530	10001524	Neisseria meningitidis strain 3006	1	1			
3531	10001526	Salmonella thompson C1 strain IS40	1	1			
3532	10001528	Escherichia coli F515	1	1			
3533	10001530	Acinetobacter haemolyticus strain 57	1	1			
3534	10001531	Acinetobacter haemolyticus strain 61	1	1			
3535	10001556	Moraxella catarrhalis 26404	1	1			
3536	10001558	Neisseria gonorrhoeae 15253	1	1			
3537	10001560	Neisseria meningitidis M982B	2	2			
3538	10001569	Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 11	1	1			
		Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 77	1	1			
3539	10001570	Anatid herpesvirus 1 Clone-03	1	1			
3540	10001573	Classical swine fever virus LPC/AHRI	4	4			
3541	10001581	Proteus penneri 8 (O67)	1	1			
3542	10001582	Dengue virus 1 Mochizuki	4	4			
3543	10001583	Dengue virus 2 New Guinea C	1	4	1	4	
3544	10001586	Porcine reproductive and respiratory syndrome virus 07V063	3	3			
3545	10001587	Porcine reproductive and respiratory syndrome virus 08V204	2	2			
3546	10001588	Providencia stuartii O4	1	1			
		Norovirus genogroup 2 Hu/NoV/Farmington Hills/2002/USA	1	2	1	2	
3549	10001606	Junin virus strain MC2	1	1			
3550	10001614	Machupo virus strain Carvallo	1	1			
3551	10001615	Guanarito virus strain INH-95551	1	1			
3552	10001616	Whitewater Arroyo virus strain AV9310135	1	1			
3553	10001617	Pichinde virus strain Munchique	1	1			
3554	10001618	Dengue virus 3 strain 16652	16	16			
3555	10001624	Feline infectious peritonitis virus (strain KU-2)	22	43	22	43	
3556	X 10001627	Human herpesvirus 5 (strain RV798)			6		6
		Aggregatibacter actinomycetemcomitans serotype b str.					
3558	10001628	Y4	1	1			
3559	10001633	Escherichia coli 055:B5	3	3			
3560	10001635	Dengue virus 2 PL046		7		7	
3561	10001636	Dengue virus 2 S221		42		42	
3562	10001638	Streptococcus pneumoniae type 27	2	2			
3563	10001641	Streptococcus dysgalactiae subsp. equisimilis D181	1	1			
		Foot-and-mouth disease virus - type O					
3564	10001642	Wuppertal/FRG/82		1		1	
3565	10001644	Streptococcus pneumoniae CCUG 1378	1	1			
3566	10001645	Streptococcus pneumoniae CSR-SCS-2	1	1			
3567	10001646	Streptococcus pneumoniae type 37	2	2			
3568	10001648	Japanese encephalitis virus strain SA-14 -14-2	2	2			
3569	10001649	West Nile virus strain 956	1	1			
3570	10001651	Streptococcus pneumoniae type 14	19	19			
3571	10001652	Candida albicans NIH B-792 (serotype B)	1	1			
3572	10001659	Escherichia coli O125	1	1			
3573	10001662	Staphylococcus aureus Cowan 1	2	2			
3574	10001663	Streptococcus anginosus K214-2K	4	4			
3575	10001667	Helicobacter pylori 487	1	1			

3576	10001676	Streptococcus dysgalactiae subsp. equisimilis ATCC 12388	2	2			
3577	10001686	Streptococcus pneumoniae type 6A	2	2			
3578	10001687	Streptococcus pneumoniae type 6B	5	5			
3579	10001688	Pseudomonas syringae pv. atrofaciens str. IMV 7836	1	1			
3580	10001689	Pseudomonas syringae pv. atrofaciens str. IMV K-1025	1	1			
3581	10001690	Pseudomonas syringae pv. atrofaciens str. IMV 4394	1	1			
3582	10001693	Pseudomonas syringae pv. tagetis str. ICMP 6370	1	1			
3583	10001697	Pseudomonas syringae pv. phaseolicola str. IMV 120a	1	1			
		Pseudomonas syringae pv. morsprunorum str. GSPB					
3584	10001698	883	1	1			
		Pseudomonas syringae pv. morsprunorum str. CFBP					
3585	10001700	1650	1	1			
3586	10001705	Dengue virus 2 strain 43	1	1			
3587	10001713	Neisseria meningitidis serogroup W-135	1	1			
3588	10001722	Salmonella 'group D'	3	3			
3589	10001730	Streptococcus pneumoniae type 6C	1	1			
3590	10001731	Streptococcus pneumoniae type 2	8	8			
3592	10001740	Candida glabrata IFO 0622	1	1			
3593	10001747	Candida parapsilosis M1015	1	1			
3594	10001761	BK polyomavirus strain Dunlop		1	1		
3595	10001762	JC polyomavirus strain MAD1		1	1		
3596	10001763	Simian virus 40 strain 776		1	1		
3597	10001764	Classical swine fever virus Margarita (AJ704817)	4	1	4	1	
3598	10001768	Dengue virus 2 S-16803		1	1		
		Porcine reproductive and respiratory syndrome virus					
3599	10001771	HuN4-F112	4	1	4	1	
3600	10001783	Neisseria meningitidis serogroup C strain C11	1	1	1	1	
3601	10001792	Streptococcus pneumoniae type 3	6	6			
3602	10001794	Helicobacter pylori B128 Gerbil-adapted variant 7.13	1	1			
3604	10001797	Neisseria meningitidis serogroup C strain MC19	1	1			
		Porcine transmissible gastroenteritis coronavirus strain					
3605	10001798	Pur46-MAD	4	4			
		Porcine reproductive and respiratory syndrome virus					
3606	10001800	HuN4	1	4	1	4	
3607	X 10001801	Streptococcus pneumoniae type 8			10	10	
3608	10001831	Moraxella catarrhalis serotype B	1	1			
3609	10001835	Proteus penneri 7 (O61)	2	2			
3610	10001836	Proteus penneri 14 (O59)	2	2			
3611	10001837	Proteus penneri 15 (O52)	2	2			
3612	10001847	Clostridium difficile BI / NAP1/ 027	1	1			
3613	10001849	Moraxella catarrhalis serotype A	3	3			
3614	10001851	Moraxella catarrhalis serotype C	1	1			
3615	10001860	Neisseria meningitidis serogroup X	3	3			
3616	10001879	West Nile virus strain 68856	2	2			
3617	10001881	Porcine circovirus 2 -A	3	3			
3619	10001886	Brucella ovis 020	2	2			
3620	10001887	Brucella ovis Reo 198	1	1			
3621	10001888	Brucella ovis 63/290	1	1			
3623	10001895	Yersinia pseudotuberculosis str. 32777		1	1		
3624	10001900	Streptococcus agalactiae serogroup III M781	1	1	1	1	
3625	10001902	Human enterovirus 71 NUH0083/SIN/08	4	4			
3626	10001913	Lactobacillus johnsonii JCM 1022	3	3			
3627	10001918	Muscovy duck reovirus S12	2	2			
3628	10001929	Equine rhinitis B virus 2 strain 313/75	5	5			
3629	10001930	Equine rhinitis B virus 3 isolate 2225AS	5	5			
3630	10001934	Chikungunya virus Singapore/11/2008	3	3			
3631	10001943	Dengue virus 4 Burma/63632/1976	3	3			
3632	10001944	Dengue virus 3 Thailand/PaH881/1988	2	2			
3633	10001945	Dengue virus 1 PVP159	2	2			
3634	10001946	Foot-and-mouth disease virus - type Asia 1 YS/CHA/05	4	4			
3635	10001964	Porcine circovirus 1 strain 1/G	7	7			
3636	10001965	Avian leukosis virus strain NX0101	1	1			
3637	10001967	Avian leukosis virus isolate CAUHM01	1	1			
3638	10001973	Vaccinia virus Acambis 2000	8	8			
3639	10001975	Streptococcus salivarius JCM 5707	1	1			

3640	10001997	Chikungunya virus strain LR2006_OPY1 IMT/Reunion Island/2006	1	1			
3641	10001999	Reticuloendotheliosis virus strain HLJ07I	1	1			
3642	10002000	Porcine epidemic diarrhea virus CH/SHH/06	1	1			
3643	10002003	Campylobacter jejuni subsp. jejuni serotype HS:15	1	1			
3644	10002006	Bluetongue virus 16 BN96/16	2	2			
3645	10002007	Plasmodium falciparum isolate UAS22	4	4			
3646	10002008	Plasmodium falciparum isolate UAS31	1	1			
3647	10002009	Plasmodium falciparum isolate UAS29	2	2			
3648	10002010	Dengue virus 2 D2/SG/05K4155DK1/2005	49	49			
3649	10002011	Plasmodium falciparum R29/IT4	1	1			
3650	10002015	Human coxsackievirus A16 shzh05-1	92	92			
3651	10002018	Bovine coronavirus Kakegawa	1	1			
3652	10002020	Foot-and-mouth disease virus - type Asia 1 Nepal 29/97	4	4			
3653	10002022	Escherichia coli O6 O6:K15:H31	1	1			
3654	10002026	Murine norovirus 1 Mu/NoV/GV/MNV1/2002/USA	1	1			
3655	10002027	Bluetongue virus 16 Kumamoto/1985	2	2			
3656	10002028	Bluetongue virus 16 Beatrice Hill/1987	2	2			
3657	10002034	Fish	4	4			
3658	10002052	Toxoplasma gondii Gansu Jingtai	27	27			
3659	10002056	Enterovirus A71 TW/2086/98	1	1			
3660	10002069	Bordetella pertussis 509	7	7			
3661	10002079	Clostridium difficile VPI 10463	2	2			
3662	10002082	Rhesus rotavirus MMU 18006	3	3			
3663	10002089	Porcine reproductive and respiratory syndrome virus SY0608	17	17			
3664	10002090	Influenza A virus (A/swine/Denmark/101310-1/2011(H1N1))	7	7			
3665	10002111	Dengue virus 4 TVP-376	1	1			
3666	10002112	Dengue virus 4 1036	1	1			
3667	10002121	Staphylococcus aureus Reynolds	2	2			
3668	10002122	Staphylococcus aureus Becker	2	2			
3669	10002123	Peste-des-petits-ruminants virus China/Tibet/Geg/07-30	53	53			
3670	10002127	Escherichia coli O86:B7	1	1			
3671	10002129	Staphylococcus aureus RN4850	1	1			
3672	10002132	Duck hepatitis A virus 1 HP-1	2	2			
3673	10002148	Dengue virus 4 Mexico/BC287/1997	1	1			
3674	10002151	Duck hepatitis A virus 1 LY0801	1	1			
3675	10002152	Duck hepatitis A virus 3 SD1201	1	1			
3676	X 10002161	Streptococcus pneumoniae type 1		5	5		
		Avian infectious bronchitis virus (strain CHINA/Sczy3/09)	2	2			
3677	10002165						
3678	10002169	Avian infectious bronchitis virus (strain Holte)	2	2			
3680	10002183	ZIKV/H. sapiens/French Polynesia/PF13/2013	4	4			
3681	X 10002190	ZIKV/H. sapiens/Uganda/MR-766/1947		4	4		
3682	10002192	Streptococcus suis 1178027	2	2			
3684	10002196	Hepatitis E virus type 4 JAK-Sai	1	1			
3685	10002197	Chikungunya virus MY/08/065	15	15			
3687	10002238	Influenza A virus (A/swan/Poland/305-135V08/2006(H5N1))	1	1			
3688	X 10002272	Streptococcus pneumoniae 7F		5	5		
3689	X 10002273	Influenza A virus (A/Hong Kong/4801/2014(H3N2))			1	1	
Total							
			44803	388409	50408	461207	5605
							72798

2 Website Features

There were two major releases (Releases 3.9 and 3.10) of the IEDB external website since the 2017 Annual Compendium plus numerous smaller updates made throughout the year. Changes of note include:

- A new popup export button was added to allow more export choices and format variants in the CSV export interface.
- Auto-complete for source antigens were also revised with new logic to sort by the most useful hits.
- In order to better manage and display receptor data, the underlying receptor database tables were completely redesigned and the web pages re-factored.
- The assay details page was refined to add a new collapsible table displaying detailed receptor information.

Although the major releases primarily focused on enhancing export options and improving receptor data logic and reporting, many outstanding bugs and refinements were also addressed throughout the contract year.

In addition, there were two major releases (Releases 2.19 and 2.20) of the Analysis Resource since the 2017 Annual Compendium plus numerous smaller updates made throughout the year. Changes of note include:

- Integration of netMHCpan 4.0
- Integration of BepiPred 2.0
- Introduction of length-rescaling for class I and II binding predictors
- Overhaul to the class I automated benchmarks
- Improved email notifications for many tools
- Transitioning of the code repositories from Trac/SVN to Gitlab/Git.
- Release of Standalone Immunome Browser tool that allows users to map epitope sequences to proteins and visualize assay data
- Release of MHC II NP tool for the prediction of naturally processed MHC II ligands
- Update of many backend libraries

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

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

2.1 Home Page

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

The top box in the left column contains a welcome statement that briefly describes the content of the database. It also has a “Learn More” link that brings the user to a web page containing more information about the support and user help features available, about the data itself, and about the IEDB program. This page is described in detail in Section 2.6. The Summary Metrics are displayed in the bottom box of this column. These numbers are intended to be a gauge of the volume of data available in the system. The Summary Metrics provide the number of epitopes (peptidic and non-peptidic), assays (T cell, B cell, and MHC ligand assays), epitope source organisms, restricting MHC alleles, and references. A middle box may appear when there are special messages to convey to users. The text will appear in red. The middle column contains the initial search interface that is described in detail in Section 2.2.1. 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 a blue header bar. The header includes the IEDB logo, the text "IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE", and navigation links for "Home", "Specialized Searches", and "Analysis Resource". Below the header are three main columns:

- Welcome:** Contains a brief welcome message and a "Learn More" link.
- START YOUR SEARCH HERE:** A search interface with sections for Epitope, Assay, Antigen, MHC Restriction, Host, and Disease. It includes dropdown menus, checkboxes, and input fields for searching specific epitope characteristics like sequence, organism, and restriction.
- Epitope Analysis Resource:** Links to various epitope prediction tools:
 - T Cell Epitope Prediction:** Predicts T cell epitopes based on amino acid patterns, covering MHC I Binding, MHC II Binding, MHC I Processing (Proteasome, TAP), and MHC I Immunogenicity.
 - B Cell Epitope Prediction:** Predicts linear B cell epitopes using antigen sequence properties and discontinuous B cell epitopes via Discotope and ElliPro.
 - Epitope Analysis Tools:** Analyzes epitope sets for population coverage, conservation across antigens, and clusters with similar sequences.

At the bottom, there are links for "Provide Feedback", "Help Request", "Solutions Center", and "Tool Licensing Information". A note states the page is supported by the National Institute of Allergy and Infectious Diseases. The footer indicates the data was last updated on January 13, 2019.

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 peptides at sequence at identity levels of 70%, 80%, or 90% as determined by BLAST. The IEDB categorizes all assays as T cell, B cell, or MHC ligand. The MHC ligand includes binding and elution assays. Users can also select the MHC restriction for non-B cell searches. Finally, users can select the host species and the disease.

The results of the query are displayed in 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 ?

Epitope 

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

Exact M ▾ Ex: SIINFEKL

Assay 

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

Ex: neutralization

Antigen 

- Organism

Ex: influenza, peanut

Antigen Name

Ex: core, capsid, myosin

MHC Restriction 

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

Ex: HLA-A*02:01

Host 

- Any Host
- Humans
- Mice
- Non-human Primates

Ex: dog, camel

Disease 

- Any Disease
- Infectious Disease
- Allergic Disease
- Autoimmune Disease

Ex: asthma, diabetes

Figure 2.2 Home page simple search

Once the initial results are generated, the user can filter the results using additional filtering criteria. Autocomplete 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 lefthand side of the results page that contain additional filter criteria. This includes the non-peptidic epitope field in the Epitope box, the organism and antigen name fields in the Antigen box, the T cell, B cell, and MHC ligand assay fields in the Assay box, the specific MHC restriction field in the MHC Restriction box, the specific host field in the Host box, 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)	
Go To Records Starting At <input type="text" value="1200"/> <input type="button" value="GO"/> Export Results 									
5 Records Found Page 1 of 1 25 ▾ Per Page									
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	YNAELLVAVALENQHTIDL	Hemagglutinin	Influenza A virus	1	1				

5 Records Found Page | 1 of 1 25 ▾ Per Page

[Go To Records Starting At 1200](#) 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	Y		325	1220
44920	NLVPMVATV	Y	65 kDa phosphoprotein	285	718
20354	GILGFVFTL	Y	Matrix protein 1	213	601
113645	MEVGBWYRSPFSRVVHLYRNGK	Y	Myelin-oligodendrocyte glycoprotein	189	1051
58560	SIIINFKL	Y	Gal d 2	175	472
4602	ASNENMETM	Y	Nucleoprotein	150	433
112741	2,4-dinitrophenyl group	Y		142	578
20788	GLCTLVAML	Y	mRNA export factor ICP27 homolog	131	292
24786	HSLGKWLGHPDF	Y	Myelin proteolipid protein	120	705
130694	1-O-(alpha-D-galactosyl)-N-hexacosanoylphytosphingosine	Y		119	593
48237	PKVVKONTLKLAT	Y	Hemagglutinin	115	449
6435	CINGVCIVTV	Y	Genome polyprotein	112	335
112742	2,4,6-trinitrophenyl group	Y		109	352
130649	alpha-D-Galp-(1->3)-beta-D-Galp-(1->4)-D-GlcNAc-yl group	Y		108	458
32208	KVALGINAV	Y	Genome polyprotein	100	329
53112	RAHYNIVTF	Y	Protein E7	99	259
61086	SSIEFARL	Y	Envelope glycoprotein B	93	324
16833	FLPSDFPPSV	Y	Capsid protein	91	280
65748	TPRVGGGAM	Y	65 kDa phosphoprotein	90	184
6568	CLGGLLTMV	Y	Latent membrane protein 2	88	232
61151	SSLENFRAYV	Y	Polymerase acidic protein	88	281
30001	KAIVVNFACTC	Y	Pre-glycoprotein polyprotein GP complex	86	272
7493	DAEPRHDSGYEVHHHQKLVFFAEDVGSNKGAIGLMVGGVIA	Y	Amyloid beta A4 protein	82	349
16878	FLRGRAYGL	Y	Epstein-Barr nuclear antigen 3	82	287
67436	TYQRTRALV	Y	Nucleoprotein	82	188

Figure 2.4 Epitope Detail Search input screen

Epitope 

Epitope ID Ex: 44920 

Structure Type - Any Epitopes

Organism Ex: influenza, Peanut 

Antigen Name Ex: core, capsid, myosin 

Epitope Reference Details

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

Epitope Related Object

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

Epitope Reference Details

Epitope Related Object

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 

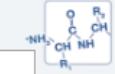
Epitope ID	Ex: 44920	
Structure Type - Discontinuous Peptides on Multi Chain		
Molecule Name	Ex: Vascular endothelial growth factor	
Discontinuous Residues	Ex: E170, E172	
 Chain 1		
Modified Residue(s)	Ex: T10	
Modification(s)	Select Multiple Options	
Organism	Ex: influenza, Peanut	
 Chain 2		
Modified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

[Epitope Reference Details](#)

[Epitope Related Object](#)

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.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

MHC Assay Detailed Search

Reset Search

Epitope

Epitope ID: Structure Type - Any

- Organism
- Antigen Name
- Epitope Reference...
- Epitope Related ...

Host

Host Organism

- Host Details
- In Vivo Process
- In Vivo Processed...
- In Vitro Administr...
- In Vitro Processe...
- Antigen Processin...

Assay

Qualitative Measurement

Assay

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

Reference

Author

Title

- Reference Details

Reference ID

Abstract

Affiliations

Date (Year)

Type - Any

Reset Search

No Filters Set

Home Specialized Searches Analysis Resource Help More IEDB

Epitopes (424719) Antigens (39280) Assays (1073280) References (2623)

Go To Records Starting At 1200 Export Results

424719 Records Found Page 1 of 16989 25 Per Page

Details	Epitope	Antigen	Organism	# References	# Assays
48237	PKYVKQNTLKLAT	Hemagglutinin	Influenza A virus	83	315
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	73	108
58580	SINFEKL	Gal d 2	Gallus gallus (chicken)	57	103
4802	ASNENMETM	Nucleoprotein	Influenza A virus	44	63
16833	FLPSDFPPSV	Capsid protein	Hepatitis B virus	39	86
27201	ILMEHIIHLK	60S ribosomal protein L19	Mus musculus (mouse)	38	51
44920	NLVPMVATV	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	34	48
55785	RRYYOKSTEL	Histone H3.1t	Homo sapiens (human)	33	59
55556	RRRFPPYYYY	Proteasome subunit beta type-1	Homo sapiens (human)	32	73
58547	SIIGRLLEV	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	Homo sapiens (human)	31	48
30820	KESTLHLVL	Ubiquitin-40S ribosomal protein S27a (UniProtJ3QTR3)	Homo sapiens (human)	30	39
89922	VMAPRTLVL			30	49
74794	YLLPAIVHII	Probable ATP-dependent RNA helicase DDX5 (UniProt:P17844)	Homo sapiens (human)	30	40
155807	AIVDKVPSV	Coatomer subunit gamma-1	Homo sapiens (human)	30	45
27125	ILKEPVHGKV	Gag-Pol polyprotein	Human immunodeficiency virus 1	29	53
101382	VMAPRTLLL	HLA class I histocompatibility antigen, A-3 alpha chain	Homo sapiens (human)	29	44
162685	KIYEGOVEV	60S ribosomal protein L5	Mus musculus (mouse)	29	36
27000	ILDKKVKEKV	Heat shock protein HSP 90-beta	Homo sapiens (human)	28	37
37182	LLDVPTAAV	Gamma-interferon-inducible lysosomal thiol reductase	Homo sapiens (human)	28	42
60887	SRYWAIWTR	Nucleoprotein	Influenza A virus	28	74
162823	KYFDDEHYEY	Cyclin-dependent kinases regulatory subunit 2	Homo sapiens (human)	28	37
419980	MRYVASYLL	60S acidic ribosomal protein P2	Homo sapiens (human)	28	48
17681	FRYNGLIHR	60S ribosomal protein L28	Homo sapiens (human)	27	37
89939	VMDSKIVQV	Imprin subunit alpha-5	Homo sapiens (human)	27	34
120105	NEICDTFRQF	V-type proton ATPase subunit F	Homo sapiens (human)	27	33

424719 Records Found Go To Records Starting At 1200 Export Results

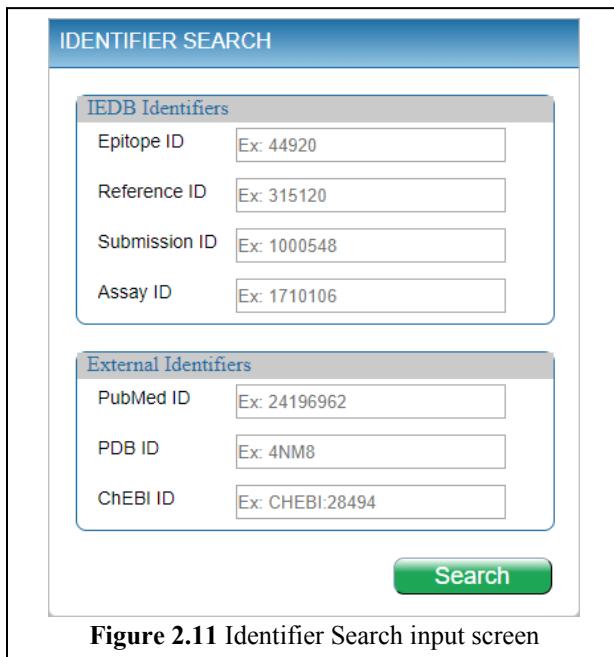
Figure 2.10 MHC Assay Detailed Search web page

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, where as for the latter, antigen in solution is bound to MHC molecules on the surface of the antigen presenting cells.



The Identifier Search input screen is 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:

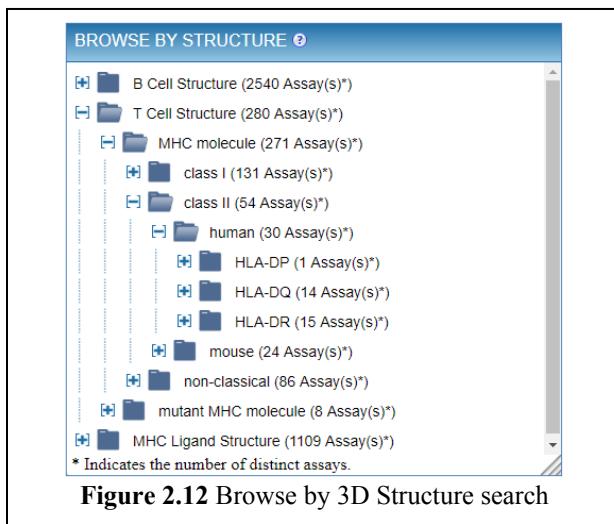
- PubMed ID: Ex: 24196962
- PDB ID: Ex: 4NM8
- ChEBI ID: Ex: CHEBI:28494

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 displays a hierarchical tree view of available 3D structures.

- B Cell Structure (2540 Assay(s)*)
- T Cell Structure (280 Assay(s)*)
- MHC molecule (271 Assay(s)*)
 - class I (131 Assay(s)*)
 - class II (54 Assay(s)*)
 - human (30 Assay(s)*)
 - HLA-DP (1 Assay(s)*)
 - HLA-DQ (14 Assay(s)*)
 - HLA-DR (15 Assay(s)*)
 - mouse (24 Assay(s)*)
 - non-classical (86 Assay(s)*)
 - mutant MHC molecule (8 Assay(s)*)
 - MHC Ligand Structure (1109 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.

Details	Epitope	Antigen	Organism	# References	# Assays
123885	cardiolipin			320	1028
44920	NLVPMVATV	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	284	699
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	209	566
113645	MEVGWYRSPFSPVVHLYRNGK	Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	187	975
58560	SIINFEKL	Gal d 2	Gallicus gallus (chicken)	173	449
4602	ASNENMETM	Nucleoprotein	Influenza A virus	146	402
112741	2,4-dinitrophenyl group			140	477
20788	GLCLTLVAML	mRNA export factor ICP27 homolog	Human herpesvirus 4 (Epstein Barr virus)	128	271
130694	1-O-(alpha-D-galactosyl)-N-hexacosanoylphosphatidoglycan			118	579
24786	HSLGKWLGHDPDKF	Myelin proteolipid protein	Mus musculus (mouse)	115	697
48237	PKYVKQNTLKLAT	Hemagglutinin	Influenza A virus	110	389
130649	alpha-D-Galp-(1->3)-beta-D-Galp-(1->4)-D-GlcNAc-yl group	Envelope glycoprotein	Murine leukemia virus	108	425
6435	CINGVCWT	Genome polyprotein	Hepatitis C virus	107	304
112742	2,4,6-trinitrophenyl group			107	310
53112	RAHYNIVTF	Protein E7	Alphapapillomavirus 9	97	243
32208	KLVALGINAV	Genome polyprotein	Hepatitis C virus	96	283
61086	SSIEFARL	Envelope glycoprotein B	Human herpesvirus 1	93	305
61151	SSLENFRAYV	Polymerase acidic protein	Influenza A virus	88	264
16833	FLPSDFPPSV	Capsid protein	Hepatitis B virus	86	246
65748	TPRVTGGAM	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	86	174
30001	KAVYNFATC	Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus	85	250
6568	CLGGLLTMV	Latent membrane protein 2	Human herpesvirus 4 (Epstein Barr virus)	84	216
16878	FLRGRAYGL	Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	82	250
7493	DAEFRHDSGYEVHHQKLVFAE DVGSNKGAIIGLMVGGVIA	Amyloid beta A4 protein	Homo sapiens (human)	81	254
17516	FQPQNQQFI	Nucleoprotein	Lymphocytic choriomeningitis mammarenavirus	80	193

Figure 2.13 The Epitope tab of the search results page

EPITOPE SUMMARY

GILGVFTL is a linear peptidic epitope (epitope ID 20354) studied as part of Matrix protein 1 from Influenza A virus. This epitope has been studied for immune reactivity in 214 publication(s), tested in 489 T cell assays, 5 B cell assays, 108 MHC ligand assays and has 3D structure(s) 2VLK, 10GA, 5JHD, 5EUQ, 5ISZ, 5TEZ, 5E6I, 2VLL, 2VLJ, 2VLR, 4NT6 and 1HHL.

COMPILED DATA

MHC Ligand Assay(s) 108	
MHC molecule	Positive / All
HLA-A*02:01	70/70
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*01:03	1/1
HLA-A*01:01	0/1
HLA-A*03:01	0/1
HLA-A*11:01	0/1
HLA-A*24:02	0/1
HLA-A3	0/1
HLA-DRA*01:01/DRB1*01:01	0/1
HLA-E	0/1

B Cell Assay(s) 5	
Assay Type	Positive / All
qualitative binding	4/4
complement-dependent cytotoxicity	1/1

T Cell Assay(s) 489	
Assay Type	Positive / All
IFNg release	142/147
qualitative binding	113/114
cytotoxicity	77/81
dissociation constant KD	28/36
off rate	14/14
on rate	14/14
proliferation	11/12
TNF α release	10/11
activation	10/10
3D structure	9/9
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
CCL4/MIP-1 β release	3/3
granzyme B release	2/2
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-4 release	0/1

EXTERNAL RESOURCES

Resource	Link
IEDB-AR: MHC-I Processing	Predict MHC class I processing
IEDB-AR: MHC-I	Predict MHC class I binding affinity
IEDB-AR: B cell scales	Predict B cell epitopes
IRD	View sequence feature Influenza A_M1_experimentally-determined-epitope_58(9) details at IRD
IRD	View sequence feature Influenza A_M1_monoclonal-antibody-binding-site_58(9) details at IRD

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.

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

MHC Restriction 

- Any MHC Restriction
- MHC Class I
- MHC Class II

Current Filters: Positive Assays Only

Epitopes (537986) **Antigens (42566)** **Assays (1235831)** **Receptors (26442)** **References (19871)**

Go To Records Starting At 1200  Export Results 

42566 Records Found Page 1 of 1703 25 Per Page

Antigen	Organism	# Epitopes	# Assays	# References
Hemagglutinin	Influenza A virus	1787	7188	649
Genome polyprotein	Hepatitis C virus	4627	13627	600
Nucleoprotein	Influenza A virus	577	2821	485
65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	367	2162	366
Matrix protein 1	Influenza A virus	331	1638	338
Large envelope protein	Hepatitis B virus	675	2915	321
Other Homo sapiens (human) protein	Homo sapiens (human)	11821	18152	295
Amyloid beta A4 protein	Homo sapiens (human)	325	1882	290
Gal d 2	Gallus gallus (chicken)	120	884	278
Genome polyprotein	Dengue virus	6981	19723	277
Envelope glycoprotein gp160	Human immunodeficiency virus 1	424	1669	258
Myelin basic protein (UniProt:P02686)	Homo sapiens (human)	400	2120	244
Protein E7	Alphapapillomavirus 9	261	1219	222
Circumsporozoite (CS) protein	Plasmodium falciparum (malaria parasite P. falciparum)	405	1999	222
Myelin-oligodendrocyte glycoprotein	Mus musculus (mouse)	73	1231	202
Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus	345	1786	196
Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	254	977	178
Capsid protein	Hepatitis B virus	247	1032	178
Immunoglobulin	Homo sapiens (human)	2482	3954	171
Glutamate decarboxylase 2	Homo sapiens (human)	388	1603	160
Polymerase acidic protein	Influenza A virus	247	1021	158
Nucleoprotein	Lymphocytic choriomeningitis mammarenavirus	224	1120	153
Myelin proteolipid protein	Mus musculus (mouse)	56	1078	152
Latent membrane protein 2	Human herpesvirus 4 (Epstein Barr virus)	156	815	145
lipopolysaccharide		200	1237	144

42566 Records Found Page 1 of 1703 25 Per Page Go To Records Starting At 1200  Export Results 

Figure 2.15 The Antigens tab of the search results page

The screenshot shows the IEDB interface with the following details:

- Pending Filters:** Includes "Reset" and "Search" buttons.
- Current Filters:** Shows "Positive Assays Only" and "Antigen: Nucleoprotein" selected.
- Navigation Tabs:** Epitopes (577), Antigens (1), Assays (2821), Receptors (2587), References (485).
- Table Headers:** Antigen, Organism, # Epitopes, # Assays, # References.
- Data Row:** Nucleoprotein, Influenza A virus, 577, 2821, 485.
- Page Navigation:** Go To Records Starting At 1200, Page 1 of 1, 25 Per Page, Export Results.
- Search Bar:** Click to search with this filter.

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, 1st In Vivo Process, Administration Details, 1st 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.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

Help | More IEDB

Pending Filters

Epitope (537986)

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

3D structure available

Amino Acid Modification

Antigen (537986)

Organism
Ex: influenza, peanut

Antigen Name
Ex: core, capsid, myosin

Receptor (537986)

Has receptor sequence

Type: Any Type

Chain: Any Type

Sequence: Exact Matches

Assay (537986)

Positive Assays Only

T Cell Assays

B Cell Assays

MHC Ligand Assays

MHC Restriction (537986)

- Any MHC Restriction
- MHC Class I
- MHC Class II

Current Filters: Positive Assays Only

Epitopes (537986) Antigens (42566) Assays (1235831) Receptors (26442) References (19871)

T Cell Assays (136542) B Cell Assays (176338) MHC Ligand Assays (922953)

Go To Records Starting At A.b Export Results

136542 Records Found Page 1 of 5462 25 Per Page

ID	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	MHC Restriction	Assay Description
1505273	P Chong; Infect Immun 1992	AGFYIYRETF CITTIV KTGQPAAD HYYSKVTA Pertussis toxin subunit 3 precursor (106-136) Bordetella pertussis	Mus musculus BALB/c	Administered in vivo with Pertussis toxin subunit 3 precursor (Source Antigen)	AGFYIYRET CITTIV KTGQPAAD HYYSKVTA 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	AICKRIPNPK KPGKKT Major surface glycoprotein G (184-198) Human respiratory syncytial virus A2	Mus musculus BALB/c	Administered in vivo with Major surface glycoprotein G (Source Antigen)	AICKRIPNPK KPGKKT Major surface glycoprotein G (184-198) Human respiratory syncytial virus A2	Epitope	H2-IEd	3H-thymidine proliferation Positive-High
1810409	Xuefeng Wang; Parasit Vectors 2010	AKOYNICCK FKELLD 22.6 kDa tegumental antigen (111-125) Schistosoma japonicum	Mus musculus C57BL/6	Administered in vivo with AKOYNICCK FKELLD (Epitope)	AKQYNNICCK FKFELLD 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	ALNNNRFQIK KVVELKS hemagglutinin (511-525) Influenza A virus	Mus musculus BALB/c	Administered in vivo with ALNNNRFQIK KVVELKS (Epitope)	ALNNNRFQIK KVVELKS hemagglutinin (511-525) Influenza A virus	Epitope	H2-d class II	3H-thymidine proliferation Positive-High
1648562	A G Paul; Int Immunol 2000	ALSTLVVNKL 60 kDa chaperonin 2 (256-265) Mycobacterium tuberculosis	Rattus norvegicus	Administered in vivo with ALSTLVVN KIRGTFK (Fragment of Source Antigen) followed by restimulation <i>in vitro</i>	ALSTLVVNKL 60 kDa chaperonin 2 (256-265) Mycobacterium tuberculosis	Epitope	RT1-Bi	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.

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 (537986)		Antigens (42566)		Assays (1235831)		Receptors (26442)		References (19871)	
T Cell Receptors (24884)		B Cell Receptors (1558)							
Go To Records Starting At: 1200 <input type="button" value="GO"/>									
Export Results									
24884 Records Found									
Page 1 of 1091									
25 Per Page									
Group ID	Species	Type	Chain 1 CDR3	Chain 2 CDR3					
47	Homo sapiens (human)	αβ	IVVRSSNTGKLI	ASSQDRDTQY					
49	Mus musculus (mouse)	αβ	AASANSHTGYQR	ASGDAGGGYEQY					
50	Mus musculus C57BL/6	αβ	AAS	ASSL					
57	Homo sapiens (human)	αβ	AALIQGAQKLV	ASTYHGTTGY					
94	Homo sapiens (human)	αβ	AVRPLLDTYIPT	ASSYLNNTGELF					
102	Mus musculus (mouse)	αβ	ALSENHYGNEKIT	ASGDASGAETLY					
103	Mus musculus (mouse)	αβ	ALSENHYGNEKIT	ASGDASGGNTLY					
104	Mus musculus (mouse)	αβ	AANSGTYQR	ASGDFWGDLY					
109	Homo sapiens (human)	αβ	IVWGGYQKV	ASRYRDDSYNEQF					
110	Homo sapiens (human)	αβ	AVTTDSWGKLQ	ASRPGLLAGGRPEQY					
111	Homo sapiens (human)	αβ	AVTTDSWGKLQ	ASRPGLMSAQPEQY					
114	Mus musculus (mouse)	αβ	AVSDPPPLT	ASGGGGTLY					
115	Mus musculus (mouse)	αβ	AVSLERPYLT	ASGGGGTLY					
116	Homo sapiens (human)	αβ	ALSGFYNTDKLI	ASPGLAGEYEQY					
117	Homo sapiens (human)	αβ	AVRPTSGGSYIPT	ASSYVGNTGELF					
118	Mus musculus (mouse)	αβ	ALFLASSFSKLV	ASSDWIVSYEQY					
125	Homo sapiens (human)	αβ	ATDTTSGTYKYI	SARDLTGANNEQF					
140	Mus musculus (mouse)	αβ	VVGDRGSAALGRHL	ASGDAGGNYAEQF					
141	Mus musculus (mouse)	αβ	VVGDRGSAALGRHL	ASSSTGLDTQY					
142	Mus musculus (mouse)	αβ	VVGDRGSAALGRHL	ASGSSLDVREVF					
143	Homo sapiens (human)	αβ	VVSDRGSTLGRILY	ASSGLRDRGLEYQY					
144	Homo sapiens (human)	αβ	VVSDRGSTLGRILY	ASSEEGALKESVGTQY					
227	Homo sapiens (human)	αβ	AVNVAGKST	AWSETGLGTGELF					

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 2.19.

IMMUNE EPITOPE DATABASE AND ANALYSIS RESOURCE

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

Pending Filters

Epitope (Any Epitopes)

Antigen (Organism: influenza, peanut; Antigen Name: 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)

MHC Restriction (Any MHC Restriction, MHC Class I, MHC Class II)

Current Filters: Positive Assays Only

Epitopes (537986) | Antigens (42566) | Assays (1235831) | Receptors (26442) | References (19871)

Go To Records Starting At: 1982 | Export Results

19871 Records Found | Page 1 of 795 | 25 Per Page

Ref ID	PMID	Author	Title	Abstract	Date
1034225	30546964	Sebastian Kruse; Marleen Büchler; Philipp Uhl; Max Sauter; Philipp Scherer; Tammy C T Lan; Samantha Zottnick; Alexandra Klevenz; Ruwen Yang; Frank Röst; Walter Mier; Angelika B Riemer	Therapeutic vaccination using minimal HPV16 epitopes in a novel MHC-humanized murine HPV tumor model.	Therapeutic vaccination as a treatment option for HPV-induced cancers is actively pursued because the two HPV proteins E6 and E7 represent ideal targets for immunotherapy, as they are non-self and exp ...more...	2019
1034260	30539581	Felicia Real-Fernández; Federico Pratesi; Paola Migliorini; Paolo Rovero	Histone Protein Epitope Mapping for Autoantibody Recognition in Rheumatoid Arthritis.	Deiminated proteins are the target of diagnostic anti-citrullinated peptide/protein autoantibodies (ACPA) in rheumatoid arthritis (RA). Deiminated histone H4 contained in the neutrophil extracellular ...more...	2019
1033402	29508533	Joël Lanoix; Chantal Durette; Mathieu Courcelles; Émilie Cossette; Simon Comtois-Marotte; Marie-Pierre Hardy; Caroline Côté; Claude Perreault; Pierre Thibault	Comparison of the MHC I Immunopeptidome Repertoire of B-Cell Lymphoblasts Using Two Isolation Methods.	Significant technological advances in both affinity chromatography and mass spectrometry have facilitated the identification of peptides associated with the major histocompatibility complex class I (M ...more...	2018
1033511	29393594	Shira Yair-Sabag; Valentina Tedeschi; Carolina Vitalano; Eilon Barnea; Fabian Glaser; Dganit Melamed Kadosh; Joel D Taurog; Maria Teresa Fiorillo; Rosa Sorrentino; Arie Admon	The Peptide Repertoire of HLA-B27 may include Ligands with Lysine at P2 Anchor Position.	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 ...more...	2018
1033513	29786170	Nicola Ternette; Marloes J M Olde Nordkamp; Julius Müller; Amanda P Anderson; Annalisa Nicastri; Adrian V S Hill; Benedikt M Kessler; Demin Li	Immunopeptidomic Profiling of HLA-A2-Positive Triple Negative Breast Cancer Identifies Potential Immunotherapy Target Antigens.	The recent development in immune checkpoint inhibitors and chimeric antigen receptor (CAR) T-cells in the treatment of cancer has not only demonstrated the potency of utilizing T-	2018

Figure 2.20 The References tab of the search results page



IMMUNE EPITOPE DATABASE
AND ANALYSIS RESOURCE

Help | More IEDB

Reference	
Article Authors	Shira Yair-Sabag; Valentina Tedeschi; Carolina Vitulano; Eilon Barnea; Fabian Glaser; Dganit Melamed Kadosh; Joel D Taurog; Maria Teresa Fiorillo; Rosa Sorrentino; Arie Admon
Article Title	The Peptide Repertoire of HLA-B27 may include Ligands with Lysine at P2 Anchor Position.

Reference Detail	
Reference ID	1033511
Abstract	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.
Affiliations	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.
Date	2018
Reference Type	Literature
PubMed ID	29393594
Journal	Proteomics
Journal Volume	18
Article Pages	e1700249
Journal ISSN	1615-9861
Curation Last Updated	2019-01-03 23:39:42

Related Information	
Epitopes	34798 (Click for related results)
Bcell Assays	0
Tcell Assays	0
MHC Ligand Assays	42431 (Click for related results)

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	HLA00005
Chain 2 Name	Beta-2-microglobulin
Chain 2 Accession	48428791

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

Peptide MHC Binding Motif ?													
9-length	10-length												
<table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="padding: 5px;">Preferred F Y</td> <td style="padding: 5px; border-left: none;">Position 2 Anchor</td> <td style="padding: 5px; border-left: none;">C-terminal Anchor</td> </tr> <tr> <td style="padding: 5px;">Position 1</td> <td style="padding: 5px; border-left: none;">Preferred LM</td> <td style="padding: 5px; border-left: none;">Preferred ILV</td> </tr> <tr> <td style="padding: 5px;">Deleterious DEP</td> <td style="padding: 5px; border-left: none;">Tolerated IQV</td> <td style="padding: 5px; border-left: none;">Tolerated AM</td> </tr> <tr> <td colspan="3" style="text-align: center; padding: 10px;"> <p>Amino Acid Binding Chart</p> </td> </tr> </table>		Preferred F Y	Position 2 Anchor	C-terminal Anchor	Position 1	Preferred LM	Preferred ILV	Deleterious DEP	Tolerated IQV	Tolerated AM	<p>Amino Acid Binding Chart</p>		
Preferred F Y	Position 2 Anchor	C-terminal Anchor											
Position 1	Preferred LM	Preferred ILV											
Deleterious DEP	Tolerated IQV	Tolerated AM											
<p>Amino Acid Binding Chart</p>													

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

- The remaining residues are designated as deleterious

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

(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:

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

2.2.3.2 Immunome Browser

The Immunome Browser is a feature integrated into the IEDB to more efficiently display large sets of immune epitope data. The purpose of the tool is to allow users to explore how often each protein region has been studied in immune assays and in how many assays the immune response was positive or negative. The Immunome Browser “maps” query results from the IEDB onto a reference proteome. A reference proteome is used because (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 GO, Export Antigens Results checked.
- Page Navigation:** 3 Records Found, Page 1 of 1, 25 Per Page.
- 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.

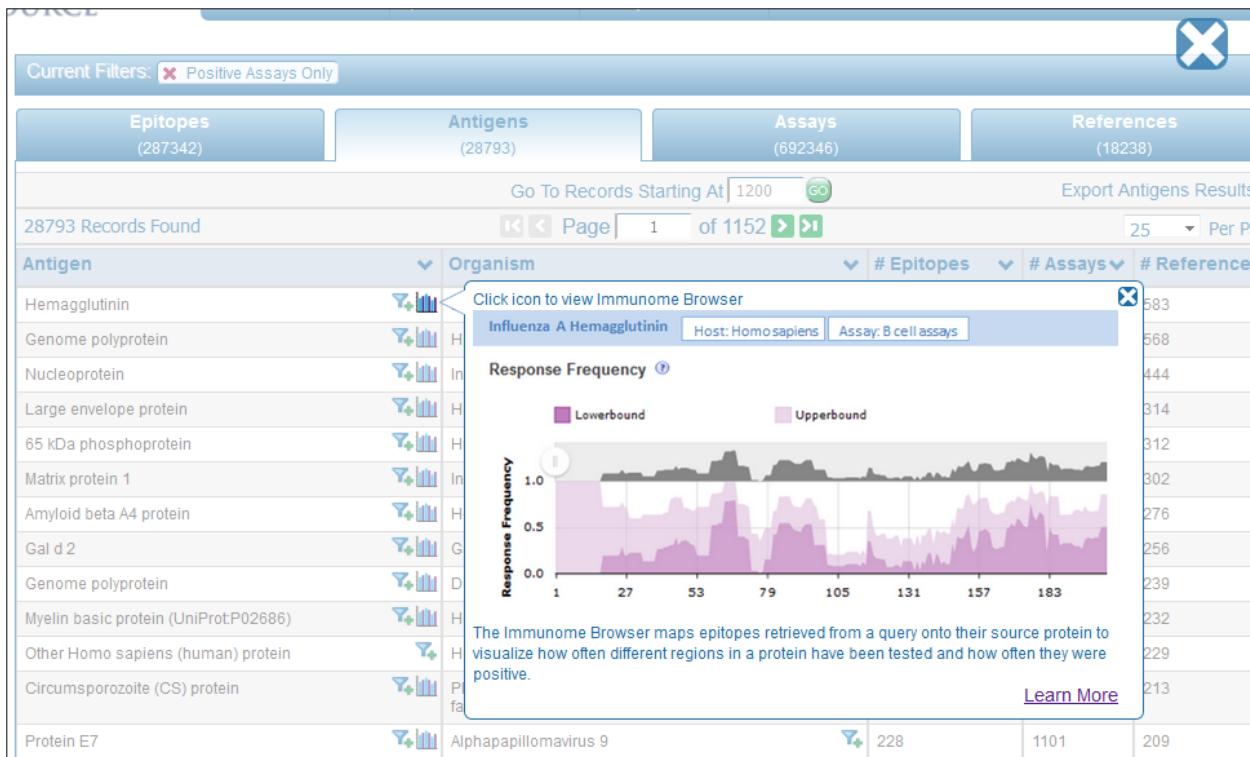


Figure 2.25 A pop-up window appears each time the user clicks on the Antigen tab on the Results page. It highlights the Immunome Browser icon and briefly explains the Immunome Browser's functionality.

In the Immunome 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 Immunome 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 <input type="checkbox"/> 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	MSTNPKPQIKTKRNTNRR	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's a search bar with the text "Current Selection(s) Papa-A*06:01". Below it are two main sections: "Search By" and "Browse by Tree (Click to Select)".

Search By: This section contains fields for "Name" (Ex: HLA-A*02:01, H-2-Kb), "Organism" (bonobo (Pan paniscus)), and "Class" (MHC class I). It includes "Clear" and "Search" buttons.

Browse by Tree (Click to Select): This section shows a hierarchical tree structure under the "MHC" category. The tree includes "MHC molecule", "class I", "bonobo", "Papa-A", "cattle", "chicken", and "chimpanzee". The entry "Papa-A*06:01" is highlighted with a green dashed border and a checkmark icon.

Search Results (Click to Select): This section displays a table of search results. The columns are Name, Type, Organism, Class, Locus, Haplotype, and Serotype. The results are:

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		

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 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, there is a 'Search Results (Click to Select)' table with one record found. The table has columns for Name, OBI ID, Method/Technique, Measurement Of, Units, and Synonyms. The single record is CCL1/TCA-3 release|ELISA, OBI:0001315, ELISA, CCL1/TCA-3 release, and ELISA, cytokine release, ELISA. There are also two pagination sections at the bottom.

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 [DOID:9351]

Reset **Apply**

Search By

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

Clear **Search**

Browse by Tree (Click to Select)

- infectious disease [DOID:0050117]
- autoimmune disease [DOID:417]
- animal model of autoimmune disease [DTRE...]
- autoimmune disease of the blood [DOID:006...]
- autoimmune disease of the cardiovascular sy...
- autoimmune disease of the central nervous s...
- autoimmune disease of the eyes, ears, nose ...
- autoimmune disease of the endocrine system...
- diabetes mellitus [DOID:9351]

Search Results (Click to Select)

4 Records Found Page 1 of 1 5 Per Page

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

Figure 2.30 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

Search By

Name: penicillin
Molecule ID: Ex: 17334

Browse by Tree (Click to Select)

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

Search Results (Click to Select)

19 Records Found

Molecule Name	Synonyms	Database ID	Organism Name
penicillin	penicillins, Penicillin, penicillins, [H][C@]1SC(C)(C)[C@@H](N1C(=O)[C@H]2NC([F])=O)C(O)=O, C9H11N2O4SR	ChEBI:17334	
penicillinate anion	C9H10N2O4SR, C9H10N2O4S, penicillin anion, penicillin, penicillin anions, [H][C@]1SC(C)(C)[C@@H](N1C(=O)[C@H]2NC([F])=O)C([O-])=O	ChEBI:51356	
benzylpenicillin	Benzylpenicillin, 2,2-dimethyl-6beta-(phenylacetamido)penam-3alpha-carboxylic acid, benzylpenicilline, 6-(2-phenylacetamido)penicillanic acid, benzilpenicilina, InChI=1S/C16H18N2O4S/c1-16(2)12(15(21)2 ...more...	ChEBI:18208	
penicillin O	6beta-[(prop-2-en-1-ylsulfanyl)acetamido]-2,2-dimethylpenam-3alpha-carboxylic acid, allylthiomethylpenicillin, (2S,5R)-6-	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 software interface. At the top, there is a search bar with the text "Current Selection(s) Voltage-gated potassium channel ★★". Below the search bar are two sections: "Search By" and "Browse by Tree (Click to Select)".

Search By:

- Name: potassium channel
- Molecule ID: Ex: P69710
- Source Organism: Ex: influenza, peanut
- Buttons: Clear, Search

Browse by Tree (Click to Select):

- material entity
 - non-peptidic material
 - protein
 - Archeobacterium protein
 - Aeropyrum pernix protein ★★
 - Branched-chain amino acid ABC transporter, permease protein ★
 - Voltage-gated potassium channel ★★ (selected)
 - Other Aeropyrum pernix protein *
 - Archaeoglobus fulgidus protein ★★★

Search Results (Click to Select):

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 ⁺ -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 ⁺ -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 2.29, a user can search the molecule tree by entering text, including synonyms, in the Name field in the upper lefthand corner of the finder. The user can also specify the source organism of the molecule of interest using the autocomplete field or the organism finder. For example, this can facilitate the specification of a hemagglutinin 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 lefthand portion of the Finder. In the example shown in Figure 2.33, a search for "dengue" is performed, which results in 45 items being found. The user can select one or more of the items by clicking on the green "+" icon or clicking a branch in the tree. The user can also choose to highlight the item in the tree, as shown in the figure, by clicking the corresponding yellow highlighter icon. Synonyms for a selection are listed next to the organism name column in the search results table. When the Organism Finder is adjacent to a Host Organism field, only the source organisms for which data exist in the IEDB are displayed in the tree structure.

ORGANISM FINDER

Current Selection(s) Dengue virus

Reset **Apply**

Search By

Name:
Organism ID:

Clear **Search**

Browse by Tree (Click to Select)

- Arterivirus
- Bacteriophage (RNA)
- Coronavirus
- Filovirus
- Flaviviridae family virus
 - Flavivirus
 - CY1014 virus
 - Carey Island virus
 - Dengue virus

Search Results (Click to Select)

45 Records Found

Organism Name	Synonyms	Organism ID
Dengue virus	<input checked="" type="checkbox"/> Dengue virus	12637
Dengue virus 1	<input checked="" type="checkbox"/> Dengue virus 1, dengue virus type 1 DEN1, type 1 dengue virus DEN-1, dengue type 1 D1 virus, Type 1 dengue virus, dengue virus-1 DEN-1, Dengue virus type 1, dengue virus type I	11053
Dengue virus 2	<input checked="" type="checkbox"/> Dengue virus 2, Dengue virus type II, dengue-2 virus, dengue-2 virus DEN-2, dengue 2 virus DEN-2, Dengue virus type 2	11060
Dengue virus 3	<input checked="" type="checkbox"/> Dengue virus 3, dengue 3 virus, Dengue virus type 3	11069
Dengue virus 4	<input checked="" type="checkbox"/> Dengue virus 4, dengue type 4 virus DEN4, Dengue virus type 4	11070

45 Records Found

Page 1 of 9

5 Per Page

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.

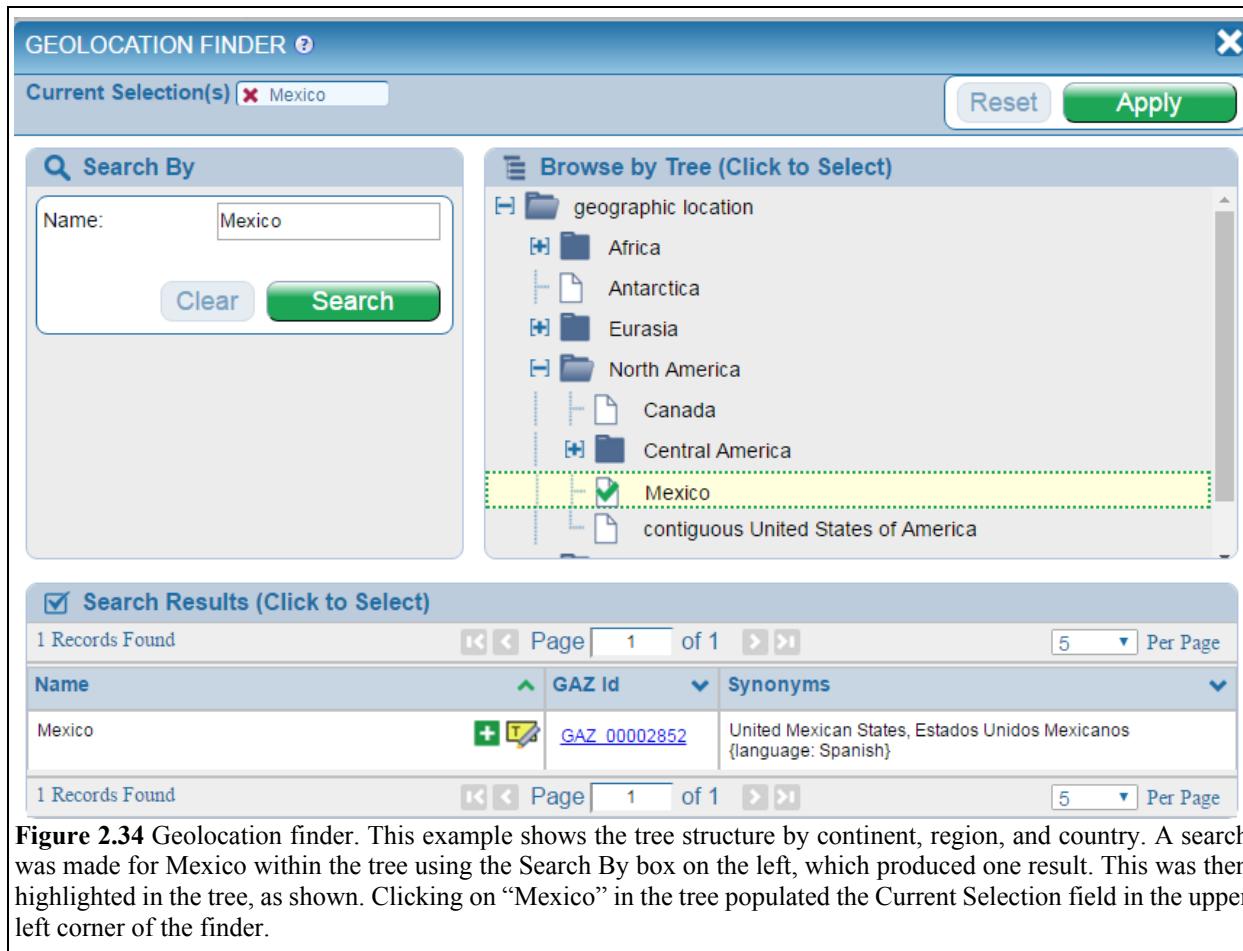


Figure 2.34 Geolocation finder. This example shows the tree structure by continent, region, and country. A search was made for Mexico within the tree using the Search By box on the left, which produced one result. This was then highlighted in the tree, as shown. Clicking on “Mexico” in the tree populated 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 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 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 describe 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 Moutafsi M et al. (Nat Biotech 2006). The methods used for Consensus are ANN, SMM, and CombLib_Sidney2008. The Consensus method uses as many of these three component methods as possible, depending on their applicability for the chosen allele and length.

NetMHCpan

NetMHCpan 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 extended data set including 10 prevalent HLA-C and 7 prevalent BoLA MHC-I molecules. The matrices of pocket-library are generated using the SMM_pmbec method described in Kim et al. (BMC Bioinformatics, 2009). 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 IC₅₀ values for each pool. IC₅₀ values for each mixture were standardized as a ratio to the geometric mean IC₅₀ value of the entire set of 180 mixtures, and then normalized at each position so that the value associated with the optimal value at each position corresponds to 1. For each position, an average (geometric) relative binding affinity (ARB) was calculated, and then the ratio of the ARB for the entire library to the ARB for each position was derived. The final results are a set of 9 by 20 scoring matrices which could predict the binding of novel peptides to MHC molecules.

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

Consensus

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

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

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

The proteasomal cleavage predictions evaluate how efficiently a peptide or its N-terminally prolonged precursors can be liberated from its source protein. The TAP transport predictions evaluate how efficiently a peptide or its N-terminal prolonged precursors are transported into the ER by TAP (Peters et al., Immunol, 2003). When this information is taken together and combined with MHC class I binding predictions, the tool yields a prediction of the efficiency with which a peptide is presented on the cell surface. The methods available are ANN, SMM, 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 takes into account the characteristics of the structurally modified proteasomes found in cells stimulated by gamma-interferon under physiological conditions. The NetChop algorithm was trained on in vitro data and MHC Class I ligand data. The use of this training set, combined with the artificial neural network methodology, makes the prediction of cleavage sites more accurate. NetChop has been trained only on human data, but since the proteasome structure is quite conserved, the algorithm developers believe that the tool is capable of making reliable predictions for at least the other mammalian proteasomes.

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

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

This web page provides information on methods for modeling and docking of antibody and protein 3D structures. The methods are available as web servers and are hosted outside the IEDB except one method, 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 Epitope Analysis Tools

2.3.3.1 Population coverage

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

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

HLA allele genotypic frequencies were obtained from Allele Frequency Net Database (<http://www.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).

2.3.3.2 Epitope conservancy

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

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.

2.3.3.3 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.

2.3.3.4 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.

2.3.3.5 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).

2.3.3.6 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.

2.3.4 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, 7 tools are currently available under the Labs designation:

Prediction LABS Tools

TepiTool
MHCII-NP
Deimmunization
CD4 T Cell Immunogenicity
LYRA

Analysis LABS Tools

RATE
ImmunomeBrowser

2.3.5 Benchmark references and data sets

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

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

- Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M. Automated benchmarking of peptide-MHC class I binding predictions. *Bioinformatics*. 2015 Jul 1;31(13):2174-81. doi: 10.1093/bioinformatics/btv123. Epub 2015 Feb 25. PubMed PMID: 25717196; PubMed Central PMCID: PMC4481849
- Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B. Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. *BMC Bioinformatics*. 2014 Jul 14;15:241. doi: 10.1186/1471-2105-15-241. PubMed PMID: 25017736; PubMed Central PMCID: PMC4111843
- Kim Y, Sidney J, Pinilla C, Sette A, Peters B. Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior. *BMC Bioinformatics*. 2009 Nov 30;10:394. PubMed PMID: 19948066.
- Peters B, Bui HH, Frankild S, Nielson M, Lundegaard C, Kostem E, Basch D, Lamberth K, Harndahl M, 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; PubMed Central 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. PubMed PMID: 21092157; PubMed Central PMCID: PMC2998531.
- Wang, P., J. Sidney, C. Dow, B. Mothe, A. Sette, B. Peters. (2008). "A Systematic Assessment of MHC Class II Peptide Binding Predictions and Evaluation of a Consensus Approach." *PLoS Computational Biology* 4(4). PMID: 18389056

For the B cell predictions, the references are:

- Krügel JV, Nielsen M, Padkjær SB, Lund O. Structural analysis of B-cell epitopes in antibody:protein complexes. *Mol Immunol*. 2013 Jan;53(1-2):24-34. doi: 10.1016/j.molimm.2012.06.001. Epub 2012 Jul 10. PubMed PMID: 22784991; PubMed Central PMCID: PMC3461403
- Krügel JV, Lundegaard C, Lund O, Nielsen M. Reliable B cell epitope predictions: impacts of method development and improved benchmarking. *PLoS Comput Biol*. 2012;8(12):e1002829. doi: 10.1371/journal.pcbi.1002829. Epub 2012 Dec 27. PubMed PMID: 23300419; PubMed Central PMCID: PMC3531324.

- Rubinstein ND, Mayrose I, Martz E, Pupko T. Epitopia: a web-server for predicting B-cell epitopes. *BMC Bioinformatics*. 2009 Sep 14;10:287. doi: 10.1186/1471-2105-10-287. PubMed PMID: 19751513; PubMed Central PMCID: PMC2751785.
- Liang S, Zheng D, Standley DM, Yao B, Zacharias M, Zhang C. EPSVR and EPMeta: prediction of antigenic epitopes using support vector regression and multiple server results. *BMC Bioinformatics*. 2010 Jul 16;11:381. doi: 10.1186/1471-2105-11-381. PubMed PMID: 20637083; PubMed Central PMCID: PMC2910724.
- Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. *BMC Struct Biol*. 2007 Oct 2;7(1):64. PMID: 17910770

2.3.6 Other Ways to Access Tools

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

The Download tab takes the user to the IEDB Tools Download web page. For users from non-commercial organizations with batch processing needs, the MHC class I and II binding prediction tools, linear B cell epitope prediction tool, ElliPro, the epitope cluster analysis tool, 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.

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 2018 event which are currently posted for user viewing are listed in Table

2.1. 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 links for Home, Specialized Searches, Analysis Resource, Help, and More IEDB. Below the navigation is a "News and Updates" section featuring a photograph of a workshop and a text block about the 2019 user workshop. To the right of this are "Latest Release Notes" for the IEDB Analysis Resource v2.21 release (March 2019) and IEDB v3.10.0 release notes. The "Support" section includes links for asking questions, browsing support topics, watching videos, and getting help with common searches. The "About the Data" section contains a figure showing pie charts for age groups (3-5, 5-18, >18) and a scatter plot of frequency within CD8+ T cells. It also links to meta-analyses, data fields, entry methods, and ontology. The "About Us" section includes links to citation guidelines, publications, acknowledgments, terms of use, and annual compendia. At the bottom right, there's a link to "View Previous Release Notes >>".

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.

Watch how to videos

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

Get help with common searches

There is a category in the Solutions Center that contains a list of common queries 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. The section also includes the IEDB System and Architecture Design document.

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 16 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 2018. This publication list was re-evaluated in December 2018 to ensure that the list was accurate and up to date. Five publications were removed and deemed non-IEDB related. Additionally, twenty-five publications that were written by the IEDB team were added after noticing that they had been overlooked in early contract years. In many cases these were also difficult to link on PubMed as well since there were typos in the contract number. As a result of this review, the publication list now contains 148 IEDB sponsored publications between program inception in 2003 and 31 December 2018.

Year	Type	Paper	PMID	Journal
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
2017	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
	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
2016	General	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
		Ebola: an analysis of immunity at the molecular level		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)		Encyclopedia of Bioimmunology
	Tools	An Ontology for Major Histocompatibility Restriction	26759709	J Biomed Semantics
		The Ontology for Biomedical Investigations	27128319	PLoS One
		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
		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
2015	General	Analysis of Human RSV immunity at the molecular level: learning from the past and present	26001197	PLoS One
		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 α -to- β (3) residue replacement for immunological recognition of peptide epitopes	25559929	ACS Chem Biol
	Tools	Automated benchmarking of peptide-MHC class I binding predictions	25717196	Bioinformatics
		Development and validation of a broad scheme for prediction of HLA class II restricted T cell epitopes	25862607	J Immunol Methods
		Automatic generation of validated specific epitope sets	26568965	J Immunol Res
		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	General	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
	Tools	MHC class II epitope predictive algorithms	20408898	Immunology
		Peptide binding predictions for HLA DR, DP and DQ molecules	21092157	BMC Bioinformatics
		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

		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
Tools		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 <i>Bacillus anthracis</i> and <i>Clostridium botulinum</i>	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
		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
Tools		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
		An analysis of the epitope knowledge related to Mycobacteria	18081934	Immunome Res
2007	General	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

		Characterization of the peptide-binding specificity of the chimpanzee class I alleles A 0301 and A 0401 using a combinatorial peptide library	17701407	Immunogenetics
2006	Tools	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
		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
2005	General	The biocurator: connecting and enhancing scientific data	17069454	PLoS Comput Biol
		The Immune Epitope Database and Analysis Resource		Conference Proceedings
		Curation of complex, context-dependent immunological data	16836764	BMC Bioinformatics
	Tools	Predicting population coverage of T-cell epitope-based diagnostics and vaccines	16545123	BMC Bioinformatics
		A community resource benchmarking predictions of peptide binding to MHC-I molecules	16789818	PLoS Comput Biol
2004	General	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
		The immune epitope database and analysis resource: from vision to blueprint	16312048	Genome Inform
	General	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 Paracoccidioides brasiliensis frequently recognized in primary peripheral blood mononuclear cell responses from sensitized individuals	15208742	Mol Med
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3.2 Publications Citing the IEDB in 2017

In 2018, the IEDB or Analysis Resource received of total of 2,215 citations. This represents an increase of 758 citations over 1,457 from the previous year (2017). The citation list includes 759 references which formally cited one or more of the 148 papers written by the IEDB team over the past sixteen years, and an additional 556 references that cited the IEDB in-text but did not cite a specific reference. Of note, this total may increase over time since these databases may not include references published late in 2018.

The formal citation list was compiled by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the 148 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 or 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). 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.

3.2.1 References Formally Citating IEDB Publications

1. Aathmanathan, V.S., Jothi, N., Prajapati, V.K., and Krishnan, M. (2018). "Investigation of immunogenic properties of Hemolin from silkworm, *Bombyx mori* as carrier protein: an immunoinformatic approach." *Scientific Reports* 8(1): 6957- [G, AR]
2. Abdallah, A.O., Coleman, H., Kamel, M., Davis, R., Landrum, T., Spencer, H., Mackintosh, S., Mahmoud, F.A., Milojkovic, N., and Wicker, C. (2018). "A novel prostate cancer immunotherapy using prostate-specific antigen peptides and *Candida* skin test reagent as an adjuvant." *SAGE open medicine* 6(2050312118800202- [G, AR]
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