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Immune Epitope Database and Analysis Resource Program

2021 Annual IEDB Compendium

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

858-752-6647
858-752-6987 (fax)
nblazeska@lji.org

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Introduction

The Immune Epitope Database and Analysis Resource (IEDB) is a public repository of immune epitope data and is sponsored by the National Institute for Allergy and Infectious Diseases (NIAID). The IEDB development started in December 2003 and it became available to the public in a beta test phase on 15 February 2006. The IEDB 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 January 2021. The second section describes the features of the IEDB 4.3 website and the Analysis Resource 2.26. The third section lists the scientific publications in 2021 for which the IEDB played a contributory role.

Since the publication of last year's 2020 Annual Compendium, the quantity of data available in the IEDB continues to increase significantly. As of January 2022, the IEDB contains data for over 1,702,000 epitopes, 74,800 antigens, 5,000,000 assays, and 173,800 receptors from more than 22,500 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 2021, 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 2020 and 2021. Of the 4,143 species/strains listed, 104 were added in 2021. 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 2021. 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 20", "T 20", "B 21", and "T 21" indicate the cumulative number of distinct B cell and T cell epitopes in the database at the end of 2020 and 2021, respectively. The two rightmost columns display the differences in the B and T cell epitope counts from 2020 to 2021. In 2021, the number of B cell epitopes increased by 77,341 from 85,646 to 162,987 and the number of T cell epitopes increased by 281,058 from 738,184 to 1,019,242.

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

ID	NEW 2021	ORGANISM ID	SPECIES / STRAIN	B 20	T 20	B 21	T 21	DELTA B	DELTA T
1		2	Bacteria	56		56			
2		106	Runella slithyformis		1		1		
3		108	Spirosoma linguale	1		1			
4		139	Borreliella burgdorferi	93	45	93	46		1
6		158	Treponema denticola		2		2		
7		160	Treponema pallidum	7	2	7	2		
8		171	Leptospira	2		2			
9		173	Leptospira interrogans	7	4	7	4		
10		195	Campylobacter coli		3		3		
11		197	Campylobacter jejuni	115	30	128	30	13	
14		210	Helicobacter pylori	88	62	88	62		
15		234	Brucella		28	1	28	1	
16		235	Brucella abortus	7	39	7	39		
17		236	Brucella ovis		3		3		
18		263	Francisella tularensis	4	16	4	16		
19		266	Paracoccus denitrificans	3		3			
20		271	Thermus aquaticus	1		1			
21		274	Thermus thermophilus	1	1	1	1		
22		280	Xanthobacter autotrophicus		1		1		
23		286	Pseudomonas	1	1	1	1		
24		287	Pseudomonas aeruginosa	97	171	98	258	1	87
25		292	Burkholderia cepacia	3	2	3	2		
26		294	Pseudomonas fluorescens		15		15		
28		300	Pseudomonas mendocina		2		2		
29		303	Pseudomonas putida	1	11	1	11		
30		306	Pseudomonas sp.		1		1		
31		312	Pseudomonas sp. RS-16	1		1			
32		316	Pseudomonas stutzeri		3		3		
33		319	Pseudomonas savastanoi pv. phaseolicola	1		1			
34		346	Xanthomonas citri		1		1		
35		354	Azotobacter vinelandii		2		2		
36		358	Agrobacterium tumefaciens	1	2	1	2		
37		382	Sinorhizobium meliloti		1		1		
38		384	Rhizobium leguminosarum		1		1		
39		446	Legionella pneumophila	1	1	1	1		
40		469	Acinetobacter		1		1		
41		470	Acinetobacter baumannii	10	8	14	10	4	2
42		471	Acinetobacter calcoaceticus		1		1		
43		480	Moraxella catarrhalis	10		10			

44		485	Neisseria gonorrhoeae	77	15	77	15		
45		487	Neisseria meningitidis	91	23	102	23	11	
46		491	Neisseria meningitidis serogroup B	46	1	47	1	1	
47		511	Alcaligenes faecalis	3	2	3	2		
48		520	Bordetella pertussis	352	218	352	218		
49		521	Bordetella avium		1		1		
51		543	Enterobacteriaceae	4		4			
52		544	Citrobacter	1		1			
53		546	Citrobacter freundii	2		2			
54		548	Klebsiella aerogenes		1		1		
55		550	Enterobacter cloacae		10		10		
56		554	Pectobacterium carotovorum	2		2			
57		556	Dickeya chrysanthemi	1		1			
58		562	Escherichia coli	279	187	280	187	1	
59		573	Klebsiella pneumoniae	29	12	33	12	4	
60		582	Morganella morganii	1		1			
61		583	Proteus	2		2			
62		584	Proteus mirabilis	7		7			
64		590	Salmonella	3		3			
65		596	Salmonella enterica subsp. enterica serovar Muenchen	1		1			
66		599	Salmonella sp.	1		1			
67		605	Salmonella enterica subsp. enterica serovar Pullorum		1		1		
68		611	Salmonella enterica subsp. enterica serovar Heidelberg	9		9			
69		615	Serratia marcescens	1	3	1	3		
70		621	Shigella boydii		4		4		
71		622	Shigella dysenteriae	6	2	6	2		
72		623	Shigella flexneri	77	11	77	11		
73		624	Shigella sonnei		1		1		
74		630	Yersinia enterocolitica	6	29	6	29		
75		632	Yersinia pestis	24	324	24	324		
76		633	Yersinia pseudotuberculosis		2		2		
78		644	Aeromonas hydrophila	9	3	9	3		
79		645	Aeromonas salmonicida	59		59			
80		659	Photobacterium phosphoreum		1		1		
81		666	Vibrio cholerae	38	92	40	92	2	
82		670	Vibrio parahaemolyticus	1	57	1	57		
83		671	Vibrio proteolyticus	1		1			
84		672	Vibrio vulnificus	1	66	2	66	1	
85		674	Vibrio mimicus	2		2			
86		686	Vibrio cholerae O1 biovar El Tor	3	1	3	1		
87		703	Plesiomonas shigelloides		2		2		
88		714	Aggregatibacter actinomycetemcomitans	1	4	1	4		
89		715	Actinobacillus pleuropneumoniae		2		2		

90		727	Haemophilus influenzae	36	72	36	72		
91		730	[Haemophilus] ducreyi	3	1	3	1		
92		731	Histophilus somni		1		1		
93		738	Glaesserella parasuis	1		1			
94		747	Pasteurella multocida	1	10	1	10		
95		769	Anaplasma centrale		2		2		
96		770	Anaplasma marginale	25	14	25	14		
97	X	774	Bartonella bacilliformis			35		35	
98		777	Coxiella burnetii	2	311	2	311		
99		779	Ehrlichia ruminantium	3	23	3	23		
100		781	Rickettsia conorii		13		13		
101		782	Rickettsia prowazekii		23		23		
102		783	Rickettsia rickettsii		1		1		
103		784	Orientia tsutsugamushi	87		87			
104		785	Rickettsia typhi		3		3		
105		787	Rickettsia australis		1		1		
106		788	Rickettsia canadensis		1		1		
107		813	Chlamydia trachomatis	241	69	241	69		
108		817	Bacteroides fragilis	27	3	27	3		
111		837	Porphyromonas gingivalis	111	22	111	22		
114		920	Acidithiobacillus ferrooxidans		1		1		
115		944	Ehrlichia canis	7	1	8	1	1	
116		945	Ehrlichia chaffeensis	14	1	14	1		
118		948	Anaplasma phagocytophilum	45		45			
119		955	Wolbachia pipientis	1		1			
120		1006	Marivirga tractuosa	1	1	1	1		
121		1018	Capnocytophaga ochracea		1		1		
122		1019	Capnocytophaga sputigena		1		1		
123		1022	Beggiatoa alba	1		1			
124		1063	Cereibacter sphaeroides		1		1		
125		1076	Rhodopseudomonas palustris		2		2		
126		1126	Microcystis aeruginosa	1		1			
127		1224	Proteobacteria	3		3			
128		1245	Leuconostoc mesenteroides	1		1			
129		1254	Pediococcus acidilactici	1		1			
130		1260	Finegoldia magna		1		1		
131		1265	Ruminococcus flavefaciens		1		1		
132		1270	Micrococcus luteus	1		1			
133		1279	Staphylococcus	1		1			
134		1280	Staphylococcus aureus	145	49	194	52	49	3
136		1292	Staphylococcus warneri	1		1			
137		1299	Deinococcus radiodurans	3		3			
138		1301	Streptococcus	3		3			

139		1303	Streptococcus oralis	12	1	12	1		
141		1305	Streptococcus sanguinis		1		1		
142		1307	Streptococcus suis	4		4			
143		1309	Streptococcus mutans	146	89	146	89		
144		1310	Streptococcus sobrinus	1		1			
145		1311	Streptococcus agalactiae	19		19			
146		1313	Streptococcus pneumoniae	95	29	96	31	1	2
147		1314	Streptococcus pyogenes	400	125	410	125	10	
148		1317	Streptococcus downei	2	1	2	1		
149		1319	Streptococcus sp. 'group B'	4		4			
151		1324	Streptococcus sp. G148	14	5	14	5		
152		1334	Streptococcus dysgalactiae	3	7	3	7		
153		1336	Streptococcus equi	22	14	22	14		
154		1349	Streptococcus uberis	8		8			
155		1351	Enterococcus faecalis	2		2			
156		1352	Enterococcus faecium	6		6			
157		1358	Lactococcus lactis		2		2		
158		1386	Bacillus		1		1		
159		1390	Bacillus amyloliquefaciens	18	3	18	3		
160		1392	Bacillus anthracis	403	209	403	209		
161		1396	Bacillus cereus	1	15	1	15		
162		1402	Bacillus licheniformis		10		10		
163		1404	Priestia megaterium		1		1		
164		1405	Bacillus mycoides		4		4		
165		1406	Paenibacillus polymyxa	1		1			
166		1408	Bacillus pumilus		1		1		
167		1422	Geobacillus stearothermophilus	2	1	2	1		
168		1423	Bacillus subtilis	2	4	2	4		
169		1428	Bacillus thuringiensis	7	10	7	10		
170		1435	Bacillus thuringiensis serovar san diego		2		2		
171		1454	Schinkia azotoformans		1		1		
172		1467	Lederbergia lentus		1		1		
173		1491	Clostridium botulinum	205	111	207	111	2	
174		1492	Clostridium butyricum		1		1		
175		1496	Clostridioides difficile	98	1	98	2		1
176		1502	Clostridium perfringens	41	2	41	2		
177		1513	Clostridium tetani	79	282	82	282	3	
178		1520	Clostridium beijerinckii	1		1			
179		1542	Clostridium novyi		1		1		
180		1585	Lactobacillus delbrueckii subsp. bulgaricus	1		1			
181		1599	Latilactobacillus sakei		1		1		
182		1604	Lactobacillus amylovorus		1		1		
183		1613	Limosilactobacillus fermentum	1		1			

185		1638	Listeria ivanovii	1	2	1	2		
186		1639	Listeria monocytogenes	24	103	25	104	1	1
187		1641	Listeria grayi		1		1		
188		1642	Listeria innocua	2	2	2	2		
189		1646	Renibacterium salmoninarum	12		12			
190		1661	Trueperella pyogenes	7		7			
191		1664	Arthrobacter glacialis		1		1		
192		1681	Bifidobacterium bifidum		1		1		
193		1685	Bifidobacterium breve		1		1		
194		1716	Corynebacterium		1		1		
195		1717	Corynebacterium diphtheriae	15	56	15	56		
196		1718	Corynebacterium glutamicum		26		26		
198		1747	Cutibacterium acnes		2		2		
199		1752	Propionibacterium freudenreichii subsp. shermanii		1		1		
200		1763	Mycobacterium	29	22	29	22		
201		1764	Mycobacterium avium	6	18	6	18		
202		1765	Mycobacterium tuberculosis variant bovis	50	327	50	327		
203		1766	Mycolicibacterium fortuitum		1		1		
204		1767	Mycobacterium intracellulare		1		1		
205		1768	Mycobacterium kansasii	9	12	9	12		
206		1769	Mycobacterium leprae	127	409	153	409	26	
207		1770	Mycobacterium avium subsp. paratuberculosis	106	15	106	15		
208		1771	Mycolicibacterium phlei		1		1		
209		1772	Mycolicibacterium smegmatis		28		29		1
210		1773	Mycobacterium tuberculosis	652	2613	677	2641	25	28
211		1774	Mycobacteroides chelonae	1		1			
212		1778	Mycobacterium gordonae	1		1			
213		1781	Mycobacterium marinum		1		2		1
214		1783	Mycobacterium scrofulaceum	4		4			
215		1795	Mycolicibacterium neoaurum		1		1		
216		1804	Mycolicibacterium gilvum		1		1		
217		1809	Mycobacterium ulcerans		11		11		
219		1828	Rhodococcus fascians		2		2		
220		1830	Rhodococcus ruber		1		1		
221		1833	Rhodococcus erythropolis		3		3		
222		1836	Saccharopolyspora erythraea	4		4			
223		1895	Streptomyces avidinii	1		1			
224		1902	Streptomyces coelicolor		2		2		
225		1916	Streptomyces lividans	10	1	11	1	1	
226		1943	Streptomyces griseoruber		1		1		
227		1946	Streptomyces kasugaensis		1		1		
228		2039	Tropheryma whipplei	1		1			
229		2097	Mycoplasma genitalium		1		1		

230		2099	Mycoplasma hyopneumoniae	3		3			
231		2100	Mycoplasma hyorhinis	1		1			
232		2104	Mycoplasma pneumoniae	16	2	20	6	4	4
234		2133	Spiroplasma citri		1		1		
235		2147	Acholeplasma	1		1			
236		2148	Acholeplasma laidlawii		2		2		
237	X	2173	Methanobrevibacter smithii				1		1
238		2190	Methanocaldococcus jannaschii		1		1		
239		2234	Archaeoglobus fulgidus	1	1	1	1		
240		2242	Halobacterium salinarum	1		1			
241		2261	Pyrococcus furiosus		1		1		
243		2287	Saccharolobus solfataricus	1		1			
244		2336	Thermotoga maritima	2		2			
245		2439	Plasmid ColB2	1		1			
246		2465	Plasmid F	1		1			
248		2736	Verrucomicrobium spinosum	1		1			
249		2759	Eukaryota	1		1			
250		2864	Dinophyceae	1		3		2	
251		2903	Emiliania huxleyi		1		1		
252		3039	Euglena gracilis	1		1			
253		3068	Volvox carteri f. nagariensis		1		1		
254		3318	Pinaceae	2		2			
255		3346	Pinus pinea	37		37			
256		3352	Pinus taeda	4		4			
257		3369	Cryptomeria japonica	45	300	45	300		
258		3469	Papaver somniferum	1		1			
259		3505	Betula pendula	88	337	91	337	3	
260		3513	Quercus alba		5		5		
261		3517	Alnus glutinosa		17		17		
262		3559	Chenopodium album	3	2	3	2		
263		3562	Spinacia oleracea	4		4			
265		3617	Fagopyrum esculentum	40		40			
266		3645	Bertholletia excelsa	7	24	7	24		
267		3656	Cucumis melo	13		13			
268		3677	Trichosanthes kirilowii	4		4			
269		3702	Arabidopsis thaliana	6	10	6	10		
270		3704	Armoracia rusticana	5		5			
271		3707	Brassica juncea	9		9			
273		3711	Brassica rapa	1		1			
274		3726	Raphanus sativus	1		1			
275		3728	Sinapis alba	2		2			
276		3750	Malus domestica	27	48	27	48		
277		3755	Prunus dulcis	19		19			

278		3758	Prunus domestica	4		4			
279		3760	Prunus persica	19	51	19	51		
280		3816	Abrus precatorius	99		99			
281		3818	Arachis hypogaea	483	263	497	263	14	
282		3847	Glycine max	611	2	649	8	38	6
283		3864	Lens culinaris	19		19			
284		3885	Phaseolus vulgaris	10	3	10	3		
286		3972	Viscum album	17		17			
287		3981	Hevea brasiliensis	212	43	212	43		
288		3988	Ricinus communis	81	6	90	6	9	
289		4012	Rhus		1		1		
290		4026	Acer pseudoplatanus	2		2			
291		4039	Daucus carota		46		46		
292		4045	Apium graveolens		14		14		
293		4081	Solanum lycopersicum	3		3			
294		4097	Nicotiana tabacum	5		5			
295		4100	Nicotiana benthamiana	5		5			
298		4146	Olea europaea	76	19	76	19		
299		4163	Digitalis	1		1			
300		4182	Sesamum indicum	11		11			
301		4212	Ambrosia artemisiifolia	4	215	5	215	1	
302		4214	Ambrosia trifida		10		10		
303		4215	Ambrosia artemisiifolia var. elatior	9	12	9	12		
304		4220	Artemisia vulgaris	1	70	4	70	3	
305		4232	Helianthus annuus	18		18			
306		4479	Poaceae	1		1			
307		4498	Avena sativa		16		16		
308		4509	Dactylis glomerata		12		12		
309		4513	Hordeum vulgare		61		61		
310		4522	Lolium perenne	44	123	44	123		
311		4530	Oryza sativa	2		2			
312		4545	Poa pratensis	34	35	34	35		
313		4550	Secale cereale	51	82	51	82		
314		4558	Sorghum bicolor		1		1		
315		4565	Triticum aestivum	651	593	656	624	5	31
316		4567	Triticum turgidum subsp. durum		1		1		
317		4568	Triticum monococcum		1		1		
319		4577	Zea mays	3	1	3	1		
320		4606	Lolium arundinaceum	1		1			
321		4615	Ananas comosus	3		3			
322		4641	Musa acuminata	50	1	50	1		
323		4751	Fungi	6		6			
324		4754	Pneumocystis carinii	2	1	2	1		

325		4903	Cyberlindnera jadinii	12		12			
326		4920	Millerozyma farinosa		1		1		
327		4932	Saccharomyces cerevisiae	32	17	37	17	5	
328		4954	Zygosaccharomyces bailii		1		1		
329		5037	Histoplasma capsulatum		1		1		
330		5039	Blastomyces dermatitidis		1		1		
331		5052	Aspergillus	4		7		3	
332		5057	Aspergillus clavatus		1		1		
333		5059	Aspergillus flavus	6	1	6	1		
334		5060	Aspergillus giganteus		4		4		
335		5061	Aspergillus niger		3		3		
336		5064	Aspergillus restrictus	1		1			
337		5067	Aspergillus parasiticus		1		1		
338		5076	Penicillium chrysogenum	45	19	45	19		
339		5077	Penicillium citrinum	13		13			
340		5141	Neurospora crassa	6	3	6	3		
341		5207	Cryptococcus neoformans	2	3	4	3	2	
342		5325	Trametes versicolor		1		1		
343		5334	Schizophyllum commune	1	1	1	1		
344		5346	Coprinopsis cinerea		1		1		
345		5476	Candida albicans	111	82	114	82	3	
346		5480	Candida parapsilosis	1		1			
347		5482	Candida tropicalis		2		2		
348		5501	Coccidioides immitis		1		1		
349		5503	Curvularia lunata	20	10	20	10		
350		5507	Fusarium oxysporum		5		5		
351		5518	Fusarium graminearum	9		9			
352		5551	Trichophyton rubrum	2	27	2	27		
353		5554	Cutaneotrichosporon cutaneum	1		1			
354		5599	Alternaria alternata	8	38	8	38		
355		5658	Leishmania	4	1	4	1		
356		5659	Leishmania amazonensis		15	5	15	5	
357		5660	Leishmania braziliensis	6		12		6	
358		5661	Leishmania donovani	30	102	30	107		5
359		5664	Leishmania major	32	186	32	186		
360		5665	Leishmania mexicana	3	3	3	3		
361		5667	Leishmania aethiopica	16		16			
362		5671	Leishmania infantum	108	9	108	9		
363		5679	Leishmania panamensis	3	7	3	18		11
364		5682	Leishmania pifanoi		20		20		
365		5691	Trypanosoma brucei	13	6	13	6		
366		5692	Trypanosoma congolense	1		1			
367		5693	Trypanosoma cruzi	164	460	164	460		

368		5702	Trypanosoma brucei brucei	5		5			
369		5722	Trichomonas vaginalis	80	1	80	1		
370		5741	Giardia intestinalis	1	13	1	13		
371		5755	Acanthamoeba castellanii	14	3	14	3		
372		5759	Entamoeba histolytica	30	14	30	14		
373		5762	Naegleria gruberi	1		1			
374		5801	Eimeria acervulina	1		1			
375		5802	Eimeria tenella	8		8			
376		5807	Cryptosporidium parvum	4	31	4	31		
377		5811	Toxoplasma gondii	99	103	99	103		
378		5820	Plasmodium	3	4	3	4		
379		5821	Plasmodium berghei	20	58	31	58	11	
380		5823	Plasmodium berghei ANKA	7	65	7	65		
381		5824	Plasmodium brasilianum	2		2			
382		5825	Plasmodium chabaudi	4	4	4	4		
383		5827	Plasmodium cynomolgi	2		2			
385		5833	Plasmodium falciparum	3380	842	3391	1053	11	211
386		5834	Plasmodium falciparum RO-33	8	1	8	1		
387		5835	Plasmodium falciparum CAMP/Malaysia	36	3	36	3		
388		5836	Plasmodium falciparum CDC/Honduras	18		18			
389		5837	Plasmodium falciparum FC27/Papua New Guinea	47	60	47	60		
390		5838	Plasmodium falciparum FCR-3/Gambia	94		94			
391		5839	Plasmodium falciparum K1	18	19	18	19		
392		5840	Plasmodium falciparum LE5		2		2		
393		5841	Plasmodium falciparum Mad20/Papua New Guinea	8	47	8	47		
394		5842	Plasmodium falciparum NF7/Ghana	4		4			
395		5843	Plasmodium falciparum NF54	21	31	21	31		
396		5846	Plasmodium falciparum T4/Thailand	25	1	25	1		
397		5848	Plasmodium falciparum isolate WELLCOME	25	51	25	51		
398		5850	Plasmodium knowlesi	2	17	2	17		
399		5851	Plasmodium knowlesi strain H	41	10	41	10		
400		5852	Plasmodium knowlesi strain Nuri		10		10		
401		5855	Plasmodium vivax	372	176	387	176	15	
402		5857	Plasmodium fragile		5		5		
403		5858	Plasmodium malariae	1		1			
404		5861	Plasmodium yoelii	17	39	19	39	2	
405		5865	Babesia bovis	5	8	5	8		
406		5866	Babesia bigemina		3		3		
407		5868	Babesia microti	5		5			
408		5872	Theileria equi	8		8			
409		5874	Theileria annulata	1		1			
410		5875	Theileria parva	28	20	28	20		
412		5970	Exophiala dermatitidis		1		1		

413		6035	Encephalitozoon cuniculi		5		5		
414		6100	Aequorea victoria	5	5	5	5		
415		6181	Schistosoma	3		3			
416		6182	Schistosoma japonicum	1207	53	1207	53		
417		6183	Schistosoma mansoni	102	52	3162	52	3060	
418		6184	Schistosoma bovis	2		2			
419		6192	Fasciola hepatica	320	28	320	28		
420		6198	Opisthorchis viverrini	4		4			
421		6203	Taenia ovis	8		8			
422		6204	Taenia solium	29	4	29	4		
423		6206	Taenia saginata	13		13			
424		6207	Taenia crassiceps	11	1	11	1		
425		6210	Echinococcus granulosus	41	2	41	2		
426		6211	Echinococcus multilocularis	14	6	22	14	8	8
427		6238	Caenorhabditis briggsae	1		1			
428		6239	Caenorhabditis elegans	2	10	2	10		
430	X	6252	Ascaris lumbricoides			11		11	
431		6253	Ascaris suum	1	1	1	349		348
432		6265	Toxocara canis	3		3			
433		6269	Anisakis simplex	38	28	40	28	2	
434		6279	Brugia malayi	10	5	10	5		
435		6280	Brugia pahangi	1		1			
436		6282	Onchocerca volvulus	4394	39	4394	39		
437		6289	Haemonchus contortus	3		3			
438		6293	Wuchereria bancrofti	13	8	13	8		
439		6299	Litomosoides carinii	3		3			
440		6334	Trichinella spiralis	18	7	18	7		
441		6339	Heligmosomoides polygyrus	3		3			
442		6421	Hirudo medicinalis		3		3		
443		6454	Haliotis rufescens	1		1			
444		6491	Conus geographus	30		30			
445		6492	Conus magus	2		2			
446		6493	Conus striatus	11		11			
448		6536	Helix pomatia	1		1			
449		6594	Macrocallista nimbosa	1		1			
450		6661	Artemia franciscana	2		2			
451		6687	Penaeus monodon	10	23	10	23		
452		6689	Penaeus vannamei	143		158	2	15	2
453		6690	Penaeus aztecus	51	31	51	31		
454		6728	Procambarus clarkii	3		3			
455		6761	Scylla serrata	13		13			
456		6850	Limulus polyphemus		1		1		
457		6853	Tachypleus tridentatus	1		1			

458		6858	Androctonus australis	9		9			
459		6860	Androctonus mauritanicus mauritanicus	1		1			
460		6878	Centruroides noxius	10		10			
461		6887	Tityus serrulatus	92		92			
462		6925	Latrodectus tredecimguttatus		1		1		
463		6938	Ornithodoros moubata	20		20			
464		6941	Rhipicephalus microplus	2		2			
465		6945	Ixodes scapularis	11		11			
466		6953	Dermatophagoides		578		578		
467		6954	Dermatophagoides farinae	58	111	58	111		
468		6956	Dermatophagoides pteronyssinus	148	326	155	326	7	
469		6958	Euroglyphus maynei		10		10		
470		6973	Blattella germanica	23	501	23	501		
471		6978	Periplaneta americana	25	6	30	6	5	
472		7088	Lepidoptera		1		1		
473		7108	Spodoptera frugiperda		4		4		
474		7130	Manduca sexta		3		3		
475		7137	Galleria mellonella	2		2			
476		7154	Chironomus thummi	2	3	2	3		
477		7155	Chironomus thummi thummi	58	27	58	27		
478		7160	Aedes albopictus	7		7			
479		7165	Anopheles gambiae	8	2	8	2		
480		7227	Drosophila melanogaster	11	17	11	17		
481		7234	Drosophila persimilis	1		1			
482		7386	Sarcophaga peregrina		1		1		
483		7441	Dolichovespula maculata	11	20	11	20		
484		7444	Vespa basalis	1		1			
485		7453	Vespula maculifrons	1		1			
486		7454	Vespula vulgaris	2	95	2	95		
487		7460	Apis mellifera	15	108	15	108		
488		7469	Apis mellifera ligustica		1		1		
489		7515	Ctenocephalides felis		2		2		
490		7719	Ciona intestinalis	2		2			
491		7726	Styela plicata	6		6			
492		7742	Vertebrata	4		4			
493		7777	Chondrichthyes	1		1			
494		7787	Tetronarce californica	151	75	151	75		
495		7788	Torpedo marmorata	3	3	3	3		
496		7955	Danio rerio	2	3	2	3		
497		7957	Carassius auratus	3	1	3	1		
498		7962	Cyprinus carpio	6	1	6	1		
499		8005	Electrophorus electricus	4		4			
500		8018	Oncorhynchus keta		6		6		

501		8022	Oncorhynchus mykiss	1		1			
502		8030	Salmo salar	35		35			
503		8049	Gadus morhua	44		44			
504		8053	Gadus morhua callarias	10		10			
505		8090	Oryzias latipes	2	1	2	1		
506		8255	Paralichthys olivaceus	1		1			
507		8342	Anura	1		1			
508		8355	Xenopus laevis	4	5	4	5		
509		8364	Xenopus tropicalis	2	2	2	2		
510		8554	Heloderma suspectum		1		1		
511		8613	Bungarus fasciatus	1		1			
512		8616	Bungarus multicinctus	17	3	17	3		
513		8620	Dendroaspis polylepis polylepis	22		22			
514		8654	Naja nigricollis	3	2	3	2		
516		8656	Naja atra	14		14			
517		8657	Naja oxiana	4		4			
518		8658	Naja pallida	1	1	1	1		
519		8663	Notechis scutatus	2		2			
520		8667	Oxyuranus scutellatus scutellatus	4		4			
521		8671	Pseudechis porphyriacus	3		3			
522		8704	Vipera ammodytes	1		1			
523		8722	Bothrops asper	28		28			
524		8724	Bothrops jararaca	5		5			
525		8725	Bothrops atrox	13		13			
526		8726	Bothrops jararacussu	13		13			
527		8732	Crotalus durissus terrificus	31		31			
528		8753	Lachesis muta muta	45		45			
529		8801	Struthio camelus	2		2			
530		8839	Anas platyrhynchos	2		2			
531		8845	Anser cygnoides	2		2			
532		8855	Cairina moschata	2	1	2	1		
533		8932	Columba livia		10		10		
534		8996	Numida meleagris	1		1			
535		9014	Colinus virginianus	1	3	1	3		
536		9031	Gallus gallus	406	371	406	2194		1823
537		9057	Phasianus colchicus colchicus	1		1			
539		9103	Meleagris gallopavo	8		9		1	
540		9258	Ornithorhynchus anatinus		1		1		
541		9322	Macropus sp.	1		1			
542		9337	Trichosurus vulpecula	45		45			
543		9397	Chiroptera	1		1			
545		9447	Lemur catta	1		1			
546		9479	Platyrrhini	1		1			

547		9483	Callithrix jacchus	1	4	1	4		
548		9488	Saguinus mystax	1		1			
549		9491	Saguinus imperator	1		1			
550		9502	Alouatta caraya	1		1			
551		9505	Aotus trivirgatus	1		1			
552		9509	Ateles geoffroyi		1		1		
553		9510	Ateles paniscus	1		1			
554		9511	Ateles sp.	1		1			
555		9515	Sapajus apella	1		1			
556		9519	Lagothrix lagotricha	1		1			
557		9521	Saimiri sciureus	1		1			
558		9534	Chlorocebus aethiops		5		5		
559		9538	Erythrocebus patas		1		1		
560		9541	Macaca fascicularis	3	4	6	4	3	
561		9544	Macaca mulatta	3	5	3	5		
563		9548	Macaca radiata	14	1	14	1		
564		9555	Papio anubis	1		1			
565		9556	Papio cynocephalus	1		1			
566		9580	Hylobates lar		1		1		
567		9593	Gorilla gorilla		2		2		
568		9595	Gorilla gorilla gorilla		6		6		
569		9597	Pan paniscus		1		1		
570		9598	Pan troglodytes	7	25	7	25		
571		9600	Pongo pygmaeus		2		2		
572		9601	Pongo abelii		2		2		
573		9606	Homo sapiens	33824	556627	34436	819449	612	262822
574		9615	Canis lupus familiaris	21	1937	24	1937	3	
575		9627	Vulpes vulpes	1		1			
576		9666	Mustela lutreola	1		1			
577		9685	Felis catus	42	117	42	117		
578		9721	Cetacea	1		1			
579		9755	Physeter catodon	2	34	2	34		
580		9796	Equus caballus	56	57	56	57		
581		9798	Equus przewalskii		1		1		
582		9823	Sus scrofa	125	55	126	55	1	
583		9825	Sus scrofa domesticus		5		5		
584		9844	Lama glama	1		1			
585		9860	Cervus elaphus	6		6			
586		9864	Cervus canadensis nelsoni	5		5			
587		9874	Odocoileus virginianus	2		2			
588		9913	Bos taurus	1345	856	1345	856		
589		9925	Capra hircus	11		11			
590		9940	Ovis aries	96	17	96	17		

591		9978	Ochotona princeps		1		1		
592		9986	Oryctolagus cuniculus	66	10	66	10		
593		10029	Cricetulus griseus	9		9			
594		10036	Mesocricetus auratus	58		58			
595		10042	Peromyscus maniculatus		1		1		
596		10090	Mus musculus	750	33667	762	43757	12	10090
597		10092	Mus musculus domesticus		12		12		
598		10114	Rattus	11		11			
599		10116	Rattus norvegicus	294	33150	295	33151	1	1
601		10141	Cavia porcellus	37	86	37	86		
602		10243	Cowpox virus		26		26		
603		10244	Monkeypox virus	5	2	5	2		
604		10245	Vaccinia virus	11	647	11	729		82
605		10247	Vaccinia virus WR 65-16		4		4		
606		10248	Vaccinia virus LC16M8		5		5		
607		10249	Vaccinia virus Copenhagen	31	851	31	851		
608		10251	Vaccinia virus IHD-J	1		1			
609		10253	Vaccinia virus Tian Tan		21		21		
610		10254	Vaccinia virus WR	31	6823	31	6823		
611		10255	Variola virus		249		250		1
612		10258	Orf virus	1		1			
613		10261	Fowlpox virus		7		7		
614		10273	Myxoma virus		4		4		
615		10276	Swinepox virus		2		2		
616		10292	Herpesviridae		1		1		
617		10298	Human alphaherpesvirus 1	183	585	183	585		
618		10299	Human alphaherpesvirus 1 strain 17	44	64	44	64		
619		10301	Human alphaherpesvirus 1 strain Angelotti		4		4		
620		10303	Human alphaherpesvirus 1 strain HFEM	2		2			
621		10304	Human alphaherpesvirus 1 strain F	17	5	17	5		
622		10306	Human alphaherpesvirus 1 strain KOS	17	4	17	4		
623		10308	Human alphaherpesvirus 1 strain Patton	3		3			
624		10309	Human alphaherpesvirus 1 strain SC16	5	2	5	2		
625		10310	Human alphaherpesvirus 2	295	229	295	229		
626		10312	Human herpesvirus 2 strain 186	1	1	1	1		
627		10313	Human herpesvirus 2 strain 333	2	5	2	5		
628		10315	Human herpesvirus 2 strain HG52		32		32		
629		10317	Cercopithecine alphaherpesvirus 2		1		1		
630		10320	Bovine alphaherpesvirus 1	7	40	7	40		
631		10323	Bovine herpesvirus type 1.1 (strain Cooper)	9	17	9	17		
632		10324	Bovine herpesvirus type 1.1 (strain P8-2)	1		1			
633		10325	Macacine alphaherpesvirus 1	366		366			
634		10326	Equid alphaherpesvirus 1	7	218	7	218		

635		10331	Equid alphaherpesvirus 4	6		6			
636		10335	Human alphaherpesvirus 3	10	132	10	132		
637		10338	Human herpesvirus 3 strain Dumas		29		29		
638		10345	Suid alphaherpesvirus 1	13	3	14	3	1	
639		10349	Suid herpesvirus 1 (strain NIA-3)	4		4			
641		10359	Human betaherpesvirus 5	124	628	126	1322	2	694
642		10360	Human herpesvirus 5 strain AD169	235	456	236	535	1	79
643		10363	Human herpesvirus 5 strain Towne	95	26	96	26	1	
644		10366	Murid betaherpesvirus 1	2	64	2	64		
645		10367	Murine cytomegalovirus (strain Smith)		32		32		
647		10369	Human herpesvirus 6 (strain GS)	2		2			
648		10370	Human herpesvirus 6 (strain Uganda-1102)	2	3	2	3		
649		10372	Human betaherpesvirus 7	2	4	2	4		
650		10373	Macaca mulatta cytomegalovirus		76		76		
651		10376	Human gammaherpesvirus 4	2367	703	2423	707	56	4
652		10377	Human herpesvirus 4 strain B95-8	187	373	187	389		16
653		10378	Human herpesvirus 4 strain RAJI	1		1			
654		10381	Saimiriine gammaherpesvirus 2		3		3		
655		10390	Gallid alphaherpesvirus 2		1		1		
656		10407	Hepatitis B virus	299	761	388	768	89	7
657		10408	Hepatitis B virus subtype adw2	82	61	82	61		
658		10409	Hepatitis B virus adr4		9		9		
659		10410	Hepatitis B virus adw/991	2	2	2	2		
660		10411	Hepatitis B virus alpha1		19		19		
661		10412	Hepatitis B virus adw/Indonesia/PIDW420		3		3		
662		10414	Hepatitis B virus LSH/chimpanzee		2		2		
663		10415	Hepatitis B virus adw/Okinawa/PODW282		5		5		
664		10418	Hepatitis B virus subtype ayw	57	185	57	185		
665		10419	Hepatitis B virus subtype adyw	4	45	4	45		
666		10430	Woodchuck hepatitis virus 1	3		3			
667		10433	Woodchuck hepatitis virus 8		34		34		
668		10479	Thermoproteus tenax virus 1	1		1			
669		10497	African swine fever virus	5	26	9	31	4	5
670		10498	African swine fever virus BA71V	56		58	106	2	106
671	X	10514	Canine adenovirus 2			2		2	
672		10515	Human adenovirus 2	28	16	28	59		43
673		10519	Human adenovirus 7	4		4			
674		10521	Human adenovirus 14	4		4			
675		10524	Human adenovirus 41	1		1			
676		10529	Human adenovirus 31		7		7		
677		10530	Murine adenovirus 1	1	2	1	2		
678		10533	Human adenovirus 1		1		1		
679		10541	Human adenovirus 11		12		12		

680		10562	Bos taurus papillomavirus 4	10	3	10	3		
681		10566	Human papillomavirus	3	1	3	1		
682		10573	human papillomavirus 13	1	1	1	1		
684		10580	human papillomavirus 11	9	43	9	43		
685		10583	Human papillomavirus type 1a	8	15	8	15		
686		10585	human papillomavirus 31	13	7	13	7		
687		10586	human papillomavirus 33	6	9	6	9		
688		10587	human papillomavirus 35	1	1	1	1		
689		10588	human papillomavirus 39	1	1	1	1		
690		10589	Human papillomavirus type 41		1		1		
691		10592	human papillomavirus 44		1		1		
692		10593	human papillomavirus 45	2	9	3	9	1	
693		10595	human papillomavirus 51	1	1	1	1		
694		10596	human papillomavirus 56	1	5	1	5		
695		10598	human papillomavirus 58	49	34	49	34		
696		10600	Human papillomavirus type 6b	11	29	11	29		
697		10611	human papillomavirus 30	1		1			
698		10614	Human papillomavirus 3		3		3		
699		10615	human papillomavirus 40	1	1	1	1		
700		10617	Human papillomavirus 4		4		4		
701		10618	human papillomavirus 52	1	36	1	36		
702		10620	Human papillomavirus type 7	1	3	1	3		
703		10623	Kappapapillomavirus 2	5	7	5	7		
704		10631	BK virus strain AS		1		1		
705		10632	JC polyomavirus	9	96	9	96		
706		10636	Murine polyomavirus strain A2	1	3	1	3		
707		10638	Kilham polyomavirus		1		1		
708		10665	Escherichia virus T4	10	20	10	20		
709		10678	Escherichia virus P1		6		6		
710		10703	Corynephage beta	2		2			
711		10710	Escherichia virus Lambda		6		6		
712		10754	Salmonella virus P22	6		6			
713		10760	Escherichia phage T7	1		1			
714		10783	Aleutian mink disease parvovirus (STRAIN G)	3		3			
715		10786	Feline panleukopenia virus		4		4		
716		10788	Canine parvovirus	23	20	24	21	1	1
717		10790	Canine parvovirus strain CPV-D CORNELL 320	1		1			
718		10791	Canine parvovirus strain N	47		47			
719		10793	Mink enteritis virus strain Abashiri	1		1			
720		10796	Porcine parvovirus	40		41		1	
721		10798	Human parvovirus B19	94	44	94	44		
722		10804	adeno-associated virus 2	42	153	42	153		
723		10847	Escherichia virus phiX174	1		1			

724		10863	Enterobacteria phage f1	1	1	1	1		
725		10864	Enterobacteria phage fd	7	1	7	1		
726		10879	Pseudomonas virus phi6	7		7			
727		10884	Mammalian orthoreovirus 1 Lang	3		3			
728		10886	Mammalian orthoreovirus 3 Dearing	1		1			
729		10891	Reovirus sp.		2		2		
730		10900	Bluetongue virus (serotype 10 / American isolate)	3		3			
731		10903	Bluetongue virus 17	4		4			
732		10904	Bluetongue virus (serotype 1 / isolate Australia)	7		7			
733		10906	Bluetongue virus 10	3		3			
734		10915	Porcine rotavirus serotype 5/strain OSU	1		1			
735		10917	Porcine rotavirus strain Gottfried	2		2			
736		10919	Porcine rotavirus strain YM	2	1	2	1		
737		10923	Simian rotavirus A/SA11	8	5	8	5		
738		10927	Bovine rotavirus	9	1	9	1		
739		10933	Bovine rotavirus strain RF	12	7	12	7		
740		10934	Bovine rotavirus strain UK/G6		1		1		
741		10941	Human rotavirus A	14	84	14	84		
742		10950	Human rotavirus (SEROTYPE 2 / STRAIN DS1)	1		1			
743		10952	Human rotavirus strain KU	9		9			
744		10957	Human rotavirus strain P	1	4	1	4		
745		10958	Human rotavirus strain RRV	1		1			
746		10960	Human rotavirus G4 strain St. Thomas 3	6		6			
747		10962	Human rotavirus strain WA	10	7	10	7		
748		10995	Infectious bursal disease virus	12		12			
749		10996	Infectious bursal disease virus 52/70		10		10		
750		10997	Infectious bursal disease virus 002-73/AUS	1		1			
751		11002	Infectious pancreatic necrosis virus	1		1			
752		11021	Eastern equine encephalitis virus	47	2	48	2	1	
753		11022	Eastern equine encephalitis virus (STRAIN VA33[TEN BROECK])		1		1		
754		11029	Ross River virus	1	1	1	1		
755		11032	Ross river virus (STRAIN T48)	11		11			
756		11033	Semliki Forest virus	36	5	36	5		
757		11034	Sindbis virus	26		26			
758		11036	Venezuelan equine encephalitis virus	2	6	2	6		
759		11037	Venezuelan equine encephalitis virus (strain TC-83)	25		25			
760		11038	Venezuelan equine encephalitis virus (strain Trinidad donkey)	15		15			
761		11039	Western equine encephalitis virus		1		1		
762		11041	Rubella virus	81	100	81	100		
763		11043	Rubella virus strain M33	3	11	3	11		
764		11044	Rubella virus vaccine strain RA27/3	2	6	2	6		
765		11045	Rubella virus strain Therien	20	35	20	35		

766		11047	Equine arteritis virus	3		3			
767		11048	Lactate dehydrogenase-elevating virus	14		14			
768		11049	Lelystad virus	66	12	66	12		
769		11053	Dengue virus 1	91	630	91	631		1
770		11057	Dengue virus 1 Thailand/AHF 82-80/1980		1		1		
771		11059	Dengue virus 1 Nauru/West Pac/1974	4	50	6	50	2	
772		11060	Dengue virus 2	193	743	199	744	6	1
773		11062	Dengue virus 2 Malaysia M2	1		1			
774		11064	Dengue virus 2 Jamaica/1409/1983	267	1254	267	1254		
775		11065	Dengue virus 2 Thailand/NGS-C/1944	20	146	20	146		
776		11066	Dengue virus 2 Puerto Rico/PR159-S1/1969	32	21	32	21		
777		11067	Dengue virus 2 Tonga/EKB194/1974		3		3		
778		11069	Dengue virus 3	129	679	129	680		1
779		11070	Dengue virus 4	85	468	85	469		1
780		11072	Japanese encephalitis virus	49	173	50	173	1	
781		11073	Japanese encephalitis virus strain SA-14	6	2	6	2		
782		11075	Japanese encephalitis virus strain JAOARS982	4	4	4	4		
783		11076	Japanese encephalitis virus strain Nakayama	2	2	2	2		
784		11077	Kunjin virus	12	1	12	1		
785		11078	Kunjin virus (STRAIN MRM61C)		4		4		
786		11079	Murray Valley encephalitis virus	21	9	21	9		
787		11080	Saint Louis encephalitis virus	9	1	9	1		
788		11081	St. Louis encephalitis virus (strain MS1-7)	7		7			
789		11082	West Nile virus	52	451	52	451		
790		11083	Powassan virus	1	3	14	3	13	
791		11084	Tick-borne encephalitis virus	18	146	18	147		1
792		11085	Langat virus		1		1		
793		11086	Louping ill virus	1		1			
794		11087	Tick-borne encephalitis virus (STRAIN SOFJIN)	6		6			
795		11089	Yellow fever virus		1364	1855	1365	1855	1
796		11090	Yellow fever virus 17D	2	583	2	688		105
797		11092	Kumlinge virus	26		26			
798		11096	Classical swine fever virus	15	4	17	4	2	
799		11098	Classical swine fever virus - Brescia	4		4			
800		11099	Bovine viral diarrhea virus 1	1	12	2	12	1	
801		11100	Bovine viral diarrhea virus 1-NADL	4	3	4	3		
802		11103	Hepacivirus C	720	1153	720	1155		2
803		11104	Hepatitis C virus (isolate 1)	37	256	37	256		
804		11105	Hepatitis C virus (isolate BK)	3	90	3	90		
805		11108	Hepatitis C virus (isolate H)	166	84	166	84		
806		11110	Hepatitis C virus HCT18	1		1			
807		11113	Hepatitis C virus isolate HC-J6	8	3	9	3	1	
808		11115	Hepatitis C virus isolate HC-J8	1	1	1	1		

809		11116	Hepatitis C virus (isolate Japanese)	6	19	6	19		
810		11120	Infectious bronchitis virus	10	5	10	9		4
811		11127	Avian infectious bronchitis virus (strain M41)	4	3	4	3		
812		11128	Bovine coronavirus	7		7			
813		11137	Human coronavirus 229E		8	5503	10	5503	2
814		11138	Murine hepatitis virus	3	31	3	31		
815		11142	Murine hepatitis virus strain A59	26	4	26	4		
816		11144	Murine hepatitis virus strain JHM	25	21	25	21		
817		11149	Transmissible gastroenteritis virus	15	1	15	1		
818		11150	Porcine transmissible gastroenteritis coronavirus strain FS772/70	2		2			
819		11151	Porcine transmissible gastroenteritis coronavirus strain Purdue	14		14			
820		11152	Turkey coronavirus	1		1			
821	X	11153	Canine coronavirus				3		3
822		11169	Mumps virus strain Kilham	1		1			
823		11173	Mumps virus strain SBL-1	6		6			
824		11177	Newcastle disease virus (STRAIN AUSTRALIA-VICTORIA/32)	4		4			
825		11178	Newcastle disease virus strain Beaudette C/45	12		12			
826		11180	Newcastle disease virus strain D26/76	4		4			
827		11186	Newcastle disease virus strain Queensland/66	4		4			
828		11191	Murine respirovirus	63	10	63	10		
829		11194	Sendai virus (strain Enders)	7	11	7	11		
830		11195	Sendai virus (strain Fushimi)		1		1		
831		11196	Sendai virus (strain Harris)	2		2			
832		11198	Sendai virus (Z)		2		2		
833		11214	Human parainfluenza virus 2 (strain Toshiba)	3		3			
834		11215	Bovine respirovirus 3	3	1	3	1		
835		11216	Human respirovirus 3	3		3			
836		11217	Human parainfluenza 3 virus (strain NIH 47885)	8	12	8	12		
837		11232	Canine morbillivirus	14	9	14	14		5
838		11233	Canine distemper virus strain Onderstepoort	6	34	6	34		
839		11234	Measles morbillivirus	64	39	64	39		
840		11235	Measles virus strain Edmonston	167	210	167	210		
841		11236	Measles virus strain Halle		34		34		
842		11241	Rinderpest morbillivirus	2	3	2	3		
843		11243	Rinderpest virus (strain L)	6		6			
844		11246	Bovine orthopneumovirus	3	2	3	2		
845		11249	Bovine respiratory syncytial virus (strain RB94)	4		4			
846		11250	Human orthopneumovirus	35	207	35	208		1
847		11251	Human respiratory syncytial virus (subgroup B / strain 18537)	2	1	2	1		
848		11252	Human respiratory syncytial virus (strain RSB642)	2		2			
850		11255	Human respiratory syncytial virus (strain RSB6190)	6		6			
851		11256	Human respiratory syncytial virus (strain RSB6256)	11		11			

852		11259	Human respiratory syncytial virus A2	98	245	111	245	13	
853		11260	Human respiratory syncytial virus A strain Long	129	94	129	94		
854		11263	Murine orthopneumovirus		14		14		
855		11269	Marburg marburgvirus	6	104	6	104		
856		11276	Vesicular stomatitis virus		10		10		
857		11277	Vesicular stomatitis Indiana virus	9	7	9	7		
858		11278	Vesicular stomatitis Indiana virus strain Glasgow		1		1		
859		11279	Vesicular stomatitis Indiana virus strain Mudd-Summers	1		1			
861		11285	Vesicular stomatitis Indiana virus strain San Juan		1		1		
862		11288	Viral hemorrhagic septicemia virus 07-71	12	1	12	1		
863		11290	Infectious hematopoietic necrosis virus	8		8			
864		11292	Rabies lyssavirus	15	26	15	26		
865		11293	Rabies virus AVO1		3		3		
866		11294	Rabies virus CVS-11	3		6		3	
867		11295	Rabies virus ERA	10	27	10	27		
868		11296	Rabies virus HEP-FLURY	7	1	7	1		
869		11298	Rabies virus Nishigahara RCEH	1		1			
870		11307	Sonchus yellow net nucleorhabdovirus		1		1		
871		11318	Dhori thogotovirus	1		1			
872		11320	Influenza A virus	78	616	78	656		40
874		11384	Influenza A virus (A/chicken/FPV/Weybridge(H7N7))		2		2		
875		11408	Influenza A virus (STRAIN A/EQUINE/NEW MARKET/76)		1		1		
876		11448	Influenza A virus (A/parrot/Ulster/73(H7N1))		1		1		
877		11484	Influenza A virus (A/whale/Maine/1/84(H13N9))	3		3			
878		11520	Influenza B virus	4	460	5	460	1	
879		11521	Influenza B virus (B/Ann Arbor/1/1986)		3		3		
880		11541	Influenza B virus (B/Oregon/5/80)	16		16			
881		11550	Influenza B virus (B/Yamagata/1/73)		3		3		
882		11552	Influenza C virus		1		1		
883		11553	Influenza C virus (C/Ann Arbor/1/50)	16		16			
884		11577	La Crosse virus	2	1	2	1		
885		11578	La Crosse virus L74		2		2		
886		11583	HoJo virus		1		1		
887		11588	Rift Valley fever virus	13	67	13	67		
888	X	11590	Toscana virus			3		3	
889		11602	Hantaan virus 76-118	14	132	14	132		
890		11605	Puumala virus Hallnas B1		1		1		
891		11607	Sapporo rat virus	1	4	1	4		
892		11610	Seoul virus SR11	1		1			
893		11620	Lassa mammarenavirus	15	707	15	707		
894		11621	Lassa virus GA391		55		55		
895		11622	Lassa virus Josiah	10	451	10	451		

896		11623	Lymphocytic choriomeningitis mammarenavirus	5	655	5	655		
897		11624	Lymphocytic choriomeningitis virus (strain Armstrong)		1158		1158		
898		11625	Lymphocytic choriomeningitis virus (strain Pasteur)		5		5		
899		11626	Lymphocytic choriomeningitis virus (strain Traub)		3		3		
900		11627	Lymphocytic choriomeningitis virus (strain WE)		74		74		
901		11628	Machupo mammarenavirus	1	801	1	801		
902		11629	Mopeia mammarenavirus		14		14		
903		11631	Tacaribe mammarenavirus		106		106		
904		11636	Reticuloendotheliosis virus	2	5	2	5		
905		11660	Caprine arthritis encephalitis virus	14	1	14	1		
906		11661	Caprine arthritis encephalitis virus strain Cork	9		9			
907		11662	Caprine arthritis encephalitis virus G63	6		6			
908		11665	Equine infectious anemia virus	93	112	93	112		
909		11670	Equine infectious anemia virus (CLONE 1369)		1		1		
910		11671	Equine infectious anemia virus (STRAIN WSU5)		19		19		
911		11673	Feline immunodeficiency virus		30		30		
912		11674	Feline immunodeficiency virus (isolate Petaluma)	2	4	2	4		
913		11675	Feline immunodeficiency virus (isolate San Diego)		1		1		
914		11676	Human immunodeficiency virus 1	314	535	319	536	5	1
915		11678	Human immunodeficiency virus type 1 BH10	2	29	2	29		
916		11679	Human immunodeficiency virus type 1 (CLONE 12)		7		7		
918		11682	Human immunodeficiency virus type 1 (BH5 ISOLATE)		1		1		
919		11683	Human immunodeficiency virus type 1 (Z2/CDC-Z34 ISOLATE)		1		1		
921		11685	HIV-1 M:B_ARV2/SF2	1	44	1	44		
922		11686	Human immunodeficiency virus type 1 (BRU ISOLATE)	1	4	1	4		
923		11687	Human immunodeficiency virus type 1 (CDC-451 ISOLATE)		3		3		
924		11688	Human immunodeficiency virus type 1 (JRCSF ISOLATE)	4	37	4	37		
925		11689	Human immunodeficiency virus type 1 (ELI ISOLATE)		7		7		
926		11690	Human immunodeficiency virus type 1 (SF33 ISOLATE)		2		2		
927		11691	Human immunodeficiency virus type 1 (SF162 ISOLATE)	2		2			
928		11694	Human immunodeficiency virus type 1 (JH3 ISOLATE)		3		3		
929		11695	Human immunodeficiency virus type 1 (NDK ISOLATE)		8		8		
930		11696	HIV-1 M:B_MN	11	27	11	27		
931		11697	Human immunodeficiency virus type 1 (MAL ISOLATE)		6		6		
932		11698	Human immunodeficiency virus type 1 (NEW YORK-5 ISOLATE)	2	2	2	2		
933		11699	Human immunodeficiency virus type 1 (OYI ISOLATE)		3		3		
934		11701	Human immunodeficiency virus type 1 (RF/HAT ISOLATE)	1	19	1	19		
935		11703	Human immunodeficiency virus type 1 (STRAIN UGANDAN / ISOLATE U455)		14		14		
936		11704	Human immunodeficiency virus type 1 (MFA ISOLATE)		2		2		
937		11705	Human immunodeficiency virus type 1 (WMJ2 ISOLATE)		1		1		

938		11706	HIV-1 M:B_HXB2R	15	18	15	18		
939		11708	Human immunodeficiency virus type 1 (ZAIRE 6 ISOLATE)		1		1		
940		11709	Human immunodeficiency virus 2	1	8	1	8		
941		11711	Simian immunodeficiency virus - mac		1		1		
942		11713	Human immunodeficiency virus type 2 (ISOLATE D194)		1		1		
943		11714	Human immunodeficiency virus type 2 (ISOLATE BEN)		12		12		
944		11715	Human immunodeficiency virus type 2 (ISOLATE CAM2)		2		2		
945		11716	Human immunodeficiency virus type 2 (ISOLATE D205,7)		2		2		
946		11717	Human immunodeficiency virus type 2 (ISOLATE GHANA-1)		7		7		
947		11718	Human immunodeficiency virus type 2 (ISOLATE SBLISY)		2		2		
948		11720	Human immunodeficiency virus type 2 (ISOLATE ROD)		2		2		
949		11723	Simian immunodeficiency virus		245		245		
950		11730	Simian immunodeficiency virus (AGM3 ISOLATE)		1		1		
953		11733	Simian immunodeficiency virus (MM142-83 ISOLATE)		102		102		
954		11734	Simian immunodeficiency virus (MM251 ISOLATE)		1		1		
955		11735	Simian immunodeficiency virus - mac K6W		125		125		
956		11736	Simian immunodeficiency virus (K78 ISOLATE)		29		29		
957		11737	Simian immunodeficiency virus (F236/SMH4 ISOLATE) (SOOTY MANGABEY)		17		17		
958		11738	Simian immunodeficiency virus (PBJ/BC13 ISOLATE) (SOOTY MANGABEY)		2		2		
959		11742	Visna lentivirus (strain 1514)	1		1			
960		11743	Visna lentivirus (strain 1514 / clone LV1-1KS1)	4		4			
961		11746	Jaagsiekte sheep retrovirus	1		1			
962		11757	Mouse mammary tumor virus		12		12		
963		11764	Baboon endogenous virus strain M7	1		1			
964		11769	Feline leukemia virus strain A/Glasgow-1	6		6			
965		11780	Snyder-Theilen feline sarcoma virus	1		1			
966		11786	Murine leukemia virus	1	23	1	25		2
967		11790	AKT8 murine leukemia virus	1		1			
968		11791	AKR (endogenous) murine leukemia virus		13		13		
969		11795	Friend murine leukemia virus	6	53	6	53		
970		11801	Moloney murine leukemia virus		5		5		
971		11812	Murine sarcoma virus 3611	4		4			
972		11824	Gardner-Arnstein feline leukemia oncovirus B	13		13			
973		11827	Human endogenous retrovirus	1	1	1	1		
974		11861	Avian erythroblastosis virus	1		1			
975		11864	Avian leukosis virus	5		5			
976		11886	Rous sarcoma virus	4	4	4	4		
977		11901	Bovine leukemia virus	108	40	108	40		
979		11908	Human T-cell leukemia virus type I	238	280	238	280		
980		11909	Human T-lymphotropic virus 2	63	2	63	2		
981		11926	Human T-cell lymphotrophic virus type 1 (strain ATK)	30	118	30	118		

982		11927	Human T-cell lymphotrophic virus type 1 (Caribbean isolate)		6		6		
983		11928	Human T-cell lymphotrophic virus type 1 (isolate MT-2)	1		1			
984		11942	Simian retrovirus 1	1		1			
985		11963	Human spumaretrovirus	1		1			
986		11966	Aids-associated retrovirus		2		2		
987		11976	Rabbit hemorrhagic disease virus	4	6	4	6		
988		11978	Feline calicivirus	4	1	4	1		
989		11980	Feline calicivirus strain Japanese F4	6		6			
990		11981	Feline calicivirus strain F9	2		2			
991		11983	Norwalk virus	4	1	4	1		
992		11984	Southampton virus	1		1			
993		12022	Escherichia phage MS2	1		1			
994		12060	Echovirus E9	1		1			
995		12063	Human parechovirus 1	7		7			
996		12064	Enterovirus E	17		17			
997		12065	Bovine enterovirus strain VG-5-27	6		6			
998		12066	Coxsackievirus	1		1			
999		12067	Coxsackievirus A9	30		30			
1000		12071	Coxsackievirus B1	12		13		1	
1001		12072	Coxsackievirus B3	7	18	7	18		
1002		12073	Coxsackievirus B4	17	51	18	51	1	
1003		12075	Swine vesicular disease virus	1		1			
1004		12076	Swine vesicular disease virus (STRAIN H/3 '76)	5		5			
1005		12077	Swine vesicular disease virus (STRAIN UKG/27/72)	3		3			
1006		12078	Echovirus E11	1		1			
1007		12080	Human poliovirus 1	6	1	6	1		
1008		12081	Human poliovirus 1 Mahoney	62	31	62	31		
1009		12082	Human poliovirus 1 strain Sabin	8		8			
1010		12086	Human poliovirus 3	5	2	5	2		
1011		12088	Poliovirus type 3 (strains P3/LEON/37 AND P3/LEON 12A[1]B)	4	15	4	15		
1012		12092	Hepatovirus A	30	22	30	22		
1013		12098	Human hepatitis A virus Hu/Australia/HM175/1976	87	83	87	96		13
1014		12104	Encephalomyocarditis virus		1		1		
1015		12107	Mengo virus	5	13	5	13		
1016		12110	Foot-and-mouth disease virus	33	5	33	6		1
1017		12111	Foot-and-mouth disease virus A	3	7	3	7		
1018		12112	Foot-and-mouth disease virus (strain A10-61)	8		8			
1019		12113	Foot-and-mouth disease virus (strain A5)	3		3			
1020		12114	Foot-and-mouth disease virus (strain A12)	21	1	21	1		
1021		12115	Foot-and-mouth disease virus (strain A24 Cruzeiro)	17	32	17	32		
1022		12116	Foot and mouth disease virus C	6	26	6	26		
1023		12117	Foot-and-mouth disease virus (strain C3 Indaial)	2		2			

1024		12118	Foot-and-mouth disease virus O	46	9	49	13	3	4
1025		12120	Foot-and-mouth disease virus (strain C1-Santa Pau)	1		1			
1026		12121	Foot-and-mouth disease virus C1	1	4	1	4		
1027		12123	Foot-and-mouth disease virus SAT 3		1		1		
1028		12124	Theiler's encephalomyelitis virus	1	18	1	18		
1029		12125	Theiler's encephalomyelitis virus (STRAIN BEAN 8386)	16	52	16	52		
1030		12126	Theiler's encephalomyelitis virus (STRAIN DA)	3	2	3	2		
1031		12130	rhinovirus A2	11		11			
1032		12131	rhinovirus B14	17	1	17	1		
1033		12132	rhinovirus A89	3		3			
1034		12134	Human rhinovirus 1A		19		19		
1035		12146	Tomato bushy stunt virus (STRAIN BS-3)	3		3			
1036		12161	Beet yellows virus	5		5			
1037		12162	Citrus tristeza virus	8		8			
1038		12211	Plum pox virus	1	1	1	1		
1039		12213	Plum pox virus isolate NAT		1		1		
1040		12216	Potato virus Y	2		2			
1041		12219	Potato virus Y strain N	1		1			
1042		12220	Potato virus Y strain O	7		7			
1043		12232	Zucchini yellow mosaic virus	1		1			
1044		12242	Tobacco mosaic virus	142	13	142	13		
1045		12243	Tobacco mosaic virus (vulgare)	1		1			
1046		12246	Tobacco mosaic virus strain Dahlemense	2		2			
1047		12260	Bean pod mottle virus	2		2			
1048		12264	Cowpea mosaic virus		1		1		
1049		12274	Grapevine fanleaf virus	1		1			
1050		12305	Cucumber mosaic virus	1		1			
1051		12455	Borna disease virus	8	4	8	4		
1052		12475	Hepatitis delta virus	56	66	56	66		
1053		12509	Human herpesvirus 4 type 2	2	10	2	10		
1054		12557	Seoul virus 80-39		3		3		
1055		12618	Chicken anemia virus	3		3			
1056		12637	Dengue virus	58	589	4429	589	4371	
1057		12639	Duck hepatitis B virus	262	20	262	20		
1058		12643	Ectromelia virus		45		45		
1059		12663	Feline coronavirus	64	2	64	2		
1060		12701	Human astrovirus 2	2		2			
1061		12721	Human immunodeficiency virus		58		58		
1062		12750	Visna/maedi virus EV1	1		1			
1063		12760	Murine hepatitis virus strain 4		5		5		
1064		12814	Respiratory syncytial virus	5	5	5	5		
1065		12870	Variola major virus		17		17		
1066		13101	Juniperus ashei	13		13			

1067		13187	Parietaria officinalis	2		2			
1068		13286	Theromyzon tessulatum	1		1			
1069		13373	Burkholderia mallei	3	50	3	50		
1070		13415	Chamaecyparis obtusa	5	68	5	68		
1071		13451	Corylus avellana	33	57	33	57		
1072		13469	Cupressus sempervirens		8		8		
1073		13557	Hapalemur griseus		1		1		
1074		13616	Monodelphis domestica	1	4	1	4		
1075		13618	Myrmecia pilosula	2		2			
1076		13677	Scomber scombrus	1		1			
1077		13684	Parastagonospora nodorum		2		2		
1078		13687	Sphingomonas	1	4	1	5		1
1080		15368	Brachypodium distachyon	1		1			
1081		15957	Phleum pratense	65	1163	65	1163		
1082		16719	Juglans nigra	1		1			
1083		27990	Plasmodium vivax-like sp.	3	1	3	1		
1084		28037	Streptococcus mitis		1		1		
1085		28038	Latilactobacillus curvatus		1		1		
1086		28080	Campylobacter upsaliensis	3		3			
1087		28108	Alteromonas macleodii		1		1		
1088		28130	Prevotella disiens		1		1		
1089		28131	Prevotella intermedia		2		2		
1092		28151	Serratia proteamaculans		1		1		
1093		28172	Vibrio metschnikovii	1		1			
1094		28227	Mycoplasma penetrans	40		40			
1095		28276	Human adenovirus 15	1		1			
1096		28280	Human adenovirus E4	1		1			
1097		28282	Human adenovirus 12	11	3	11	3		
1098		28284	Human adenovirus 40	2	1	2	1		
1099		28285	Human adenovirus 5	27	186	27	186		
1100		28295	Porcine epidemic diarrhea virus	15		16		1	
1101		28300	Heron hepatitis B virus		1		1		
1102		28314	Aleutian mink disease virus	10		10			
1103		28327	Murine rotavirus		3		3		
1104		28344	Porcine reproductive and respiratory syndrome virus	90	156	90	163		7
1105		28375	Soil-borne wheat mosaic virus	1		1			
1106		28446	Anaerotignum propionicum		2		2		
1107		28448	Komagataeibacter xylinus		1		1		
1108		28450	Burkholderia pseudomallei	19	13	65	13	46	
1109		28479	Phalaris aquatica		12		12		
1110		28869	Ovine respiratory syncytial virus	1		1			
1111		28871	Taterapox virus		4		4		
1112		28873	Camelpox virus		2		2		

1113		28875	Rotavirus A	2		2	2		2
1114		28901	Salmonella enterica		147		147		
1115		28903	Mycoplasmopsis bovis	21		21			
1116		28909	Cynodon dactylon	27	48	27	48		
1117		29073	Ursus maritimus	1		1			
1118		29159	Crassostrea gigas	7		7			
1119	X	29170	Ancylostoma caninum			1		1	
1120		29176	Neospora caninum	3	17	3	17		
1121		29271	Dasheen mosaic virus	1		1			
1122		29292	Pyrococcus abyssi		1		1		
1123		29320	Paenarthrobacter nicotinovorans	1		1			
1124		29339	Bacillus thuringiensis serovar kurstaki	3		3			
1125		29355	Ruminiclostridium cellobioparum	1		1			
1126		29362	Ruminiclostridium papyrosolvens		1		1		
1127		29388	Staphylococcus capitis	1		1			
1128		29430	Acinetobacter haemolyticus	1		1			
1129		29438	Pseudomonas savastanoi		1		1		
1130		29442	Pseudomonas tolaasii		1		1		
1131		29447	Xanthomonas albilineans		1		1		
1132		29459	Brucella melitensis	19	95	19	95		
1133		29461	Brucella suis	1	8	1	8		
1134		29477	Salmonella enterica subsp. enterica serovar Essen	1		1			
1135		29491	Aeromonas salmonicida subsp. salmonicida		1		1		
1136		29507	Leptospira kirschneri	1		1			
1137		29518	Borreliella afzelii	6	1	6	1		
1138		29519	Borreliella garinii	6	29	6	29		
1139		29661	Anthoxanthum odoratum		3		3		
1140		29679	Holcus lanatus	14	3	14	3		
1141		29715	Ambrosia psilostachya		10		10		
1142		29760	Vitis vinifera	1		1			
1143		29780	Mangifera indica	1		1			
1144		29908	Sporothrix schenckii		2		2		
1145		29916	Fusarium sp.	3		3			
1146		29918	Cladosporium herbarum		18		18		
1147		29960	Penaeus indicus	2		2			
1148		30011	Pyrophorus plagiophthalamus		1		1		
1149		30069	Anopheles stephensi	1		1			
1151		30538	Vicugna pacos	2		2			
1152		31271	Plasmodium chabaudi chabaudi		3		3		
1153		31273	Plasmodium vivax strain Belem	9	31	9	31		
1154		31276	Perkinsus marinus		1		1		
1155		31285	Trypanosoma brucei gambiense	2		2			
1156		31286	Trypanosoma brucei rhodesiense	1	9	1	9		

1157		31330	Ephydatia fluviatilis		1		1		
1158		31525	Human herpesvirus 4 strain CAO		1		1		
1159		31531	Vaccinia virus L-IPV		8		8		
1160		31545	Human adenovirus D8	1	1	1	1		
1161		31552	Human papillomavirus type 6	12	4	12	4		
1162		31560	Infectious bursal disease virus E	1		1			
1163		31569	Human rotavirus (serotype 2 / strain RV-5)	1		1			
1164		31604	Small ruminant morbillivirus	13	31	13	31		
1165		31608	Simian virus 5 (isolate canine/CPI+)	1		1			
1166		31611	Bovine respiratory syncytial virus (strain 391-2)	3		3			
1167		31615	Tacaribe virus strain V5		1		1		
1168		31616	Tacaribe virus strain V7		1		1		
1169		31621	Four Corners hantavirus	2	8	2	8		
1170		31631	Human coronavirus OC43		9	9397	11	9397	2
1171		31634	Dengue virus 2 Thailand/16681/84	32	62	36	62	4	
1172		31635	Dengue virus 2 16681-PDK53	4	80	4	80		
1173		31636	Dengue virus 2 China/D2-04		5		5		
1174		31637	Dengue virus 2 Thailand/TH-36/1958		4		4		
1175		31641	Yellow fever virus 1899/81		36		36		
1176		31644	Hepatitis C virus HCV-KF	1	1	1	1		
1177		31645	Hepatitis C virus (isolate Taiwan)	3	15	3	15		
1178		31647	Hepatitis C virus subtype 1b	609	293	612	293	3	
1179		31649	Hepatitis C virus subtype 2a	80	22	80	22		
1180		31650	Hepatitis C virus subtype 2b	103	4	103	4		
1181		31653	Hepatitis C virus subtype 4a	1	1	1	1		
1182		31654	Hepatitis C virus subtype 5a	1	1	1	1		
1183		31655	Hepatitis C virus subtype 6a		1		1		
1184		31678	Human immunodeficiency virus type 1 (WMJ1 isolate)		16		16		
1186		31682	Simian immunodeficiency virus - mac1A11		18		18		
1187		31683	Simian immunodeficiency virus - stm		7		7		
1188		31684	Simian immunodeficiency virus (isolate AGM / clone GRI-1)		2		2		
1190		31704	Coxsackievirus A16	4		5	1	1	1
1191		31708	rhinovirus A16	9	30	9	30		
1192		31715	Bean-pod mottle virus (strain Kentucky G7)	9	1	9	1		
1193		31721	Beet necrotic yellow vein virus	10		10			
1194		31767	Hepatitis E virus (strain Burma)	160		160			
1195		31768	Hepatitis E virus (strain Mexico)	31		31			
1196		32008	Burkholderia	1		1			
1197		32019	Campylobacter fetus subsp. fetus	3		3			
1198		32022	Campylobacter jejuni subsp. jejuni	2		2			
1199		32025	Helicobacter hepaticus		1		1		
1200		32049	Synechococcus sp. PCC 7002		1		1		
1201		32201	Carya illinoinensis	19		19			

1202		32278	Metapenaeus ensis	1	6	1	6		
1203		32603	Human betaherpesvirus 6A	2	7	2	7		
1204		32604	Human betaherpesvirus 6B	2	4523	2	4533		10
1205		32605	Buffalopox virus		1		1		
1206		32606	Rabbitpox virus		2		2		
1207		32614	Convict Creek 107 virus	1	3	1	3		
1208		32644	unidentified		23254		23528		274
1211		33075	Acidobacterium capsulatum		1		1		
1212		33090	Viridiplantae	1		1			
1213		33127	Parietaria judaica	65	2	65	2		
1214		33178	Aspergillus terreus	2		2			
1215		33703	Suid herpesvirus 1 strain Kaplan	4		4			
1216		33706	Caviid betaherpesvirus 2	3	3	3	3		
1217		33708	Murid gammaherpesvirus 4	1	54	1	54		
1218		33717	Bluetongue virus (serotype 13 / isolate USA)	2		2			
1219		33718	Bluetongue virus (serotype 17 / isolate USA)	4		4			
1220		33727	Marburg virus - Musoke, Kenya, 1980	3	84	3	84		
1221		33728	Lake Victoria marburgvirus - Popp	3	15	3	15		
1222		33734	Feline infectious peritonitis virus (strain 79-1146)	15	14	15	14		
1223		33741	Dengue virus 1 Singapore/S275/1990		244		244		
1224		33745	Hepatitis C virus genotype 4	1	10	1	10		
1225		33746	Hepatitis C virus genotype 5		2		2		
1226		33747	Simian T-lymphotropic virus 1		14		14		
1227		33758	Echovirus		1		1		
1228		33892	Mycobacterium tuberculosis variant bovis BCG	13	288	13	296		8
1229		33934	Anoxybacillus flavithermus		1		1		
1230		33959	Lactobacillus johnsonii	1		1			
1231		33990	Rickettsia bellii	1	3	1	3		
1232		34054	Yersinia enterocolitica (type O:8)		1		1		
1233		34245	Zinnia elegans		1		1		
1234		34610	Amblyomma variegatum	1		1			
1235		34613	Ixodes ricinus	2		2			
1236		34631	Rhipicephalus appendiculatus	2		2			
1237		34632	Rhipicephalus sanguineus	1		1			
1238		34828	Eulemur mongoz	1		1			
1239		34862	Otospermophilus beecheyi		1		1		
1240		35241	Lactococcus phage Tuc2009	1		1			
1241		35258	Lambdapapillomavirus 2		25		25		
1242		35269	Woodchuck hepatitis virus	4	6	4	6		
1243		35275	Murine endogenous retrovirus		14		14		
1244		35288	Grapevine virus A	12		12			
1245		35292	Foot-and-mouth disease virus SAT 2	1	1	1	1		
1246		35297	Striped jack nervous necrosis virus	1		1			

1247		35305	California encephalitis virus		1		1		
1248		35327	Bluetongue virus 1	4		5		1	
1249		35329	Bluetongue virus 11	6		6			
1250		35330	Bluetongue virus 13	1		1			
1251		35331	Bluetongue virus 15	7		7			
1252		35336	Rotavirus G4		1		1		
1253		35345	Lactococcus phage TP901-1	3		3			
1254		35670	Naja naja	3		3			
1255		35725	Macrophomina phaseolina		1		1		
1256		35788	Rickettsia africae		1		1		
1257		35791	Rickettsia massiliae		1		1		
1258		35793	Rickettsia sibirica		6		6		
1259		35795	Ehrlichia muris	2	3	2	3		
1261		36080	Mucor circinelloides		3		3		
1262	X	36087	Trichuris trichiura			15		15	
1263		36329	Plasmodium falciparum 3D7	1176	281	1183	394	7	113
1264		36351	Human herpesvirus 6 strain Z29	1	146	1	146		
1265		36352	Human herpesvirus 4 type 1	4	14	4	14		
1266		36372	Feline immunodeficiency virus (strain UK8)		1		1		
1267		36374	Visna/maedi virus EV1 KV1772	2		2			
1268		36375	Human immunodeficiency virus type 1 (KB-1 isolate)		2		2		
1269		36386	Louping ill virus (strain 31)	1		1			
1270		36409	Rinderpest virus (strain RBOK)	33	5	33	5		
1271		36412	Human parainfluenza 1 virus (strains A1426 / 86-315 / 62M-753)		1		1		
1272		36418	Influenza A virus (A/chicken/Brescia/1902(H7N7))		1		1		
1273		36420	H1N1 swine influenza virus		13		13		
1274		36421	African horse sickness virus 4	42	4	42	4		
1275		36439	Bovine rotavirus strain NCDV/G6	1		1			
1276		36470	Streptococcus sp. 'group A'	21		21			
1277		36596	Prunus armeniaca	4		4			
1278		36809	Mycobacteroides abscessus		19		19		
1279		36826	Clostridium botulinum A	46		46			
1280		36827	Clostridium botulinum B	29		29			
1281		36829	Clostridium botulinum D	2		2			
1282		36830	Clostridium botulinum E	3	3	3	3		
1283		36831	Clostridium botulinum F	3		3			
1284		36855	Brucella canis		4		4		
1285		36911	Clavispora lusitaniae	1	1	1	1		
1286		36914	Lodderomyces elongisporus		3		3		
1287		36936	Lepidoglyphus destructor	5	10	5	10		
1289		37111	Human papillomavirus 28		1		1		
1290		37112	Human papillomavirus 29		1		1		
1291		37115	human papillomavirus 59	2	1	2	1		

1292		37120	human papillomavirus 67	2		2			
1293		37121	human papillomavirus 69		1		1		
1294		37124	Chikungunya virus	83	22	87	22	4	
1295		37128	Potato mop-top virus	8		8			
1296		37132	Rabies virus Ontario fox	3		3			
1297		37137	Simian rotavirus A/SA11-both	20	2	20	2		
1298		37207	Rio Segundo hantavirus	1		1			
1299		37296	Human gammaherpesvirus 8	26	488	26	489		1
1300		37325	Muscovy duck parvovirus	11		11			
1301		37326	Nocardia brasiliensis	6		6			
1302		37329	Nocardia farcinica		1		1		
1303		37347	Tupaia belangeri		1		1		
1304		37546	Glossina morsitans morsitans	2		2			
1306		37731	Secale strictum subsp. africanum		2		2		
1307		37734	Enterococcus casseliflavus		1		1		
1308		37762	Escherichia coli B	1		1			
1309		37769	Cryptococcus gattii VGI		1		1		
1310		38020	marmosets	3		3			
1311		38033	Chaetomium globosum	1		1			
1312		38171	Avian reovirus strain S1133	6		6			
1313		38251	Goose parvovirus	10		10			
1314		38289	Corynebacterium jeikeium		1		1		
1315		38323	Bartonella henselae	1		1			
1316		38347	Leptospira interrogans serovar Hardjo-prajitno	1		1			
1317		38832	Micromonas		1		1		
1318		38873	Fraxinus excelsior		3		3		
1319		38973	Influenza A virus (A/Memphis/4/1973(H3N2))		2		2		
1320		39002	Puumala virus sotkamo/v-2969/81	196		196			
1321		39015	Human T-cell lymphotropic virus type 1 (african isolate)		2		2		
1322		39054	Enterovirus A71	129	1	129	1		
1324		39152	Methanococcus maripaludis	1		1			
1325		39414	Plantago lanceolata		2		2		
1326		39442	Mus musculus musculus		1		1		
1327		39457	Human papillomavirus type 70		1		1		
1329	X	39584	Juniperus virginiana			1		1	
1330		39803	Escherichia virus Qbeta		2		2		
1331		39947	Oryza sativa Japonica Group	5	1	5	1		
1332		40051	Bluetongue virus	12	1	12	1		
1333		40214	Acinetobacter johnsonii		1		1		
1334		40271	Hepatitis C virus genotype 2	42	6	42	6		
1335		40324	Stenotrophomonas maltophilia	1		1			
1336		40674	Mammalia	6	2	6	2		
1337		40697	Blomia tropicalis	31	6	31	6		

1338		41514	Salmonella enterica subsp. arizonae serovar 62:z4,z23:-		4		4		
1339		41846	Echovirus E30	2		2			
1340		41856	Hepatitis C virus genotype 1	4	178	27	178	23	
1341		41857	Influenza A virus H3N2	6	50	6	50		
1342		41858	Simian foamy virus-gorilla	1		1			
1343		41953	Pseudo-nitzschia	1		1			
1344		41997	Enterococcus saccharolyticus		1		1		
1345		42097	Isla Vista hantavirus	1	2	1	2		
1346		42182	Hepatitis C virus genotype 6		7		7		
1347		42229	Prunus avium	3	1	3	1		
1348		42345	Phoenix dactylifera		3		3		
1349		42358	Hantavirus Monongahela-3		5		5		
1350		42374	Candida dubliniensis		2		2		
1351		42764	Oliveros mammarenavirus		2		2		
1352		42769	Coxsackievirus A10	3		4		1	
1353		42782	Coxsackievirus A20	1		1			
1354		42789	enterovirus D68	16		16			
1355		42792	Hepatitis C virus subtype 3g	1		1			
1356		42862	Rickettsia felis		1		1		
1357		42897	Shigella flexneri 2a	35		36		1	
1358		43304	Mycolicibacterium peregrinum	2		2			
1359		43765	Corynebacterium amycolatum		1		1		
1360		43767	Rhodococcus hoagii	18	3	18	3		
1361		43852	Toxicodendron	1	1	1	1		
1362		43853	Toxicodendron radicans	1		1			
1363		44026	Sepik virus		1		1		
1364		44088	Canarypox virus		8		8		
1365		44104	Vibrio cholerae 569B	37		37			
1366		44271	Leishmania chagasi	3		3			
1367		44275	Leptospira interrogans serovar Copenhageni	2		2			
1368		44276	Leptospira interrogans serovar Pomona	2	3	2	3		
1369		44386	Haemaphysalis longicornis	1		1			
1370		44561	Murine type C retrovirus		1		1		
1371		44689	Dictyostelium discoideum	1	1	1	1		
1372		44755	New York hantavirus		2		2		
1373		45029	Bluetongue virus 16	3		3			
1374		45201	Mannheimia haemolytica serotype 1	82		82			
1375		45219	Guanarito mammarenavirus		842		842		
1376		45240	human papillomavirus 68		1		1		
1377		45409	Feline immunodeficiency virus (isolate wo)	3		3			
1378		45410	Hepatitis B virus adw4/Brazil/isolate w4b		12		12		
1379		45455	Macacine gammaherpesvirus 4		27		27		
1380		45582	[Candida] saitoana	1		1			

1381		45617	Human endogenous retrovirus K	14		14			
1382		45659	Human adenovirus B3	29	2	29	2		
1384		46015	Autographa californica nucleopolyhedrovirus		1		1		
1385		46221	Porcine circovirus	1	49	1	49		
1386		46242	Spodoptera litura nucleopolyhedrovirus		2		2		
1387		46245	Drosophila pseudoobscura pseudoobscura	1		1			
1388		46290	Foot-and-mouth disease virus C3	4	1	4	1		
1389		46457	Cycloclasticus oligotrophus		1		1		
1391		46506	Bacteroides stercoris		1		1		
1392		46771	Simian virus 12	1		1			
1393		46835	Fasciola gigantica	3		3			
1394		46919	Whitewater Arroyo mammarenavirus		349		349		
1395		46920	Rio Mamore hantavirus	1	1	1	1		
1396		46921	Human adenovirus D13	1		1			
1397		46941	Human adenovirus 46	1		1			
1399		47466	Borrelia miyamotoi	73		73			
1400	X	47516	Echovirus E3			1		1	
1402		47929	Macacine betaherpesvirus 3		101		101		
1403		48409	Salmonella enterica subsp. enterica serovar Virchow		1		1		
1404		48483	Reclinomonas americana		1		1		
1405		48935	Novosphingobium aromaticivorans		1		1		
1406		49011	Hesperocyparis arizonica	2	6	2	6		
1407		49511	Piper longum	1		1			
1409		50557	Insecta	7		7			
1410	X	51022	Ancylostoma duodenale			8		8	
1411		51031	Necator americanus	17		25		8	
1412		51033	human papillomavirus 73		1		1		
1413		51240	Juglans regia	34	19	34	19		
1414		53182	Feline foamy virus	7		7			
1415		53258	Variola minor virus		93		93		
1416	X	53326	Ancylostoma ceylanicum			3		3	
1417		53751	Echinacea purpurea	1		1			
1418		54290	GB virus C	16		16			
1419		54315	Bovine viral diarrhea virus 2	1		1			
1420		54388	Salmonella enterica subsp. enterica serovar Paratyphi A		4		4		
1421		54390	Micrurus corallinus	125		125			
1422		54736	Salmonella bongori		1		1		
1423		55097	Mobala mammarenavirus	1		1			
1425		55513	Pistacia vera		6		6		
1426		55532	Influenza A virus (A/swine/Quebec/1192/1986(H1))		1		1		
1427		55601	Vibrio anguillarum	1		1			
1428		55635	Inula helenium		1		1		
1429		55951	Grapevine leafroll-associated virus 3	1		1			

1430		56636	Aeropyrum pernix	3	2	3	2		
1431	X	56950	Border disease virus strain Moredun			3		3	
1432		57068	Acanthisitta chloris		1		1		
1433		57266	Plasmodium falciparum 7G8	43	52	43	59		7
1434		57270	Plasmodium falciparum Palo Alto/Uganda	38		38			
1435		57278	Human herpesvirus 7 strain JI		1		1		
1437		57372	Mycoplasma suis	3		3			
1438		57482	European bat 1 lyssavirus		1		1		
1439		57486	Mus musculus molossinus		1		1		
1440		57667	Simian-Human immunodeficiency virus	1	5	1	5		
1441		57678	Leptospira interrogans serovar Lai	10	10	10	10		
1442		57975	Burkholderia thailandensis		2		2		
1443		58024	Spermatophyta	4	1	4	1		
1444		58216	Loxosceles gaucho	1		1			
1445		58217	Loxosceles laeta	2		2			
1446		58218	Loxosceles intermedia	83		83			
1447		58291	Rhizopus microsporus		1		1		
1448		59201	Salmonella enterica subsp. enterica		18		18		
1449		59202	Salmonella enterica subsp. salamae		1		1		
1450		59203	Salmonella enterica subsp. arizonae		1		1		
1451		59205	Salmonella enterica subsp. houtenae		1		1		
1452		59300	Getah virus	9		9			
1453		59301	Mayaro virus	1		11		10	
1454		59375	Influenza A virus (A/South Carolina/1/1918(H1N1))	9	1	9	1		
1455		59538	Pantholops hodgsonii		1		1		
1456		59729	Taeniopygia guttata		1		1		
1457		59799	Angomonas deanei		2		2		
1458		60189	Rhipicephalus decoloratus	6		6			
1460		60552	Burkholderia vietnamiensis		2		2		
1461		60876	Pixuna virus		1		1		
1462		60879	Cabassou virus		1		1		
1463		60893	Desulfobacca acetoxidans		1		1		
1464		61466	Gnathostoma binucleatum	10		10			
1465		61673	Porcine endogenous retrovirus	2	11	2	11		
1466		62319	Halococcus saccharolyticus		1		1		
1467		62322	Shewanella baltica		1		1		
1468		62330	Fagopyrum tataricum	5		8		3	
1469		62446	Influenza A virus (A/Argentina/3779/94(H3N2))		1		1		
1470		62478	Influenza A virus (A/Kitakyushu/93(H3N2))		1		1		
1471		62488	Influenza A virus (A/Nanchang/58/1993(H3N2))		1		1		
1472		62496	Influenza A virus (A/New_York/17/94(H3N2))		1		1		
1473		62503	Influenza A virus (A/Ohio/3/95(H3N2))		1		1		
1474		62512	Influenza A virus (A/Shangdong/5/94(H3N2))		1		1		

1475		62541	Influenza A virus (A/Christchurch/2/1988(H3N2))		1		1		
1476		62549	Influenza A virus (A/Fukuoka/C29/1985(H3N2))	5		5			
1477		62559	Influenza A virus (A/Los Angeles/1987(H3N2))	5		5			
1478		62564	Influenza A virus (A/New_York/15/94(H3N2))		1		1		
1479		62575	Influenza A virus (A/Sichuan/2/1987(H3N2))		5		5		
1480		62596	Influenza A virus (A/USSR/26/1985(H3N2))		1		1		
1482		63106	Influenza A virus (A/Wuhan/359/1995(H3N2))	5		5			
1483		63330	Hendra henipavirus	9	2	9	2		
1484		63363	Aquifex aeolicus	2	7	2	7		
1485		63421	Swine hepatitis E virus	12		12			
1486		63673	Turbo cornutus	2		2			
1487		63737	Nostoc punctiforme PCC 73102		2		2		
1488		63746	Hepatitis C virus (isolate H77)	177	208	183	210	6	2
1489		64284	Saboya virus		1		1		
1490		64289	Carey Island virus		2		2		
1491		64293	Tembusu virus	2	10	3	11	1	1
1492		64320	Zika virus	124	650	1279	747	1155	97
1493		64382	Human Endogenous Retrovirus IDDMK1,2-22	3		3			
1494		64495	Rhizopus arrhizus	4	1	4	1		
1495		65690	AK7 murine leukemia virus		1		1		
1496		65699	Neisseria meningitidis serogroup A	5		5			
1497		65743	Blackcurrant reversion virus	2		2			
1498		66692	Alkalihalobacillus clausii KSM-K16		1		1		
1499	X	66976	Legionella pneumophila serogroup 1				7		7
1500		67351	Streptomyces californicus	1		1			
1501		68621	Classical swine fever virus strain Riems		5		5		
1502		68825	Rasamsonia emersonii		1		1		
1503		68887	Torque teno virus	5	94	5	94		
1504		68909	Deinococcus geothermalis	1		1			
1505		69008	Juniperus oxycedrus		3		3		
1506		69153	Human enterovirus 71 (strain BRCR)	1		1			
1507		69156	Murine cytomegalovirus (strain K181)	2	15	2	15		
1508		69245	Lechiguanas virus		9		9		
1510		69247	Oran virus		2		2		
1511		69248	Pergamino virus		1		1		
1512		70146	Measles virus strain Edmonston-B	2	78	2	78		
1513		70149	Measles virus strain Edmonston-Zagreb	1		1			
1514		70175	Androctonus australis hector	24		24			
1515		70203	Vibrio virus fs1		1		1		
1516		70865	Murine rotavirus EDIM		27		27		
1517		71238	Pseudomonas sp. G-179		1		1		
1518		71366	Staphylococcus phage PVL	1		1			
1519		71421	Haemophilus influenzae Rd KW20		3		3		

1522		72132	Rotavirus G1	1	1	1	1		
1523		72539	Physalis mottle virus	2		2			
1524		72556	Achromobacter piechaudii	1		1			
1525		72590	Salmonella sp. 'group B'	6		6			
1526		72664	Eutrema salsugineum	2		2			
1527		73036	Rotavirus G3		1		1		
1528		73239	Plasmodium yoelii yoelii	22	42	23	42	1	
1529		73482	Foot-and-mouth disease virus (strain O1)	38	1	38	1		
1530		73484	Human immunodeficiency virus type 2 (isolate KR)		3		3		
1531		74537	Vladivostok virus	1		1			
1532		74722	Stachybotrys chartarum	11		11			
1533		74942	Hantavirus CRF355		1		1		
1535		75325	Orf virus strain D1701		36		36		
1536		75922	Mycolicibacterium tusciae		2		2		
1538		76777	Malassezia sympodialis	1		1			
1539		76832	Myroides odoratimimus		1		1		
1541		77009	Hordeum vulgare subsp. spontaneum		2		2		
1542		77044	Rosellinia necatrix		1		1		
1543		77095	Prevotella bryantii		2		2		
1544		77153	Muscovy duck reovirus	1		1			
1545		77643	Mycobacterium tuberculosis complex		5		5		
1546		78245	Xanthobacter autotrophicus Py2		1		1		
1547		79692	Human respiratory syncytial virus B1	1	25	1	25		
1548		79695	Influenza A virus (A/Memphis/1/71H-A/Bellamy/42N)		1		1		
1549		79698	Merluccius bilinearis	1		1			
1550		79889	Bovine herpesvirus type 1.1	2		2			
1551		79923	Clonorchis sinensis	2	1	2	1		
1552		80365	Laminaria digitata	2		2			
1553		80859	Streptomyces ribosidificus		1		1		
1554		80956	Pomacentrus moluccensis		1		1		
1556		81475	Frateuria aurantia	1		1			
1557		81847	Trichophyton quinckeanum	1		1			
1558		81985	Capsella rubella	1		1			
1559		82070	Squilla maritima	1		1			
1560		82300	adeno-associated virus 5	9		9			
1561		82372	Influenza A virus (A/Sydney/05/97-like(H3N2))		1		1		
1562		82470	Bovine viral diarrhea virus strain Oregon C24V	5	3	5	3		
1563		82639	Coxsackievirus B2	2		2			
1564		82658	Lordsdale virus		1		1		
1565		82659	Sapporo virus-Manchester		1		1		
1566		82823	Bovine respiratory syncytial virus strain lelystad	1		1			
1567		82824	Bovine respiratory syncytial virus strain snook	1	75	1	75		
1568		82830	Epstein-barr virus strain ag876	16	1	16	1		

1569		82831	Equid herpesvirus type 2 strain 86/87	1		1			
1571		83192	Topografov hantavirus	1		1			
1572		83206	Influenza A virus (A/swine/Scotland/410440/94(H1N2))		5		5		
1573		83262	Mycobacteroides immunogenum		5		5		
1574		83331	Mycobacterium tuberculosis CDC1551		42		42		
1575		83332	Mycobacterium tuberculosis H37Rv	62	975	62	993		18
1576		83333	Escherichia coli K-12	33	19	33	19		
1577		83334	Escherichia coli O157:H7	3	123	3	123		
1578		83455	Myxococcus stipitatus		1		1		
1579		83554	Chlamydia psittaci	102	6	102	6		
1580		83555	Chlamydia abortus	32		32			
1581		83556	Chlamydia felis	12		12			
1582		83557	Chlamydia caviae	14		14			
1583		83558	Chlamydia pneumoniae	110	24	110	24		
1584		83559	Chlamydia suis	19		19			
1585		83560	Chlamydia muridarum	17	3	17	3		
1586		83810	Thosea asigna virus		1		1		
1587		85057	Trypanosoma cruzi cruzi		1		1		
1588		85106	Adeno-associated virus - 1		11		11		
1589		85223	Laurus nobilis		1		1		
1590		85552	Scylla paramamosain	95		95			
1591		85569	Salmonella enterica subsp. enterica serovar Typhimurium str. DT104	1		1			
1592		85698	Achromobacter xylosoxidans	1		1			
1593		85708	Porcine circovirus 2	36	1	36	1		
1594		85709	Porcine circovirus type 2-B	18		18			
1595		85777	Agelas mauritiana		1		1		
1596		85929	Sphaerulina musiva		1		1		
1597		85962	Helicobacter pylori 26695	40	10	40	10		
1598		85963	Helicobacter pylori J99		53		53		
1599		85991	Chlamydia pecorum	142		142			
1600		86049	Cladophialophora carrionii		2		2		
1601		86107	Coxsackievirus A6	1		1			
1602		86385	Porcine circovirus type 2-D	1		1			
1603		86600	Discosoma sp.		1		1		
1604		86782	Amur virus		35		35		
1606		87883	Burkholderia multivorans	1	2	1	2		
1607		88036	Selaginella moellendorffii		1		1		
1608		88085	Lachesis stenophrys	13		13			
1609		88086	Protobothrops elegans	7		7			
1610		88087	Protobothrops flavoviridis	3		3			
1611		88103	Influenza A virus (A/Hong Kong/532/1997(H5N1))		1		1		
1612		88104	Influenza A virus (A/Hong Kong/483/1997(H5N1))	3	10	3	10		

1613		88776	Influenza A virus (A/Brevig Mission/1/1918(H1N1))		1	1	1	1	
1614		89059	Ligilactobacillus acidipiscis		1		1		
1615		89169	Influenza A virus (A/Chicken/Pennsylvania/13552-1/98 (H7N2NSB))	1		1			
1616		89172	Influenza A virus (A/quail/Arkansas/16309-7/94 (H7N3NSA))	1		1			
1618		89462	Bubalus bubalis	7	1	7	1		
1620		90370	Salmonella enterica subsp. enterica serovar Typhi	15	112	22	119	7	7
1621		90371	Salmonella enterica subsp. enterica serovar Typhimurium	16	76	16	76		
1622		91465	Pseudomonas sp. MIS38		1		1		
1623		91626	Mucor ambiguus		1		1		
1624		92050	Macruronus magellanicus	2		2			
1625		92637	Metarhizium acridum		1		1		
1626		92652	Shrimp white spot syndrome virus	3		3			
1627		93061	Staphylococcus aureus subsp. aureus NCTC 8325	5	1	5	1		
1628		93062	Staphylococcus aureus subsp. aureus COL	17		17			
1629		93621	Heteropneustes fossilis		1		1		
1630		93678	TTV-like mini virus		1		1		
1631		93838	Influenza A virus (A/goose/Guangdong/1/1996(H5N1))	1	10	1	10		
1632		94432	Human rotavirus MP409	1	1	1	1		
1633		94966	Bluetongue virus 12	15		15			
1634		94967	Bluetongue virus 4	7		7			
1637		95486	Burkholderia cenocepacia	1	1	1	1		
1638		95602	Eriocheir sinensis	10		10			
1639		95888	Influenza A virus (A/mallard duck/PA/10218/84(H5N2))	8		8			
1641		97138	Clostridium sp. MD294				3		3
1642	X	97253	Eubacterium plexicaudatum				4		4
1643		97348	Influenza A virus (A/Chicken/Hong Kong/G23/97(H9N2))		1		1		
1644		97353	Influenza A virus (A/Chicken/Hong Kong/739/94(H9N2))		1		1		
1645		97477	Acetomicrobium mobile		1		1		
1646		98360	Salmonella enterica subsp. enterica serovar Dublin		1		1		
1647		99287	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2		78		78		
1648		99586	Echis ocellatus	5		5			
1649		99875	Leishmania donovani donovani	1		1			
1650		99883	Tetraodon nigroviridis		2		2		
1651		100226	Streptomyces coelicolor A3(2)	1	1	1	1		
1652		100835	Influenza A virus (A/Chicken/Hong Kong/258/97 (H5N1))	1		1			
1653		101350	Porcine rotavirus strain A253	2		2			
1654		102617	Helicobacter pylori SS1	4	3	4	3		
1655		102793	H5N1 subtype	27	40	27	40		
1656		102796	H9N2 subtype	2		3	1	1	1
1657		102862	Proteus penneri	1		1			
1658		103448	Pleistophora sp. LS		1		1		

1659		103903	Coxsackievirus B3 (strain Nancy)	13	32	13	32		
1660		103905	Coxsackievirus B4 (strain E2)	7	41	7	41		
1661		103906	Coxsackievirus B4 (strain JVB / Benschoten / New York/51)		76		76		
1662		103920	Guinea pig cytomegalovirus (strain 22122 / ATCC VR682) (GPCMV)	1		1			
1663		103922	Human enterovirus 71 (strain 7423/MS/87)	4		4			
1664		103929	Rabies virus strain Pasteur vaccin	2	1	2	1		
1665		103930	Rhesus cytomegalovirus strain 68-1		18		18		
1666		104102	Acetobacter tropicalis		1		1		
1667		104355	Gloeophyllum trabeum		1		1		
1668		105751	Aeromonas bestiarum		1		1		
1669	X	106276	Mimachlamys nobilis			7		7	
1670		106654	Acinetobacter nosocomialis		1		1		
1671		106820	Hepatitis B virus subtype adr	23	25	23	25		
1672		106821	Hepatitis B virus subtype adw	17	76	17	76		
1673		107404	Influenza B virus (B/Beijing/184/93)		1		1		
1674		107406	Influenza B virus (B/Chiba/447/98)		1		1		
1675		107493	Influenza A virus (A/Cordoba/3278/96(H3N2))		1		1		
1676		107558	Influenza A virus (A/France/75/97(H3N2))		1		1		
1677		107819	Clostridium perfringens D	45		45			
1678		108098	Human mastadenovirus B	1		1			
1679		110195	Foot-and-mouth disease virus Asia 1	10	3	10	3		
1680		110321	Sinorhizobium medicae		1		1		
1681		112509	Hordeum vulgare subsp. vulgare		26		26		
1682		114497	Cordyceps fumosorosea		1		1		
1683		114727	H1N1 subtype	16	49	23	49	7	
1684		114729	H2N2 subtype		1		1		
1685		114742	Pythium insidiosum	2		2			
1686		115711	Chlamydia pneumoniae AR39	1		1			
1687		115713	Chlamydia pneumoniae CWL029	73	48	73	48		
1688		117125	Cucumber mosaic virus (strain Pepo)	1		1			
1689		117187	Fusarium verticillioides	1		1			
1690		117204	African horse sickness virus 3	21		21			
1691		118161	Pleurocapsa sp. PCC 7319		1		1		
1692		119210	H3N2 subtype	6	23	6	23		
1693		119211	H3N8 subtype	1		1			
1694		119215	H7N3 subtype	2		2			
1695		119218	H7N7 subtype		1		1		
1696		119220	H5N2 subtype	1		1			
1697		119602	Streptococcus dysgalactiae subsp. equisimilis	21		22		1	
1698		119856	Francisella tularensis subsp. tularensis		5		5		
1699		119912	Salmonella enterica subsp. enterica serovar Choleraesuis		2		2		
1700		120505	Baboon cytomegalovirus		1		1		
1701		121224	Pediculus humanus corporis	2		2			

1702		121723	Photobacterium sp. SKA34		1		1		
1703		121759	Paracoccidioides brasiliensis	4	16	4	16		
1704		121791	Nipah henipavirus	7	11	7	11		
1705		122291	Kappapapillomavirus 1	2		2			
1706		122355	Pseudomonas psychrophila	1		1			
1707		122586	Neisseria meningitidis MC58	18		18			
1708		122928	Norovirus GI	2		2			
1709		122929	Norovirus GII	2	19	2	19		
1710	X	123734	Hypoderma bovis			1		1	
1712		126283	Herpes simplex virus unknown type		1		1		
1713		126793	Plasmodium vivax Sal-1	24		24			
1714		126794	Vaccinia virus Ankara		127		127		
1715		127886	Alkalihalobacillus hemicellulosilyticus		1		1		
1716		127906	Vibrio cholerae O1	9		9			
1717		127999	Tanacetum parthenium		1		1		
1718		128947	Ebola virus - Gabon (1994-1997)		18		18		
1719		128948	Sudan virus - Boniface, Sudan,1976	3	1	3	1		
1720		128949	Sudan ebolavirus - Maleo (1979)		30		30		
1721		128951	Ebola virus - Zaire (1995)		3		3		
1722		128952	Ebola virus - Mayinga, Zaire, 1976	40	13	70	13	30	
1723		128982	Influenza A virus (A/Swine/Indiana/9K035/99 (H1N2))		2		2		
1724		128987	Grass carp reovirus		1		1		
1725		128999	Tai Forest virus - Cote d'Ivoire, Cote d'Ivoire, 1994	1	3	1	3		
1726		129000	Ebola virus - Eckron (Zaire, 1976)		12		12		
1727		129003	Reston ebolavirus - Reston	2	27	2	27		
1728		129052	Catelliglobosispora koreensis		1		1		
1729		129138	Pseudomonas amygdali pv. morsprunorum	2		2			
1730		129727	Bovine papular stomatitis virus		2		2		
1731		129788	Ruditapes philippinarum	3		3			
1732		129875	Human mastadenovirus A		1		1		
1733		129951	Human mastadenovirus C	1	3	1	3		
1734		130663	Fowl aviadenovirus 4	3		3			
1735		130760	Influenza A virus (A/Hong Kong/1073/99(H9N2))	1	25	1	25		
1736		130763	Influenza A virus (A/Hong Kong/156/97(H5N1))	4	26	4	26		
1737		131110	Schaalia radingae		1		1		
1738		132475	Yaba-like disease virus		3		3		
1739		132487	Measles virus strain Schwarz	1	1	1	1		
1740		132504	Influenza A virus (A/X-31(H3N2))	78	189	78	193		4
1742		132783	Influenza A virus (A/Netherlands/626/89 (H3N2))		1		1		
1743		132841	Influenza A virus (A/Netherlands/785e/90 (H3N2))		1		1		
1744		132884	Influenza A virus (A/Netherlands/458/98 (H3N2))		1		1		
1745		133704	Porcine circovirus 1	6		6			

1746		133926	Olsenella uli		1		1		
1747		134537	Paraburkholderia fungorum	1		1			
1749		135661	Influenza A virus (A/environment/Hong Kong/437-10/99 (H5N1))		1		1		
1750		135720	Neisseria meningitidis serogroup C	3		3			
1751		136371	Umbilicaria papulosa	1		1			
1752		136474	Influenza A virus (A/Swine/Colorado/23619/99(H3N2))		1		1		
1753		136966	SEN virus		7		7		
1754		137578	Influenza A virus (A/England/939/69 x A/PR/8/34)		2		2		
1755		137885	Influenza A virus (A/parakeet/Chiba/1/97(H9N2))		4		4		
1756		137886	Influenza A virus (A/parakeet/Narita/92A/98(H9N2))		2		2		
1757		138948	Enterovirus A	8		8			
1758		138949	Enterovirus B	7		7			
1759		138950	Enterovirus C	13	3	13	3		
1760		138951	Enterovirus D	7		7			
1762		142786	Norovirus		8		8		
1763		142948	Influenza A virus (A/ruddy turnstone/Delaware/67/1998(H12N4))		1		1		
1764		144549	Mycolicibacterium fortuitum subsp. fortuitum		1		1		
1765		145262	Methanothermobacter thermautotrophicus		1		1		
1766		145306	Influenza A virus (A/swine/Hong Kong/10/98(H9N2))	5		5			
1767		145307	Influenza A virus (A/swine/Hong Kong/9/98(H9N2))	2		2			
1768		147095	Influenza A virus (A/Swine/Italy/25823/94(H3N2))		2		2		
1769		147272	Paspalum notatum		16		16		
1770	X	147711	Rhinovirus A				21		21
1771		148360	Watermelon mosaic virus 2 (isolate USA)	2		2			
1772		148363	Helicoverpa armigera nucleopolyhedrovirus G4	2		2			
1773		149539	Salmonella enterica subsp. enterica serovar Enteritidis	1	3	1	3		
1774		150080	Norovirus isolates	1		1			
1775		150127	Influenza B virus (B/Osaka/983/97-V3)	1		1			
1776		150340	Vibrio antiquarius		15		15		
1777		150846	Enterovirus 5865/sin/000009	2		2			
1778		151250	Kali turgidum	1	22	1	22		
1779		152219	Menangle virus	2		2			
1780		152794	Corynebacterium efficiens		5		5		
1781		153496	Kozakia baliensis		1		1		
1782		153969	Influenza A virus (A/Hong Kong/497/97(H3N2))		1		1		
1783		154540	Influenza A virus (A/Kayano/57(H2N2))		1		1		
1784		155091	Secale cereale subsp. afghanicum		2		2		
1785		155218	Influenza A virus (A/Hong Kong/482/97(H5N1))	7	1	7	1		
1786		155220	Influenza A virus (A/Hong Kong/542/97(H5N1))	1		1			
1787		155222	Influenza A virus (A/Hong Kong/488/97(H5N1))		1		1		
1788		155225	Influenza A virus (A/Hong Kong/507/97(H5N1))		5		5		
1789		155226	Influenza A virus (A/Hong Kong/514/97(H5N1))		1		1		

1790		155227	Influenza A virus (A/Hong Kong/516/97(H5N1))		2		2		
1791		155864	Escherichia coli O157:H7 str. EDL933	4	32	4	32		
1792		155917	Influenza A virus (A/NWS/33HA-A/tern/Australia/G70C/75NA(H1N9))	1		1			
1793		156230	Karenia brevis	1		1			
1795		157703	Murine polyomavirus strain A3		4		4		
1796		157914	Ziziphus mauritiana	4		4			
1797		158306	Influenza A virus (A/swine/Cotes d'Armor/800/00(H1N2))		1		1		
1798		158465	Human calicivirus Hu/NLV/GII/MD145-12/1987/US	1	1	1	1		
1799		158474	Bovine viral diarrhea virus strain Trangie Y546	1		1			
1800		158879	Staphylococcus aureus subsp. aureus N315		5		5		
1801		158899	Collimonas fungivorans		2		2		
1802		159091	Pseudomonas sp. KIE171		1		1		
1803		159449	Embleya scabrispora	1		1			
1804		159471	Influenza A virus (A/eq/Sussex/89/(H3N8))	4		4			
1805		159479	Saaremaa hantavirus		21		21		
1806		160490	Streptococcus pyogenes M1 GAS	13	2	13	2		
1807		160491	Streptococcus pyogenes str. Manfredo	3	35	3	35		
1808		160691	Tiger frog virus		1		1		
1809		160753	Simian immunodeficiency virus 17E-Fr		2		2		
1810		161502	Influenza A virus (A/swine/Italy/1509-6/97(H1N1))		15		15		
1811		161600	Yellow grouper nervous necrosis virus	1		1			
1812		161727	Foot-and-mouth disease virus A10/Holland	11	14	11	14		
1813		161934	Beta vulgaris	5		5			
1814		162145	Human metapneumovirus	8	130	8	130		
1815		162326	Influenza A virus (A/Hong Kong/1143/99(H3N2))	1		1			
1816		162425	Aspergillus nidulans		1		1		
1817		163164	Wolbachia endosymbiont of Drosophila melanogaster		1		1		
1818		164326	Influenza A virus (A/Hong Kong/1131/1998(H1N1))	1	1	1	1		
1819		164756	Mycobacterium sp. MCS		73		73		
1820		164757	Mycobacterium sp. JLS		77		77		
1821	X	165179	Prevotella copri				5		5
1822		165420	Influenza A virus (A/Turkey/MO/24093/99(H1N2))		4		4		
1823		165512	Influenza A virus (A/goose/Guangdong/3/1997(H5N1))	3	1	3	1		
1826		167758	TTV-like virus DXL1		10		10		
1827		168278	Influenza A virus (A/swine/Finistere/127/99(H3N2))		4		4		
1828		168807	Escherichia coli O127:H6	1		1			
1829		169166	Influenza A virus (A/swine/Italy/1521/98(H1N2))		4		4		
1830		169169	Influenza A virus (A/swine/Cotes d'Armor/1482/1999(H1N1))		1		1		
1831		169173	Choclo virus		3		3		
1833		169963	Listeria monocytogenes EGD-e	5	64	5	64		
1835		170187	Streptococcus pneumoniae TIGR4		2		2		
1836		170325	Canid alphaherpesvirus 1		1		1		

1837		170342	Influenza A virus (A/swine/Italy/1654-1/99(H1N2))		1		1		
1838		170500	H1N9 subtype	1		1			
1839		170525	Measles virus genotype D4	1		1			
1840		170529	Measles virus genotype D7	1		1			
1841		170955	Amur virus Solovey/AP63/1999		2		2		
1842		171101	Streptococcus pneumoniae R6	1	12	2	12	1	
1843		171264	Measles virus genotype D3	1		1			
1844		171425	Influenza B virus (B/Kobe/87/2001)	1		1			
1845		171631	Fusarium oxysporum species complex	8		8			
1846		171929	Anacardium occidentale	64	10	65	10	1	
1847		172148	Alkhumra hemorrhagic fever virus		4		4		
1848		172149	Influenza A virus (A/swine/Quebec/192/81(H1N1))	1		1			
1849		173473	Influenza A virus (A/swine/Hong Kong/2106/98(H9N2))		2		2		
1850		173477	Influenza A virus (A/swine/Hong Kong/3297/98(H9N2))		3		3		
1851		176275	Beauveria bassiana		1		1		
1852	X	176279	Staphylococcus epidermidis RP62A				1		1
1853		176672	Influenza A virus (A/Duck/Hong Kong/ww461/2000(H5N1))		1		1		
1855		177128	Influenza A virus (A/SW/MN/12883/00(H1N2))		2		2		
1856		177131	Influenza A virus (A/SW/KS/13481-T/00(H1N2))		1		1		
1857		177188	Influenza A virus (A/SW/MN/3227/00(H1N2))		1		1		
1858		177416	Francisella tularensis subsp. tularensis SCHU S4		92	44	92	44	
1859		178876	Cryptococcus neoformans var. grubii	1		1			
1860		180454	Anopheles gambiae str. PEST	6	2	6	2		
1861		180498	Jatropha curcas	6		6			
1862		182082	Chlamydia pneumoniae TW-183	7		7			
1863		182781	Influenza A virus (A/Goose/Hong Kong/385.3/2000(H5N1))		1		1		
1864		182785	Mycobacterium tuberculosis subsp. tuberculosis		1		1		
1865		183741	Influenza A virus (A/Chicken/Shanghai/F/98(H9N2))	5		5			
1866		183764	Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1))	7	100	7	100		
1867		183778	Influenza A virus (A/quail/Hong Kong/SF550/00(H6N1))		2		2		
1868		183783	Influenza A virus (A/duck/Hong Kong/3096/99(H6N2))		2		2		
1869		184816	Influenza B virus (B/Kadoma/122/99)	2		2			
1870		184922	Giardia lamblia ATCC 50803		249		249		
1871		185431	Trypanosoma brucei brucei TREU927		1		1		
1872		185579	Hepatitis E virus type 1	3		3			
1873		185580	Hepatitis E virus type 4	1		1			
1874		185794	Influenza A virus (A/mallard/NZ/1/97(H5N2))		1		1		
1875		185894	rhinovirus A15	3		3			
1876		185905	rhinovirus A34		54		54		
1877		185907	rhinovirus A39		1		1		
1878		185949	Sphingomonas aurantiaca		1		1		

1879		186460	Influenza A virus (A/swine/New Jersey/11/1976(H1N1))	1		1			
1880		186536	Ebolavirus	61	1	61	1		
1881		186538	Zaire ebolavirus	128	898	128	901		3
1882		186539	Reston ebolavirus	1	11	1	11		
1883		186540	Sudan ebolavirus	6	292	7	292	1	
1884		186541	Tai Forest ebolavirus		1		1		
1885		187164	Influenza A virus (A/Swine/Minnesota/55551/2000(H1N2))		1		1		
1886		187410	Yersinia pestis KIM10+		11		11		
1887		187420	Methanothermobacter thermautotrophicus str. Delta H		1		1		
1888		188538	Human parainfluenza virus 1 strain Washington/1964		11		11		
1889		188763	Panine betaherpesvirus 2		4		4		
1890		189518	Leptospira interrogans serovar Lai str. 56601	1		1			
1891		189918	Mycobacterium sp. KMS		69		69		
1892	X	190063	Fowl aviadenovirus C			1		1	
1893		191090	Influenza A virus (A/Weiss/1943(H1N1))		1		1		
1894		191218	Bacillus anthracis str. A2012		29		29		
1895		192087	Pseudomonas syringae pv. atrofaciens	4		4			
1896		192222	Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819	10	22	13	22	3	
1897		192535	Influenza A virus (A/Saudi Arabia/7971/2000(H1N1))		1		1		
1898		192549	Influenza A virus (A/Egypt/96/2002(H1N2))		1		1		
1899		192720	Influenza A virus (A/Saudi Arabia/2581/2001(H1N2))		1		1		
1901		194601	Vipera aspis aspis	3		3			
1902		194958	Porcine endogenous retrovirus A	2		2			
1903		194959	Porcine endogenous retrovirus B	1		1			
1904		195055	Human parechovirus 3	4		4			
1905		195099	Campylobacter jejuni RM1221		13		13		
1906		195102	Clostridium perfringens str. 13		1		1		
1907		195700	Avian rotavirus PO-13	6		6			
1908		196164	Corynebacterium efficiens YS-314		4		4		
1909		196403	Baboon endogenous virus	1	1	1	1		
1910		196462	Influenza A virus (A/chicken/California/1002a/00(H6N2))	1	1	1	1		
1911		196600	Vibrio vulnificus YJ016		75		75		
1912		196620	Staphylococcus aureus subsp. aureus MW2		7		7		
1913		196627	Corynebacterium glutamicum ATCC 13032		14		14		
1914		197575	Haemophilus aegyptius	1		1			
1915		197579	Influenza A virus (A/Chicken/Guangdong/11/97(H9N2))		1		1		
1916		197585	Influenza A virus (A/chicken/Shandong/6/96(H9N2))	1		1			
1917		197589	Influenza A virus (A/Quail/Shanghai/8/96(H9N2))		1		1		
1918		197780	Bluetongue virus 8	2	21	2	21		
1919		198059	Influenza A virus (A/England/627/01(H1N2))		2		2		
1920		198094	Bacillus anthracis str. Ames		2		2		
1921		198214	Shigella flexneri 2a str. 301		4		4		

1922		198215	Shigella flexneri 2a str. 2457T		2		2		
1923		199306	Coccidioides posadasii		10		17		7
1924		199310	Escherichia coli CFT073	1	2	1	2		
1925		199738	uncultured Chlamydia sp.	2		2			
1926		200454	Pseudomonas tremae		1		1		
1927		201444	Aracatuba virus		5		5		
1928		202812	Adeno-associated virus - 7		2		2		
1929		202813	Adeno-associated virus - 8	17	14	17	14		
1930		202950	Acinetobacter baylyi		2		2		
1931		203119	Acetivibrio thermocellus ATCC 27405		1		1		
1932		203124	Trichodesmium erythraeum IMS101		2		2		
1933		203126	Influenza A virus (A/Kamata/14/91(H3N2))	1		1			
1934		203129	Influenza A virus (A/Aichi/2/1994(H3N2))		1		1		
1935		203172	Camelpox virus CMS		28		28		
1936		203173	Camelpox virus M-96		133		133		
1937		203174	Camelpox virus CP1		1		1		
1939		204038	Dickeya dadantii	2		2			
1940		204428	Chlamydiae	16		16			
1941		204711	Theilovirus		10		10		
1942		204722	Brucella suis 1330	1	29	1	29		
1944		205488	Ebola virus sp.		2		2		
1945		205913	Bifidobacterium longum DJO10A		2		2		
1946		205914	Histophilus somni 129PT		1		1		
1947		205920	Ehrlichia chaffeensis str. Arkansas	23		23			
1948		205946	Influenza A virus (A/Chicken/Beijing/1/95(H9N2))		1		1		
1950		206203	Influenza B virus (B/Hong Kong/330/2001)		23		23		
1951		207401	Influenza A virus (A/finch/Canada/NS1301/2001(H3N8))		1		1		
1952		208226	Alkaliphilus metalliredigens		1		1		
1953		208435	Streptococcus agalactiae 2603V/R	1	2	1	2		
1954		208726	Human hepatitis A virus	4	1	4	1		
1955		208893	Human respiratory syncytial virus A	31	4	32	4	1	
1957		208899	Cupixi mammarenavirus		1		1		
1958		208963	Pseudomonas aeruginosa UCBPP-PA14		23		23		
1959		208964	Pseudomonas aeruginosa PAO1	2	38	2	38		
1960		209261	Salmonella enterica subsp. enterica serovar Typhi str. Ty2		16		16		
1962		209841	Actinobacillus pleuropneumoniae serovar 7	1		1			
1963		209882	Fusobacterium nucleatum subsp. vincentii ATCC 49256		2		2		
1964		210655	Influenza A virus (A/Duck/Shantou/2144/00(H9N2))		1		1		
1965		210656	Influenza A virus (A/Duck/Shantou/1881/00(H9N2))		1		1		
1966		210659	Influenza A virus (A/Duck/Shantou/2088/01(H9N2))		1		1		
1967		210663	Influenza A virus (A/Duck/Shantou/2134/00(H9N2))		1		1		
1968		211044	Influenza A virus (A/Puerto Rico/8/1934(H1N1))	36	546	37	552	1	6

1969		211110	Streptococcus agalactiae NEM316		1		1		
1970		211882	Leptospira interrogans serovar Australis	2		2			
1971		212042	Anaplasma phagocytophilum str. HZ	21		21			
1972		212045	Bacillus anthracis str. Western North America USA6153		1		1		
1973		212361	Anabaena aequalis	1		1			
1974		212717	Clostridium tetani E88		16		16		
1975		214092	Yersinia pestis CO92	39	22	53	22	14	
1976		214675	Leptospira interrogans serovar Manilae	1		1			
1977		214697	Musa acuminata AAA Group	1		1			
1979		214856	Alistipes finegoldii		1		1		
1980		215243	Exophiala oligosperma		1		1		
1981		215358	Larimichthys crocea	3		3			
1982		215862	Influenza A virus (A/Chicken/Nanchang/2-220/2001(H3N6))		1		1		
1984		216466	Streptococcus agalactiae serogroup V	1		1			
1985		216495	Streptococcus agalactiae serogroup III	14		14			
1986		216592	Escherichia coli 042	2		2			
1987		216594	Mycobacterium marinum M		29		29		
1988		216597	Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344		2		2		
1989		216600	Streptococcus pneumoniae 23F	6		7		1	
1990		216877	Influenza A virus (A/quail/Hong Kong/FY298/00(H9N2))		4		4		
1991		216895	Vibrio vulnificus CMCP6		53		53		
1992		217686	Little cherry virus 1		1		1		
1993		217992	Escherichia coli O6		7		7		
1994		218497	Chlamydia abortus S26/3	29		29			
1995		220341	Salmonella enterica subsp. enterica serovar Typhi str. CT18		92		92		
1996		220837	Cryptosporidium sp. MNJ-1		1		1		
1997		220977	Influenza A virus (A/England/10/67(H2N2))		1		1		
1998		221012	Influenza A virus (A/Rio/6/69(H3N2))		1		1		
1999		221703	Simian foamy virus Pongo pygmaeus pygmaeus	2		2			
2000		221918	Bovine viral diarrhea virus VEDEVAC	6		6			
2001		223337	Tobacco leaf curl Zimbabwe virus		1		1		
2002		223926	Vibrio parahaemolyticus RIMD 2210633	2	17	2	17		
2003		223931	Influenza A virus (A/Bangkok/10/1983(H1N1))		1		1		
2005		223935	Influenza A virus (A/Okuda/1957(H2N2))	1	9	1	9		
2006		223947	Influenza A virus (A/Hokkaido/20/89(H3N2))		3		3		
2007		223997	Murine norovirus 1	8	1	8	1		
2008		224197	Influenza C virus (C/Nara/1/85)		1		1		
2009		224206	Simian immunodeficiency virus - mon		1		1		
2010		224308	Bacillus subtilis subsp. subtilis str. 168		1		1		
2011		224324	Aquifex aeolicus VF5	2	1	2	1		
2012		224326	Borreliella burgdorferi B31	113	10	114	19	1	9
2013		224819	Influenza A virus (A/Nagasaki/76/98(H3N2))		1		1		

2014		224914	Brucella melitensis bv. 1 str. 16M	6	14	6	14		
2015		224964	Influenza B virus (B/Johannesburg/5/99)	1		1			
2016		225071	Influenza A virus (A/Tokyo/1566/98(H3N2))		1		1		
2017		225085	Influenza A virus (A/Aichi/2/68 (Ao))		9		9		
2018		225088	Influenza A virus (A/Kitakyushu/159/93(H3N2))		1		1		
2019		225089	Influenza A virus (A/equine/NewMarket/D64/79(H3N8))		1		1		
2020		226186	Bacteroides thetaiotaomicron VPI-5482		1		1		
2021		226900	Bacillus cereus ATCC 14579		1	1	1	1	
2022		227377	Coxiella burnetii RSA 493		13		13		
2023		227941	Chlamydia caviae GPIC	11		11			
2024		227984	SARS coronavirus Tor2	177	2205	2723	2205	2546	
2025		228330	SARS coronavirus Urbani	26	67	28	67	2	
2026		228399	Actinobacillus pleuropneumoniae serovar 1 str. 4074	2	1	2	1		
2027		228400	Histophilus somni 2336	1		1			
2028		228407	SARS coronavirus BJ01	68	28	68	28		
2029	X	228415	SARS coronavirus CUHK-W1			1		1	
2030		228928	Influenza A virus (A/Memphis/31/98(H3N2))	6		6			
2031		229032	Porcine epidemic diarrhea virus CV777	10		10			
2032		229051	Influenza A virus (A/81/HO)		6		6		
2033		229992	SARS coronavirus Frankfurt 1	5	26	5	26		
2034		231428	Avian infectious bronchitis virus (strain Vic S)	11	8	11	8		
2035		231455	Dyella japonica	1		1			
2036		231851	Influenza A virus (A/Hong Kong/1774/99(H3N2))		1		1		
2037		233262	Bovine enteric coronavirus (strain 98TXSF-110-ENT)		1		1		
2038		233412	[Haemophilus] ducreyi 35000HP	1		1			
2039		233413	Mycobacterium tuberculosis variant bovis AF2122/97		54		54		
2040		234267	Candidatus Solibacter usitatus Ellin6076		2		2		
2041		234603	Sapovirus Mc114		1		1		
2042		234826	Anaplasma marginale str. St. Maries	16	28	16	28		
2043		235279	Helicobacter hepaticus ATCC 51449	2		2			
2044		235455	Adeno-associated virus 9	10		10			
2046		237561	Candida albicans SC5314		3		3		
2047		237609	Pseudomonas alkylphenolica		1		1		
2048		237631	Ustilago maydis 521		2		2		
2049		237895	Cryptosporidium hominis		3		3		
2051	X	239935	Akkermansia muciniphila				9		9
2052		240426	Squirrelpox virus		1		1		
2054		242619	Porphyromonas gingivalis W83	4		4			
2056		243160	Burkholderia mallei ATCC 23344		40		40		
2057		243161	Chlamydia muridarum str. Nigg	11	72	11	72		
2058		243164	Dehalococcoides mccartyi 195		1		1		
2059		243230	Deinococcus radiodurans R1	2		2			

2060		243232	Methanocaldococcus jannaschii DSM 2661	3	1	3	1		
2061		243243	Mycobacterium avium 104		43		43		
2062		243273	Mycoplasma genitalium G37	8	1	8	1		
2063		243274	Thermotoga maritima MSB8	1		1			
2064		243276	Treponema pallidum subsp. pallidum str. Nichols	283	9	283	9		
2065		243277	Vibrio cholerae O1 biovar El Tor str. N16961	4	3	4	3		
2066	X	243678	Influenza A virus (A/chicken/Jiangsu/JS-1/2002(H9N2))			1	1	1	1
2067		244320	Escherichia coli O55:H7		1		1		
2068		244367	Foot-and-mouth disease virus C-S8c1	15	18	15	18		
2069		246196	Mycolicibacterium smegmatis MC2 155		61		61		
2070		246202	Streptococcus sobrinus 6715	4	4	4	4		
2071		246437	Tupaia chinensis	1	1	1	1		
2072		246618	Bifidobacterium thermacidophilum	1		1			
2073		246878	Canine parvovirus 2	3		3			
2074		249372	Influenza A virus (A/duck/Hokkaido/13/00(H9N2))	2		2			
2075		251297	Influenza A virus (A/Netherlands/127/03(H7N7))		1		1		
2076		253182	Human Respiratory syncytial virus 9320	1		1			
2077		253446	Avian orthoreovirus strain 1017-1	1		1			
2078		253682	Influenza A virus (A/swine/Hong Kong/5190/99(H3N2))		3		3		
2079		253686	Influenza A virus (A/swine/Hong Kong/74/02(H3N2))		1		1		
2080		254252	Lactococcus virus P2	2		2			
2081		254355	Small ruminant lentivirus	1		1			
2082		255681	Influenza A virus (A/Yokohama/22/2002(H1N2))		2		2		
2083		255682	Influenza A virus (A/Yokohama/47/2002(H1N2))		1		1		
2084		256045	Influenza A virus (A/swine/Chiai/77-10/2001(H3N1))		1		1		
2085		256080	Influenza B virus (B/Kobe/1/2003)	1		1			
2087	X	257309	Corynebacterium diphtheriae NCTC 13129			118		118	
2088		257313	Bordetella pertussis Tohama I		15		15		
2089		257363	Rickettsia typhi str. Wilmington		6		6		
2090		260799	Bacillus anthracis str. Sterne	5	4	5	4		
2091		260806	Influenza A virus (A/FPV/Dutch/1927(H7N7))	1		1			
2092		260965	Cercopithecine herpesvirus 1 (strain E2490)	18		18			
2093		261202	Alto Paraguay hantavirus		3		3		
2094		261204	Itapua hantavirus		10		10		
2095		261594	Bacillus anthracis str. 'Ames Ancestor'		1		1		
2096		261658	Cavenderia fasciculata		1		1		
2097		262307	Measles virus genotype A	4		4			
2098		262316	Mycobacterium avium subsp. paratuberculosis K-10	4	58	4	58		
2099		262698	Brucella abortus bv. 1 str. 9-941		1		1		
2100		262722	Mycoplasma hyopneumoniae 7448	1		1			
2101		262724	Thermus thermophilus HB27	1		1			
2102		262727	Haemophilus influenzae R2846		6		6		

2103		262728	Haemophilus influenzae R2866		2		2		
2104		263683	Bovine herpesvirus 5 strain TX89	2		2			
2105		263815	Pneumocystis murina	3		3			
2106		264202	Chlamydia felis Fe/C-56	14		14			
2107		264510	Influenza A virus (A/chicken/Thailand/LV1NF/2004(H5N1))		1		1		
2109		264635	Acholeplasma granularum	1		1			
2110		264732	Moorella thermoacetica ATCC 39073		1		1		
2111		265120	Influenza A virus (A/turkey/Italy/214845/2002(H7N3))	1		1			
2112		265619	Ornithodoros erraticus	22		22			
2113		265669	Listeria monocytogenes serotype 4b str. F2365		7		7		
2114		265872	Cowpox virus (Brighton Red)		1		1		
2115		266093	Influenza A virus (A/chicken/Yamaguchi/7/2004(H5N1))	3		4		1	
2116		266264	Cupriavidus metallidurans CH34		3		3		
2117		266779	Chelativorans sp. BNC1		4		4		
2118		266827	Influenza A virus (A/Thailand/1(KAN-1)/2004(H5N1))	4		4	16		16
2119		266834	Sinorhizobium meliloti 1021		3		3		
2120		266940	Kineococcus radiotolerans SRS30216 = ATCC BAA-149		2		2		
2121		267212	Neisseria bacilliformis	1		1			
2122		267377	Methanococcus maripaludis S2	1		1			
2123		267409	Listeria monocytogenes serotype 1/2a str. F6854		3		3		
2124		267410	Listeria monocytogenes serotype 4b str. H7858		24		24		
2125		267671	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	11		11			
2126		269482	Burkholderia vietnamiensis G4		9		9		
2127		269484	Ehrlichia canis str. Jake	16		16			
2128		269638	Bovine enterovirus type 2	2		2			
2129		269798	Cytophaga hutchinsonii ATCC 33406		1		1		
2131		269801	Bacillus cereus G9241		39		39		
2132		270338	Human poliovirus 3 strain Sabin	80	1	80	1		
2133		270473	Pneumonia virus of mice J3666		10		10		
2134		270478	Zantedeschia mild mosaic virus	1		1			
2135		270484	Influenza A virus (A/tiger/Thailand/CU-LV/2004(H5N1))		2		2		
2136		270490	Influenza A virus (A/chicken/Nakorn-Patom/Thailand/CU-K3/2004(H5N1))		1		1		
2137		270510	Influenza A virus (A/chicken/Vietnam/HD1/2004(H5N1))		3		3		
2138		270945	Influenza A virus (A/Thailand/4(SP-528)/2004(H5N1))		21		21		
2139		271108	Bombyx mori nucleopolyhedrovirus	2		2			
2140		272560	Burkholderia pseudomallei K96243	3	735	3	735		
2141		272561	Chlamydia trachomatis D/UW-3/CX	51	26	51	26		
2142		272562	Clostridium acetobutylicum ATCC 824		1		1		
2143		272563	Clostridioides difficile 630	1		1			
2144		272564	Desulfitobacterium hafniense DCB-2		3		3		
2145	X	272569	Haloarcula marismortui ATCC 43049			1		1	

2146		272620	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	28		28			
2148		272624	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	1		1			
2149		272627	Magnetospirillum magnetotacticum MS-1		5		5		
2150		272631	Mycobacterium leprae TN		30		30		
2151		272634	Mycoplasma pneumoniae M129	9		9			
2152		272636	Adeno-associated virus		18		18		
2153		272831	Neisseria meningitidis FAM18	1		1			
2154		272843	Pasteurella multocida subsp. multocida str. Pm70		5		5		
2155		272943	Cereibacter sphaeroides 2.4.1		1		1		
2156		272944	Rickettsia conorii str. Malish 7		5		5		
2157		272947	Rickettsia prowazekii str. Madrid E		8		8		
2158		272951	Rickettsia sibirica 246		25		25		
2159		272989	Salmonella enterica subsp. enterica serovar Enteritidis str. LK5		1		1		
2160		273123	Yersinia pseudotuberculosis IP 32953		1		1		
2162		273371	Candida orthopsilosis		1		1		
2163		274828	Influenza A virus (A/duck/Fujian/13/2002(H5N1))		1		1		
2164		274829	Influenza A virus (A/duck/Fujian/17/2001(H5N1))		2		2		
2165		277944	Human coronavirus NL63		5	5623	8	5623	3
2166		278137	Mycolicibacterium gilvum Spyr1		53		53		
2167		279150	Classical swine fever virus 96TD	2		7		5	
2168		279329	Influenza B virus (B/Shandong/7/97)	1	1	1	1		
2169		279797	Influenza A virus (A/egret/Hong Kong/757.3/2002(H5N1))		3		3		
2171		279889	Triticum spelta var. arduini		3		3		
2172		280240	Nocardiopsis baichengensis	1		1			
2173		280463	Emiliania huxleyi CCMP1516		1		1		
2174		280855	Seoul virus BjHD01	2		2			
2175		281310	Haemophilus influenzae 86-028NP	13		13			
2176		281689	Desulfuromonas acetoxidans DSM 684		1		1		
2177		282124	Influenza A virus (A/mallard/Alberta/127/00(H3N8))		1		1		
2178		282458	Staphylococcus aureus subsp. aureus MRSA252	86		86			
2179		283166	Bartonella henselae str. Houston-1		1		1		
2180		283643	Cryptococcus neoformans var. neoformans B-3501A	1	3	1	3		
2181		283877	Leucobacter chromiireducens		1		1		
2182		284168	Influenza A virus (A/Ck/HK/2133.1/2003(H5N1))		1		1		
2183		284177	Influenza A virus (A/Ck/HK/YU22/2002(H5N1))	1		1			
2184		284190	Influenza A virus (A/Ck/Viet Nam/36/2004(H5N1))	1		1			
2185		284195	Influenza A virus (A/Ck/YN/115/2004(H5N1))		1		1		
2186		284202	Influenza A virus (A/Dk/ST/5048/2001(H3N8))	1		1			
2187		284218	Influenza A virus (A/Viet Nam/1203/2004(H5N1))	74	134	76	134	2	
2188		284581	Priestia koreensis		1		1		
2189		284672	SARS coronavirus TJF		14		14		

2190		284813	Encephalitozoon cuniculi GB-M1		28		28		
2191		285006	Saccharomyces cerevisiae RM11-1a		2		2		
2192		286239	Influenza A virus (A/red knot/Delaware/2561/1987(H10N5))		1		1		
2193		286542	Soochong virus-2		1		1		
2194		286636	Streptococcus pyogenes MGAS10394		1		1		
2195		286783	Salmonella enterica subsp. enterica serovar Indiana		1		1		
2196		288118	Mandrillus leucophaeus foamy virus	1		1			
2197		289338	Influenza B virus (B/Nanchang/12/98)		1		1		
2198		289365	Human parvovirus 4		3		3		
2199		290028	Human coronavirus HKU1		6	4851	6	4851	
2201		290512	Prosthecochloris aestuarii DSM 271		1		1		
2202		291592	Influenza A virus (A/crow/Kyoto/53/2004(H5N1))	1		1			
2203		292039	Influenza A virus (A/chicken/HongKong/SF1/03(H9N2))	1		1			
2204		292045	Influenza A virus (A/chicken/HongKong/YU427/03(H9N2))	1		1			
2205		292348	Canine calicivirus (strain 48)	2		2			
2206		292349	Feline calicivirus (strain Urbana)	3		3			
2207		292590	Influenza A virus (A/swine/Ontario/42729A/01(H3N3))	1		1			
2208		292633	Dragon grouper nervous necrosis virus	20		20			
2209		293054	Influenza A virus (A/turkey/Ontario/6213/66(H5N?))	1		1			
2210		293055	Influenza A virus (A/mallard/Ohio/556/1987(H5N9))		1		1		
2211		293090	Influenza A virus (A/Fujian/411/2002(H3N2))		1		1		
2212		293614	Rickettsia akari str. Hartford		1		1		
2213		294381	Entamoeba histolytica HM-1:IMSS		103		103		
2214		295027	Human herpesvirus 5 strain Merlin	2	3	4	3	2	
2215		295319	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150		3		3		
2216		295358	Mycoplasma hyopneumoniae 232	21		21			
2217		298339	Pan troglodytes foamy virus	1		1			
2218		298653	Frankia sp. EAN1pec		2		2		
2219		298713	Influenza A virus (A/chicken/Korea/SNU0091/00(H9N2))		1		1		
2220		298716	Influenza A virus (A/chicken/Korea/SNU1035C/00(H9N2))		1		1		
2221		299386	Equine arteritis virus Bucyrus	2		2			
2222		299390	Influenza A virus (A/Viet Nam/HN/2004(H5N1))		6		6		
2223		299730	Influenza A virus (A/chicken/Viet Nam/AG-010/2004(H5N1))		1		1		
2225		300015	Lactate dehydrogenase elevating virus C	1		1			
2226		300016	Lactate dehydrogenase elevating virus Plagemann	1		1			
2227		300180	Mopeia Lassa virus reassortant 29		4		4		
2228		300267	Shigella dysenteriae Sd197		5		5		
2229		300268	Shigella boydii Sb227		3		3		
2230		300269	Shigella sonnei Ss046		9		9		
2231		300559	PRRSV VR2332	21	7	21	7		
2232		300563	PRRSV HB-1(sh)/2002	1		1			

2233		300748	Influenza A virus (A/swine/Korea/S190/2004(H9N2))		3		3		
2234		300749	Influenza A virus (A/swine/Korea/S452/2004(H9N2))		1		1		
2235		300750	Influenza A virus (A/chicken/Korea/S1/2003(H9N2))		1		1		
2236		300852	Thermus thermophilus HB8		1		1		
2237		301448	Streptococcus pyogenes serotype M3	1		1			
2238		301449	Streptococcus pyogenes serotype M5	56	57	56	57		
2239		301450	Streptococcus pyogenes serotype M6	9	7	9	7		
2240		301451	Streptococcus pyogenes serotype M18	1		1			
2241		301452	Streptococcus pyogenes serotype M49	1		1			
2242		301478	Murray valley encephalitis virus (strain MVE-1-51)	11	14	11	14		
2243		301964	CY1014 virus		1		1		
2244		302272	Sendai virus (strain Ohita)	1		1			
2245		303316	Influenza A virus (A/Hatay/2004/(H5N1))	3		3			
2246		304883	Influenza A virus (A/Belfast/53582/2004(H3N?))		2		2		
2247		304895	Catenulispora acidiphila		1		1		
2248		305674	Deerpox virus W-848-83		2		2		
2249		306061	Influenza A virus (A/swine/IDT/Bakum1832/2000(H1N2))		1		1		
2250		306254	Campylobacter coli RM2228		2		2		
2251		306263	Campylobacter lari RM2100		1		1		
2252		306264	Campylobacter upsaliensis RM3195		1		1		
2253		307044	West Nile virus strain 385-99	22	12	22	12		
2254		307685	Merluccius australis polylepis	1		1			
2255		307819	Influenza A virus (A/Jiangsu/38/2004(H3N2))		1		1		
2256		308061	Hantavirus HPR/02-73		1		1		
2257		308159	Araucaria virus		6		6		
2258		310542	Chimpanzee adenovirus	2		2			
2259		311169	Influenza A virus (A/duck/Korea/S10/03(H3N2))		1		1		
2260		311339	Human herpesvirus 5 strain Toledo	9		9			
2261		311410	Roseibium album		1		1		
2262		311596	Influenza A virus (A/New York/18/2003(H3N2))		9		9		
2263		311695	Influenza A virus (A/New York/124/2001(H3N2))		1		1		
2265		311775	Influenza A virus (A/New York/205/2001(H1N1))		12		12		
2266		313589	Janibacter sp. HTCC2649		1		1		
2267		313596	Robiginitalea biformata HTCC2501		1		1		
2268		313606	Microscilla marina ATCC 23134		1		1		
2269		313627	Bacillus sp. NRRL B-14911		2		2		
2270		314262	Roseobacter sp. MED193		1		1		
2271		314275	Alteromonas mediterranea		1		1		
2272		314278	Nitrococcus mobilis Nb-231		1		1		
2273		314283	Reinekea blandensis MED297		1		1		
2274		314285	Congregibacter litoralis KT71		1		1		
2275		314288	Vibrio alginolyticus 12G01		3		3		

2276		314291	Vibrio splendidus 12B01		2		2		
2277		314292	Photobacterium angustum S14		1		1		
2278		315277	Chlamydia trachomatis A/HAR-13	6	1	6	1		
2279		315456	Rickettsia felis URRWXCal2		7		7		
2280		315730	Bacillus mycoides KBAB4		2		2		
2281		315749	Bacillus cytotoxicus NVH 391-98		1		1		
2282		316056	Rhodopseudomonas palustris BisB18		1		1		
2283		316068	Leadbetterella byssophila		1		1		
2284		316287	Ceratogyrus marshalli	1		1			
2285		316385	Escherichia coli str. K-12 substr. DH10B		3		3		
2286		316401	Escherichia coli ETEC H10407	64	31	64	31		
2287		316407	Escherichia coli str. K-12 substr. W3110		1		1		
2288		317652	Influenza A virus (A/Hong Kong/2/68(H3N2))		4		4		
2289		317655	Sphingopyxis alaskensis RB2256		1		1		
2290		318586	Paracoccus denitrificans PD1222		2		2		
2291		319224	Shewanella putrefaciens CN-32		1		1		
2292		320306	Influenza A virus (A/crested eagle/Belgium/01/2004(H5N1))	2		2			
2293		320372	Burkholderia pseudomallei 1710b		1		1		
2294		320373	Burkholderia pseudomallei 668		9		9		
2295		320374	Burkholderia pseudomallei S13		2		2		
2296		320388	Burkholderia mallei SAVP1		29		29		
2297		320390	Burkholderia mallei GB8 horse 4		1		1		
2298		320483	Anaplasma marginale str. Florida	19	61	19	61		
2299		320667	Trichosanthes dioica	1		1			
2300		321314	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67		5		5		
2301		322053	Konjac mosaic virus	1		1			
2302		322564	Influenza A virus (A/tiger/Thailand/CU-T4/04(H5N1))		5		5		
2303		322566	Influenza A virus (A/tiger/Thailand/CU-T6/04(H5N1))		1		1		
2304		322710	Azotobacter vinelandii DJ		2		2		
2306		325240	Shewanella baltica OS155		2		2		
2307		327105	HIV-1 O_ANT70	1		1			
2308		327205	Influenza A virus (A/New York/348/2003(H1N1))		150		150		
2309		327310	Influenza A virus (A/Kinmen/645/04(H3N2))		1		1		
2310		327311	Influenza A virus (A/Yilan/515/03(H3N2))		1		1		
2311		328670	Banana streak GF virus	4		4			
2312		328671	Banana streak OL virus	4		4			
2313	X	328812	Parabacteroides goldsteinii				1		1
2315		329389	Hepatitis C virus (isolate Glasgow)	3	4	3	4		
2316		329593	Influenza A virus (A/chicken/Fujian/25/00(H9N2))		6		6		
2317		329854	Bacteroides intestinalis		1		1		
2318		330879	Aspergillus fumigatus Af293		18		18		
2319		331111	Escherichia coli O139:H28 str. E24377A		36		36		

2320		331112	Escherichia coli HS		14		14		
2321		331271	Burkholderia cenocepacia AU 1054		7		7		
2322		331272	Burkholderia cenocepacia HI2424		1		1		
2323		331635	Chlamydia pecorum E58	29		29			
2324		331636	Chlamydia psittaci 6BC	1		1			
2325		331978	Burkholderia pseudomallei Pasteur 52237		1		1		
2326		332162	Candidatus Solibacter		1		1		
2327		332193	Vaccinia Virus Acambis 3000 MVA		20		20		
2329		332747	Influenza A virus (A/swine/Tennessee/25/1977(H1N1))	1		1			
2330		332884	Norovirus Hu/GII.4/Sydney715D/04S/AU		1		1		
2331		333278	H7N9 subtype	7	26	12	26	5	
2332		333284	Hepatitis C virus (isolate Con1)	4	3	4	3		
2333		333367	Enterocloster asparagiformis		1		1		
2334		333668	Theileria parva strain Muguga	14	19	14	51		32
2335		333751	Human papillomavirus type 2		7		7		
2336		333754	Alphapapillomavirus 10	4		4			
2337		333760	Human papillomavirus type 16	350	492	351	523	1	31
2338		333761	Human papillomavirus type 18	26	104	28	104	2	
2339		333762	Human papillomavirus type 26		1		1		
2340		333763	Human papillomavirus type 32	1	1	1	1		
2341		333765	Human papillomavirus type 53		1		1		
2342		333849	Enterococcus faecium DO		1		1		
2343		333923	Human papillomavirus 5	1		1			
2344		333990	Carnobacterium sp. AT7	1		1			
2345		334203	Mupapillomavirus 1	1	38	1	38		
2346		334380	Orientia tsutsugamushi str. Ikeda		1		1		
2347		334426	Angiostrongylus costaricensis	1	1	1	1		
2348	X	334440	Palythoa tuberculosa			1		1	
2350		334590	Influenza A virus (A/Moscow/343/2003(H3N2))		1		1		
2351		334802	Burkholderia mallei FMH		1		1		
2352		334803	Burkholderia mallei JHU		2		2		
2353		335333	Influenza A virus (A/New York/384/2005(H3N2))		64		64		
2354		335337	Influenza A virus (A/New York/388/2005(H3N2))		14		14		
2355		335358	Influenza A virus (A/New York/232/2004(H3N2))		110		110		
2356		335812	Influenza B virus (B/Shanghai/361/2002)	1		1			
2357		336092	Influenza A virus (A/black-headed goose/Qinghai/1/2005(H5N1))	2		2			
2358		336205	Influenza A virus (A/swine/Bakum/5/95(H1N1))		2		2		
2359		336207	Influenza A virus (A/swine/Bakum/1832/2000(H1N2))		3		3		
2360		336238	Influenza A virus (A/Bar-headed Goose/Qinghai/61/05(H5N1))		8		8		
2361		336306	Enterobacter cloacae subsp. cloacae		1		1		
2362		336407	Rickettsia bellii RML369-C		4		4		
2363		336794	Influenza A virus (A/equine/Massachussetts/213/2003(H3N8))		1		1		

2364		336800	Influenza A virus (A/equine/New York/1/1999(H3N8))		3		3		
2365		336982	Mycobacterium tuberculosis F11		24		24		
2366		337042	Alphapapillomavirus 7	11		11			
2367		337043	Alphapapillomavirus 4		1		1		
2368		337052	Deltapapillomavirus 4	24		24			
2369		337090	Chlorobium chlorochromatii		1		1		
2370		338079	African green monkey simian foamy virus	3		3			
2371		338188	Bacteroides finegoldii		1		1		
2372		338478	Macaque simian foamy virus	1		1			
2373		338966	Pelobacter propionicus DSM 2379		3		3		
2374		339670	Burkholderia ambifaria AMMD		4		4		
2375		339854	Bacillus thuringiensis serovar israelensis ATCC 35646		4		4		
2376		340177	Chlorobium chlorochromatii CaD3		1		1		
2377		340184	Escherichia coli B7A		5		5		
2378		340185	Escherichia coli E22		13		13		
2379		340186	Escherichia coli E110019		2		2		
2380		340197	Escherichia coli F11		12		12		
2382		341663	Aspergillus terreus NIH2624	2		2			
2383		341946	Woodchuck hepatitis virus 2	4		4			
2384		341980	Human herpesvirus 3 strain Oka vaccine	4	151	4	276		125
2385		342023	Streptococcus pyogenes serotype M12	3	1	3	1		
2386		342137	Influenza A virus (A/chicken/CA/375TR/2002(H6N2))		1		1		
2387		342145	Influenza A virus (A/turkey/MN/735/79(H6N2))		2		2		
2388		342207	Influenza A virus (A/shorebird/Delaware/141/2002(H9N9))		1		1		
2389		342210	Influenza A virus (A/shorebird/Delaware/275/2001(H9N7))		1		1		
2390		342221	Influenza A virus (A/chicken/Korea/S4/2003(H9N2))		1		1		
2391		342396	Influenza A virus (A/turkey/Canada-Ontario/NS-01839-1/05(H3))		1		1		
2392		342409	White spot syndrome virus	1		1			
2393		342508	Influenza A virus (A/New York/444/2001(H1N1))		25		25		
2395		342610	Pseudoalteromonas atlantica T6c		1		1		
2396		342613	Streptococcus agalactiae 18RS21	2		2			
2397		342614	Streptococcus agalactiae 515	1		1			
2398		342615	Streptococcus agalactiae H36B	1		1			
2399		342617	Streptococcus agalactiae CJB111	2		2			
2400		343462	Human adenovirus 11p	7		7			
2401		343463	Human adenovirus 11a	1		1			
2402		344598	Influenza A virus (A/whooper swan/Mongolia/6/05(H5N1))		1		1		
2403		344601	Escherichia coli B171		25		25		
2404		344609	Shigella boydii CDC 3083-94		20		20		
2405		344610	Escherichia coli 53638		1		1		
2406		345072	Vibrio cholerae MO10		1		1		
2407		345073	Vibrio cholerae O395		4		4		

2408		345074	Vibrio cholerae RC385		2		2		
2409		345075	Vibrio cholerae V51		3		3		
2410		345076	Vibrio cholerae V52		32		32		
2411		345840	Palaemon modestus	74		74			
2412		347257	Mycoplasmopsis agalactiae PG2	3		3			
2413		347495	Bacillus cereus F837/76		1		1		
2414		347515	Leishmania major strain Friedlin	29	38	29	38		
2415		348776	Mycobacterium tuberculosis C		177		177		
2416		349101	Cereibacter sphaeroides ATCC 17029		1		1		
2417		349163	Acidiphilium cryptum JF-5		1		1		
2418		349344	Bat SARS CoV Rp3/2004		1		1		
2419		349741	Akkermansia muciniphila ATCC BAA-835		4		4		
2420		349746	Yersinia pestis Angola		3		3		
2421		349747	Yersinia pseudotuberculosis IP 31758		9		9		
2422		349966	Yersinia frederiksenii ATCC 33641		2		2		
2423		349967	Yersinia mollaretii ATCC 43969		3		3		
2424		349968	Yersinia bercovieri ATCC 43970		5		5		
2425		350054	Mycolicibacterium gilvum PYR-GCK		64		64		
2426		350058	Mycolicibacterium vanbaalenii PYR-1		55		55		
2427		350702	Burkholderia cenocepacia PC184		1		1		
2428		350703	Pseudomonas aeruginosa 2192		2		2		
2429		350704	Pseudomonas aeruginosa C3719		2		2		
2430		351071	Newcastle disease virus AF2240	1		1			
2431		351073	Mammalian orthoreovirus		1		1		
2432		351277	Influenza A virus (A/Nanchang/0058/1994(H3N2))		1		1		
2433		351581	Francisella tularensis subsp. holarctica FSC200		1		1		
2434		351607	Acidothermus cellulolyticus 11B		2		2		
2435		351627	Caldicellulosiruptor saccharolyticus DSM 8903		1		1		
2436		351745	Shewanella sp. W3-18-1		1		1		
2437		351746	Pseudomonas putida F1		5		5		
2438		352034	Influenza A virus (A/duck/Potsdam/1402-6/1986(H5N2))	1		1			
2439		352348	Influenza A virus (A/chicken/Hong Kong/17/1977(H6N1))		1		1		
2440		352520	Influenza A virus (A/mallard/Alberta/35/1976(H1N1))	1	6	1	6		
2441		352561	Influenza A virus (A/duck/Australia/341/1983(H15N8))		1		1		
2442		352564	Influenza A virus (A/mallard/Astrakhan/263/1982(H14N5))	1		1			
2443		352764	Influenza A virus (A/mallard/Alberta/202/1996(H2N5))	1		1			
2444		352914	Plasmodium yoelii yoelii 17XNL	6	3	6	3		
2445		352963	Influenza A virus (A/California/7/2004(H3N2))		1		1		
2446		353152	Cryptosporidium parvum Iowa II		84		84		
2447		353153	Trypanosoma cruzi strain CL Brener	2059	12	2127	12	68	
2448		353154	Theileria annulata strain Ankara		4		4		
2449		353253	Influenza A virus (A/duck/Novosibirsk/56/2005(H5N1))	6	2	6	2		

2450		353466	Influenza A virus (A/Canterbury/236/2005(H3N2))		1		1		
2451		354228	Influenza A virus (A/Gf/HK/SSP607/2003(H9N2))		1		1		
2452		354235	Influenza A virus (A/Ck/HK/CSW161/2003(H9N2))		1		1		
2453		354242	Campylobacter jejuni subsp. jejuni 81-176		4		4		
2454		355315	Streptococcus agalactiae serogroup Ia	1		1			
2456		356114	Hepatitis C virus genotype 3	121	20	121	20		
2457		356386	Hepatitis C virus (isolate India)		1		1		
2458		356391	Hepatitis C virus (isolate 6a33)		11		11		
2459		356410	Hepatitis C virus (isolate HC-G9)	1	1	1	1		
2460		356411	Hepatitis C virus JFH-1	8	5	8	5		
2461		356413	Hepatitis C virus (isolate BEBE1)		14		14		
2462		356415	Hepatitis C virus (isolate NZL1)	1	3	1	3		
2463		356416	Hepatitis C virus (isolate HCV-K3a/650)		21		21		
2464		356417	Hepatitis C virus (isolate JK049)		6		6		
2465		356418	Hepatitis C virus ED43	3	1	3	1		
2466		356419	Hepatitis C virus (isolate EUH1480)		5		5		
2467		356421	Hepatitis C virus (isolate Th580)		7		7		
2468		356424	Hepatitis C virus (isolate VN004)		1		1		
2469		356426	Hepatitis C virus subtype 3a	12	105	12	105		
2470		357205	Influenza A virus (A/chicken/Hong Kong/3123.1/2002(H5N1))		1		1		
2471		357208	Influenza A virus (A/Vietnam/CL26/2004(H5N1))		79		79		
2472		357210	Influenza A virus (A/Vietnam/CL100/2004(H5N1))	1		1			
2473		357244	Orientia tsutsugamushi str. Boryong	2	2	2	2		
2474		357348	Burkholderia pseudomallei 1106a		2		2		
2475		357355	Hepatitis C virus (isolate Tr Kj)		3		3		
2476		358708	Shigella dysenteriae 1012		1		1		
2477		358709	Escherichia coli 101-1		5		5		
2478		358769	Classical swine fever virus - Alfort/187	70		70			
2479		358805	Classical swine fever virus - Alfort/Tuebingen	5		5			
2480		358812	Classical swine fever virus - C	2		2			
2481		359391	Brucella abortus 2308		31		31		
2482		359787	Staphylococcus aureus subsp. aureus JH1	1	1	1	1		
2483		359921	Influenza A virus (A/Australian shelduck/Western Australia/1756/1983(H15N2))	1		1			
2484		360095	Bartonella bacilliformis KC583		1		1		
2485		360102	Yersinia pestis Antiqua		36		36		
2486		360112	Campylobacter jejuni subsp. jejuni HB93-13		2		2		
2487		360115	Coxiella burnetii RSA 331		8		8		
2488		360116	Coxiella burnetii 'MSU Goat Q177'		7		7		
2489		360117	Coxiella burnetii Q321		14		14		
2490		360118	Burkholderia pseudomallei 406e		2		2		
2491		360549	Themiste hennahi	1		1			
2492		362242	Mycobacterium ulcerans Agy99		15		15		

2493		362651	Human immunodeficiency virus type 1 (isolate YU2)	16	21	16	21		
2494		362663	Escherichia coli 536		65		65		
2495		363020	Avian leukosis virus HPRS103	1		1			
2497		364106	Escherichia coli UTI89		2		2		
2498		364132	Influenza A virus (A/New York/504/1998(H3N2))		1		1		
2499		365044	Polaromonas naphthalenivorans CJ2		2		2		
2501		365078	Influenza A virus (A/duck/Guangxi/1586/2004(H5N1))		1		1		
2502		365080	Influenza A virus (A/duck/Guangxi/1793/2004(H5N1))		1		1		
2503		365129	Influenza A virus (A/chicken/Vietnam/DT171/2004(H5N1))		1		1		
2506		367120	Influenza A virus (A/Fort Monmouth/1/1947(H1N1))	1		1			
2507		367400	Neembucu hantavirus		5		5		
2508		367737	Aliarcobacter butzleri RM4018	1		1			
2509		367830	Staphylococcus aureus subsp. aureus USA300	1		2		1	
2510		368445	Crocodilepox virus		2		2		
2511		370127	Influenza A virus (A/Victoria/1968(H3N2))		1		1		
2512		370128	Influenza A virus (A/Northern Territory/60/1968(H3N2))		3		3		
2513		370354	Entamoeba dispar SAW760		19		19		
2514		370810	Influenza A virus (A/Anhui/1/2005(H5N1))	7		7			
2515		370811	Influenza A virus (A/Anhui/2/2005(H5N1))	1		1			
2516		370813	Influenza A virus (A/duck/IT/701/2005(H10N7))		1		1		
2517		370830	Hantaan virus Q32		4		4		
2518		371082	Influenza A virus (A/Taiwan/2/2006(H1N1))		7		7		
2519		371094	Chikungunya virus strain S27-African prototype	24		24			
2520		371214	Influenza A virus (A/chicken/Taiwan/0329/01(H6N1))	5		5			
2521		371601	Bacteroides xylanisolvens	1		1			
2522		373098	Gambierdiscus toxicus	7		7			
2524		373153	Streptococcus pneumoniae D39		60		60		
2525		373384	Shigella flexneri 5 str. 8401		23		23		
2526		373665	Yersinia pestis biovar Orientalis str. IP275		1		1		
2527		374405	Influenza C virus (C/Yamagata/15/2004)	2		2			
2528		374507	Human rotavirus G9 isolate F45	7		7			
2529		374927	Haemophilus influenzae 22.1-21		3		3		
2530		374928	Haemophilus influenzae PittAA		1		1		
2531		374931	Haemophilus influenzae PittGG		1		1		
2532		374932	Haemophilus influenzae PittHH	1		1			
2533		374933	Haemophilus influenzae PittII		3		3		
2534		375177	Haemophilus influenzae 3655	6	1	6	1		
2535		375432	Haemophilus influenzae R3021		2		2		
2536		375450	Yersinia pestis FV-1		2		2		
2537		376619	Francisella tularensis subsp. holarctica LVS	10	291	10	301		10
2538		376721	Influenza A virus (A/chicken/Kurgan/05/2005(H5N1))	1		1			
2539		377628	Yersinia pestis Nepal516		135		135		

2540		378131	Influenza A virus (A/Memphis/13/1978(H1N1))		1		1		
2541		378139	Influenza A virus (A/Memphis/1/1978(H1N1))		7		7		
2542		378809	Ravn virus - Ravn, Kenya, 1987	2	32	2	32		
2543		378830	Lake Victoria marburgvirus - Angola2005	8	18	8	18		
2545		380210	Influenza A virus (A/England/333/1980(H1N1))	1	1	1	1		
2546		380213	Influenza A virus (A/Taiwan/1/1986(H1N1))		1		1		
2547		380217	Influenza A virus (A/swine/Hong Kong/4/1976(H3N2))		1		1		
2548		380282	Influenza A virus (A/Fort Monmouth/1/1947-mouse adapted(H1N1))		47		47		
2549		380284	Influenza A virus (A/England/268/1996(H7N7))	1	1	1	1		
2550		380285	Influenza A virus (A/turkey/Ireland/1378/1983(H5N8))		1		1		
2551		380299	Influenza A virus (A/turkey/Wisconsin/1968(H5N9))		1		1		
2552		380301	Influenza A virus (A/turkey/Ontario/7732/1966(H5N9))	5	8	5	8		
2553		380330	Influenza A virus (A/goose/Hong Kong/8/1976(H1N1))		2		2		
2554		380332	Influenza A virus (A/swine/Hong Kong/273/1994(H1N1))		1		1		
2555		380337	Influenza A virus (A/equine/Prague/1/1956(H7N7))		1		1		
2556		380339	Influenza A virus (A/equine/Tennessee/5/1986(H3N8))		1		1		
2557		380340	Influenza A virus (A/equine/London/1416/1973(H7N7))	1	1	1	1		
2558		380342	Influenza A virus (A/swine/Iowa/15/1930(H1N1))	1		1			
2559		380343	Influenza A virus (A/ruddy turnstone/New Jersey/47/1985(H4N6))		2		2		
2560		380346	Influenza A virus (A/Wisconsin/3523/1988(H1N1))	2		2			
2562		380836	Influenza A virus (A/chicken/Vietnam/5/2003(H5N1))		1		1		
2563		380842	Influenza A virus (A/duck/Vietnam/15/2003(H5N1))		3		3		
2564		380905	Influenza A virus (A/X-47(H3N2))	3	2	3	2		
2565		380950	Influenza A virus (A/Beijing/32/1992(H3N2))		54		54		
2566		380951	Influenza A virus (A/Hebei/19/1995(H3N2))	1		1			
2567		380960	Influenza A virus (A/Tokyo/3/1967(H2N2))	2		2			
2568		380964	Influenza A virus (A/Texas/36/1991(H1N1))		1		1		
2569		380978	Influenza A virus (A/Wisconsin/4755/1994(H1N1))		5		5		
2570		380979	Influenza A virus (A/Wisconsin/4754/1994(H1N1))		1		1		
2571		380982	Influenza A virus (A/WSN(H1N1))		1		1		
2572		380984	Influenza A virus (A/Leningrad/134/17/1957(H2N2))		3		3		
2573		380985	Influenza A virus (A/Chile/1/1983(H1N1))		4		4		
2574		381512	Influenza A virus (A/New Caledonia/20/1999(H1N1))	39	247	40	247	1	
2575		381513	Influenza A virus (A/Panama/2007/1999(H3N2))	10	16	10	16		
2576		381516	Influenza A virus (A/USSR/90/1977(H1N1))	12		12			
2577		381517	Influenza A virus (A/Udorn/307/1972(H3N2))		5		5		
2578		381518	Influenza A virus (A/Wilson-Smith/1933(H1N1))	1	158	1	158		
2579		381666	Cupriavidus necator H16		1		1		
2580		382781	Influenza A virus (A/Singapore/1/1957(H2N2))	1	32	1	32		
2581		382813	Influenza A virus (A/Japan/305+/1957(H2N2))	2		2			
2582		382825	Influenza A virus (A/Philippines/2/1982(H3N2))	1	1	1	1		

2583		382828	Influenza A virus (A/RI/5-/1957(H2N2))		1		1		
2584		382832	Influenza A virus (A/VM113-V1(H1N1))	1		1			
2585		382835	Influenza A virus (A/WSN/1933(H1N1))	13	3	13	3		
2586		382842	Influenza A virus (A/swine/29/1937(H1N1))		2		2		
2587		382848	Influenza A virus (A/swine/Hong Kong/126/1982(H3N2))		1		1		
2588		383028	Influenza A virus (A/New York/687/1995(H3N2))	1		1			
2589		383121	Influenza A virus (A/Waikato/7/2000(H3N2))		2		2		
2590		383152	Influenza A virus (A/Wellington/22/2001(H3N2))		1		1		
2591		383231	Influenza A virus (A/Wellington/8/2004(H3N2))		2		2		
2592		383281	Influenza A virus (A/Otago/5/2005(H1N1))		1		1		
2593		383379	Toxoplasma gondii RH	27	23	27	23		
2594		383531	Influenza A virus (A/swine/Italy/2/1979(H1N1))		5		5		
2595		383537	Influenza A virus (A/swine/Iowa/1946(H1N1))		1		1		
2596		383550	Influenza A virus (A/duck/England/1/1956(H11N6))		2		2		
2598		383561	Influenza A virus (A/swine/Italy/1850/1977(H3N2))		1		1		
2599		383566	Influenza A virus (A/swine/Italy/425/1976(H1N1))		1		1		
2600		383568	Influenza A virus (A/Shanghai/11/1987(H3N2))		1		1		
2602		383571	Influenza A virus (A/Memphis/6/1986(H3N2))	4	1	4	1		
2603		383574	Influenza A virus (A/Memphis/2/1985(H3N2))	1		1			
2604		383577	Influenza A virus (A/Memphis/1/1990(H3N2))		1		1		
2605		383578	Influenza A virus (A/Memphis/4/1980(H3N2))		1		1		
2606		383586	Influenza A virus (A/Memphis/1/1971(H3N2))	19	11	19	11		
2607		383602	Influenza A virus (A/Anas acuta/Primorje/695/1976(H2N3))		17		17		
2608		383603	Influenza A virus (A/turkey/Minnesota/833/1980(H4N2))		1		1		
2610		384483	Influenza A virus (A/swine/Hong Kong/127/1982(H3N2))		1		1		
2611		384484	Influenza A virus (A/swine/Hong Kong/81/1978(H3N2))		12		12		
2612		384487	Influenza A virus (A/Swine/Indiana/1726/1988(H1N1))		2		2		
2613		384493	Influenza A virus (A/seal/Mass/1/1980(H7N7))	1	1	1	1		
2614		384495	Influenza A virus (A/Kiev/59/1979(H1N1))		5		5		
2615		384498	Influenza A virus (A/Ann Arbor/6/1960(H2N2))		271		271		
2616		384499	Influenza A virus (A/gull/Maryland/704/1977(H13N6))		1		1		
2617		384500	Influenza A virus (A/Beijing/11/1956(H1N1))		30		30		
2619		384505	Influenza A virus (A/nt/60/1968(H3N2))	1	70	1	70		
2620		384509	Influenza A virus (A/tern/Australia/G70C/1975(H11N9))	9		9			
2621		384510	Influenza A virus (A/tern/South Africa/1961(H5N3))	1		1			
2622		384527	Influenza A virus (A/Cameron/1946(H1N1))		1		1		
2623		384676	Pseudomonas entomophila L48		1		1		
2624		384946	Influenza A virus (A/duck/Hungary/1/1970(H6N2))		1		1		
2625		385576	Influenza A virus (A/Alaska/6/1977(H3N2))		2		2		
2626		385580	Influenza A virus (A/duck/Ukraine/1/1963(H3N8))	3		3			
2627		385583	Influenza A virus (A/Denver/1957(H1N1))		2		2		

2628		385585	Influenza A virus (A/equine/Jilin/1/1989(H3N8))	1		1			
2629		385586	Influenza A virus (A/chicken/Pennsylvania/1/1983(H5N2))		1		1		
2630		385587	Influenza A virus (A/budgerigar/Hokkaido/1/1977(H4N6))		10		10		
2631		385599	Influenza A virus (A/udorn/1972(H3N2))		1		1		
2632		385600	Influenza A virus (A/Puerto Rico/8/1934(Cambridge)(H1N1))	1		1			
2633		385605	Influenza A virus (A/equine/Kentucky/2/1986(H3N8))		3		3		
2634		385616	Influenza A virus (A/ruddy turnstone/NJ/60/1985(N9))		1		1		
2635		385617	Influenza A virus (A/chicken/Pennsylvania/1370/1983(H5N2))	1		1			
2636		385624	Influenza A virus (A/Port Chalmers/1/1973(H3N2))	7	1	7	1		
2637		385630	Influenza A virus (A/Bangkok/1/1979(H3N2))	1	7	1	7		
2638		385640	Influenza A virus (A/Memphis/102/1972(H3N2))		8		8		
2639		385644	Influenza A virus (A/swine/Ukkel/1/1984(H3N2))		1		1		
2640		386032	Reston ebolavirus - Reston (1989)		4		4		
2641		386033	Sudan ebolavirus - Uganda (2000)	1	6	1	6		
2642		386043	Listeria welshimeri serovar 6b str. SLCC5334		3		3		
2643		386056	Paraburkholderia ferrariae		1		1		
2644		386415	Clostridium novyi NT		2		2		
2645		386585	Escherichia coli O157:H7 str. Sakai		17		17		
2646		386656	Yersinia pestis Pestoides F		2		2		
2647		387090	Phocaeicola coprophilus		2		2		
2648		387093	Sulfurovum sp. NBC37-1		1		1		
2649		387139	Influenza A virus (A/Aichi/2/1968(H3N2))	12	11	12	11		
2650		387147	Influenza A virus (A/England/878/1969(H3N2))	1	2	1	2		
2651		387156	Influenza A virus (A/Harbin/1/1988(H1N2))		17		17		
2652		387161	Influenza A virus (A/Japan/305/1957(H2N2))	5	29	5	29		
2653		387191	Influenza A virus (A/camel/Mongolia/1982(H1N1))		8		8		
2654		387203	Influenza A virus (A/duck/Bavaria/2/1977(H1N1))		1		1		
2655		387207	Influenza A virus (A/duck/Hokkaido/8/1980(H3N8))		6		6		
2657		387213	Influenza A virus (A/equine/Alaska/1/1991(H3N8))		1		1		
2658		387223	Influenza A virus (A/equine/Miami/1963(H3N8))	5		5			
2659		387239	Influenza A virus (A/gull/Delaware/475/1986(H2N2))		1		1		
2660		387243	Influenza A virus (A/herring gull/DE/677/1988(H2N8))		1		1		
2661		388041	Influenza A virus (A/bar-headed goose/Qinghai/1A/2005(H5N1))	1		1			
2662		388272	Pseudomonas aeruginosa PACS2		12		12		
2663		388634	Bombyx mandarina nuclear polyhedrosis virus		1		1		
2664		388799	HIV-1 group O	1		1			
2665		389259	Influenza A virus (A/Nagasaki/N03/2005(H3N2))		1		1		
2666		390157	Senecavirus A	8		8			
2667		390236	Borreliella afzelii PKo	2		2			
2668	X	390333	Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842 = JCM 1002			1		1	
2669		391646	Hepatitis B virus ayw3	1		1			

2670		391647	Hepatitis B virus ayw2	8		8			
2671		391650	Hepatitis B virus ayw4	1		1			
2672		391896	Rickettsia bellii OSU 85-389		3		3		
2673		392021	Rickettsia rickettsii str. 'Sheila Smith'	1	9	1	9		
2674		392734	Terriglobus roseus		1		1		
2675		392809	Influenza A virus (A/Victoria/3/1975(H3N2))	45	13	45	13		
2676		392810	Influenza A virus (A/chicken/Rostock/8/1934(H7N1))	2	4	2	4		
2677		392811	Influenza A virus (A/Udorn/8/1972(H3N2))	1		1			
2678		393011	Francisella tularensis subsp. holarctica OSU18		6		6		
2679		393115	Francisella tularensis subsp. tularensis FSC198		85		85		
2680		393117	Listeria monocytogenes FSL J1-194		2		2		
2681		393124	Listeria monocytogenes FSL N3-165		2		2		
2682		393125	Listeria monocytogenes FSL R2-503		1		1		
2683		393126	Listeria monocytogenes FSL R2-561		1		1		
2684		393128	Listeria monocytogenes F6900		1		1		
2685		393130	Listeria monocytogenes J0161		6		6		
2686		393133	Listeria monocytogenes 10403S		4		4		
2687		393305	Yersinia enterocolitica subsp. enterocolitica 8081		15		15		
2689		393548	Influenza A virus (A/chicken/Tula/Russia/Oct-5/2005(H5N1))		1		1		
2690		393557	Influenza A virus (A/Leningrad/1954/1(H1N1))		8		8		
2691		393697	Influenza A virus (A/Liaoning/25/2000(H1N1))		1		1		
2692		393902	Influenza A virus (A/Wisconsin/67/2005(H3N2))	1	5	1	5		
2693		395095	Mycobacterium tuberculosis str. Haarlem		127		127		
2694		395494	Gallionella capsiferriformans ES-2		1		1		
2695		395841	Influenza A virus (A/duck/Hokkaido/1130/01(H1N1))		1		1		
2696		395842	Influenza A virus (A/tern/Australia/1/04(H2N5))		1		1		
2697		397342	Horsepox virus		6		6		
2699		398031	Toxoplasma gondii type III		1	6	1	6	
2700		398812	TGEV virulent Purdue	4		4			
2701		400331	Influenza A virus (A/New South Wales/15/1999(H3N2))		1		1		
2702		400667	Acinetobacter baumannii ATCC 17978	10	13	13	15	3	2
2703		400788	Influenza A virus (A/Indonesia/5/2005(H5N1))	1	3	1	3		
2704		400810	Influenza A virus (A/Indonesia/CDC594/2006(H5N1))	1		1			
2705		400828	Influenza A virus (A/Indonesia/CDC669/2006(H5N1))	5		5			
2706		400830	Influenza A virus (A/Indonesia/CDC699/2006(H5N1))	2		2			
2708		401650	Listeria monocytogenes HPB2262		3		3		
2709		401671	HIV-1 M:B_89.6		1		1		
2710		402194	Influenza A virus (A/Istanbul/CTF/10/2004(H3N2))		1		1		
2711		402464	Influenza A virus (A/gray teal/Australia/2/1979(H4N4))		1		1		
2712		402489	Influenza A virus (A/turkey/Minnesota/1200/1980(H7N3))		1		1		
2713		402518	Influenza A virus (A/Canada/rv504/2004(H7N3))	1		1			

2714		402527	Influenza A virus (A/chicken/Scotland/1959(H5N1))		1		1		
2715		402648	Streptomyces hainanensis		1		1		
2716		402938	Influenza A virus (A/Michigan/2/2003(H1N2))	1		1			
2717		404137	Influenza A virus (A/chicken/Beijing/nl/2002(H9N2))		1		1		
2719		404150	Influenza A virus (A/chicken/Hubei/wk/1997(H5N1))		2		2		
2721		404155	Influenza A virus (A/chicken/Hunan/fg/2004(H5N1))		2		2		
2722		404163	Influenza A virus (A/chicken/Jilin/hg/2002(H5N1))		1		1		
2723		404330	Streptococcus pyogenes serotype M2	2		2			
2724		404331	Streptococcus pyogenes serotype M4	2		2			
2725		404408	Influenza A virus (A/chicken/Shanxi/2/2006(H5N1))	1		1			
2726		404573	Influenza A virus (A/chicken/Netherlands/03010132/03(H7N7))	1		1			
2727		404974	Vibrio cholerae AM-19226		1		1		
2728		405050	Influenza A virus (A/tern/Australia/1402/2004(H2N5))		1		1		
2729		405531	Bacillus cereus G9842		3		3		
2730		405532	Bacillus cereus B4264		1		1		
2731		405533	Bacillus cereus AH1134		3		3		
2732		405536	Bacillus anthracis str. Tsiankovskii-I		1		1		
2733		405917	Bacillus cereus W		1		1		
2734		405955	Escherichia coli APEC O1		8		8		
2735		406269	West Nile virus strain PTRoxo		12		12		
2736		407134	Yellow fever virus strain Ghana/Asibi/1927		5		5		
2737		407141	Yellow fever virus isolate Ethiopia/Couma/1961		2		2		
2738		407148	Campylobacter jejuni subsp. jejuni 81116		14		14		
2739		407418	Influenza A virus (A/chicken/Guiyang/2147/2005(H5N1))		1		1		
2740		408599	Human rotavirus G9P[8]	1		1			
2741		408685	Dengue virus 1 Brazil/97-11/1997		1058		1058		
2742		408686	Dengue virus 4 Philippines/H241/1956	4	947	4	947		
2743		408687	Dengue virus 4 Singapore/8976/1995		5		5		
2744		408688	Dengue virus 4 Thailand/0348/1991		15		15		
2745		408689	Dengue virus 4 Thailand/0476/1997		3		3		
2746		408690	Dengue virus 3 China/80-2/1980		84		84		
2747		408691	Dengue virus 3 Martinique/1243/1999		889		889		
2748		408692	Dengue virus 3 Sri Lanka/1266/2000		66		66		
2749		408693	Dengue virus 3 Singapore/8120/1995		69		69		
2750		408694	Dengue virus 2 Peru/IQT2913/1996		87		87		
2751		408870	Dengue virus 3 Philippines/H87/1956	8	13	8	13		
2752		408871	Dengue virus 4 Dominica/814669/1981	1	256	1	256		
2753		410069	Streptococcus pyogenes serotype M80	1		1			
2754		410072	Coprococcus comes	1		1			
2755		410078	Human respiratory syncytial virus S2	1		1			
2756		410289	Mycobacterium tuberculosis variant bovis BCG str. Pasteur 1173P2	1	230	1	230		
2757		411157	Influenza A virus (A/Thailand/271/2005(H1N1))	1		1			

2758		411167	Influenza A virus (A/Queensland/11/2001(H3N2))		1		1		
2759		411662	Influenza A virus (A/Hanoi/TN405/2005(H3N2))		1		1		
2760		412022	Burkholderia mallei NCTC 10229		9		9		
2761		412419	Borrelia duttonii Ly	12		12			
2762		412420	Yersinia pestis CA88-4125		21		21		
2763		412614	Vibrio cholerae 2740-80		44		44		
2764		412694	Bacillus thuringiensis str. Al Hakam		7		7		
2765		412883	Vibrio cholerae MZO-3		1		1		
2766		412966	Vibrio cholerae 1587		3		3		
2767		412967	Vibrio cholerae MAK 757		9		9		
2768		413502	Cronobacter turicensis	1		1			
2769		413999	Clostridium botulinum A str. ATCC 3502		3		3		
2770		414044	Influenza A virus (A/Thailand/1(KAN-1A)/2004(H5N1))	1		1			
2771		415166	Influenza A virus(A/swine/Henan/2/2004(H9N2))		2		2		
2772		415167	Influenza A virus(A/swine/Henan/3/2004(H9N2))		1		1		
2773		415169	Influenza A virus(A/swine/Henan/5/2004(H9N2))		1		1		
2774		415172	Influenza A virus(A/swine/Henan/8/2004(H9N2))		2		2		
2775		415176	Influenza A virus(A/swine/Shandong/fNY/2003(H9N2))		3		3		
2776		415177	Influenza A virus(A/swine/Shandong/fZC/2003(H9N2))		7		7		
2777		416035	Norovirus Hu/GII.4/DenHaag89/2006/NL	1		1			
2778		416276	Rickettsia massiliae MTU5		2		2		
2779		416674	Influenza B virus (B/Yamagata/16/1988)	4	1	5	1	1	
2780		416730	Influenza A virus (A/Memphis/10/1996(H1N1))		1		1		
2781		417398	Vibrio cholerae MZO-2		2		2		
2782		417399	Vibrio cholerae NCTC 8457		1		1		
2783		417400	Vibrio cholerae B33		5		5		
2784		417758	Influenza A virus (A/quail/Shantou/1475/2004(H9N2))	1		1			
2785		418136	Francisella tularensis subsp. tularensis WY96-3418		2		2		
2786		418868	Influenza A virus (A/Egypt/14724-NAMRU3/2006(H5N1))	1		1			
2787		419109	Vibrio parahaemolyticus AQ3810		38		38		
2788		419612	Camelus ferus		1		1		
2789		419947	Mycobacterium tuberculosis H37Ra		130		130		
2790		420174	Hepatitis C virus isolate HC-J4	23	163	23	180		17
2791		420245	Leishmania braziliensis MHOM/BR/75/M2904	14	18	14	18		
2792		420246	Geobacillus thermodenitrificans NG80-2	2		2			
2793		420521	Expression vector pNIC-NHT-CF	1		1			
2794		420662	Methylibium petroleiphilum PM1		1		1		
2795		421472	Influenza A virus (A/Indonesia/CDC1032N/2007(H5N1))	3		3			
2796		421877	Hepatitis C virus isolate HC-J1	3	26	3	26		
2797		421901	Influenza A virus (A/Egypt/0636-NAMRU3/2007(H5N1))	2	1	2	1		
2798		423368	Salmonella enterica subsp. enterica serovar Newport str. SL254		1		1		

2799		424362	Bat coronavirus HKU4-4		1		1		
2800		424717	Shigella flexneri 3a	4		4			
2801		424718	Shigella flexneri 5a	2		2			
2802		424720	Shigella flexneri Y	8		8			
2803		425067	Burkholderia pseudomallei 305		2		2		
2804		425088	Tanganya virus		1		1		
2805		425551	Influenza A virus (A/AA/Huston/1945(H1N1))	1		1			
2806		425557	Influenza A virus (A/California/10/1978(H1N1))		1		1		
2807		426430	Staphylococcus aureus subsp. aureus str. Newman	7		7			
2808		426738	Influenza A virus (A/swine/Miyagi/5/2003(H1N2))		2		2		
2809		427773	Influenza A virus (A/Thailand/SP83/2004(H5N1))	1		1			
2810		427826	Influenza B virus (B/Hong Kong/8/1973)		1		1		
2811		427890	Influenza A virus (A/Viet Nam/JP4207/2005(H5N1))	1		1			
2813		430066	Brucella abortus S19		15		15		
2814		430417	Influenza A virus (A/Wyoming/3e5/2003(H3))	1		1			
2815		430511	Juquitiba virus		2		2		
2816		430557	Francisella tularensis subsp. tularensis FSC033		27		27		
2817		431944	Magnetospirillum gryphiswaldense MSR-1		1		1		
2818		431947	Porphyromonas gingivalis ATCC 33277	20	4	20	4		
2819		432070	Influenza A virus (A/Hong Kong/213/2003(H5N1))	1	4	1	4		
2820		432094	Influenza A virus (A/Wyoming/3/2003-X-147(H3N2))		1		1		
2821		432359	Toxoplasma gondii VEG	14		14			
2822		434922	Coxiella burnetii Dugway 5J108-111		8		8		
2823		434923	Coxiella burnetii CbuG_Q212		1		1		
2824		434924	Coxiella burnetii CbuK_Q154		1		1		
2825		435258	Leishmania infantum JPCM5	28	15	28	19		4
2826		435359	Influenza A virus (A/chicken/Hebei/706/2005(H5N1))		2		2		
2827		436004	Influenza A virus (A/kunke/1/71(H3N2))		1		1		
2828		439184	Escherichia coli RS218	1		1			
2829		439220	Streptococcus caballi		1		1		
2830		439235	Desulfatibacillum alkenivorans AK-01		1		1		
2831		439843	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633		1		1		
2832		439847	Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29		1		1		
2833		440534	Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701		1		1		
2834		441158	Burkholderia pseudomallei 9		1		1		
2835		441159	Burkholderia pseudomallei 91		2		2		
2836		441160	Burkholderia pseudomallei 14		1		1		
2837		441769	Bacillus coahuilensis m4-4		1		1		
2838		441771	Clostridium botulinum A str. Hall	45		45			
2839		441962	Influenza A virus (A/duck/Mongolia/47/2001(H7N1))		3		3		
2840		443149	Mycobacterium tuberculosis CCDC5079		3		3		
2841	X	443239	Human coronavirus HKU1 (isolate N1)			1		1	

2842	X	443240	Human coronavirus HKU1 (isolate N2)			1		1	
2843	X	443241	Human coronavirus HKU1 (isolate N5)			1		1	
2844		444178	Brucella ovis ATCC 25840		8		8		
2845		444185	Simian rotavirus A strain RRV	10	1	10	1		
2846		444186	Simian rotavirus A strain TUCH		5		5		
2847		444318	Influenza A virus (A/Texas/1/1977(H3N2))	1	15	1	15		
2848		444793	Influenza A virus (A/Auckland/590/2000(H1N1))		1		1		
2849		444922	Psychromonas ossibalaenae		1		1		
2850		445027	Influenza A virus (A/Beijing/01/2003(H5N1))	1		1			
2851		445335	Clostridium botulinum NCTC 2916		2		2		
2852		445338	Clostridium botulinum str. Iwanei E	6		6			
2853		445983	Borreliella burgdorferi 156a	1		1			
2854		445985	Borreliella burgdorferi ZS7	3	45	3	45		
2855		446023	Influenza A virus (A/Hong Kong/68(H3N2))	1		1			
2856		446679	Nostoc sphaeroides		1		1		
2858		447095	Blastomyces dermatitidis ATCC 26199		1		1		
2859		447106	Leptospira licerasiae		1		1		
2860		447133	Influenza A virus (A/chicken/Japan/1925(H7N7))	1		1			
2861		447188	Influenza A virus (A/duck/Tasmania/277/2007(H7N2))	1		1			
2862		448058	Influenza A virus (A/swine/Guangdong/01/2005(H3N2))		1		1		
2863		449278	West Nile virus SPU116/89		1		1		
2864		449656	Influenza A virus (A/chicken/Taiwan/2838V/00(H6N1))	15		15			
2865		451515	Staphylococcus aureus subsp. aureus USA300_FPR3757		1		1		
2866	X	451516	Staphylococcus aureus subsp. aureus USA300_TCH1516			1		1	
2867		451707	Bacillus cereus NVH0597-99		7		7		
2868		451708	Bacillus cereus H3081.97		12		12		
2869		451709	Bacillus cereus 03BB108		8		8		
2870		451804	Aspergillus fumigatus A1163		13		13		
2871		452646	Neogale vison		1		1		
2872		452652	Kitasatospora setae KM-6054		1		1		
2873		452659	Rickettsia rickettsii str. Iowa		1		1		
2874		453057	Influenza A virus (A/Indonesia/CDC540/2006(H5N1))	1		1			
2875		453927	Juniperus formosana	1		1			
2876		456999	Rhizoctonia solani		1		1		
2877		458234	Francisella tularensis subsp. holarctica FTNF002-00		1		1		
2878		458678	Hantaanvirus CGRn93P8		2		2		
2879		461739	Influenza B virus (B/Florida/4/2006)	1		4		3	
2880		461772	Influenza A virus (A/Wisconsin/43/2006(H3N2))	1		1			
2881		462695	Influenza A virus (A/Hiroshima/52/2005(H3))	2		2			
2882	X	463676	Rhinovirus C				14		14
2883		463722	Murine norovirus GV/CR6/2005/USA		1		1		
2884		464314	Influenza A virus (A/Anhui/T2/2006(H5N1))	1		1			

2885		464417	Influenza B virus (B/Malaysia/2506/2004)	1		1			
2886		464622	Influenza A virus (A/Solomon Islands/3/2006 (Egg passage)(H1N1))	1		1			
2887		464623	Influenza A virus (A/Solomon Islands/3/2006(H1N1))	17		18		1	
2888		465541	Streptomyces sp. Mg1		1		1		
2889		467144	Modified Vaccinia Ankara virus		23		23		
2890		468968	Influenza A virus (A/Indonesia/560H/2006(H5N1))	1		1			
2891		470137	Brucella suis ATCC 23445	1	5	1	5		
2892		471223	Geobacillus sp. WCH70		2		2		
2893		471721	HIV-1 CRF01_AE	1		1			
2894		472511	Influenza A virus (A/Indonesia/TLL007/2006(H5N1))	1		1			
2895		475478	Influenza A virus (A/equine/New Market/1/1979(H3N8))	1		1			
2896		475493	Influenza A virus (A/equine/California/8560/2002(H3N8))		2		2		
2897		476176	Moraea pallida	1		1			
2899		476294	Influenza A virus (A/Brisbane/10/2007(H3N2))	5		5			
2900		476303	Influenza A virus (A/California/04/2007(H1N1))		1		1		
2901		478005	Escherichia coli O157:H7 str. EC4486		1		1		
2902		478006	Escherichia coli O157:H7 str. EC4501		2		2		
2903		478008	Escherichia coli O157:H7 str. EC869		13		13		
2904		479022	Influenza A virus (A/chicken/Korea/IS/2006(H5N1))	1		1			
2905		479935	Gluconobacter morbifer		1		1		
2906		480019	Influenza A virus (A/Moscow/10/1999(H3N2))		2	1	2	1	
2907		480024	Influenza A virus (A/Wyoming/03/2003(H3N2))		8		8		
2908		480116	Hepatitis B virus adw2/Rutter/1979		1		1		
2909		481805	Escherichia coli ATCC 8739		1		1		
2910		482134	Hepatitis B virus adw/Japan/Nishioka/1983		1		1		
2911		482628	Campylobacter jejuni subsp. jejuni BH-01-0142		1		1		
2912		482957	Burkholderia lata		2		2		
2913		483179	Brucella canis ATCC 23365		9		9		
2914		484021	Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044		1		1		
2915		486280	Torque teno virus VT416		3		3		
2916		486619	Bacillus anthracis str. A0193		3		3		
2917		486620	Bacillus anthracis str. A0465		5		5		
2918		486621	Bacillus anthracis str. A0442		1		1		
2919		486623	Bacillus anthracis str. A0389		5		5		
2920		486624	Bacillus anthracis str. A0488		91		91		
2921		487067	Torque teno virus Human/Ghana/GH1/1996		3		3		
2922		487317	Aequorivita capsosiphonis		1		1		
2923		487521	Mycobacterium intracellulare ATCC 13950	1		1			
2924		488233	Influenza A virus (A/Iran/1/1957(H2N2))		1		1		
2925		488241	Influenza A virus (A/Korea/426/1968(H2N2))		2		2		
2926		489455	hepatitis B virus genotype A	1		1	1		1
2927		489460	HBV genotype B	1	10	1	18		8

2928		489466	HBV genotype C	10	28	21	29	11	1
2929		489469	Hepatitis B virus ayw/China/Tibet127/2002	1		1			
2930		489483	HBV genotype D	1	9	1	9		
2931		489821	Norovirus GII.4	2	16	3	16	1	
2932		489822	Norovirus Hu/Houston/TCH186/2002/US	2		2			
2933		490039	Norovirus GII.2	1		1			
2934		490041	Norovirus GII.3	1		1			
2935		490133	Hepatitis B virus ayw/France/Tiollais/1979		4		4		
2936		493803	Merkel cell polyomavirus	2	30	2	30		
2937		496036	Influenza A virus (A/duck/Vietnam/37/2007(H5N1))		1		1		
2938		497976	Salmonella enterica subsp. enterica serovar Typhi str. E00-7866		1		1		
2939		497977	Salmonella enterica subsp. enterica serovar Typhi str. 404ty		1		1		
2940		499191	Norovirus GII.1	1		1			
2941		499286	Influenza A virus (A/Hong Kong/CUHK13527/2003(H3N2))		2		2		
2942		502057	Vaccinia virus GLV-1h68		2		2		
2943		502780	Paracoccidioides brasiliensis Pb18	1	1	1	1		
2944		502790	Aeromonas diversa		1		1		
2945		503386	Influenza B virus (B/Kobe/3/2004)	1		1			
2946		504660	Influenza B virus (B/Kobe/67/2005)	1		1			
2947		504662	Influenza B virus (B/Kobe/39/2005)	1		1			
2948		504664	Influenza B virus (B/Kobe/113/2005)	1		1			
2949		504666	Influenza B virus (B/Kobe/115/2005-T1)	1		1			
2950		504697	Influenza A virus (A/Cygnus olor/Czech Republic/10732/07(H5N1))		1		1		
2951		504904	Influenza A virus (A/Brisbane/59/2007(H1N1))	26	14	26	14		
2952		504910	Influenza A virus (A/Wellington/75/2006(H1N1))		1		1		
2953		505184	HIV-1 M:A	9	1	9	1		
2954		505185	HIV-1 M:B	8	25	8	25		
2955		505186	HIV-1 M:C	11		11			
2956		505228	HIV-1 M:G	4		4			
2957		506282	Influenza A virus (A/unknown/New York/11646-5/2005(H7N2))	1		1			
2958		506350	Influenza A virus (A/Hong Kong/1/1968(H3N2))	22	3	22	3		
2960		506380	Influenza A virus (A/Hong Kong/1-4-MA21-1/1968(H3N2))	1		1			
2961		507601	Toxoplasma gondii GT1		205		205		
2963		508767	Clostridium botulinum E3 str. Alaska E43		1		1		
2964		508771	Toxoplasma gondii ME49	21	89	21	89		
2965		508775	Norovirus GII.9	1	1	1	1		
2966		509173	Acinetobacter baumannii AYE		1		1		
2967		509628	Hepatitis E virus type 3		1	1	1	1	
2968		510222	Influenza A virus (A/duck/Vietnam/NCVD-9/2007(H5N1))	1		1			
2969		510670	Hepatitis delta virus dTk6		1		1		
2970		511145	Escherichia coli str. K-12 substr. MG1655		31		31		
2971		511839	Influenza A virus (A/turkey/England/N28/1973(H5N2))	1		1			

2972		514118	Influenza A virus (A/BRISBANE/9/2006(H3N2))		1		1		
2973		514193	Influenza A virus (A/CHU/2-524/2005(H3N2))		2		2		
2974		515581	Influenza A virus (A/swine/Ohio/24366/2007(H1N1))		2		2		
2976		515817	Amphioctopus fangsiao	1		1			
2977		518922	Influenza A virus (A/Beijing/262/1995(H1N1))	4		5		1	
2978		518968	Influenza A virus (A/X-31B(Puerto Rico/8/1934-Aichi/2/1968)(H3N2))	1		2		1	
2979		518987	Influenza B virus (B/Lee/1940)	5	3	5	3		
2980		519082	Influenza A virus (A/New York/107/2003(H7N2))	1		1			
2981		519424	Alkalihalobacillus trypoxylicola		1		1		
2983		520450	Brucella abortus bv. 2 str. 86/8/59		1		1		
2984		520464	Brucella melitensis bv. 1 str. Rev.1	1		1			
2985		520963	Norovirus GII.11	1		1			
2986		520964	Norovirus GII.18	1		1			
2987		521004	Haemophilus influenzae 6P18H1		1		1		
2988		521005	Haemophilus influenzae 7P49H1		1		1		
2989		521007	Borreliella burgdorferi N40	4	3	4	3		
2990		522740	Influenza A virus (A/swine/Hannover/1/1981(H1N1))		12		12		
2991		524364	Norovirus Hu/1968/US	6	1	6	1		
2992	X	524651	Muromegalovirus WP15B				1		1
2993		525281	Escherichia coli 83972		3		3		
2994		525368	Mycobacterium parascrofulaceum ATCC BAA-614		35		35		
2995		525374	Staphylococcus epidermidis BCM-HMP0060		1		1		
2996		526974	Bacillus cereus BDRD-ST24		1		1		
2997		526977	Bacillus cereus ATCC 4342		1		1		
2999		527024	Bacillus thuringiensis serovar tochigiensis BGSC 4Y1		1		1		
3000		527026	Bacillus thuringiensis serovar sotto str. T04001		1		1		
3002		528354	Neisseria gonorrhoeae MS11	8		8			
3003		529058	Influenza A virus (A/Uruguay/716/2007(H3N2))	1		1			
3004		529507	Proteus mirabilis HI4320	1		1			
3005		533026	Influenza A virus (A/turkey/Ohio/313053/2004(H3N2))	1	2	1	2		
3006		535026	Bacillus subtilis subsp. subtilis NCIB 3610 = ATCC 6051 = DSM 10		1		1		
3007		535852	Influenza A virus (A/California/06/2008(H1N1))		1		1		
3008		538555	Influenza A virus (A/swine/Korea/Hongsong2/2004(H1N2))		2		2		
3009		543153	Mycobacterium phage Predator		1		1		
3010		543824	Synechocystis aquatilis		2		2		
3011		545501	Oceanobacillus oncorhynchi		1		1		
3012		546980	Norovirus Hu/GII-4/Saga1/2006/JP	1	1	1	1		
3013		548470	Staphylococcus aureus subsp. aureus MN8	11		11			
3014	X	548473	Staphylococcus aureus subsp. aureus TCH60			47		47	
3015		549169	Pseudogulbenkiania ferrooxidans		1		1		
3017		552536	Listeria monocytogenes HCC23		2		2		
3018	X	552592	Norovirus GII.17			1		1	

3019		553345	Influenza A virus (A/Aichi/72/2007(H3N2))	1		1			
3020		553583	Staphylococcus aureus A9635	1		1			
3021		554290	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601		3		3		
3022		556277	Influenza A virus (A/swine/Guangdong/02/2005(H3N2))	1		1			
3023		557433	Limosilactobacillus reuteri JCM 1112	3		3			
3024		557599	Mycobacterium kansasii ATCC 12478	1		1			
3025		558177	Influenza A virus (A/mallard/Bavaria/10/2007(H5N1))		1		1		
3026	X	558553	Crassostrea angulata			15		15	
3027		559292	Saccharomyces cerevisiae S288C	15	2	16	2	1	
3028		559561	Aureobasidium namibiae		2		2		
3029		560463	Influenza A virus (A/Taiwan/VGHYM0325-06/2002(H3N2))		1		1		
3032		562988	Influenza A virus (A/Egypt/2289-NAMRU3/2008(H5N1))	1		1			
3033		562992	Influenza A virus (A/Egypt/3300-NAMRU3/2008(H5N1))	1		1			
3034		563041	Helicobacter pylori G27	2		2			
3035		563466	Scedosporium apiospermum		1		1		
3036		563773	Vibrio parahaemolyticus AN-5034		4		4		
3037		565995	Bundibugyo ebolavirus	15		17		2	
3039		566466	gamma proteobacterium NOR5-3		1		1		
3040		567106	Campylobacter jejuni subsp. jejuni IA3902		1		1		
3041		568206	Bacillus anthracis str. CDC 684		3		3		
3042		568819	Listeria monocytogenes serotype 4b str. CLIP 80459		6		6		
3043		568833	Influenza A virus (A/chicken/Jiangsu/7/2002(H9N2))		1		1		
3044		568987	Candidatus Hamiltonella		1		1		
3045		571800	Psychrobacter sp. G	1		1			
3046		572264	Bacillus cereus 03BB102		2		2		
3047		572307	Neospora caninum Liverpool		1		1		
3048		573729	Thermothelomyces thermophilus ATCC 42464	1		1			
3049		573797	Influenza A virus (A/England/654/2007(H1N1))		1		1		
3050		573977	Human bocavirus 2	4		4			
3051		574556	Anaplasma centrale str. Israel		2		2		
3052		575591	Brucella abortus NCTC 8038		1		1		
3053		575788	Vibrio atlanticus LGP32		1		1		
3055		577543	Influenza A virus (A/Xinjiang/1/2006(H5N1))	4		4			
3056		578079	Influenza A virus (A/ferret/Maryland/P10-UMD/2008(H9N2))		1		1		
3057	X	578831	Rotavirus A human/USA/D/1974 G1P1A[8]				23		23
3058		580047	Chlamydia trachomatis A2497	3		3			
3059		580165	Bacillus cytotoxicus		2		2		
3060		585034	Escherichia coli IAI1	3		3			
3061		586029	Fowl adenovirus 8b	2		2			
3062		587200	Variola virus human/India/Ind3/1967		4		4		
3063		587884	Influenza A virus (A/Sydney/5/1997(H3N2))	7		7			
3064		588533	Norovirus Hu/GII/GZ-1/2008/CHN	1		1			

3065		588596	Rhizophagus irregularis		1		1		
3066		591020	Shigella flexneri 2002017		1		1		
3067		592021	Bacillus anthracis str. A0248		1		1		
3068		592313	Vibrio cholerae 12129(1)		1		1		
3070		595609	Recombinant Hepatitis C virus HK6a/JFH-1	8		8			
3071		598745	Giardia intestinalis ATCC 50581		7		7		
3072		604436	Influenza B virus (B/Brisbane/60/2008)	14		14			
3073		614035	Influenza A virus (A/swine/Belgium/1/1998(H1N1))	1		1			
3074		616922	Influenza A virus (A/chicken/Anhui/1/1998(H9N2))		1		1		
3075		617102	Yellow fever virus 17D/Tiantan	4	5	4	5		
3076		619693	Prevotella sp. oral taxon 472 str. F0295	1		1			
3078		627442	SARS coronavirus P2	1		1			
3079		627611	Vibrio parahaemolyticus K5030		22		22		
3080		630277	Tarsius lariang		1		1		
3081		632134	Influenza A virus (A/chicken/Pakistan/UDL-01/2008(H9N2))	7		7			
3082		632955	Acinetobacter rudis		1		1		
3083	X	633137	SARS coronavirus MA15			1		1	
3084		633557	Infectious bronchitis virus CK/CH/LHLJ/04V	1		1			
3085		634464	Chlamydia trachomatis Sweden2	1		1			
3086		637383	Helicobacter pylori NCTC 11639		8		8		
3087		638313	Human bocavirus 3	6		6			
3088		641140	Brucella abortus str. 2308 A		1		1		
3089		641501	Influenza A virus (A/California/04/2009(H1N1))	124	128	128	128	4	
3090		641809	Influenza A virus (A/California/07/2009(H1N1))	35	50	36	68	1	18
3091		641812	Influenza A virus (A/Texas/05/2009(H1N1))	1		1			
3092		642261	Influenza A virus (A/California/08/2009(H1N1))	8		8			
3093		642794	Influenza A virus (A/Auckland/1/2009(H1N1))		1		1		
3094		643212	Influenza A virus (A/Netherlands/602/2009(H1N1))	2	14	7	14	5	
3095		643680	Saccharomyces cerevisiae EC1118		1		1		
3096		644289	Influenza A virus (A/Korea/01/2009(H1N1))	4		4			
3097		644788	Influenza A virus (A/Vietnam/1194/2004(H5N1))	14	10	14	10		
3098		645463	Clostridioides difficile R20291	5		25		20	
3099		645724	Influenza A virus (A/Hong Kong/01/2009(H1N1))	3		3			
3100		645771	Influenza A virus (A/Catalonia/63/2009(H1N1))		1		1		
3101		647096	Influenza A virus (A/Beijing/01/2009(H1N1))		35		35		
3102		647343	Norovirus Hu/GII.4/Hiroshima/48/2004/JPN		1		1		
3103		647514	Norovirus GI.1	1		1			
3104		647515	Norovirus GI.2	1		1			
3105		647516	Norovirus GI.3		1		1		
3106		647519	Norovirus GI.5	1		1			
3107		647521	Norovirus GI.7	1		1			
3108		647923	Influenza A virus (A/reassortant/NYMC X-179A(California/07/2009 x NYMC X-157)(H1N1))	16		16	6		6

3109		648194	Neisseria meningitidis serogroup Y	3		3			
3110		648856	Influenza A virus (A/Beijing/501/2009(H1N1))	1		1			
3112		650131	Equine rhinitis B virus 1 strain P1436/71	6		6			
3113		651183	Aurantimonas manganoxydans		1		1		
3114		652616	Mycobacterium tuberculosis str. Erdman = ATCC 35801	15	19	15	19		
3116		654811	Influenza A virus (A/Perth/16/2009(H3N2))	5		6		1	
3117		655288	Influenza A virus (A/mallard/Quebec/10969/2006(H2N3))		1		1		
3118		655827	Metarhizium acridum CQMa 102	1		1			
3119		655863	Grosmannia clavigera kw1407		1		1		
3120		657165	Influenza A virus (A/Hong Kong/213/03)	2	2	2	2		
3121		658578	Influenza A virus (A/duck/Beijing/MG0617/2005(H9N2))		1		1		
3122		658655	Lachnospiraceae bacterium 1_4_56FAA		1		1		
3123		658858	Giardia lamblia P15		1		1		
3124		660658	Norovirus Hu/GII.4/CHDC4108/1987/US		2		2		
3126		661367	Legionella longbeachae NSW150		1		1		
3128		667015	Phocaeicola salanitronis DSM 18170		1		1		
3129		672161	Chlamydia trachomatis B/TZ1A828/OT	3		3			
3130		673446	Influenza A virus (A/reassortant/NYMC X-181(California/07/2009 x NYMC X-157)(H1N1))	1		2		1	
3131		679206	Escherichia coli MS 119-7		1		1		
3132		679716	Trypanosoma brucei gambiense DAL972		1		1		
3133		680689	Influenza A virus (A/England/AV877/1996(H7N7))		1		1		
3134		680690	Influenza A virus (A/Hong Kong/1074/1999(H9N2))	2	1	2	1		
3135		680692	Influenza A virus (A/Hong Kong/485/1997(H5N1))	1	1	1	1		
3136		680693	Influenza A virus (A/Netherlands/219/2003(H7N7))	1		14		13	
3137		680729	Influenza A virus (A/chicken/Italy/1067/1999(H7N1))		20		20		
3138		680739	Influenza A virus (A/chicken/Mexico/37821-771/1996(H5N2))		1		1		
3139		680767	Influenza A virus (A/duck/Hong Kong/140/1998(H5N1))		1		1		
3140		680785	Influenza A virus (A/environment/Hong Kong/156/1997(H5N1))	1		1			
3141		680789	Influenza A virus (A/environment/Viet Nam/1203/2004(H5N1))	1		1			
3142		680799	Influenza A virus (A/goose/Hong Kong/437-6/1999(H5N1))		1		1		
3143		680803	Influenza A virus (A/goose/Hong Kong/739.2/2002(H5N1))		1		1		
3144		682728	Influenza A virus (A/Quebec/144147/2009(H1N1))	10		10			
3145		683780	Influenza A virus (A/wild bird/Korea/A81/2009(H5N2))	1		1			
3146		687340	Torque teno virus 1		3		3		
3147		687341	Torque teno virus 2		4		4		
3148		687342	Torque teno virus 3		4		4		
3149		687343	Torque teno virus 4		6		6		
3150		687345	Torque teno virus 6		2		2		
3151		687346	Torque teno virus 7		3		3		
3152		687347	Torque teno virus 8		6		6		

3153		687350	Torque teno virus 11		1		1		
3154		687353	Torque teno virus 14		5		5		
3155		687354	Torque teno virus 15		3		3		
3156		687355	Torque teno virus 16		4		4		
3157		687358	Torque teno virus 19		5		5		
3158		687359	Torque teno virus 20		2		2		
3159		687360	Torque teno virus 21		2		2		
3160		687362	Torque teno virus 23		2		2		
3161		687363	Torque teno virus 24		3		3		
3162		687364	Torque teno virus 25		3		3		
3163		687365	Torque teno virus 26		5		5		
3164		687366	Torque teno virus 27		5		5		
3165		687367	Torque teno virus 28		3		3		
3166		687368	Torque teno virus 29		4		4		
3167		687369	Torque teno mini virus 1		1		1		
3168		687371	Torque teno mini virus 3		2		2		
3169		687375	Torque teno mini virus 7		2		2		
3170		687376	Torque teno mini virus 8		2		2		
3171		687382	Torque teno tamarin virus		2		2		
3172		687383	Torque teno douroucouli virus		5		5		
3173		687384	Torque teno felis virus		1		1		
3174		687385	Torque teno canis virus		1		1		
3175		687386	Torque teno sus virus 1a	12	1	12	1		
3176		689403	Human bocavirus 1	8		8			
3179		693999	Scotophilus bat coronavirus 512		1		1		
3180	X	694003	Betacoronavirus 1			260		260	
3182	X	694007	Tylonycteris bat coronavirus HKU4			2		2	
3183		694008	Pipistrellus bat coronavirus HKU5		1	1	1	1	
3184	X	696863	Carp sprivivirus				1		1
3185		696871	Vaccinia virus Western Reserve		31		31		
3186	X	697298	Giant panda rotavirus A				1		1
3187		697610	Influenza A virus (A/India/GWMH05/2009(H1N1))		1		1		
3188		703352	Brucella melitensis M5-90	5	26	5	26		
3189		707424	Norovirus Hu/GII-4/Ehime4/2007/JP		1		1		
3191		707488	Norovirus Hu/GII-4/Nagano3/2007/JP		4		4		
3192		707882	Duck astrovirus 1	1		1			
3193		708187	Colletotrichum chlorophyti		1		1		
3194		714978	Human adenovirus 55	4		4			
3195		715091	Influenza A virus (A/Roma/ISS1941/2009(H1N1))		1		1		
3196		715494	Influenza A virus (A/Hong Kong/33982/2009(H9N2))		3		3		
3197		722438	Mycoplasma pneumoniae FH	3		3			
3198		742305	Influenza A virus (A/slaty-backed gull/Japan/6KS0185/2006(H4N8))		1		1		
3199		742503	Tokudaia muenninki		1		1		

3200		743722	Sphingobacterium sp. 21	1		1			
3201		743973	Taylorella equigenitalis ATCC 35865	1		1			
3202		746128	Aspergillus fumigatus	136	88	136	88		
3203		747305	Norovirus GII.10	7		7			
3204		754027	Treponema phagedenis F0421		1		1		
3205		754366	Influenza A virus (A/Ontario/309862/2009(H1N1))	1		1			
3206		754503	Mycoplasma hyopneumoniae 7422	1		1			
3207		759272	Chaetomium thermophilum var. thermophilum DSM 1495	1		1			
3208		759363	Chlamydia trachomatis D-EC	3		3			
3209		759851	Sporosarcina newyorkensis		2		2		
3210		760591	Influenza A virus (A/Egypt/N03072/2010(H5N1))	1		1			
3211		761193	Runella slithyformis DSM 19594		1		1		
3212		761251	Influenza A virus (A/Mexico City/WR1704T/2009(H1N1))		1		1		
3213		762377	Influenza A virus (A/bar-headed goose/Qinghai/1-HVRI/2006(H5N1))		5		5		
3214		762378	Influenza A virus (A/bar-headed goose/Qinghai/3/2005(H5N1))		1		1		
3216		763552	Mus musculus papillomavirus type 1		4		4		
3218		768646	Influenza A virus (A/chicken/Uchal/8293/2006(H9N2))		1		1		
3219		768647	Influenza A virus (A/chicken/Uchal/8286/2006(H9N2))		1		1		
3220		857099	Streptococcus mutans OMZ175	2	1	2	1		
3221		857571	Moraxella catarrhalis O35E	27		27			
3222		862909	Trichodysplasia spinulosa-associated polyomavirus	2		2			
3223		863370	Meiothermus granaticius		1		1		
3224		866344	Helicobacter pylori F16	2		2			
3227		870484	Nonlabens agnitus		1		1		
3228		871575	Ogataea parapolymorpha DL-1		1		1		
3229		874269	African swine fever virus Georgia 2007/1	15		15	1		1
3230		875328	Mycolicibacter sinensis		10		10		
3232		885311	Entamoeba histolytica KU27		1		1		
3233		887118	Influenza A virus (A/Mexico/UASLP-012/2008(H3N2))		1		1		
3234		908203	Influenza A virus (A/Thailand/CU-H126/2009(H1N1))		1		1		
3235		909420	Neisseria meningitidis H44/76	2		2			
3236		913028	Yersinia enterocolitica W22703		1		1		
3237		914129	Streptococcus pneumoniae 2061376		1		1		
3238		915014	Influenza A virus (A/swine/Heilongjiang/44/2009(H1N1))	1		1			
3239		928301	Fowlpox virus strain NVSL		3		3		
3240	X	928303	Hendra virus horse/Australia/Hendra/1994			3		3	
3241		928313	Tacaribe virus strain Franze-Fernandez		6		6		
3242		929439	Leishmania mexicana MHOM/GT/2001/U1103		1		1		
3243		932622	Influenza A virus (A/chicken/Huadong/4/2008(H5N1))	1		1			
3244		935198	Clostridium botulinum B str. Eklund 17B (NRP)		1		1		
3245		936115	Influenza A virus (A/Netherlands/18/1994(H3N2))		1		1		

3246		940614	Granulicella mallensis		1		1		
3247		947939	Influenza A virus (A/aquatic bird/Korea/w44/2005(H7N3))		1		1		
3248		981087	Leishmania donovani BPK282A1		9		9		
3249	X	981676	Bovine viral diarrhea virus 1b				28		28
3250		986174	Influenza A virus (A/swine/Korea/4382/2009(H1N2))		1		1		
3251		991335	Influenza A virus (A/swine/Hong Kong/71/2009(H1N1))		1		1		
3252		992121	Helicobacter pylori Hp M5	1		1			
3253		996581	Influenza A virus (A/chicken/Shanghai/Q0808-1/2008(H9N2))		1		1		
3254		1003835	Severe fever with thrombocytopenia syndrome virus	1		1			
3255		1004253	Cyberlindnera mrakii	1	1	1	1		
3256		1005048	Collimonas fungivorans Ter331		1		1		
3257		1005962	Ogataea parapolymorpha		1		1		
3258		1006061	Duck hepatitis A virus 1	1		1			
3259		1006581	Mycoplasma gallisepticum S6	1		1			
3260		1009714	Pseudomonas aeruginosa PAK	7	3	7	3		
3261		1016852	Banana streak CA virus	5		5			
3262		1016853	Banana streak IM virus	10		10			
3263		1016998	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7		11		11		
3264		1035514	Plasmodium vivax North Korean	1		1			
3265	X	1036723	Plasmodium falciparum Vietnam Oak-Knoll (FVO)				2		2
3266		1041522	Mycobacterium colombiense CECT 3035		20		20		
3267		1041990	Influenza A virus (A/Guangdong/15/2007(H3N2))	3		3			
3268	X	1045010	Escherichia coli O157			1		1	
3269		1045775	Paenibacillus catalpae	1		1			
3270		1046049	Norovirus Hu/GII.12/HS206/2010/USA		1		1		
3271		1047168	Zymoseptoria brevis		1		1		
3272		1050221	Chlamydia psittaci NJ1	10		10			
3273		1053141	Recombinant Hepatitis C virus J6/JFH1-J6	2		2			
3274		1055687	Trypanosoma vivax Y486	1		1			
3275		1068705	Influenza A virus (A/swine/Guangdong/221/2009(H1N1))		1		1		
3277		1071379	Tetrapisispora blattae		1		1		
3278		1077587	Influenza B virus (B/Victoria/2/1987)	2	4	2	4		
3279		1081253	Influenza A virus (A/Indiana/08/2011(H3N2))		6		6		
3280		1082519	Influenza A virus (A/chicken/Taixing/10/2010(H9N2))	2		2			
3281		1086859	Influenza A virus (A/Bilthoven/4791/1981(H3N2))		3		3		
3282		1091045	Cutibacterium acnes subsp. defendens ATCC 11828	5		5			
3283		1093545	Influenza A virus (A/shorebird/Delaware Bay/277/2000(H9N7))		1		1		
3284		1112244	Chlamydia psittaci 06-1683	3		3			
3285		1112253	Chlamydia psittaci 02DC14	1		1			
3286		1112254	Chlamydia psittaci 02DC15	19		19			
3287		1112258	Chlamydia psittaci 02DC22	2		2			

3288		1112262	Chlamydia psittaci 03DC29	1		1			
3289		1112269	Chlamydia psittaci 09DC78	1		1			
3290		1117322	Glaesserella parasuis str. Nagasaki	1		1			
3291	X	1118369	Wobbly possum disease virus				14		14
3292		1122279	Influenza A virus (A/equine/Guangxi/3/2011(H9N2))		1		1		
3293		1125722	Porphyromonas gingivalis W50		36		36		
3294		1126212	Macrophomina phaseolina MS6		1		1		
3295		1129345	Influenza A virus (A/little yellow-shouldered bat/Guatemala/153/2009(H17N10))		3		3		
3297		1133319	Bacteroides reticulotermitis		1		1		
3298		1133363	Schmallenberg virus	6		6			
3299		1133968	Babesia microti strain RI	3		3			
3300		1144025	Influenza A virus (A/Shandong/9/1993(H3N2))	13		13			
3301		1146883	Blastococcus saxobsidens DD2		1		1		
3302		1156983	Norovirus Hu/GII.4/Minerva/CS1258/2006/USA	1		1			
3304		1163697	Influenza A virus (A/Oklahoma/309/2006(H3N2))	4	3	4	3		
3305		1169127	Clostridioides difficile genomovar ribotype_087	1		1			
3306		1171336	Influenza A virus (A/swine/Nebraska/A01116984/2011(H3N2))		1		1		
3307		1172206	Neisseria meningitidis NMB	1		1			
3308	X	1173018	Phlebovirus WCH/97/HN/China/2011			19		19	
3309		1173701	Colletotrichum sublineola		1		1		
3310		1176042	Influenza A virus (A/swine/Italy/1513-1/1998(H1N1))		1		1		
3311		1178016	Encephalitozoon romaleae SJ-2008		1		1		
3312		1179777	Mycoplasma feriruminatoris		1		1		
3313		1182143	Norovirus Hu/GII.4/Farmington Hills/2004/USA	2		2			
3314		1182144	Norovirus Hu/GII.4/Minerva/2006/USA	2		2			
3315		1184252	Streptococcus suis S735	2		2			
3316		1184593	Influenza A virus (A/Victoria/210/2009(H3N2))	16		16			
3317		1186058	Trichosporon asahii var. asahii CBS 2479		1		1		
3318		1193095	Paucilactobacillus hokkaidonensis		1		1		
3319		1193576	Staphylococcus aureus subsp. aureus CN1		3		3		
3320		1197131	Escherichia coli F576	1		1			
3321		1198627	Mycobacteroides abscessus subsp. massiliense str. GO 06		1		1		
3322		1198676	Streptococcus mutans GS-5		14		14		
3323		1207470	Streptococcus pyogenes M1 476	1		1			
3324		1209523	Toxoplasma gondii type II		2	11	2	11	
3325		1209525	Toxoplasma gondii type I		2	10	2	10	
3326		1209926	Colletotrichum orchidophilum		1		1		
3327		1214154	Streptococcus suis 2651	1		1			
3328		1214159	Streptococcus suis 13730	2		2			
3329		1214225	Acidocella sp. MX-AZ02	1		1			
3330		1218488	Torque teno sus virus k2	11		11			
3331		1219377	rhinovirus C3		52		52		

3332		1225860	Porcine torque teno virus 1	2		2			
3333		1229831	Chlamydia avium 10DC88	2		2			
3334		1235801	Ligilactobacillus murinus ASF361		2		2		
3335		1235802	Eubacterium plexicaudatum ASF492		2		2		
3336	X	1235803	Parabacteroides sp. ASF519				8		8
3337		1235996	Human betacoronavirus 2c EMC/2012	11	26	11	26		
3338		1236180	Halopelagius longus		1		1		
3339		1236978	Staphylococcus epidermidis JCM 2414	1		1			
3340		1239567	Mamastrovirus 3	2		2			
3341		1241973	Norovirus Hu/GII.4/Sydney/NSW0514/2012/AU	4	31	8	31	4	
3342		1254407	Norovirus Hu/GII.4/N3/2008/HuZhou		1		1		
3344		1263102	Prevotella copri CAG:164		1		1		
3345		1263720	Betacoronavirus England 1	11		13		2	
3346		1268303	Rhodococcus sp. AW25M09	1	1	1	1		
3347		1268360	Influenza A virus (A/Victoria/361/2011(H3N2))	5		8		3	
3348		1278073	Myxococcus stipitatus DSM 14675		1		1		
3349		1281454	Rodent hepacivirus		8		12		4
3350		1285028	Influenza A virus (A/American black duck/New Brunswick/00464/2010(H4N6))	1		1			
3351		1285600	Nile crocodilepox virus		2		2		
3352		1285902	Artificial vector pGEX-2T	1		1			
3353		1286616	Norovirus Hu/GII.3/693/425/2008/AU	6		6			
3354		1286635	Desulfotignum phosphitoxidans DSM 13687		1		1		
3355		1288825	Shigella flexneri 2b	2		2			
3356		1289562	Influenza A virus (A/swine/Spain/SF11131/2007(H1N1))		3		3		
3357		1291361	Leptospira interrogans serovar Naam str. Naam	1		1			
3358		1291821	Norovirus Hu/GII/20144/2009/VNM		1		1		
3359		1291870	Norovirus Hu/GII/20457/2010/VNM		1		1		
3360		1303514	Diaporthe toxica	1		1			
3361		1310532	Influenza A virus (A/chicken/West Java/Sbg-29/2007(H5N1))	7		7			
3362	X	1314758	Influenza A virus (A/Hangzhou/1/2013(H7N9))				1		1
3363		1318439	Influenza A virus (A/Washington/05/2011(H1N1))	1		1			
3364		1318464	Bovine Schmallenberg virus BH80/Germany/2011	2		2			
3365		1321009	Influenza A virus (A/Texas/50/2012(H3N2))	2		6		4	
3366		1321999	Norovirus Hu/GII.6/Ehime120246/2012/JP	2		2			
3368		1330520	Enterovirus F	1		1			
3369	X	1331831	Influenza A virus (A/Taiwan/1/2013(H7N9))			2		2	
3370		1332244	Influenza A virus (A/Shanghai/02/2013(H7N9))	66		66			
3371		1335626	Middle East respiratory syndrome-related coronavirus	11	25	15636	26	15625	1
3372		1337063	Puumala virus bank vole/CG1820/Russia/1984		1		1		
3373		1337393	Helicobacter pylori PZ5056	1		1			
3374		1342397	Influenza A virus (A/chicken/Hong Kong/TP38/2003(H9N2))		3		3		
3375		1342434	Influenza A virus (A/turkey/Minnesota/511/1978(H9N2))		1		1		

3376		1345266	HIV-1 M:CRF01_AE	1		1			
3377		1346336	Influenza A virus (A/Fort Monmouth/1-JY2/1947(H1N1))		1		1		
3379		1350216	Norovirus Hu/GII.12/Texas/E13842/USA/2000		1		1		
3380		1352357	Helicobacter pylori SouthAfrica50	1		1			
3381		1355477	Bradyrhizobium diazoefficiens		1		1		
3382		1380386	Mycobacterium sp. URHB0044		1		1		
3384		1384672	Mumps virus genotype G		82		83		1
3385		1389959	Mycobacterium tuberculosis variant bovis AN5	9	28	9	28		
3386		1391655	Influenza A virus (A/Aichi/2-1/1968(H3N2))	1		1			
3387		1391998	Mycobacterium avium subsp. paratuberculosis 08-8281	1		1			
3388		1392869	Escherichia coli K1		1		1		
3390		1395982	Influenza A virus (A/tree sparrow/Shanghai/01/2013(H7N9))	1		1			
3391		1398154	Sporothrix brasiliensis 5110		4		4		
3392		1399582	Duck Tembusu virus	7		8		1	
3393		1401444	Avian leukosis virus ev/J	5		6		1	
3394		1403335	Porphyromonas gingivalis 381	71	55	71	55		
3395		1403514	Influenza A virus (A/chicken/Jiangsu/x1/2004(H9N2))	7		8		1	
3396		1405296	Chlamydia suis MD56	1		1			
3397		1406148	Norovirus Hu/GII.3/Jingzhou/2013402/CHN	2		2			
3398		1408475	Taylorella asinigenitalis ATCC 700933	1		1			
3399		1413188	Influenza A virus (A/Anhui/PA-1/2013(H7N9))	1	3	1	3		
3400		1416333	Trypanosoma cruzi Dm28c	2		2			
3401		1420840	Influenza A virus (A/Luxembourg/46/2009(H1N1))		1		1		
3402		1423732	Lacticaseibacillus casei DSM 20011 = JCM 1134 = ATCC 393	2		2			
3403		1427371	Chlamydia pecorum VR629	5		5			
3404		1432052	Eisenbergiella tayi		3		3		
3405		1432555	Escherichia coli ISC7		1		1		
3406		1440122	Murid herpesvirus 68		2		2		
3407		1447813	Influenza A virus (A/Shanghai/5190T/2013(H7N9))		6		6		
3408		1451093	Influenza A virus (A/chicken/Taiwan/67/2013(H6N1))		5		5		
3409		1457141	Chlamydia avium	1		1			
3410		1457153	Chlamydia gallinacea	3		3			
3411		1458279	Staphylococcus aureus USA300-ISMMS1	1		1			
3412	X	1458555	Influenza A virus (A/Jiangxi/IPB13/2013(H10N8))			1		1	
3413		1463841	Streptomyces sp. NRRL F-2580		1		1		
3414		1464048	Micromonospora parva		1		1		
3415		1470614	Influenza A virus (A/swine/Thailand/CU-S3673N/2012(H3N2))		1		1		
3416		1472713	Norovirus Hu/GII/Amsterdam/1994		1		1		
3417		1476909	Banana streak MY virus	39		39			
3418		1481964	Influenza A virus (A/Anhui/1-DEWH730/2013(H7N9))	1	35	1	35		
3419		1481966	Influenza A virus (A/Anhui/1-JCVI1_RG2/2013(H7N9))	3		3			

3420	X	1481987	Influenza A virus (A/Anhui/1-BALF_RG44/2013(H7N9))			1		1	
3421		1498499	Legionella norrlandica		1		1		
3422		1498657	Norovirus Hu/GII.4/Chiba5/2010/JP		2		2		
3423		1501332	Oribacterium asaccharolyticum		1		1		
3424		1507381	Influenza A virus (A/Minnesota/11/2010(H3N2))	19		19			
3426	X	1507390	Influenza A virus (A/reassortant/NYMC X-217A(A/Puerto Rico/8/1934 x A/Victoria/361/2011)(H3N2))			1		1	
3428	X	1508227	Bat SARS-like coronavirus			646		646	
3430		1562038	Norway rat hepacivirus 1		5		5		
3432		1566201	Pseudomonas sp. NFACC45		2		2		
3433		1566298	Paraiso Escondido virus		1		1		
3434		1570291	Ebola virus	3	142	3	142		
3435		1581419	Amblyomma sculptum	1		1			
3436		1586324	Porcine deltacoronavirus	1		3		2	
3437		1590370	Betacoronavirus HKU24		3		3		
3438		1631247	Mesorhizobium delmotii		1		1		
3439		1634342	Norovirus Hu/GII/JP/2015/GII.P17_GII.17/Kawasaki308	1		1			
3440		1663864	Influenza A virus (A/Anhui/1-YK_RG134/2013(H7N9))		1		1		
3441		1663934	Influenza A virus (A/Anhui/1-YK_RG64/2013(H7N9))		2		2		
3442		1663996	Influenza A virus (A/Anhui/1-YK_RG01/2013(H7N9))	1		1			
3443		1665645	Norovirus GI/Hu/NL/2012/GI.6/Groningen		1		1		
3444		1671798	Human papillomavirus type 54		1		1		
3445		1678143	Orthohepevirus A	153	91	153	91		
3446		1678144	Orthohepevirus B	20		20			
3447		1727172	Influenza A virus (A/duck/Bavaria/1/1977(H1N1))		2		2		
3448		1737357	Rhizobium wenxiniae		1		1		
3449		1763596	Guertu virus	32		32			
3450	X	1777792	Influenza A virus (A/Michigan/45/2015(H1N1))			1		1	
3451		1783360	Comamonas sediminis		1		1		
3453		1835656	Rotavirus A RVA/Cow-tc/USA/B223/1983/G10P[11]	2		2			
3455		1855372	bacterium JGI 053		1		1		
3456		1868221	Porcine circovirus 3	4		4			
3457	X	1868482	Carlito syrichta			1		1	
3458		1885248	Variegated squirrel bornavirus 1		1		1		
3459		1891187	Zaire ebolavirus Makona	48	57	55	57	7	
3460		1891729	Mesocricetus auratus polyomavirus 1	11		11			
3461		1891730	Mus musculus polyomavirus 1	4	30	4	37		7
3462		1891762	Human polyomavirus 1	4	78	4	81		3
3463		1891767	Macaca mulatta polyomavirus 1	16	42	16	42		
3464		1898104	Bacteroidetes bacterium	1	1	1	1		
3465		1898112	Rhodospirillaceae bacterium		1		1		
3466		1898203	Lachnospiraceae bacterium		1		1		

3467	X	1907210	Human adenovirus sp.				4		4
3469	X	1914447	Atypical porcine pestivirus			3		3	
3470	X	1933298	Tomato spotted wilt orthotospovirus			1		1	
3471		1933300	Watermelon silver mottle orthotospovirus	3		3			
3472		1965067	Porcine reproductive and respiratory syndrome virus 2		41		41		
3473	X	1968303	Influenza A virus (A/chicken/Guangdong/GD15/2016(H7N9))			2		2	
3475		1972699	Norovirus Hu/GII.3/3-34/2015/HNZZ/CHN	11		11			
3476		1977402	Escherichia virus M13		1		1		
3477		1978231	Acidobacteria bacterium		1		1		
3478		1980442	Orthohantavirus		13		13		
3479		1980456	Andes orthohantavirus	2	79	2	79		
3480		1980459	Bayou orthohantavirus	1		1			
3481		1980463	Cano Delgadito orthohantavirus		1		1		
3482		1980467	Dobrava-Belgrade orthohantavirus		25		25		
3483		1980468	El Moro Canyon orthohantavirus		2		2		
3484		1980471	Hantaan orthohantavirus	2	63	4	69	2	6
3485		1980475	Khabarovsk orthohantavirus		1		1		
3486		1980476	Laguna Negra orthohantavirus		12		12		
3487		1980481	Montano orthohantavirus	3		3			
3488		1980485	Prospect Hill orthohantavirus	1	2	1	2		
3489		1980486	Puumala orthohantavirus	32	20	33	20	1	
3490		1980489	Sangassou orthohantavirus		6		6		
3491		1980490	Seoul orthohantavirus		5		5		
3492		1980491	Sin Nombre orthohantavirus	1	35	1	35		
3493		1980494	Tula orthohantavirus	1	14	1	14		
3494		1980519	Crimean-Congo hemorrhagic fever orthonairovirus	95	18	95	18		
3496	X	2016460	Giant panda anellovirus				1		1
3497	X	2016461	Giant panda associated gemycircularvirus				1		1
3498	X	2016463	Giant panda polyomavirus				1		1
3500	X	2019571	Influenza A virus (A/reassortant/IDCDC-RG56B(Hong Kong/125/2017 X Puerto Rico/8/1934)(H7N9))			2		2	
3501		2024894	Acidimicrobiaceae bacterium		1		1		
3503		2026033	Influenza A virus (A/chicken/Hunan/S12753/2016(H7N9))	2		2			
3505		2029108	Bacillus sp. UMB0899	1		1			
3506		2043570	Zika virus ZIKV/H. sapiens/FrenchPolynesia/10087PF/2013	20	54	26	75	6	21
3507	X	2044587	Schaedlerella arabinosiphila				5		5
3508		2066070	Mesorhizobium japonicum		1		1		
3509		2070132	Influenza A virus (A/chicken/Jiangsu/W1-8/2015(H7N9))	6		6			
3510		2115988	Swine acute diarrhea syndrome related coronavirus	1		1			
3511		2116544	Synechococcus lacustris	1		1			
3512		2169971	Visna-maedi virus	5	7	5	7		
3513		2169986	Barley yellow dwarf virus PAV	1		1			
3514		2169991	Argentinian mammarenavirus	8	873	8	873		

3515		2169992	Brazilian mammarenavirus		879		879		
3516		2169993	Cali mammarenavirus		11		11		
3517		2169994	Paraguayan mammarenavirus		1		1		
3518		2169996	Serra do Navio mammarenavirus		3		3		
3519		2170197	Guenon simian foamy virus	1		1			
3520		2170200	Spider monkey simian foamy virus	1		1			
3521		2170201	Squirrel monkey simian foamy virus	1		1			
3522		2170206	Yellow-breasted capuchin simian foamy virus	1		1			
3523		2282107	Pyrrhoderma noxium		1		1		
3524		2316109	Zika virus ZIKV/Human/Cambodia/FSS13025/2010		2		2		
3525		2478486	Holophagales bacterium		1		1		
3526		2487134	Clostridium sp. E02		1		1		
3527		2492960	Bacillus yapensis		1		1		
3528		2501420	Yak coronavirus		1		1		
3529		2560319	Avian orthoavulavirus 1	21	5	26	5	5	
3530		2560525	Human orthorubulavirus 2	10		10			
3531		2560580	Mammalian orthorubulavirus 5	1	1	1	1		
3532		2560602	Mumps orthorubulavirus	3	2	3	22		20
3533		2560645	Porcine orthorubulavirus	3		3			
3535	X	2593991	Peste des petits ruminants virus				1		1
3536		2594813	Fusarium fasciculatum		1		1		
3537		2599941	Oligoflexia bacterium		1		1		
3538		2630493	unclassified Granulicatella		1		1		
3539		2678873	Trimerodytes annularis	1		1			
3540		2697049	Severe acute respiratory syndrome coronavirus 2	200	660	7625	3166	7425	2506
3541		2707005	Paenibacillus lutimineralis		1		1		
3542	X	2708335	Pangolin coronavirus			1782	1	1782	1
3543	X	2709072	Bat coronavirus RaTG13			687		687	
3544		2758382	Bos taurus papillomavirus 2	15		15			
3546		2847087	GB virus-B		4		4		
3547		2847144	hepatitis C virus genotype 1a	206	399	216	399	10	
3550		10000000	Mus musculus BALB/c		3		3		
3551		10000055	Mus musculus DBA/2	1		1			
3552		10000067	Mus musculus C57BL/6		381	1	381	1	
3553		10000187	Sus scrofa Landrace X Large White	1		1			
3554	X	10000225	Mus musculus C57BL/6N				1		1
3555		10000291	Bacillus anthracis str. Sterne 34F2	1		1			
3556		10000293	Clostridium botulinum A 1	1		1			
3557		10000294	Clostridium botulinum A 2	2		2			
3558		10000295	Clostridium botulinum B 111	2		2			
3559		10000296	Clostridium botulinum D 1873	2		2			
3560		10000297	Clostridium botulinum C 92-13	5		5			
3561		10000299	Clostridium botulinum E Beluga	2		2			

3562		10000301	Clostridium botulinum A str. Hall hyper	3		3			
3563		10000302	Clostridium botulinum A Kyoto-F	1		1			
3564		10000303	Clostridium botulinum B Lammana	1		1			
3565		10000304	Clostridium botulinum F NCTC 10281	1		1			
3566		10000305	Clostridium botulinum B Okra	3		3			
3567		10000306	Clostridium botulinum C Stockholm	2		2			
3568		10000307	Clostridium difficile BART'S W1	1		1			
3569		10000308	Listeria monocytogenes ATCC 35967		1		1		
3570		10000309	Listeria monocytogenes ATCC 43251		3		3		
3571		10000313	Mycobacterium avium serovar 1	1		1			
3572		10000314	Mycobacterium avium serovar 2	1		1			
3573		10000316	Mycobacterium avium serovar 25	1		1			
3574		10000317	Mycobacterium avium serovar 26	1		1			
3575		10000318	Mycobacterium avium serovar 4	2		2			
3576		10000319	Mycobacterium avium serovar 8	1	1	1	1		
3577		10000320	Mycobacterium avium serovar 9	1		1			
3578		10000323	Mycobacterium bovis T/91/1378		6		6		
3579		10000328	Mycobacterium avium subsp. paratuberculosis Strain Ben		1		1		
3580		10000329	Mycobacterium tuberculosis 103	1		1			
3581		10000331	Mycobacterium gastri W471	1		1			
3582		10000335	Candida albicans A-9 (serotype B)	1		1			
3583		10000337	Candida albicans KIT 1113	1		1			
3584		10000339	Candida albicans serotype A	1		1			
3585		10000341	Leishmania donovani donovani 1S2D	1		1			
3586		10000345	Leishmania infantum LEM 75	14		14			
3587		10000348	Trypanosoma cruzi G	1		1			
3588		10000351	Trypanosoma cruzi Y	1		1			
3589		10000352	Entamoeba histolytica YS-27	1		1			
3590		10000353	Toxoplasma gondii 76K	5	5	5	5		
3591		10000354	Toxoplasma gondii BK	1	1	1	1		
3592		10000355	Toxoplasma gondii Prugniaud		1		1		
3593		10000356	Plasmodium berghei NK65	2	2	2	2		
3594		10000357	Plasmodium chabaudi adami DS	2	37	2	37		
3595		10000358	Plasmodium falciparum 366		1		1		
3599		10000363	Plasmodium falciparum Brazil-608	1	1	1	1		
3600		10000366	Plasmodium falciparum FCB-2	1		1			
3601		10000369	Plasmodium falciparum FVO		5		5		
3602		10000370	Plasmodium falciparum GAM5		1		1		
3603		10000371	Plasmodium falciparum Indochina I/CDC	32		32			
3604		10000373	Plasmodium falciparum ItG2G1		1		1		
3605		10000375	Plasmodium falciparum RO71	1	1	1	1		
3606		10000376	Plasmodium falciparum UF-5	2		2			
3607		10000378	Plasmodium vivax NK		2		2		

3608		10000381	Plasmodium yoelii yoelii YM	1	5	1	5		
3609		10000382	Babesia bovis Mexico	3	4	3	4		
3610		10000383	Babesia bovis Mexico Mo7	1	33	1	33		
3611		10000385	Schistosoma mansoni Puerto Rico	20	7	20	7		
3612		10000386	Monkeypox virus USA_2003_039		1		1		
3613		10000388	Vaccinia virus NYCBH - Dryvax		29		29		
3614		10000390	Variola major virus India-1967		1		1		
3615		10000391	Equid herpesvirus 2 ER32	1		1			
3616		10000394	Human herpesvirus 1 103/65	1		1			
3617		10000396	Human herpesvirus 1 McIntyre		1		1		
3618		10000398	Human herpesvirus 1 NS	1		1			
3619		10000404	Bovine herpesvirus 1 Lam	1		1			
3620		10000405	Equid herpesvirus 4 TH20	2		2			
3621		10000406	Human herpesvirus 3 H-551	26	15	26	15		
3622		10000408	Human herpesvirus 5 TB40		1		1		
3623		10000411	Murid herpesvirus 1 deltaMS94.5		2		2		
3624		10000412	Murid herpesvirus 1 Isolate G4		1		1		
3625		10000413	Murid herpesvirus 1 Isolate K6		1		1		
3627		10000420	Human herpesvirus 4 BL74		1		1		
3628		10000421	Human herpesvirus 4 CKL		10		10		
3629		10000424	Human herpesvirus 4 GD1	4	1	4	1		
3630		10000427	Human herpesvirus 4 type A		5		5		
3632	X	10000431	Hepatitis B virus ay/ad			4		4	
3633	X	10000432	Hepatitis B virus genotype A			1		1	
3634		10000436	Hepatitis B virus subtype AY	7		7			
3635		10000437	Hepatitis B virus subtype AYR		1		1		
3636		10000438	Human parvovirus B19 genotype 1	1		1			
3637		10000439	Eastern equine encephalitis virus SV	8		8			
3638		10000440	Dengue virus type 1 Hawaii	29	22	29	22		
3639		10000442	Dengue virus type 3 CH53489		7		7		
3640		10000444	Japanese encephalitis virus CH2195LA	1		1			
3641		10000445	Japanese encephalitis virus JaOH0566	1		1			
3642		10000447	West Nile virus 3000.0259	2		2			
3643		10000449	Tick-borne encephalitis virus (WESTERN SUBTYPE) - Neudoerfl	10		10			
3644		10000451	Classical swine fever virus Shimen	16		19		3	
3645		10000453	Hepatitis C virus subtype 1a (isolate Gla)	5		5			
3646		10000455	Hepatitis C virus subtype 1a 1/910		18		18		
3647		10000456	Hepatitis C virus subtype 1b AD78	71		71			
3648		10000457	Hepatitis C virus subtype 1a Chiron Corp.	1	1	1	1		
3650		10000460	Hepatitis C virus subtype 1b JK1	13		13			
3651		10000462	Measles virus CAM/RB		1		1		
3652		10000463	Phocine distemper virus 2558/Han 88	5		5			
3653		10000465	Rinderpest virus LATC	2		2			

3654		10000467	Rabies virus CVS	14		14			
3655		10000470	Rabies virus Flury LEP		1		1		
3656		10000471	Rabies virus RC-HL	4		4			
3657		10000472	Bovine ephemeral fever virus BB7721	2		2			
3658		10000474	Influenza A virus H3N2 (A/Resvir-9 (H3N2))		10		10		
3659		10000477	H1N1 subtype Influenza A virus (A/Netherlands/306/00 (H1N1))		1		1		
3660		10000482	Rift Valley fever virus ZH501	2		2	42		42
3661		10000483	Puumala virus CG18-20	4		4			
3662		10000484	Puumala virus Kazan	26	7	26	7		
3663		10000485	Puumala virus (STRAIN HALLNAS B1) Vranica/Hallnas	4		4			
3664		10000487	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 4)	1		1			
3665		10000488	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 53b)		61		61		
3666		10000490	Lymphocytic choriomeningitis virus A22.2b		1		1		
3667		10000491	Lymphocytic choriomeningitis virus Docile		2		2		
3668		10000494	Lymphocytic choriomeningitis virus (strain WE) variant 8.7		1		1		
3669		10000495	Lymphocytic choriomeningitis virus (strain WE) WE CL1.2		1		1		
3670		10000496	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 3)		1		1		
3671		10000497	Lymphocytic choriomeningitis virus (strain Armstrong) (clone 5)	1		1			
3672		10000499	Equine infectious anemia virus PV		2		2		
3673		10000500	Human immunodeficiency virus 1 IIIB	1	2	1	2		
3674		10000501	Simian immunodeficiency virus - mac - mac 239	1	474	1	474		
3675		10000502	Simian immunodeficiency virus - mac - mac 32H		9		9		
3676		10000503	Simian immunodeficiency virus - mac - mac BK28		4		4		
3677		10000504	Simian immunodeficiency virus - mac - mac F965		2		2		
3679		10000506	Simian immunodeficiency virus - sm - sm PT573		3		3		
3680		10000507	Rabbit hemorrhagic disease virus Olot/89	1		1			
3681		10000513	Foot-and-mouth disease virus (strain O1) (O1 Kaufbeuren)	43	8	43	8		
3682		10000514	Foot-and-mouth disease virus (strain O1) (O1BFS 1860)	9		9			
3683		10000515	Foot-and-mouth disease virus (strain O1) (O1BFS)	5		5			
3684		10000516	Foot-and-mouth disease virus (strain O1) (O1 Campos)	18	19	18	19		
3685		10000518	Borna disease virus Giessen strain He/80	6		6			
3686		10000519	Hepatitis E virus China Xinjiang	1		1			
3687		10000520	Hepatitis E virus SAR-55	2	6	2	6		
3688		10000523	Hepatitis delta virus TW2667		5		5		
3689		10000524	Equid herpesvirus 2 691	1		1			
3690		10000525	Equid herpesvirus 2 16V	1		1			
3691		10000526	Equid herpesvirus 2 5FN	1		1			
3692		10000527	Equid herpesvirus 2 FIN60	1		1			
3693		10000528	Porcine respiratory and reproductive syndrome virus BJ-4	2		2			
3694		10000529	Porcine respiratory and reproductive syndrome virus CH-1a	7	1	7	1		
3695		10000530	Borrelia garinii IP90	3		3			

3696	X	10000532	Peste-des-petits-ruminants virus Sungri-96				11		11
3697		10000535	Human herpesvirus 6B HST	1		1			
3698		10000536	Murid herpesvirus 4 G2.4		3		3		
3699		10000537	Murid herpesvirus 4 WUMS		19		19		
3700		10000542	Streptococcus pyogenes serotype M3 D58	4		4			
3701		10000544	Sin Nombre virus NM H10	4		4			
3702		10000547	Human enterovirus 71 Subgenogroup B5	12		12			
3703		10000548	Human enterovirus 71 Subgenogroup C2	19		19			
3704		10000549	Human enterovirus 71 Subgenogroup C4	11		12		1	
3705		10000550	Influenza A virus H3N2 (A/Netherlands/9/03 (H3N2))		1		1		
3706		10000553	Andes virus CHI-7913	53		53			
3707		10000554	Salmonella enterica subsp. enterica serovar Minnesota R595	2		2			
3708		10000555	Plasmodium yoelii yoelii 265BY		1		1		
3709		10000556	Foot-and-mouth disease virus (strain O1) Kaufbeuren	44	12	44	12		
3710		10000559	Chlamydophila abortus B-577	11		11			
3711		10000560	Norovirus genogroup 3 Bo/Jena/1980/DE	1		1			
3712		10000566	Paracoccidioides brasiliensis B339		8		8		
3713		10000567	Vibrio cholerae O1 serotype Inaba	1		1			
3714		10000568	Vibrio cholerae O1 serotype Ogawa	5		6		1	
3715		10000571	Cowpox virus (Brighton Red) White-pock		1		1		
3716	X	10000632	Mus musculus NOD				578		578
3717		10000662	Rattus norvegicus Lewis		1		1		
3718		10000675	Borrelia burgdorferi CA12		6		6		
3719		10000679	Campylobacter jejuni subsp. jejuni 16971.94GSH (O:41)	2		2			
3720		10000718	Helicobacter pylori J223	2		2			
3721		10000720	Helicobacter pylori UA948	2		2			
3722		10000721	Helicobacter pylori UA955	1		1			
3723		10000723	Pseudomonas aeruginosa Immunotype 4	4		4			
3724		10000727	Escherichia coli 180/C3	1		1			
3725		10000728	Escherichia coli B B/r CM6		1		1		
3726		10000733	Escherichia coli O5:K4:H4	1		1			
3727		10000734	Escherichia coli O65:K-:H-	1		1			
3728		10000738	Salmonella typhimurium PL5 (O9,12)	1		1			
3729		10000739	Salmonella typhi 620Ty	1		1			
3730		10000740	Salmonella typhi Ty21a		6		6		
3731		10000742	Salmonella typhimurium SH 4809	4		4			
3732		10000743	Salmonella typhimurium SL3261		4		4		
3733		10000748	Shigella dysenteriae serotype 1	3		3			
3734		10000749	Shigella dysenteriae serotype 1 114Sd	1		1			
3735		10000752	Shigella flexneri 5b	1		1			
3736		10000754	Shigella flexneri X	1		1			
3737		10000756	Yersinia pestis KIM 5	21		21			
3738		10000757	Yersinia pestis 195/P	5		5			

3739		10000759	Pasteurella multocida X-73	2		2			
3740		10000760	Anaplasma marginale South Idaho		2		2		
3741		10000761	Orientia tsutsugamushi Karp	1		1			
3742		10000763	Chlamydia trachomatis Serovar C	16	1	16	1		
3743		10000764	Chlamydia trachomatis Serovar E	19	2	19	2		
3744		10000765	Chlamydia trachomatis Serovar H	7		7			
3745		10000766	Chlamydia trachomatis Serovar I	10		10			
3746		10000767	Chlamydia trachomatis serovar K	14		14			
3747		10000768	Chlamydia trachomatis Serovar L2	15	12	15	12		
3748		10000769	Chlamydia trachomatis Serovar L3	2		2			
3749		10000773	Streptococcus mutans MT 8148	40	12	40	12		
3750		10000775	Streptococcus pyogenes 156	1		1			
3751		10000776	Streptococcus pyogenes 88/25	1		1			
3752		10000777	Streptococcus pyogenes 88/30	1		1			
3753		10000778	Streptococcus pyogenes 88/544	1		1			
3754		10000779	Streptococcus pyogenes 90/85	1		1			
3755		10000780	Streptococcus pyogenes serotype M12 A374	1		1			
3756		10000781	Streptococcus pyogenes BSA10	3		3			
3757		10000782	Streptococcus pyogenes NS1	1		1			
3758		10000783	Streptococcus pyogenes NS14	1		1			
3759		10000784	Streptococcus pyogenes NS27	1		1			
3760		10000785	Streptococcus pyogenes NS5	1		1			
3761		10000786	Streptococcus pyogenes serotype M11	2		2			
3762		10000787	Streptococcus pyogenes serotype M13	1		1			
3763		10000788	Streptococcus pyogenes serotype M22	1		1			
3764		10000789	Streptococcus pyogenes serotype M24	6	2	6	2		
3765		10000790	Streptococcus pyogenes serotype M30	1		1			
3766		10000791	Streptococcus pyogenes serotype M41	1		1			
3767		10000792	Streptococcus pyogenes serotype M52	1		1			
3768		10000793	Streptococcus pyogenes serotype M54	1		1			
3769		10000794	Streptococcus pyogenes serotype M55	1		1			
3770		10000795	Streptococcus pyogenes serotype M57	1		1			
3771		10000796	Streptococcus pyogenes serotype M60	1		1			
3772		10000797	Streptococcus pyogenes serotype M75	1		1			
3773		10000798	Streptococcus pyogenes serotype M8	1		1			
3774		10000801	Foot-and-mouth disease virus - type O (O/SKR/2002)	1		1			
3775		10000802	Taenia crassiceps Strain ORF	3	3	3	3		
3776		10000804	Chlamydia trachomatis Serovar B	47	5	47	5		
3777		10000806	Foot-and-mouth disease virus (strain O1) (O1 Manisa)	6	1	6	1		
3778		10000807	Haemophilus influenzae NTHi UC19	2	2	2	2		
3779		10000809	Swine vesicular disease virus ITL/1/66	1		1			
3780		10000814	Leptospira interrogans serovar Lai str. HY-1	1		1			
3781		10000815	Pseudomonas aeruginosa PAO	2	2	2	2		

3782		10000816	Plasmodium falciparum T9/96	1	1	1	1		
3783		10000817	Pseudomonas aeruginosa KB7	2		2			
3784		10000818	Pseudomonas aeruginosa P1	1		1			
3785		10000820	Foot-and-mouth disease virus (strain O1) (O/Taiwan/1/97)	1		1			
3786		10000822	Pseudomonas aeruginosa Immunotype 3	1		1			
3787		10000824	Streptococcus pyogenes serotype M6 strain D471	4		4			
3788		10000825	Infectious bronchitis virus Avian strain D207	11		11			
3789		10000828	Ajellomyces dermatitidis ATCC 60636		2		2		
3790		10000829	Norovirus genogroup 2 Mexico type strain 36	3		3			
3791		10000832	Norovirus genogroup 2 Camberwell 1890	1		1			
3792		10000833	Haemophilus influenzae NTHi 1128	6		6			
3793		10000835	Equine rhinitis A virus 393/76	4		4			
3794		10000836	Foot-and-mouth disease virus C1 CS8	22	24	23	24	1	
3795		10000840	Foot-and-mouth disease virus C1 Brescia It/64	2		2			
3796		10000842	Swine vesicular disease virus NET/1/92	1		1			
3797		10000843	Neisseria meningitidis serogroup B H44/76	74	22	74	22		
3798		10000845	Chlamydia trachomatis Serovar F	3		3			
3799		10000848	Theileria sergenti Type B1		1		1		
3800		10000849	Theileria sergenti Type B2		2		2		
3801		10000850	Theileria sergenti Type C		5		5		
3802		10000851	Theileria sergenti Type I		1		1		
3803		10000852	Chlamydophila pneumoniae Kajaani 6		7		7		
3804		10000853	Chlamydia trachomatis Serovar L1	21	3	21	3		
3805		10000855	Theiler's murine encephalomyelitis virus (strain BeAn 8386) (variant M2)		1		1		
3806		10000856	Foot-and-mouth disease virus - type O isolate O/UKG/35/2001		14		14		
3808		10000858	Chlamydia trachomatis B/Jali-20/OT	2		2			
3809		10000859	Porcine respiratory and reproductive syndrome virus JA142	1		1			
3810		10000860	Haemophilus influenzae Serotype B	18	9	18	9		
3811		10000861	Haemophilus influenzae Variant d1	18		18			
3812		10000862	Plasmodium vivax VK247	1		1			
3813		10000863	Neisseria gonorrhoeae 4505	1		1			
3814		10000864	Porcine respiratory and reproductive syndrome virus MD-001	2		2			
3815		10000865	Influenza A virus H3N2 (A/Kiev/301/94)	3		3			
3816		10000888	Porcine respiratory and reproductive syndrome virus Olot/91	3	5	3	5		
3817		10000890	Porcine respiratory and reproductive syndrome virus SD92-23983		33		33		
3818		10000960	Human respiratory syncytial virus A Mon/3/88	6		6			
3819		10000961	Dengue virus type 1 strain 16007	15		15			
3820		10000964	Foot-and-mouth disease virus (strain O1) (O1 Brugge)	2		2			
3821		10000965	Dengue virus type 1 FGA/89	4		4			
3822		10000968	Hepatitis C virus subtype 1b isolate BE-11	3		3			
3823		10000969	Porcine respiratory and reproductive syndrome virus 111/92	9		9			
3824		10000971	West Nile virus NY-99	15	21	15	21		

3825		10000972	Neisseria meningitidis serogroup B Strain B16.B6	1		1			
3826		10000979	Neisseria meningitidis serogroup B Strain 8047	4		4			
3827		10000980	Arcanobacterium pyogenes Strain 42	4		4			
3828		10000986	Foot-and-mouth disease virus C1 CS30	1		1			
3829		10000987	Human rhinovirus 2 Vienna	5		5			
3830		10000989	Foot-and-mouth disease virus - type A (strain A22)	10	6	10	6		
3831		10000991	Foot-and-mouth disease virus - type A (strain A22 Iraq)	5	1	5	1		
3832		10000992	Foot-and-mouth disease virus - type SAT 1 (Strain Bot 1/68)	1		1			
3833		10000993	Foot-and-mouth disease virus - type SAT 2 (Strain Ken 3/57)	1		1			
3834		10000994	Foot-and-mouth disease virus - type SAT 3 (Strain Bec 1/65)	1		1			
3835		10000995	Foot-and-mouth disease virus - type Asia 1 Pakistan	1		1			
3836		10001000	Foot-and-mouth disease virus - type SAT 2 (strain Rho 1/48)	4		4			
3837		10001002	Swine vesicular disease virus SPA/1/93	16		16			
3838		10001003	Neisseria meningitidis serogroup B CU385	2		2			
3839		10001004	Human T-cell lymphotrophic virus type 1 (Caribbean isolate) (Strain HS35)	1		1			
3840		10001006	Proteus mirabilis CFT322	1		1			
3841		10001008	Chlamydia trachomatis Serovar J	6		6			
3842		10001019	Mus musculus B10.D2		1		1		
3843		10001020	Peste-des-petits-ruminants virus (strain Nigeria 75/1)		1		1		
3844		10001021	Treponema pallidum subsp. pallidum (strain Chicago)	19		19			
3845		10001025	Classical swine fever virus Glentorf		26		26		
3846		10001027	Vaccinia virus Connaught	1		1			
3847		10001028	Human poliovirus 2 (strain MEF-1)	1		1			
3848		10001032	Newcastle disease virus (strain La Sota)	17		17			
3849		10001039	Foot-and-mouth disease virus C3 (strain Resendne-Br/55)	1		1			
3850		10001040	Human poliovirus 2 (strain Sabin)	2	7	2	7		
3851		10001042	Haemophilus influenzae NTHi 1479	12	4	12	4		
3852		10001044	Neisseria meningitidis serogroup C MC51	1		1			
3853		10001047	West Nile virus strain 2741	32		32			
3854		10001049	Neisseria meningitidis serogroup B Strain S3446	1		1			
3855		10001050	Neisseria meningitidis serogroup B Strain 7967	1		1			
3856		10001051	Neisseria meningitidis serogroup A Strain 8659	1		1			
3857		10001053	Haemophilus influenzae MinnA	9		9			
3858		10001055	Haemophilus influenzae 6U	2		2			
3859		10001056	Haemophilus influenzae ATCC 9795	2		2			
3860		10001057	Pseudomonas aeruginosa CD4	1		1			
3861		10001058	Pseudomonas aeruginosa K122-4	1		1			
3862		10001077	Neisseria gonorrhoeae SU89	1		1			
3863		10001078	Neisseria gonorrhoeae SU96	3		3			
3864		10001081	Porphyromonas gingivalis HG66	2		2			
3865		10001085	Chlamydia trachomatis Serovar D	3		3			

3866		10001091	Borrelia burgdorferi BEP4	1		1			
3867		10001097	Sus scrofa Yorkshire	1		1			
3868		10001100	Plum pox virus (strain W)	6		6			
3869		10001102	Foot-and-mouth disease virus (strain O1) O/UKG/11/2001	1	2	1	3		1
3870		10001116	Norovirus genogroup 1 isolates 96-908	4		4			
3871		10001118	Foot-and-mouth disease virus - type O (strain HKN/14/82)	2		2			
3872		10001120	Cryptococcus neoformans var. neoformans Serotype D	1		1			
3873		10001121	Chlamydia trachomatis Serovar Da	1		1			
3874		10001130	Feline leukemia virus subtype A	2		2			
3875		10001132	Cryptococcus neoformans var. neoformans Serotype A	1		1			
3876		10001133	Rattus norvegicus DA		3		3		
3877		10001138	Newcastle disease virus (strain Eaves)	1		1			
3878		10001140	Newcastle disease virus (strain WA2116)	1		1			
3879		10001141	Chlamydia trachomatis Serovar A	22	8	22	8		
3880		10001145	Escherichia coli 1471	2		2			
3881		10001149	Haemophilus influenzae Subtype 1H	23		23			
3882		10001150	Haemophilus influenzae Strain Eagan	58		58			
3883		10001154	Transmissible gastroenteritis virus MAD88	8	1	8	1		
3884		10001155	Haemophilus influenzae strain 1479	2		2			
3885		10001156	Hepatitis B virus subtype AD	3	2	3	2		
3886		10001157	H3N2 subtype Influenza A virus (A/Hong Kong(H3N2))		15		15		
3887		10001161	Neisseria meningitidis serogroup B Strain 2996	1		1			
3888		10001162	Neisseria meningitidis serogroup B Strain M1239	4		4			
3889		10001207	Murine leukemia virus LP-BM5		1		1		
3890		10001209	Tobacco mosaic virus (strain PM5)	1		1			
3891		10001210	Tobacco mosaic virus (strain Ni568)	1		1			
3892		10001213	Human coxsackievirus B3 (strain RK)	1		1			
3893		10001215	Human rotavirus G9 WI61	1		1			
3894		10001216	Rotavirus G3 strain RV-3	1		1			
3895		10001223	Porphyromonas gingivalis OMZ 409	23		23			
3896		10001225	H1N1 subtype Influenza A/Oklahoma/7485/01		5		5		
3897		10001238	Puumala virus (strain Umea/hu)	1		1			
3898		10001239	Porcine circovirus strain ISU31	7		7			
3899		10001243	Theileria parva strain Marikebuni		1		1		
3900		10001307	Small ruminant lentivirus strain It-561	1		1			
3901		10001308	Small ruminant lentivirus strain It-Pi1	1		1			
3902		10001315	H1N1 swine influenza virus (A/swine/Korea/S10/2004(H1N1))		3		3		
3903		10001316	H1N1 swine influenza virus (A/swine/Korea/S175/2004(H1N1))		1		1		
3904		10001317	H9N2 subtype Influenza A virus (A/swine/Korea/S81/2004(H9N2))		1		1		
3905		10001318	H9N2 subtype Influenza A virus (A/swine/Korea/S83/2004(H9N2))		2		2		
3906		10001335	Japanese encephalitis virus Vellore P20778	1	1	1	1		
3907		10001392	Human adenovirus B strain Harbin04B	5		5			

3908		10001396	Murine cytomegalovirus (strain Smith) MW97.01		5		5		
3909		10001412	Rattus norvegicus Wistar-Furth		11		11		
3910		10001424	Brucella abortus W99	1		1			
3911		10001431	Infectious bronchitis virus CK/CH/LDL/97I	1		1			
3912		10001439	Streptococcus sanguinis strain BD113-20		6		6		
3913		10001456	Human respiratory syncytial virus A strain RGH	1		1			
3914		10001459	Babesia bovis Argentina R1A	4		4			
3915		10001484	Norovirus genogroup 1 GI.12	1		1			
3916		10001485	Norovirus genogroup 3 GIII.1	1		1			
3917		10001489	Proteus vulgaris Strain 5/43	1		1			
3918		10001490	Proteus mirabilis O24	1		1			
3919		10001491	Proteus mirabilis O29	1		1			
3920		10001492	Salmonella enterica subsp. enterica serovar Enteritidis SH1262	3		3			
3922		10001498	Proteus mirabilis O23	1		1			
3923		10001499	Proteus mirabilis O6	1		1			
3924		10001500	Proteus mirabilis O43	1		1			
3925		10001501	Proteus penneri ATCC 33519	1		1			
3926		10001502	Escherichia coli J-5	1		1			
3927		10001503	Acinetobacter lwoffii F78	1		1			
3928		10001504	Yokenella regensburgei PCM 2476	1		1			
3929		10001505	Yokenella regensburgei PCM 2477	1		1			
3930		10001511	Salmonella 'group A'	2		2			
3931		10001514	Providencia stuartii O33	1		1			
3932		10001519	Pseudomonas aeruginosa serotype O11	1		1			
3933		10001520	Haemophilus influenzae strain RM7004	1		1			
3934		10001523	Haemophilus influenzae strain I-69 Rd-/b+	4		4			
3935		10001524	Neisseria meningitidis strain 3006	1		1			
3936		10001526	Salmonella thompson C1 strain IS40	1		1			
3937		10001528	Escherichia coli F515	1		1			
3938		10001530	Acinetobacter haemolyticus strain 57	1		1			
3939		10001531	Acinetobacter haemolyticus strain 61	1		1			
3940		10001556	Moraxella catarrhalis 26404	1		1			
3941		10001558	Neisseria gonorrhoeae 15253	1		1			
3942		10001560	Neisseria meningitidis M982B	5		5			
3943		10001569	Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 11	1		1			
3944		10001570	Salmonella enterica subsp. enterica serovar Gallinarum/pullorum str. 77	1		1			
3945		10001573	Anatid herpesvirus 1 Clone-03	1		1			
3946		10001578	Classical swine fever virus LPC/AHRI	4		5		1	
3947		10001581	Proteus penneri 8 (O67)	1		1			
3948		10001582	Dengue virus 1 Mochizuki	4		4			
3949		10001583	Dengue virus 2 New Guinea C	1	38	1	38		
3950		10001586	Porcine reproductive and respiratory syndrome virus 07V063	3		3			

3951		10001587	Porcine reproductive and respiratory syndrome virus 08V204	2		2			
3952		10001588	Providencia stuartii O4	1		1			
3954		10001606	Norovirus genogroup 2 Hu/NoV/Farmington Hills/2002/USA	1	2	1	17		15
3955		10001614	Junin virus strain MC2		1		1		
3956		10001615	Machupo virus strain Carvallo		1		1		
3957		10001616	Guanarito virus strain INH-95551		1		1		
3958		10001617	Whitewater Arroyo virus strain AV9310135		1		1		
3959		10001618	Pichinde virus strain Munchique		1		1		
3960		10001619	Dengue virus 3 strain 16652	16		16			
3961		10001624	Feline infectious peritonitis virus (strain KU-2)	22	43	22	43		
3962		10001627	Human herpesvirus 5 (strain RV798)		6		6		
3963		10001628	Aggregatibacter actinomycetemcomitans serotype b str. Y4	1		1			
3964		10001633	Escherichia coli 055:B5	3		3			
3965		10001635	Dengue virus 2 PL046		7		7		
3966		10001636	Dengue virus 2 S221		42		42		
3967		10001638	Streptococcus pneumoniae type 27	2		2			
3968		10001641	Streptococcus dysgalactiae subsp. equisimilis D181	1		1			
3969		10001642	Foot-and-mouth disease virus - type O Wuppertal/FRG/82		1		1		
3970		10001644	Streptococcus pneumoniae CCUG 1378	1		1			
3971		10001645	Streptococcus pneumoniae CSR-SCS-2	1		1			
3972		10001646	Streptococcus pneumoniae type 37	2		2			
3973		10001648	Japanese encephalitis virus strain SA-14 -14-2	2		2			
3974		10001649	West Nile virus strain 956	1		1			
3975		10001651	Streptococcus pneumoniae type 14	25		26		1	
3976		10001652	Candida albicans NIH B-792 (serotype B)	1		1			
3977		10001659	Escherichia coli O125	1		1			
3978		10001662	Staphylococcus aureus Cowan 1	2		2			
3979		10001663	Streptococcus anginosus K214-2K	4		4			
3980		10001667	Helicobacter pylori 487	1		1			
3981		10001676	Streptococcus dysgalactiae subsp. equisimilis ATCC 12388	2		2			
3983		10001686	Streptococcus pneumoniae type 6A	2		2			
3984		10001687	Streptococcus pneumoniae type 6B	5		5			
3985		10001688	Pseudomonas syringae pv. atrofaciens str. IMV 7836	1		1			
3986		10001689	Pseudomonas syringae pv. atrofaciens str. IMV K-1025	1		1			
3987		10001690	Pseudomonas syringae pv. atrofaciens str. IMV 4394	1		1			
3988		10001693	Pseudomonas syringae pv. tagetis str. ICMP 6370	1		1			
3989		10001697	Pseudomonas syringae pv. phaseolicola str. IMV 120a	1		1			
3990		10001698	Pseudomonas syringae pv. morsprunorum str. GSPB 883	1		1			
3991		10001700	Pseudomonas syringae pv. morsprunorum str. CFBP 1650	1		1			
3992		10001705	Dengue virus 2 strain 43	2		2			
3993		10001713	Neisseria meningitidis serogroup W-135	1		1			

3994		10001722	Salmonella 'group D'	3		3			
3995		10001730	Streptococcus pneumoniae type 6C	1		1			
3996		10001731	Streptococcus pneumoniae type 2	8		8			
3998		10001740	Candida glabrata IFO 0622	1		1			
3999		10001747	Candida parapsilosis M1015	1		1			
4000		10001761	BK polyomavirus strain Dunlop		1		1		
4001		10001762	JC polyomavirus strain MAD1		1		1		
4002		10001763	Simian virus 40 strain 776		1		1		
4003		10001764	Classical swine fever virus Margarita (AJ704817)	4	1	4	1		
4004		10001768	Dengue virus 2 S-16803	1		1			
4005		10001771	Porcine reproductive and respiratory syndrome virus HuN4-F112	4	1	4	5		4
4006		10001783	Neisseria meningitidis serogroup C strain C11	1	1	1	1		
4007		10001792	Streptococcus pneumoniae type 3	6		6			
4008		10001794	Helicobacter pylori B128 Gerbil-adapted variant 7.13	1		1			
4010		10001797	Neisseria meningitidis serogroup C strain MC19	1		1			
4011		10001798	Porcine transmissible gastroenteritis coronavirus strain Pur46-MAD	4		4			
4012		10001800	Porcine reproductive and respiratory syndrome virus HuN4	4	4	4	4		
4013		10001801	Streptococcus pneumoniae type 8	10		10			
4014		10001831	Moraxella catarrhalis serotype B	1		1			
4015		10001833	Streptococcus pneumoniae type 19F	1		1			
4016	X	10001834	Streptococcus pneumoniae type 19A			2		2	
4017		10001835	Proteus penneri 7 (O61)	2		2			
4018		10001836	Proteus penneri 14 (O59)	2		2			
4019		10001837	Proteus penneri 15 (O52)	2		2			
4020		10001847	Clostridium difficile BI / NAP1/ 027	1		1			
4021		10001849	Moraxella catarrhalis serotype A	3		3			
4022		10001851	Moraxella catarrhalis serotype C	1		1			
4023		10001860	Neisseria meningitidis serogroup X	3		4		1	
4024		10001879	West Nile virus strain 68856	2		2			
4025		10001881	Porcine circovirus 2 -A	5		5			
4027		10001886	Brucella ovis 020	2		2			
4028		10001887	Brucella ovis Reo 198	1		1			
4029		10001888	Brucella ovis 63/290	1		1			
4031		10001895	Yersinia pseudotuberculosis str. 32777		1		1		
4032		10001900	Streptococcus agalactiae serogroup III M781	1	1	1	1		
4033		10001902	Human enterovirus 71 NUH0083/SIN/08	4		4			
4034		10001913	Lactobacillus johnsonii JCM 1022	3		3			
4035		10001918	Muscovy duck reovirus S12	4		4			
4036		10001929	Equine rhinitis B virus 2 strain 313/75	5		5			
4037		10001930	Equine rhinitis B virus 3 isolate 2225AS	5		5			
4038		10001934	Chikungunya virus Singapore/11/2008	8		8			
4039		10001943	Dengue virus 4 Burma/63632/1976	3		3			

4040		10001944	Dengue virus 3 Thailand/PaH881/1988	2		2			
4041		10001945	Dengue virus 1 PVP159	2		2			
4042		10001946	Foot-and-mouth disease virus - type Asia 1 YS/CHA/05	4		4			
4043		10001964	Porcine circovirus 1 strain 1/G	7		7			
4044		10001965	Avian leukosis virus strain NX0101	1		1			
4045		10001967	Avian leukosis virus isolate CAUHM01	1		1			
4046		10001973	Vaccinia virus Acambis 2000	8		8			
4047		10001975	Streptococcus salivarius JCM 5707	1		1			
4048		10001997	Chikungunya virus strain LR2006_OPY1 IMT/Reunion Island/2006	1		1			
4049		10001999	Reticuloendotheliosis virus strain HLJ07I	1		1			
4050		10002000	Porcine epidemic diarrhea virus CH/SHH/06	1		1			
4051		10002003	Campylobacter jejuni subsp. jejuni serotype HS:15	1		1			
4052		10002006	Bluetongue virus 16 BN96/16	2		2			
4053		10002007	Plasmodium falciparum isolate UAS22	4		4			
4054		10002008	Plasmodium falciparum isolate UAS31	1		1			
4055		10002009	Plasmodium falciparum isolate UAS29	2		2			
4056		10002010	Dengue virus 2 D2/SG/05K4155DK1/2005		49		49		
4057		10002011	Plasmodium falciparum R29/IT4	1		1			
4058		10002015	Human coxsackievirus A16 shzh05-1	92		92			
4059		10002018	Bovine coronavirus Kakegawa	1		1			
4060		10002020	Foot-and-mouth disease virus - type Asia 1 Nepal 29/97	4		4			
4061		10002022	Escherichia coli O6 O6:K15:H31		1		1		
4062		10002026	Murine norovirus 1 Mu/NoV/GV/MNV1/2002/USA		1		1		
4063		10002027	Bluetongue virus 16 Kumamoto/1985	2		2			
4064		10002028	Bluetongue virus 16 Beatrice Hill/1987	2		2			
4065		10002034	Fish	4		4			
4066		10002052	Toxoplasma gondii Gansu Jingtai	27		27			
4067		10002056	Enterovirus A71 TW/2086/98	1		1			
4068		10002069	Bordetella pertussis 509		7		7		
4069		10002079	Clostridium difficile VPI 10463	2		2			
4070		10002082	Rhesus rotavirus MMU 18006		3		3		
4071		10002089	Porcine reproductive and respiratory syndrome virus SY0608	17		17			
4072		10002090	Influenza A virus (A/swine/Denmark/101310-1/2011(H1N1))		7		7		
4073		10002111	Dengue virus 4 TVP-376	1		1			
4074		10002112	Dengue virus 4 1036	1		1			
4075	X	10002120	Human metapneumovirus A2 TN/94-49				7		7
4076		10002121	Staphylococcus aureus Reynolds	2		2			
4077		10002122	Staphylococcus aureus Becker	2		2			
4078		10002123	Peste-des-petits-ruminants virus China/Tibet/Geg/07-30	53		53			
4079		10002127	Escherichia coli O86:B7	1		1			
4080		10002129	Staphylococcus aureus RN4850	1		1			
4081	X	10002131	Foot-and-mouth disease virus A/HuBWH/CHA/2009			1		1	

4082		10002132	Duck hepatitis A virus 1 HP-1	2		2			
4083		10002144	Chikungunya virus CHIKV/SL/2006 SL15649		26		26		
4084		10002148	Dengue virus 4 Mexico/BC287/1997	1		1			
4085		10002151	Duck hepatitis A virus 1 LY0801	1		1			
4086		10002152	Duck hepatitis A virus 3 SD1201	1		1			
4087		10002161	Streptococcus pneumoniae type 1	5		5			
4088		10002165	Avian infectious bronchitis virus (strain CHINA/Sczy3/09)	2		2			
4089		10002169	Avian infectious bronchitis virus (strain Holte)		2		2		
4091	X	10002180	ZIKV/H. sapiens/China/SZ01/2016				40		40
4092		10002183	ZIKV/H. sapiens/French Polynesia/PF13/2013	4		4			
4093		10002188	ZIKV/H. sapiens/PRI/PRVABC59/2015		12		12		
4094		10002190	ZIKV/H. sapiens/Uganda/MR-766/1947	5	1	5	1		
4095		10002192	Streptococcus suis 1178027	2		2			
4097		10002196	Hepatitis E virus type 4 JAK-Sai	1		1			
4098		10002197	Chikungunya virus MY/08/065	15		15			
4100		10002238	Influenza A virus (A/swan/Poland/305-135V08/2006(H5N1))	1		1			
4101	X	10002244	Influenza A virus (A/Taiwan/2/2013(H6N1))			1		1	
4102	X	10002270	Foot-and-mouth disease virus O/Tibet/CHA/99			3		3	
4103		10002272	Streptococcus pneumoniae 7F	5		5			
4104		10002273	Influenza A virus (A/Hong Kong/4801/2014(H3N2))		1		1		
4105		10002285	Yellow fever virus CNYF01/2016	1		1			
4106		10002287	Salmonella enterica subsp. enterica serovar Typhi str. Quailes		1		1		
4107		10002289	Enterobacteria phage PRD1	2		2			
4108	X	10002301	ZIKV/H. sapiens/Suriname/Z1106033/2015			1		1	
4109		10002308	West Nile virus goshawk/Austria/2008		61		61		
4110		10002309	Andes orthohantavirus CHI-9717869	11		11			
4111		10002310	Canine Distemper Virus strain PS	2		2			
4112		10002313	Porcine epidemic diarrhea virus strain HeB/TS/2016/325b	1		1			
4113		10002314	Streptococcus pneumoniae type 10A	1		1			
4114		10002316	SARS-CoV1	179	507	10594	510	10415	3
4115		10002317	ZIKV/H. sapiens/Brazil/BEH823339/2015	1		1			
4116	X	10002321	Severe acute respiratory syndrome coronavirus 2 Wuhan/IVDC-HB-01/2019			2		2	
4117		10002329	Severe acute respiratory syndrome coronavirus 2 USA-WA1/2020		27	10	27	10	
4118	X	10002330	Severe acute respiratory syndrome coronavirus 2 Australia/VIC01/2020			4		4	
4119	X	10002332	Severe acute respiratory syndrome coronavirus 2 Victoria/01/2020				22		22
4120		10002337	Anogeissus	1		1			
4121		10002345	Influenza B virus (B/Phuket/3073/2013)	2		3		1	
4122	X	10002359	Influenza A virus (A/Serbia/NS-601/2014 (H1N1))			1		1	
4123	X	10002360	Influenza A virus (A/chicken/Anhui/BRI99/2016(H9N2))			1		1	
4124	X	10002361	Eastern equine encephalitis virus (strain FL93-939)			10		10	
4125	X	10002365	Nipah henipavirus strain NiV Malaysia			2		2	

4126	X	10002370	Severe acute respiratory syndrome coronavirus 2 Wuhan/Hu-1/2019			57	33	57	33
4127	X	10002371	Dengue virus 2 East Timor/ET300/2000			1		1	
4128	X	10002377	Mus musculus PWK/Ph			1		1	
4129	X	10002380	Severe acute respiratory syndrome coronavirus 2 ITA/INMI1/2020			4		4	
4130	X	10002384	Influenza A virus (A/Switzerland/9715293/2013(H3N2))			3		3	
4131	X	10002394	Severe acute respiratory syndrome coronavirus 2 England/MIG457/2020			3		3	
4133	X	10002407	Foot-and-mouth disease virus O/HN/CHA/93			9		9	
4134	X	10002408	Foot-and-mouth disease virus A/GDMM/CHA/2013			2		2	
4135	X	10002414	Avian leukosis virus strain HB2018003			1		1	
4137	X	10002422	Bordetella pertussis 186			2		2	
4139	X	10002442	Severe acute respiratory syndrome coronavirus 2 DEU/Vero E6 cells/2021			8		8	
4140	X	10002444	Porcine reproductive and respiratory syndrome virus JXA1-R			6		6	
4141	X	10002450	African swine fever virus pig/China/HLJ/18			5		5	
4143	X	10002484	Porcine astrovirus 1 Guangxi/Nanning/PAstV-1/2013			2		2	

2 Website Features

In 2021, the IEDB continued the agile, continuous deployment methodology, whereby weekly, iterative updates were deployed to the IEDB external website (4.3). Changes of note include:

- Completed and deployed Filter Options assay filters on Results page which allow limiting size of filter fields based on Assay Type.
- Retired Advanced Epitope and Assay Searches from Specialized Searches menu as most important data can now be accessed via homepage searches.
- Retired EpiFilter feature from CSV export menu as this functionality has been mostly integrated into new Filter Options.
- Completed the first release of API Postgres table structure and PostgREST interface and released the beta version on production in June 2021.
- Updated ImmunomeBrowser to handle guides for mutant SARS-CoV-2 variants and updated the legend to explain the variant guidelines. Updated amcharts version for ImmunomeBrowser.
- Developed new Excel exports with dynamically selectable columns (pending future release).
- Added Reference Type and Journal, removed Article Abstract from Reference tab to speed up searches. Also replaced Article Abstract with Journal in all API tables.
- Updated full B cell export on Database Export page to include a multi-file zip to get around Excel size limits.
- Updated the red homepage banner to show the new locally hosted COVID myocarditis paper.
- Added a 3D viewer option in the ImmunomeBrowser for the SARS-CoV-2 spike glycoprotein antigen and included the latest omicron variant data.

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

In addition, there were two major releases (Releases 2.25 and 2.26) of the Analysis Resource since the 2020 Annual Compendium plus numerous smaller updates made throughout the year. Changes of note include:

- NEW: TCRMatch tool added for prediction of TCR specificity based on sequence similarity to TCRs with known specificity
- Deimmunization tool stability updates
- NEW: AxelF tool to enhance MHC-peptide binding predictions using expression data
- TCRMatch updated to version 1.0.2 with a significant speed increase
- Immunomebrowser chart download enabled
- Log4j vulnerabilities patched
- Additional bug fixes and performance improvements

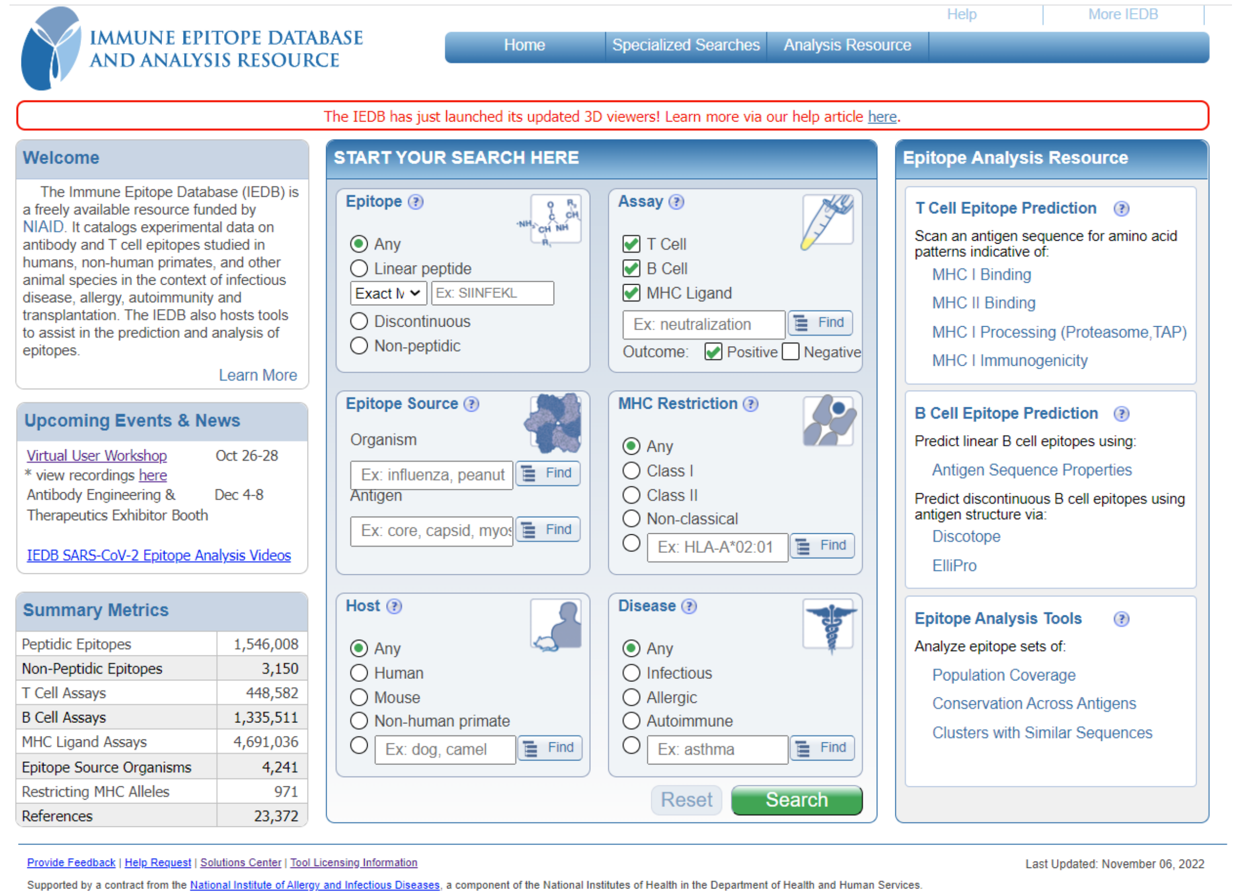
The IEDB website functionality can be divided into five categories – Home Page (Section 2.1), Specialized Searches (Section 2.2.2) however this was retired in 2021, Analysis Resource (Section 2.3), Help (Section 2.4), and More IEDB (Section 2.5), which largely correspond to the pull-down menus at the 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 (as shown in Figure 2.10) 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 IEDB has just launched its updated 3D viewers! Learn more via our help article here.

Welcome

The Immune Epitope Database (IEDB) is a freely available resource funded by NIAID. It catalogs experimental data on antibody and T cell epitopes studied in humans, non-human primates, and other animal species in the context of infectious disease, allergy, autoimmunity and transplantation. The IEDB also hosts tools to assist in the prediction and analysis of epitopes.

Upcoming Events & News

Virtual User Workshop * view recordings here	Oct 26-28
Antibody Engineering & Therapeutics Exhibitor Booth	Dec 4-8

IEDB SARS-CoV-2 Epitope Analysis Videos

Summary Metrics

Peptidic Epitopes	1,546,008
Non-Peptidic Epitopes	3,150
T Cell Assays	448,582
B Cell Assays	1,335,511
MHC Ligand Assays	4,691,036
Epitope Source Organisms	4,241
Restricting MHC Alleles	971
References	23,372

Scan an antigen sequence for amino acid patterns indicative of:

Predict linear B cell epitopes using:

Predict discontinuous B cell epitopes using antigen structure via:

Analyze epitope sets of:

Last Updated: November 06, 2022

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

Figure 2.10 IEDB 4.3 Home page

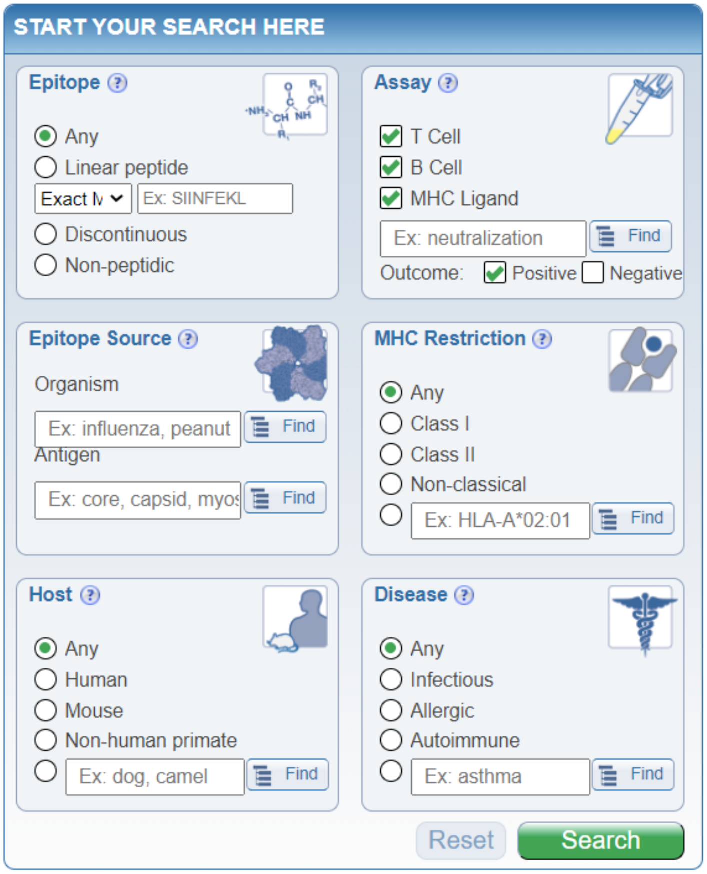
2.2 Query

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 could previousl be accessed on the Search pull-down menu and consisted 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, however most of these features were retired in 2021 due to low usability. Now only “Identifier Search” and “Browse by 3D Structure” can be accessed from the Specialized Searches menu.

2.2.1 Perform a Home Page Search

The home page search feature available in the center of the home page (Figure 2.11) is designed to simplify the search process for many commonly asked queries by immunologists. It is the most frequently used query mode. The approach it takes is analogous to many travel and shopping websites. IEDB users can start their search by specifying a number of fundamental and common search parameters on the home page. On the subsequent results page, users can then apply additional and more specific filters. The epitope structure choices include linear epitopes, discontinuous epitopes, and non-peptidic epitopes. For the linear epitope search, the user can prescribe the type of search desired - an exact match to the entered sequence, a substring search (described below), or a homologous peptide sequence at identity levels of 70%, 80%, or 90% as determined by BLAST. The IEDB categorizes all assays as T cell, B cell, or MHC ligand. The MHC ligand includes binding and elution assays. Users can also select the MHC restriction for non-B cell searches. Finally, users can select the host species and the disease.

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



START YOUR SEARCH HERE

Epitope
● Any
○ Linear peptide
Exact M | Ex: SIINFEKL
○ Discontinuous
○ Non-peptidic

Assay
☑ T Cell
☑ B Cell
☑ MHC Ligand
Ex: neutralization | Find
Outcome: ☑ Positive ☐ Negative

Epitope Source
Organism
Ex: influenza, peanut | Find
Antigen
Ex: core, capsid, myos | Find

MHC Restriction
● Any
○ Class I
○ Class II
○ Non-classical
○ Ex: HLA-A*02:01 | Find

Host
● Any
○ Human
○ Mouse
○ Non-human primate
○ Ex: dog, camel | Find

Disease
● Any
○ Infectious
○ Allergic
○ Autoimmune
○ Ex: asthma | Find

Reset Search

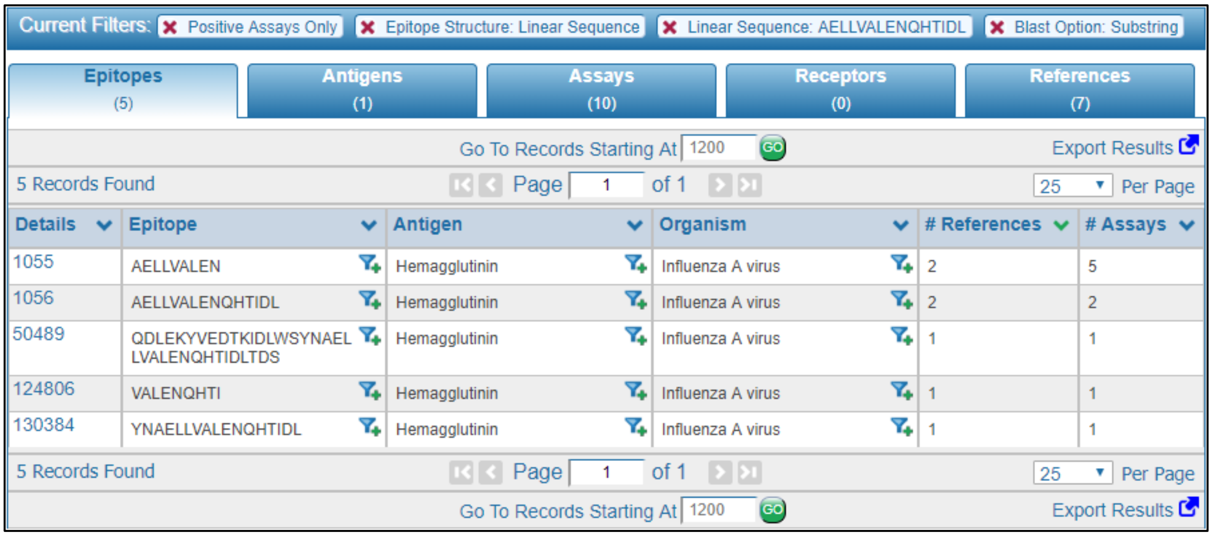
Figure 2.11 Home page simple search

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

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

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

In addition to finding peptides in the database that contain the specified amino acid sequence, the substring search also finds epitopes within the input sequence itself. For example, when the sequence AELLVALENQHTIDL is submitted for a substring search, the query results, shown in Figure 2.12, yields five peptide sequences. Three of them (the second, third, and fifth) contain the input sequence. The two others (the first and fourth) are substrings of the input sequence that are also epitopes contained in the IEDB.

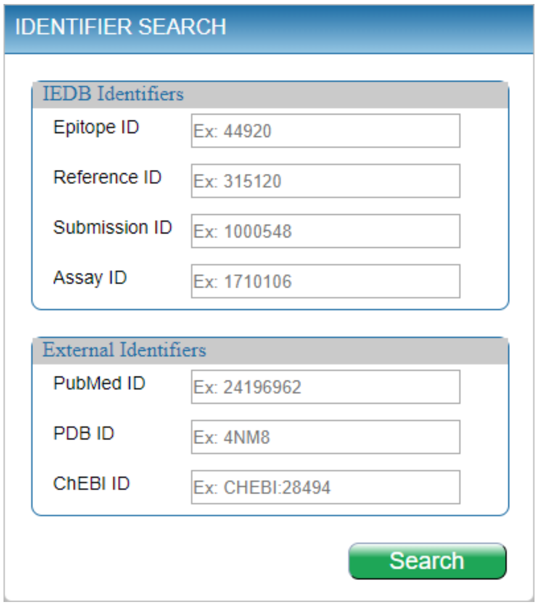


Details	Epitope	Antigen	Organism	# References	# Assays
1055	AELLVALEN	Hemagglutinin	Influenza A virus	2	5
1056	AELLVALENQHTIDL	Hemagglutinin	Influenza A virus	2	2
50489	QDLEKYVEDTKIDLWSYNAEL LVALENQHTIDLTDS	Hemagglutinin	Influenza A virus	1	1
124806	VALENQHTI	Hemagglutinin	Influenza A virus	1	1
130384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

Figure 2.12 Query results for a substring search performed on the input sequence AELLVALENQHTIDL

2.2.2 Specialized Searches

The Specialized Searches feature was largely retired in 2021 due to underutilization by the scientific community and high cost of maintenance. As a result, this section has been downscaled in the Annual Compendium. The two remaining features of the Specialized Searches includes the Identifier Search shown in Figure 2.13. 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.



IDENTIFIER SEARCH

IEDB Identifiers

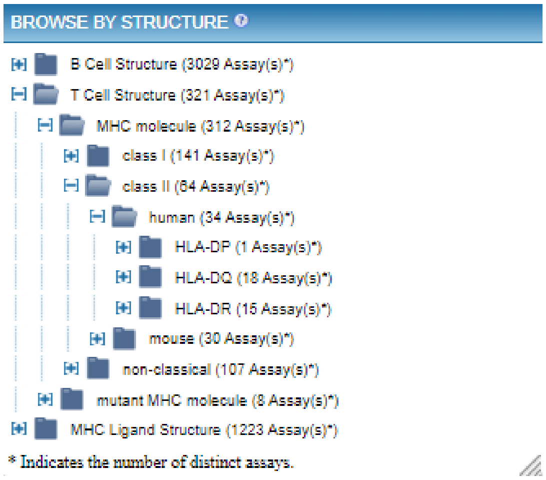
Epitope ID: Ex: 44920
Reference ID: Ex: 315120
Submission ID: Ex: 1000548
Assay ID: Ex: 1710106

External Identifiers

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

Figure 2.13 Identifier Search input screen

The Browse by 3D Structure selection screen in shown in Figure 2.14. Users can select 3D structure of interest to them based on available structures within the database.



BROWSE BY STRUCTURE

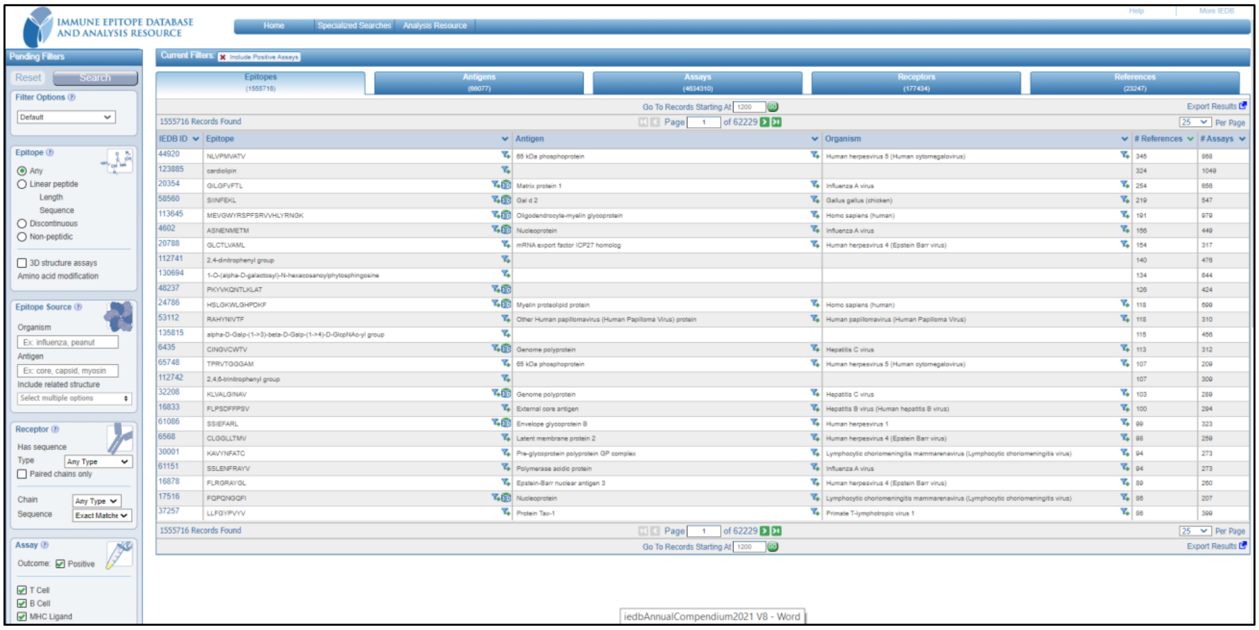
- B Cell Structure (3029 Assay(s)*)
- T Cell Structure (321 Assay(s)*)
  - MHC molecule (312 Assay(s)*)
    - class I (141 Assay(s)*)
    - class II (64 Assay(s)*)
      - human (34 Assay(s)*)
        - HLA-DP (1 Assay(s)*)
        - HLA-DQ (18 Assay(s)*)
        - HLA-DR (15 Assay(s)*)
      - mouse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

* Indicates the number of distinct assays.

Figure 2.14 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 2.15. The search criteria are listed in the Current Filters section above the results table. There are five tabs for the results. Figure 2.15 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 2.16. The bottom section of the figure contains links to relevant tools in the Analysis Resource. The user can also refine the search results by clicking on the filter icon in the epitope, antigen, and organism fields.

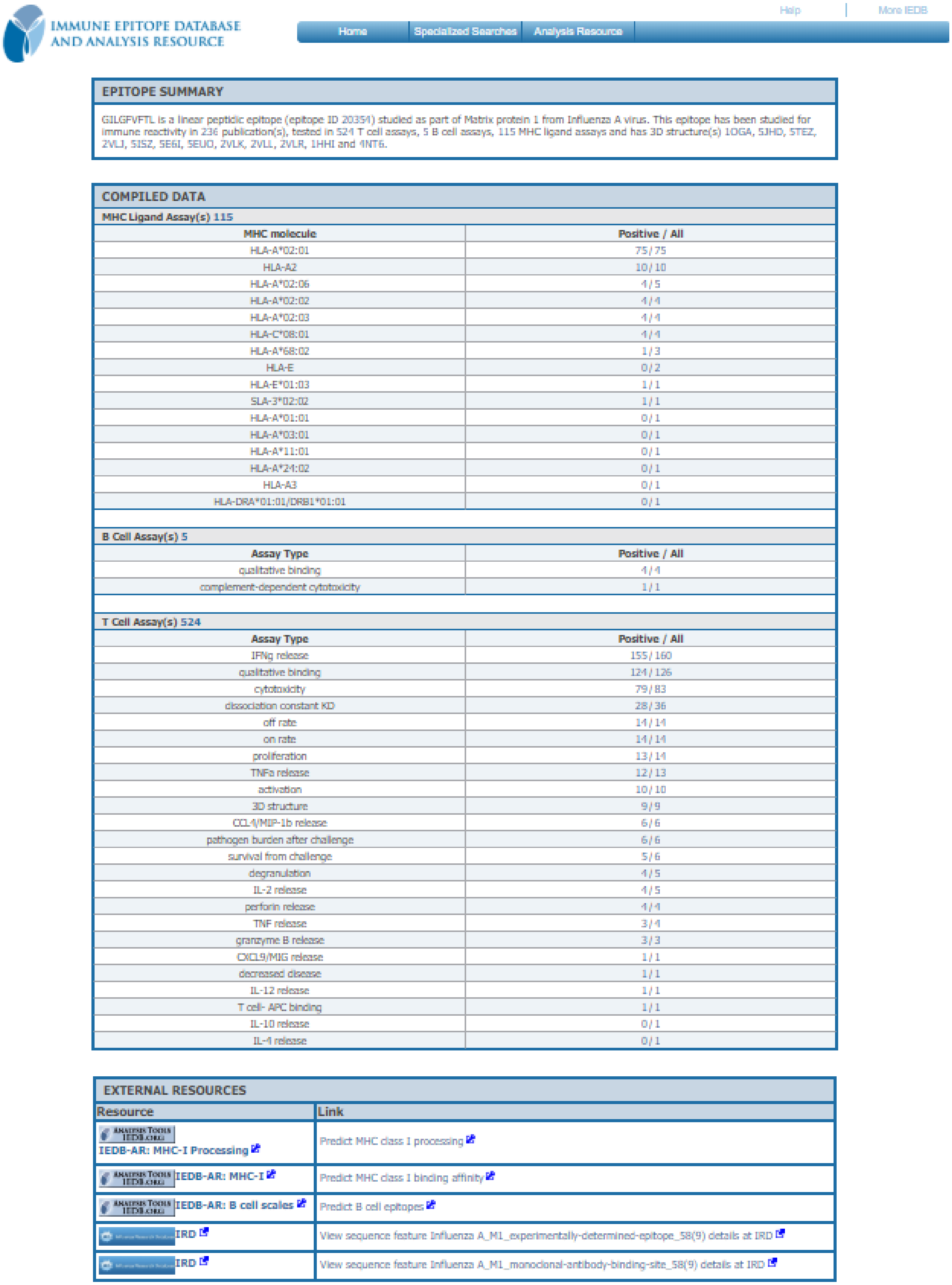


1555716 Records Found

IEDB ID	Epitope	Antigen	Organism	# References	# Assays
44920	NLVPMVATV	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	345	868
123885	cardiolipin			324	1049
20354	GILGFVFTL	Matrix protein 1	Influenza A virus	254	656
58560	SIINFEKL	Gal d 2	Gallus gallus (chicken)	219	547
113645	MEVGWYRSPFSRVVHLYRNGK	Oligodendrocyte-myelin glycoprotein	Homo sapiens (human)	191	979
4602	ASNENMETM	Nucleoprotein	Influenza A virus	156	449
20788	GLCTLVAML	mRNA export factor ICP27 homolog	Human herpesvirus 4 (Epstein Barr virus)	154	317
112741	2,4-dinitrophenyl group			140	476
130694	1-O-(alpha-D-galactosyl)-N-hexacosanoylphytosphingosine			134	644
48237	PKYVKQNTLKLAT			126	424
24786	HSLGKWLGHPDKF	Myelin proteolipid protein	Homo sapiens (human)	118	699
53112	RAHYNIVTF	Other Human papillomavirus (Human Papilloma Virus) protein	Human papillomavirus (Human Papilloma Virus)	118	310
135815	alpha-D-Galp-(1->3)-beta-D-Galp-(1->4)-D-GlcpNAc-yl group			115	456
6435	CINGVCWTV	Genome polyprotein	Hepatitis C virus	113	312
65748	TPRVTGGGAM	65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	107	209
112742	2,4,6-trinitrophenyl group			107	309
32208	KLVALGINAV	Genome polyprotein	Hepatitis C virus	103	289
16833	FLPSDFFPSV	External core antigen	Hepatitis B virus (Human hepatitis B virus)	100	294
61086	SSIEFARL	Envelope glycoprotein B	Human herpesvirus 1	99	323
6568	CLGGLLTMV	Latent membrane protein 2	Human herpesvirus 4 (Epstein Barr virus)	98	259
30001	KAVYNFATC	Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus (Lymphocytic choriomeningitis virus)	94	273
61151	SSLENFRAYV	Polymerase acidic protein	Influenza A virus	94	273
16878	FLRGRAYGL	Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	89	260
17516	FQPQNGQFI	Nucleoprotein	Lymphocytic choriomeningitis mammarenavirus (Lymphocytic choriomeningitis virus)	86	207
37257	LLFGYPVYV	Protein Tax-1	Primate T-lymphotropic virus 1	86	399

1555716 Records Found

Figure 2.15 The Epitope tab of the search results page



EPITOPE SUMMARY

GILGFVFTL 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 236 publication(s), tested in 524 T cell assays, 5 B cell assays, 115 MHC ligand assays and has 3D structure(s) 1OGA, 5JHD, 5TEZ, 2VLJ, 5ISZ, 5E6I, 5EUO, 2VLK, 2VLL, 2VLR, 1HHI and 4NT6.

COMPILED DATA

MHC Ligand Assay(s) 115

MHC molecule	Positive / All
HLA-A*02:01	75 / 75
HLA-A2	10 / 10
HLA-A*02:06	4 / 5
HLA-A*02:02	4 / 4
HLA-A*02:03	4 / 4
HLA-C*08:01	4 / 4
HLA-A*68:02	1 / 3
HLA-E	0 / 2
HLA-E*01:03	1 / 1
SLA-3*02:02	1 / 1
HLA-A*01:01	0 / 1
HLA-A*03:01	0 / 1
HLA-A*11:01	0 / 1
HLA-A*24:02	0 / 1
HLA-A3	0 / 1
HLA-DRA*01:01/DRB1*01:01	0 / 1

B Cell Assay(s) 5

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

T Cell Assay(s) 524

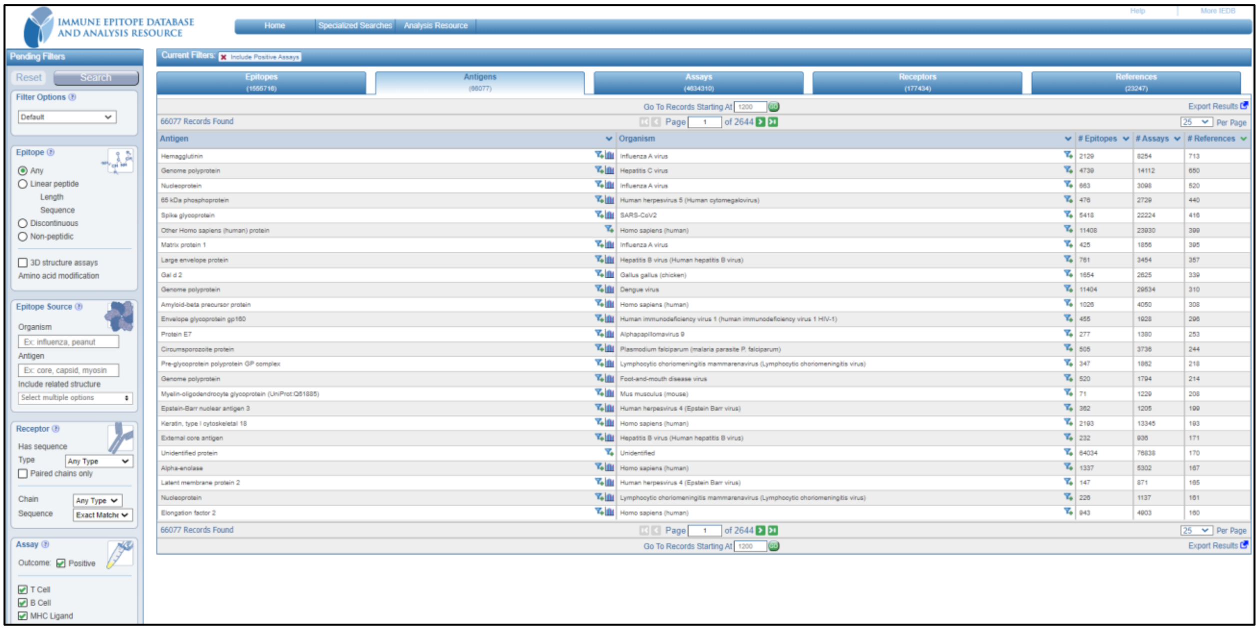
Assay Type	Positive / All
IFNg release	155 / 160
qualitative binding	124 / 126
cytotoxicity	79 / 83
dissociation constant KD	28 / 36
off rate	14 / 14
on rate	14 / 14
proliferation	13 / 14
TNFa release	12 / 13
activation	10 / 10
3D structure	9 / 9
CCL4/MIP-1b release	6 / 6
pathogen burden after challenge	6 / 6
survival from challenge	5 / 6
degranulation	4 / 5
IL-2 release	4 / 5
perforin release	4 / 4
TNF release	3 / 4
granzyme B release	3 / 3
CXCL9/MIG release	1 / 1
decreased disease	1 / 1
IL-12 release	1 / 1
T cell- APC binding	1 / 1
IL-10 release	0 / 1
IL-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 2.16 An example of the epitope detail page

The second tab on the results page is the Antigens tab (Figure 2.17). 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 2.18.

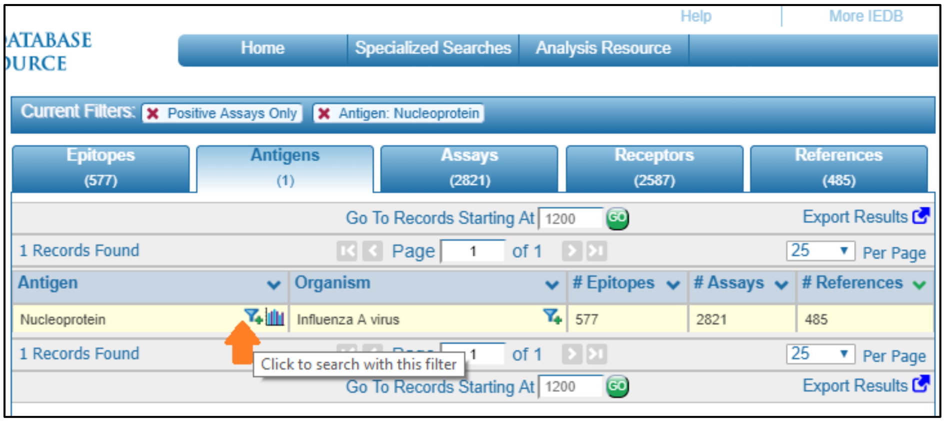


66077 Records Found

Antigen	Organism	# Epitopes	# Assays	# References
Hemagglutinin	Influenza A virus	2129	8254	713
Genome polyprotein	Hepatitis C virus	4739	14112	650
Nucleoprotein	Influenza A virus	663	3098	520
65 kDa phosphoprotein	Human herpesvirus 5 (Human cytomegalovirus)	476	2729	440
Spike glycoprotein	SARS-CoV2	5418	22224	416
Other Homo sapiens (human) protein	Homo sapiens (human)	11408	23930	399
Matrix protein 1	Influenza A virus	425	1856	395
Large envelope protein	Hepatitis B virus (Human hepatitis B virus)	761	3454	357
Gal d 2	Gallus gallus (chicken)	1654	2625	339
Genome polyprotein	Dengue virus	11404	29534	310
Amyloid-beta precursor protein	Homo sapiens (human)	1026	4050	308
Envelope glycoprotein gp160	Human immunodeficiency virus 1 (human immunodeficiency virus 1 HIV-1)	455	1928	296
Protein E7	Alphapapillomavirus 9	277	1380	253
Circumsporozoite protein	Plasmodium falciparum (malaria parasite P. falciparum)	505	3736	244
Pre-glycoprotein polyprotein GP complex	Lymphocytic choriomeningitis mammarenavirus (Lymphocytic choriomeningitis virus)	347	1862	218
Genome polyprotein	Foot-and-mouth disease virus	520	1794	214
Myelin-oligodendrocyte glycoprotein (UniProt:Q61885)	Mus musculus (mouse)	71	1229	208
Epstein-Barr nuclear antigen 3	Human herpesvirus 4 (Epstein Barr virus)	362	1205	199
Keratin, type I cytoskeletal 18	Homo sapiens (human)	2193	13345	193
External core antigen	Hepatitis B virus (Human hepatitis B virus)	232	936	171
Unidentified protein	Unidentified	64034	76838	170
Alpha-enolase	Homo sapiens (human)	1337	5302	167
Latent membrane protein 2	Human herpesvirus 4 (Epstein Barr virus)	147	871	165
Nucleoprotein	Lymphocytic choriomeningitis mammarenavirus (Lymphocytic choriomeningitis virus)	226	1137	161
Elongation factor 2	Homo sapiens (human)	943	4903	160

66077 Records Found

Figure 2.17 The Antigens tab of the search results page



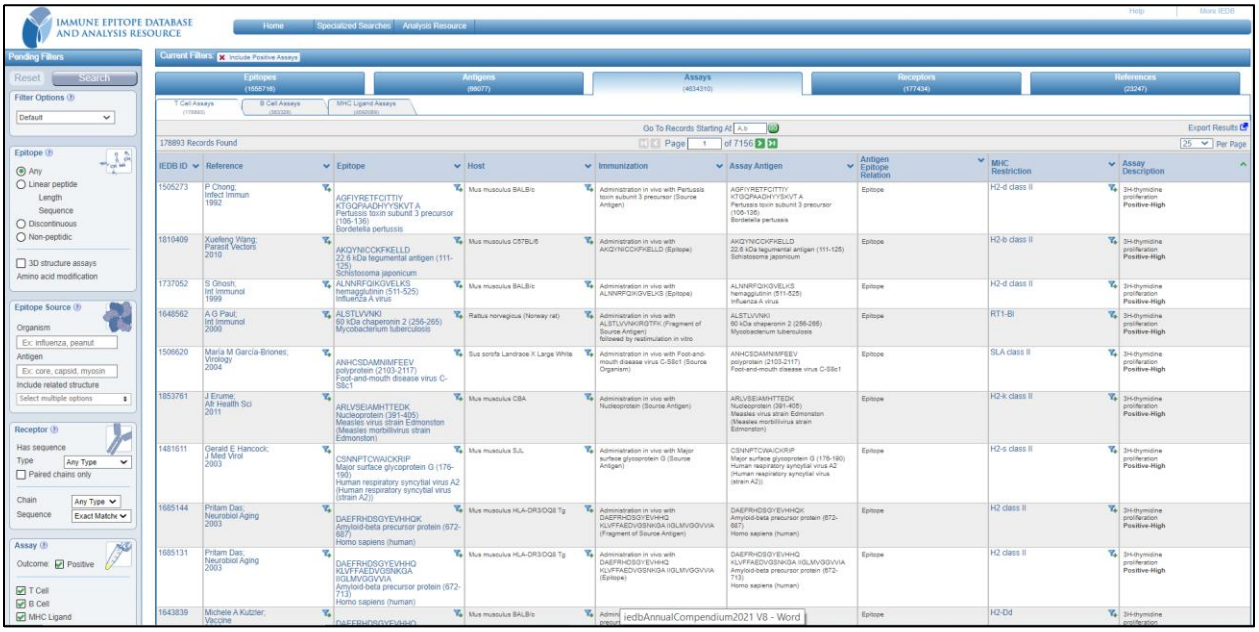
1 Records Found

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

1 Records Found

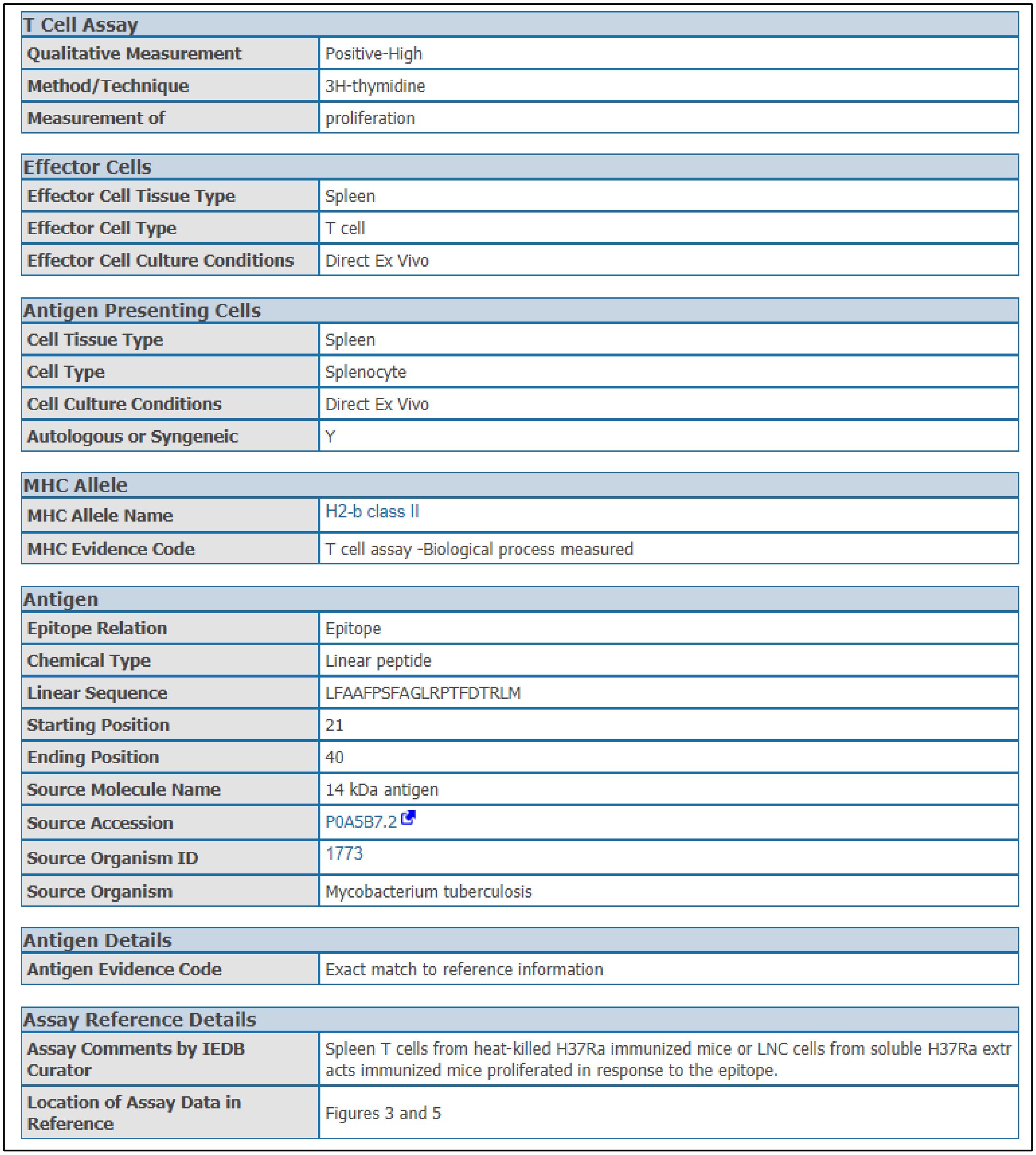
Figure 2.18 The Results filtered by the Nucleoprotein of the Influenza A virus. This was achieved by clicking on the filter icon in the antigen column. The content of the other tabs contain data specific to this antigen.

The third tab on the results page is the Assays tab (Figure 2.19). 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 2.20. 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.



IEDB ID	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	MHC Restriction	Assay Description
1505273	P Chong; Infect Immun 1992	AGFIYRETFCITTIY KTGQPAADHYYSKVT A Pertussis toxin subunit 3 precursor (106-136) Bordetella pertussis	Mus musculus BALB/c	Administration in vivo with Pertussis toxin subunit 3 precursor (Source Antigen)	AGFIYRETFCITTIY KTGQPAADHYYSKVT A Pertussis toxin subunit 3 precursor (106-136) Bordetella pertussis	Epitope	H2-d class II	3H-thymidine proliferation **Positive-High**
1810409	Xuefeng Wang; Parasit Vectors 2010	AKQYNICCKFKELLD 22.6 kDa tegumental antigen (111-125) Schistosoma japonicum	Mus musculus C57BL/6	Administration in vivo with AKQYNICCKFKELLD (Epitope)	AKQYNICCKFKELLD 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	ALNNRFQIKGVELKS hemagglutinin (511-525) Influenza A virus	Mus musculus BALB/c	Administration in vivo with ALNNRFQIKGVELKS (Epitope)	ALNNRFQIKGVELKS hemagglutinin (511-525) Influenza A virus	Epitope	H2-d class II	3H-thymidine proliferation **Positive-High**
1648562	A G Paul; Int Immunol 2000	ALSTLVVNKI 60 kDa chaperonin 2 (256-265) Mycobacterium tuberculosis	Rattus norvegicus (Norway rat)	Administration in vivo with ALSTLVVNKIRGTFK (Fragment of Source Antigen) followed by restimulation in vitro	ALSTLVVNKI 60 kDa chaperonin 2 (256-265) Mycobacterium tuberculosis	Epitope	RT1-Bl	3H-thymidine proliferation **Positive-High**
1506620	María M García-Briones; Virology 2004	ANHCSDAMNIMFEEV polyprotein (2103-2117) Foot-and-mouth disease virus C-S8c1	Sus scrofa Landrace X Large White	Administration in vivo with Foot-and-mouth disease virus C-S8c1 (Source Organism)	ANHCSDAMNIMFEEV polyprotein (2103-2117) Foot-and-mouth disease virus C-S8c1	Epitope	SLA class II	3H-thymidine proliferation **Positive-High**
1853761	J Erume; Afr Health Sci 2011	ARLVSEIAMHTTEDK Nucleoprotein (391-405) Measles virus strain Edmonston (Measles morbillivirus strain Edmonston)	Mus musculus CBA	Administration in vivo with Nucleoprotein (Source Antigen)	ARLVSEIAMHTTEDK Nucleoprotein (391-405) Measles virus strain Edmonston (Measles morbillivirus strain Edmonston)	Epitope	H2-k class II	3H-thymidine proliferation **Positive-High**
1481611	Gerald E Hancock; J Med Virol 2003	CSNNPTCWAICKRIP Major surface glycoprotein G (176-190) Human respiratory syncytial virus A2 (Human respiratory syncytial virus (strain A2))	Mus musculus SJL	Administration in vivo with Major surface glycoprotein G (Source Antigen)	CSNNPTCWAICKRIP Major surface glycoprotein G (176-190) Human respiratory syncytial virus A2 (Human respiratory syncytial virus (strain A2))	Epitope	H2-s class II	3H-thymidine proliferation **Positive-High**
1685144	Pritam Das; Neurobiol Aging 2003	DAEFRHDSGYEVHHQK Amyloid-beta precursor protein (672-687) Homo sapiens (human)	Mus musculus HLA-DR3/DQ8 Tg	Administration in vivo with DAEFRHDSGYEVHHQ KLVFFAEDVGSNKGA IIGLMVGGVVIA (Fragment of Source Antigen)	DAEFRHDSGYEVHHQK Amyloid-beta precursor protein (672-687) Homo sapiens (human)	Epitope	H2 class II	3H-thymidine proliferation **Positive-High**
1685131	Pritam Das; Neurobiol Aging 2003	DAEFRHDSGYEVHHQ KLVFFAEDVGSNKGA IIGLMVGGVVIA Amyloid-beta precursor protein (672-713) Homo sapiens (human)	Mus musculus HLA-DR3/DQ8 Tg	Administration in vivo with DAEFRHDSGYEVHHQ KLVFFAEDVGSNKGA IIGLMVGGVVIA (Epitope)	DAEFRHDSGYEVHHQ KLVFFAEDVGSNKGA IIGLMVGGVVIA Amyloid-beta precursor protein (672-713) Homo sapiens (human)	Epitope	H2 class II	3H-thymidine proliferation **Positive-High**
1643839	Michele A Kutzler; Vaccine	DAEFRHDSGYEVHHQ	Mus musculus BALB/c	Admini		Epitope	H2-Dd	3H-thymidine proliferation

Figure 2.19 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

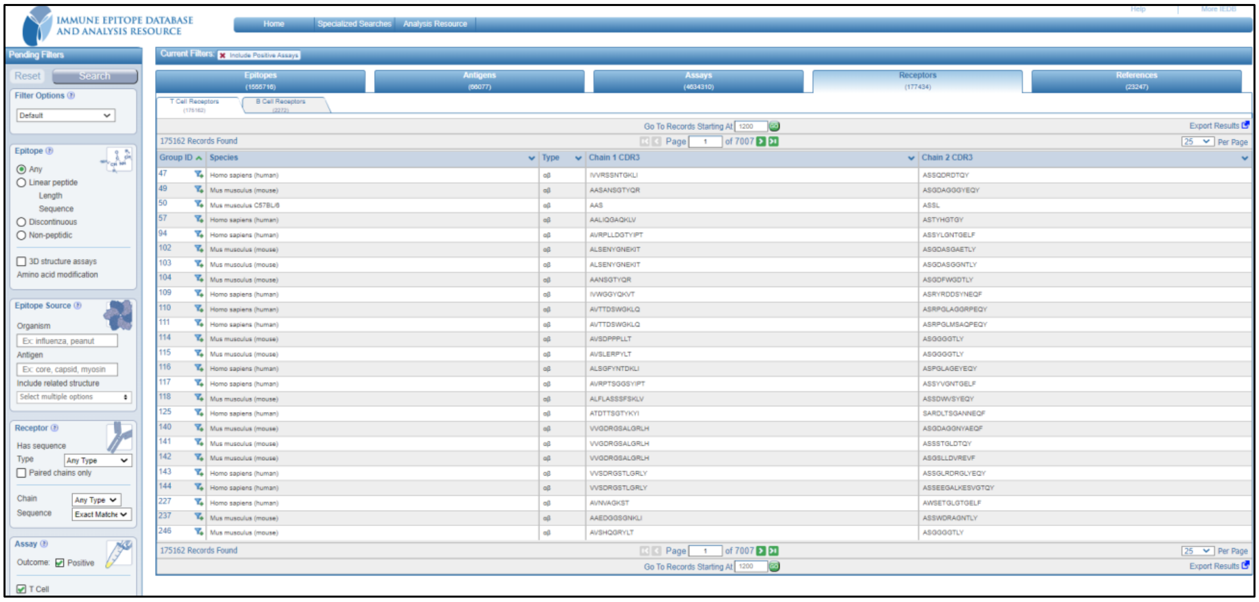
Antigen	
Epitope Relation	Epitope
Chemical Type	Linear peptide
Linear Sequence	LFAAFPSFAGLRPTFDTRLM
Starting Position	21
Ending Position	40
Source Molecule Name	14 kDa antigen
Source Accession	P0A5B7.2
Source Organism ID	1773
Source Organism	Mycobacterium tuberculosis

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

The fourth tab on the results page is the Receptors tab (Figure 2.21). 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.



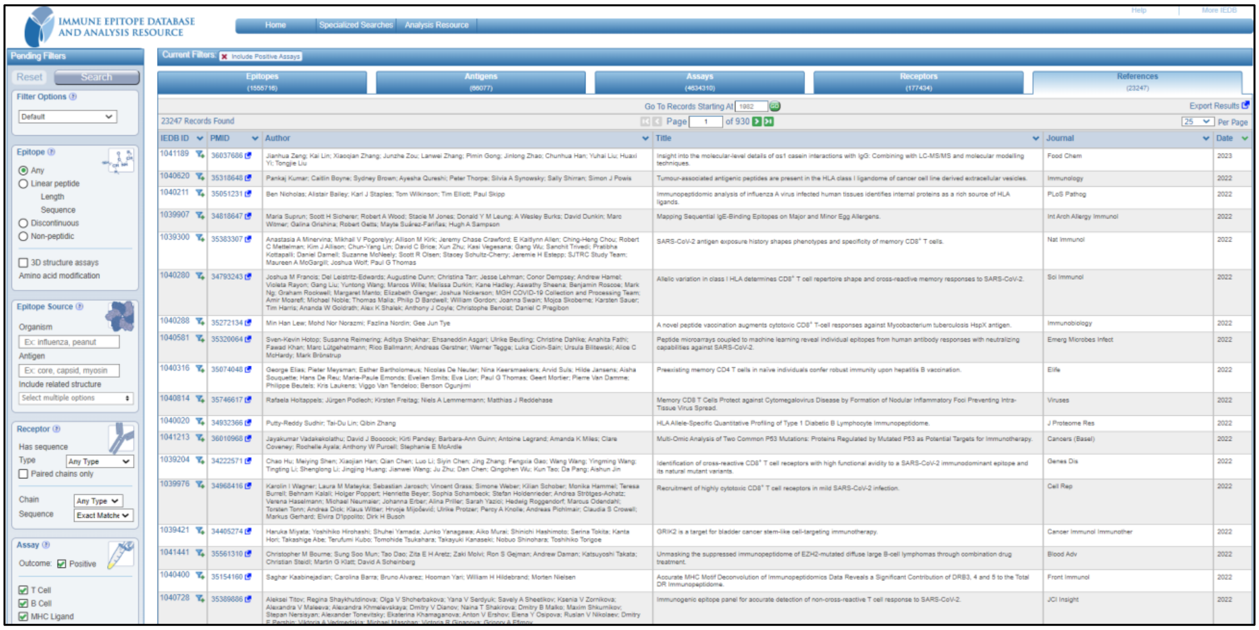
175162 Records Found

Group ID	Species	Type	Chain 1 CDR3	Chain 2 CDR3
47	Homo sapiens (human)	αβ	IVVRSSNTGKLI	ASSQDRDTQY
49	Mus musculus (mouse)	αβ	AASANSGTYQR	ASGDAGGGYEQY
50	Mus musculus C57BL/6	αβ	AAS	ASSL
57	Homo sapiens (human)	αβ	AALIQGAQKLV	ASTYHGTGY
94	Homo sapiens (human)	αβ	AVRPLLDGTYIPT	ASSYLGNTGELF
102	Mus musculus (mouse)	αβ	ALSENYGNEKIT	ASGDASGAETLY
103	Mus musculus (mouse)	αβ	ALSENYGNEKIT	ASGDASGGNTLY
104	Mus musculus (mouse)	αβ	AANSGTYQR	ASGDFWGDTLY
109	Homo sapiens (human)	αβ	IVWGGYQKVT	ASRYRDDSYNEQF
110	Homo sapiens (human)	αβ	AVTTDSWGKLQ	ASRPGLAGGRPEQY
111	Homo sapiens (human)	αβ	AVTTDSWGKLQ	ASRPGLMSAQPEQY
114	Mus musculus (mouse)	αβ	AVSDPPPLLT	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	ALFLASSSFSKLV	ASSDWVSYEQY
125	Homo sapiens (human)	αβ	ATDTTSGTYKYI	SARDLTSGANNEQF
140	Mus musculus (mouse)	αβ	VVGDRGSALGRLH	ASGDAGGNYAEQF
141	Mus musculus (mouse)	αβ	VVGDRGSALGRLH	ASSSTGLDTQY
142	Mus musculus (mouse)	αβ	VVGDRGSALGRLH	ASGSLLDVREVF
143	Homo sapiens (human)	αβ	VVSDRGSTLGRLY	ASSGLRDRGLYEQY
144	Homo sapiens (human)	αβ	VVSDRGSTLGRLY	ASSEEGALKESVGTQY
227	Homo sapiens (human)	αβ	AVNVAGKST	AWSETGLGTGELF
237	Mus musculus (mouse)	αβ	AAEDGGSGNKLI	ASSWDRAGNTLY
246	Mus musculus (mouse)	αβ	AVSHQGRYLT	ASGGGGTLY

175162 Records Found

Figure 2.21 The Receptors tab of the search results page

The fifth tab on the results page is the References tab (Figure 2.22). 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 (Figure 2.23).



23247 Records Found

IEDB ID	PMID	Author	Title	Journal	Date
1041189	36037686	Jianhua Zeng; Kai Lin; Xiaoqian Zhang; Junzhe Zou; Lanwei Zhang; Pimin Gong; Jinlong Zhao; Chunhua Han; Yuhai Liu; Huaxi Yi; Tongjie Liu	Insight into the molecular-level details of αs1 casein interactions with IgG: Combining with LC-MS/MS and molecular modelling techniques.	Food Chem	2023
1040620	35318648	Pankaj Kumar; Caitlin Boyne; Sydney Brown; Ayesha Qureshi; Peter Thorpe; Silvia A Synowsky; Sally Shirran; Simon J Powis	Tumour-associated antigenic peptides are present in the HLA class I ligandome of cancer cell line derived extracellular vesicles.	Immunology	2022
1040211	35051231	Ben Nicholas; Alistair Bailey; Karl J Staples; Tom Wilkinson; Tim Elliott; Paul Skipp	Immunopeptidomic analysis of influenza A virus infected human tissues identifies internal proteins as a rich source of HLA ligands.	PLoS Pathog	2022
1039907	34818647	Maria Suprun; Scott H Sicherer; Robert A Wood; Stacie M Jones; Donald Y M Leung; A Wesley Burks; David Dunkin; Marc Witmer; Galina Grishina; Robert Getts; Mayte Suárez-Fariñas; Hugh A Sampson	Mapping Sequential IgE-Binding Epitopes on Major and Minor Egg Allergens.	Int Arch Allergy Immunol	2022
1039300	35383307	Anastasia A Minervina; Mikhail V Pogorelyy; Allison M Kirk; Jeremy Chase Crawford; E Kaitlynn Allen; Ching-Heng Chou; Robert C Mettelman; Kim J Allison; Chun-Yang Lin; David C Brice; Xun Zhu; Kasi Vegesana; Gang Wu; Sanchit Trivedi; Pratibha Kottapalli; Daniel Darnell; Suzanne McNeely; Scott R Olsen; Stacey Schultz-Cherry; Jeremie H Estepp; SJTRC Study Team; Maureen A McGargill; Joshua Wolf; Paul G Thomas	SARS-CoV-2 antigen exposure history shapes phenotypes and specificity of memory CD8$^+$ T cells.	Nat Immunol	2022
1040280	34793243	Joshua M Francis; Del Leistritz-Edwards; Augustine Dunn; Christina Tarr; Jesse Lehman; Conor Dempsey; Andrew Hamel; Violeta Rayon; Gang Liu; Yuntong Wang; Marcos Wille; Melissa Durkin; Kane Hadley; Aswathy Sheena; Benjamin Roscoe; Mark Ng; Graham Rockwell; Margaret Manto; Elizabeth Gienger; Joshua Nickerson; MGH COVID-19 Collection and Processing Team; Amir Moarefi; Michael Noble; Thomas Malia; Philip D Bardwell; William Gordon; Joanna Swain; Mojca Skoberne; Karsten Sauer; Tim Harris; Ananda W Goldrath; Alex K Shalek; Anthony J Coyle; Christophe Benoist; Daniel C Pregibon	Allelic variation in class I HLA determines CD8$^+$ T cell repertoire shape and cross-reactive memory responses to SARS-CoV-2.	Sci Immunol	2022
1040288	35272134	Min Han Lew; Mohd Nor Norazmi; Fazlina Nordin; Gee Jun Tye	A novel peptide vaccination augments cytotoxic CD8$^+$ T-cell responses against Mycobacterium tuberculosis HspX antigen.	Immunobiology	2022
1040581	35320064	Sven-Kevin Hotop; Susanne Reimering; Aditya Shekhar; Ehsaneddin Asgari; Ulrike Beutling; Christine Dahlke; Anahita Fathi; Fawad Khan; Marc Lütgehetmann; Rico Ballmann; Andreas Gerstner; Werner Tegge; Luka Cicin-Sain; Ursula Bilitewski; Alice C McHardy; Mark Brönstrup	Peptide microarrays coupled to machine learning reveal individual epitopes from human antibody responses with neutralizing capabilities against SARS-CoV-2.	Emerg Microbes Infect	2022
1040316	35074048	George Elias; Pieter Meysman; Esther Bartholomeus; Nicolas De Neuter; Nina Keersmaekers; Arvid Suls; Hilde Jansens; Aisha Souquette; Hans De Reu; Marie-Paule Emonds; Evelien Smits; Eva Lion; Paul G Thomas; Geert Mortier; Pierre Van Damme; Philippe Beutels; Kris Laukens; Viggo Van Tendeloo; Benson Ogunjimi	Preexisting memory CD4 T cells in naïve individuals confer robust immunity upon hepatitis B vaccination.	Elife	2022
1040814	35746617	Rafaela Holtappels; Jürgen Podlech; Kirsten Freitag; Niels A Lemmermann; Matthias J Reddehase	Memory CD8 T Cells Protect against Cytomegalovirus Disease by Formation of Nodular Inflammatory Foci Preventing Intra-Tissue Virus Spread.	Viruses	2022
1040020	34932366	Putty-Reddy Sudhir; Tai-Du Lin; Qibin Zhang	HLA Allele-Specific Quantitative Profiling of Type 1 Diabetic B Lymphocyte Immunopeptidome.	J Proteome Res	2022
1041213	36010968	Jayakumar Vadakekolathu; David J Boocock; Kirti Pandey; Barbara-Ann Guinn; Antoine Legrand; Amanda K Miles; Clare Coveney; Rochelle Ayala; Anthony W Purcell; Stephanie E McArdle	Multi-Omic Analysis of Two Common P53 Mutations: Proteins Regulated by Mutated P53 as Potential Targets for Immunotherapy.	Cancers (Basel)	2022
1039204	34222571	Chao Hu; Meiying Shen; Xiaojian Han; Qian Chen; Luo Li; Siyin Chen; Jing Zhang; Fengxia Gao; Wang Wang; Yingming Wang; Tingting Li; Shenglong Li; Jingjing Huang; Jianwei Wang; Ju Zhu; Dan Chen; Qingchen Wu; Kun Tao; Da Pang; Aishun Jin	Identification of cross-reactive CD8$^+$ T cell receptors with high functional avidity to a SARS-CoV-2 immunodominant epitope and its natural mutant variants.	Genes Dis	2022
1039976	34968416	Karolin I Wagner; Laura M Mateyka; Sebastian Jarosch; Vincent Grass; Simone Weber; Kilian Schober; Monika Hammel; Teresa Burrell; Behnam Kalali; Holger Poppert; Henriette Beyer; Sophia Schambeck; Stefan Holdenrieder; Andrea Strötges-Achatz; Verena Haselmann; Michael Neumaier; Johanna Erber; Alina Priller; Sarah Yazici; Hedwig Roggendorf; Marcus Odendahl; Torsten Tonn; Andrea Dick; Klaus Witter; Hrvoje Mijočević; Ulrike Protzer; Percy A Knolle; Andreas Pichlmair; Claudia S Crowell; Markus Gerhard; Elvira D'Ippolito; Dirk H Busch	Recruitment of highly cytotoxic CD8$^+$ T cell receptors in mild SARS-CoV-2 infection.	Cell Rep	2022
1039421	34405274	Haruka Miyata; Yoshihiko Hirohashi; Shuhei Yamada; Junko Yanagawa; Aiko Murai; Shinichi Hashimoto; Serina Tokita; Kanta Hori; Takashige Abe; Terufumi Kubo; Tomohide Tsukahara; Takayuki Kanaseki; Nobuo Shinohara; Toshihiko Torigoe	GRIK2 is a target for bladder cancer stem-like cell-targeting immunotherapy.	Cancer Immunol Immunother	2022
1041441	35561310	Christopher M Bourne; Sung Soo Mun; Tao Dao; Zita E H Aretz; Zaki Molvi; Ron S Gejman; Andrew Daman; Katsuyoshi Takata; Christian Steidl; Martin G Klatt; David A Scheinberg	Unmasking the suppressed immunopeptidome of EZH2-mutated diffuse large B-cell lymphomas through combination drug treatment.	Blood Adv	2022
1040400	35154160	Saghar Kaabinejadian; Carolina Barra; Bruno Alvarez; Hooman Yari; William H Hildebrand; Morten Nielsen	Accurate MHC Motif Deconvolution of Immunopeptidomics Data Reveals a Significant Contribution of DRB3, 4 and 5 to the Total DR Immunopeptidome.	Front Immunol	2022
1040728	35389886	Aleksei Titov; Regina Shaykhutdinova; Olga V Shcherbakova; Yana V Serdyuk; Savely A Sheetikov; Ksenia V Zornikova; Alexandra V Maleeva; Alexandra Khmelevskaya; Dmitry V Dianov; Naina T Shakirova; Dmitry B Malko; Maxim Shkurnikov; Stepan Nersisyan; Alexander Tonevitsky; Ekaterina Khamaganova; Anton V Ershov; Elena Y Osipova; Ruslan V Nikolaev; Dmitry	Immunogenic epitope panel for accurate detection of non-cross-reactive T cell response to SARS-CoV-2.	JCI Insight	2022

Figure 2.22 The References tab of the search results page

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.

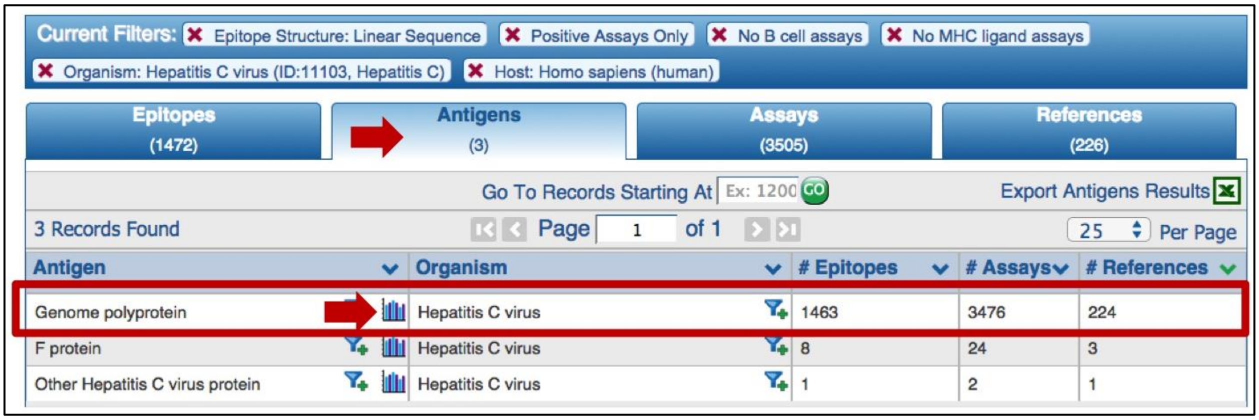
Reference Detail	
Reference ID	1033511
Abstract	The HLA-B*27 peptidome has drawn significant attention due to the genetic association between some of the HLA-B*27 alleles and the inflammatory rheumatic disease ankylosing spondylitis (AS), for which a comprehensive biological explanation is still lacking. 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 2.23 An example of the Reference detail page

2.2.3.1 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.

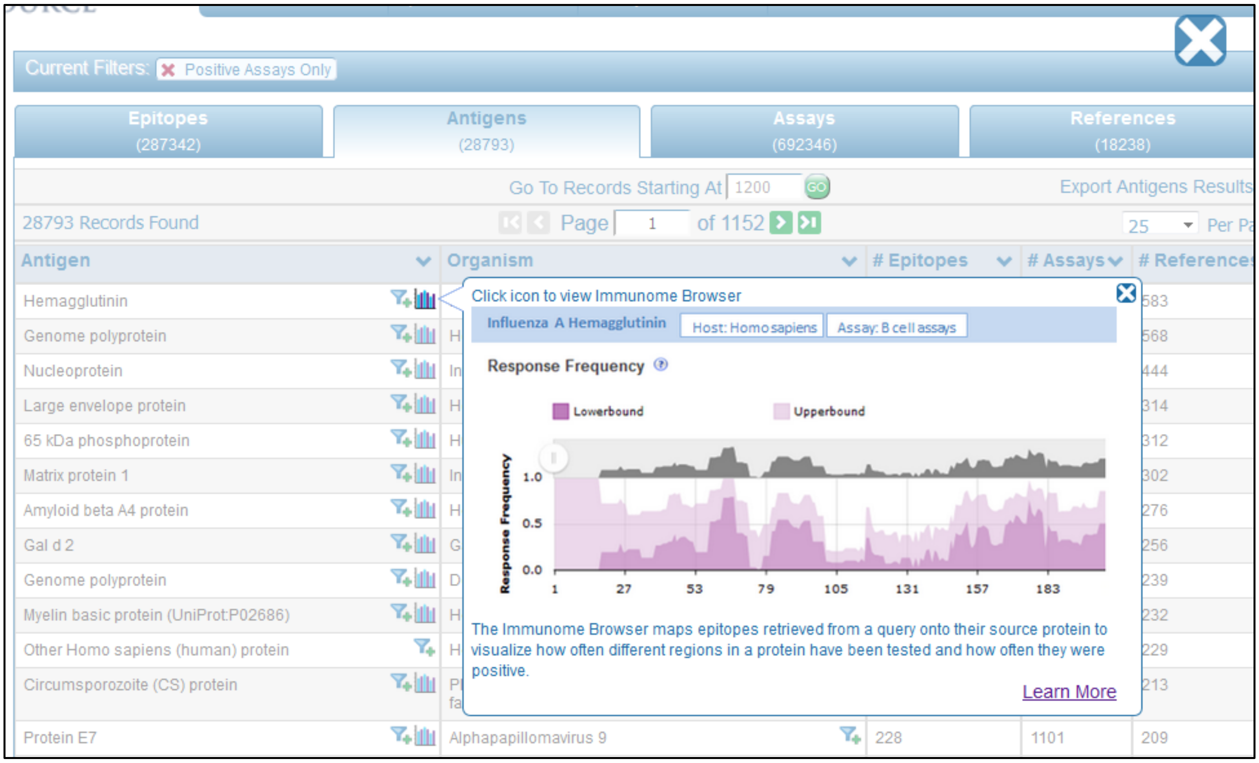


3 Records Found

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 2.2 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 2.3. It can be easily dismissed by clicking on the large X in the upper right-hand corner or clicking anywhere else on the window.



28793 Records Found

Click icon to view Immunome Browser

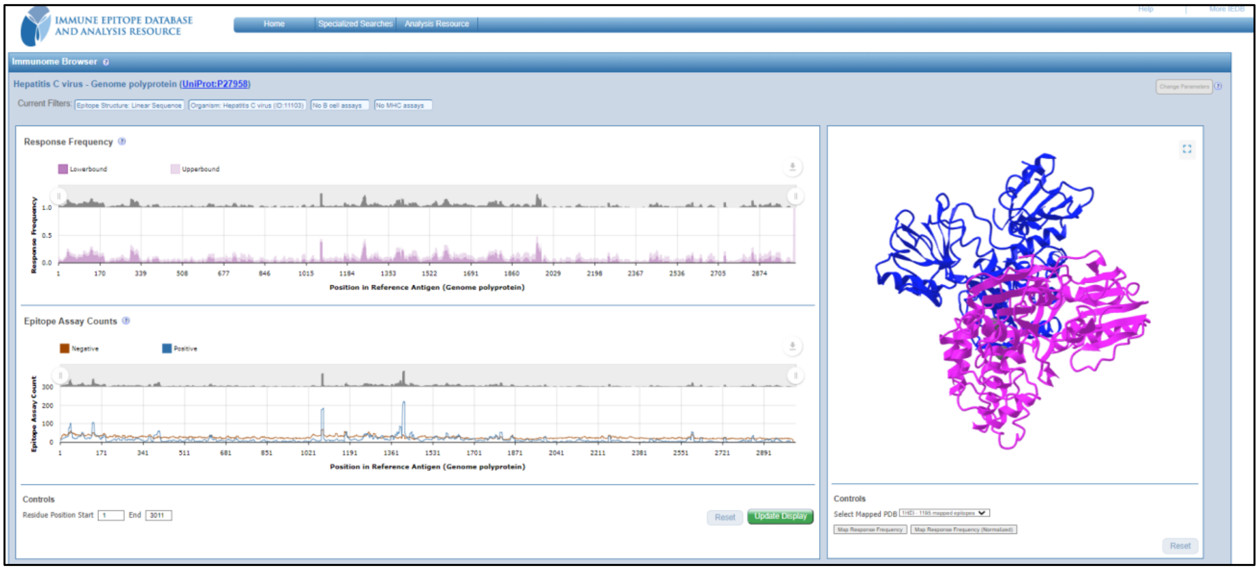
Influenza A Hemagglutinin | Host: Homo sapiens | Assay: B cell assays

The Immunome Browser maps epitopes retrieved from a query onto their source protein to visualize how often different regions in a protein have been tested and how often they were positive.

Antigen	Organism	# Epitopes	# Assays	# Reference
Hemagglutinin				583
Genome polyprotein	H			568
Nucleoprotein	In			444
Large envelope protein	H			314
65 kDa phosphoprotein	H			312
Matrix protein 1	In			302
Amyloid beta A4 protein	H			276
Gal d 2	G			256
Genome polyprotein	D			239
Myelin basic protein (UniProt:P02686)	H			232
Other Homo sapiens (human) protein	H			229
Circumsporozoite (CS) protein	Pl fa			213
Protein E7	Alphapapillomavirus 9	228	1101	209

Figure 2.3 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 is shown in Figure 2.4.



Hepatitis C virus - Genome polyprotein (UniProt:P27958)

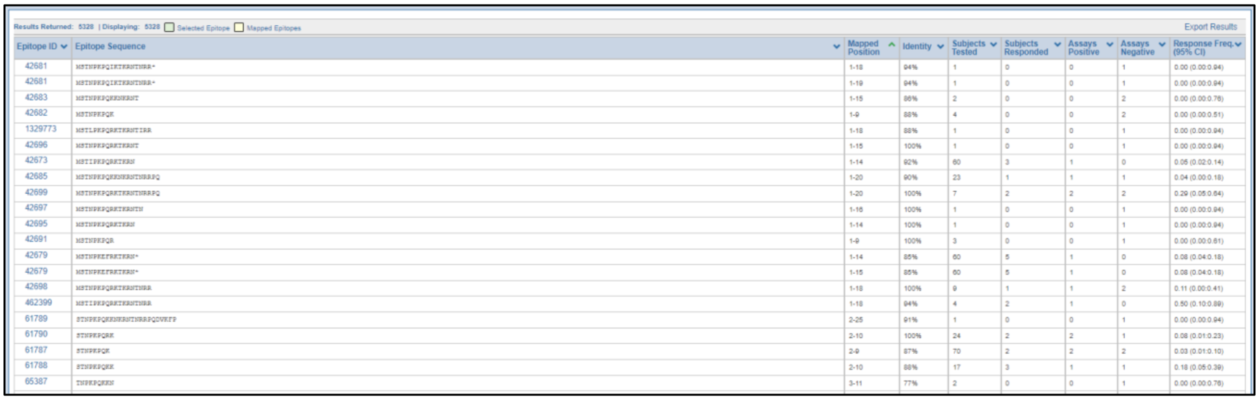
Current Filters: Epitope Structure: Linear Sequence | Organism: Hepatitis C virus (ID:11103) | No B cell assays | No MHC assays

Residue Position Start 1 End 3011

Select Mapped PDB 1HEI - 1195 mapped epitopes

Figure 2.4 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: 5328 | Displaying: 5328 ☐ Selected Epitope ☐ Mapped Epitopes

Epitope ID	Epitope Sequence	Mapped Position	Identity	Subjects Tested	Subjects Responded	Assays Positive	Assays Negative	Response Freq. (95% CI)
42681	MSTNPKPQIKTKRNTNRR*	1-18	94%	1	0	0	1	0.00 (0.00:0.94)
42681	MSTNPKPQIKTKRNTNRR*	1-19	94%	1	0	0	1	0.00 (0.00:0.94)
42683	MSTNPKPQKKNKRNT	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)
1329773	MSTLPKPQRKTKRNTIRR	1-18	88%	1	0	0	1	0.00 (0.00:0.94)
42696	MSTNPKPQRKTKRNT	1-15	100%	1	0	0	1	0.00 (0.00:0.94)
42673	MSTIPKPQRKTKRN	1-14	92%	60	3	1	0	0.05 (0.02:0.14)
42685	MSTNPKPQKKNKRNTNRRPQ	1-20	90%	23	1	1	1	0.04 (0.00:0.18)
42699	MSTNPKPQRKTKRNTNRRPQ	1-20	100%	7	2	2	2	0.29 (0.05:0.64)
42697	MSTNPKPQRKTKRNTN	1-16	100%	1	0	0	1	0.00 (0.00:0.94)
42695	MSTNPKPQRKTKRN	1-14	100%	1	0	0	1	0.00 (0.00:0.94)
42691	MSTNPKPQR	1-9	100%	3	0	0	1	0.00 (0.00:0.61)
42679	MSTNPKEFRKTKRN*	1-14	85%	60	5	1	0	0.08 (0.04:0.18)
42679	MSTNPKEFRKTKRN*	1-15	85%	60	5	1	0	0.08 (0.04:0.18)
42698	MSTNPKPQRKTKRNTNRR	1-18	100%	9	1	1	2	0.11 (0.00:0.41)
462399	MSTIPKPQRKTKRNTNRR	1-18	94%	4	2	1	0	0.50 (0.10:0.89)
61789	STNPKPQKKNKRNTNRRPQDVKFP	2-25	91%	1	0	0	1	0.00 (0.00:0.94)
61790	STNPKPQRK	2-10	100%	24	2	2	1	0.08 (0.01:0.23)
61787	STNPKPQK	2-9	87%	70	2	2	2	0.03 (0.01:0.10)
61788	STNPKPQKK	2-10	88%	17	3	1	1	0.18 (0.05:0.39)
65387	TNPKPQKKN	3-11	77%	2	0	0	1	0.00 (0.00:0.76)

Figure 2.5 Immunome Browser tabular output.

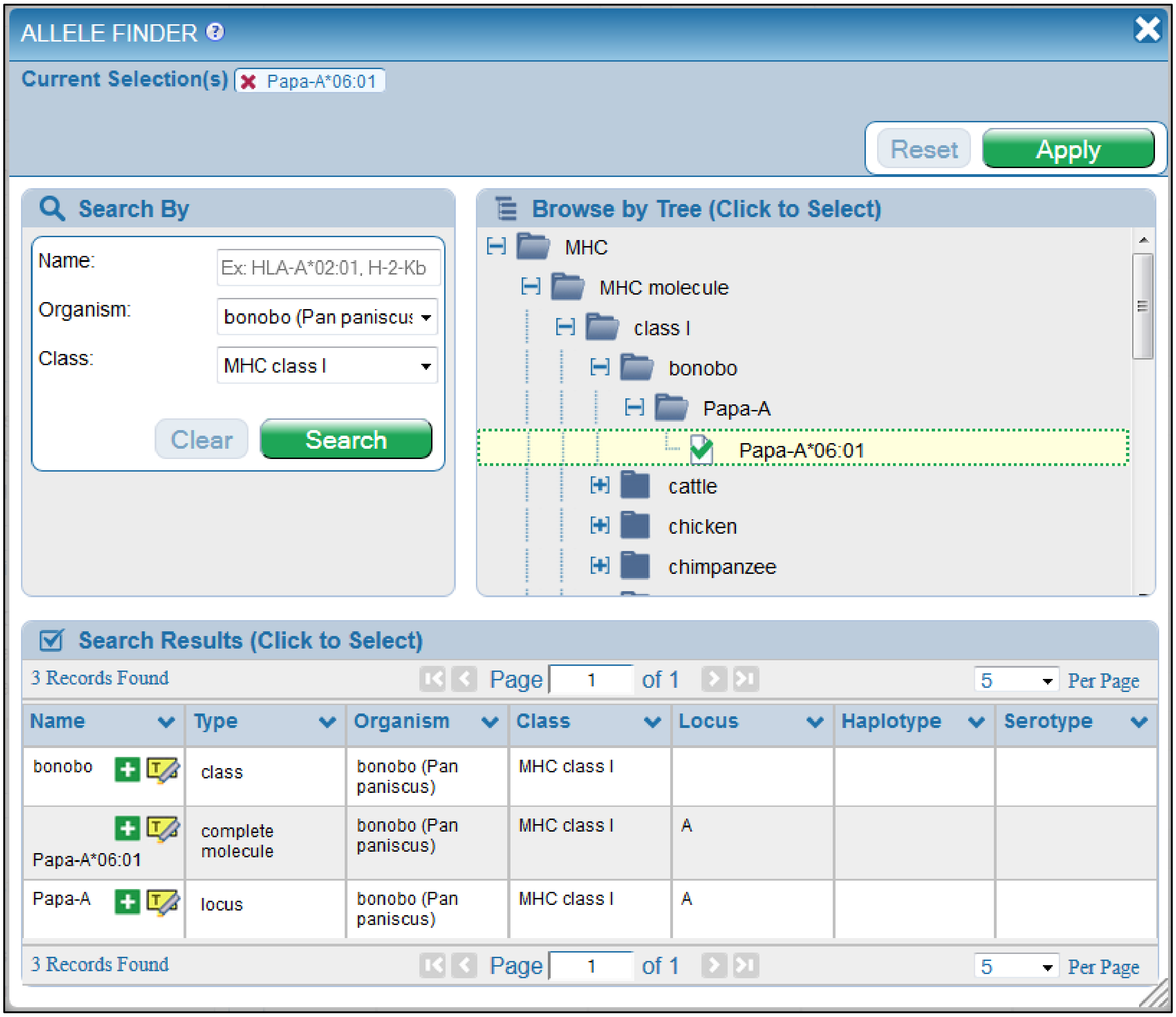
In addition to the plots, a table is generated that displays the epitope ID, sequence, position, and identity, as well as the number of subjects tested, the number who responded, and number of positive and negative assays, and the response frequency (Figure 2.5). The user can interactively zoom in and 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 2.6. 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.



Current Selection(s) Papa-A*06:01

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

3 Records Found

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

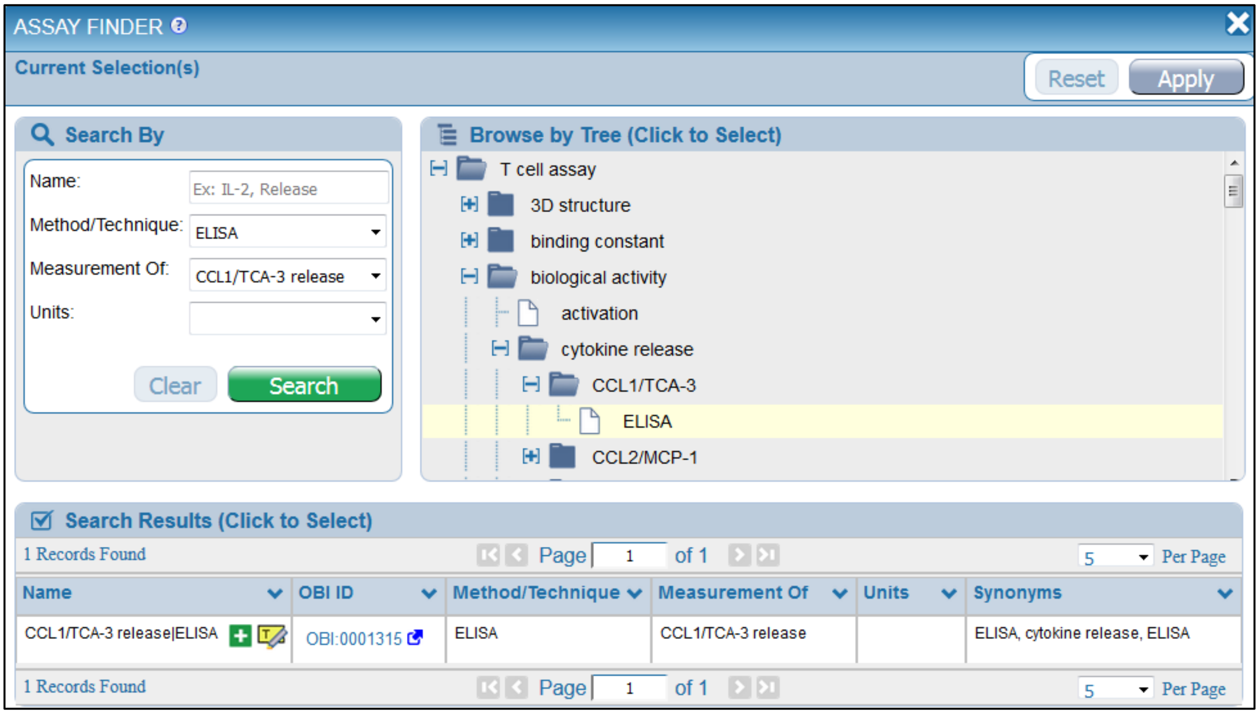
3 Records Found

Figure 2.6 Allele Finder. Alleles are displayed in a tree structure and users can search by allele name, source organism, and MHC class (I, II, or non-classical)

2.2.4.2 Assay Finder

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

The Assay Finder is used to facilitate the selection of one or more assay types and lists all assay types in the selected assay category. The Assay Finder for T Cell, B cell, and MHC Ligand assays can be found in the Assay section on the home page search interface, the left-hand side of the Results page, and on their respective Specialized Search pages. These versions of the Assay Finder organize and display assays in a tree structure, as seen in Figure 2.7 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.



Name: Ex: IL-2, Release

Method/Technique: ELISA

Measurement Of: CCL1/TCA-3 release

Units:

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 2.7 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 IEDB-specific identifier that will be updated later with a DOID number when the Disease Ontology incorporates the terms.

Current Selection(s) ✖ diabetes mellitus

Disease Name: diabetes

Disease ID: Ex: 9415

ID Source:

- additional diseases by category
  - disease of anatomical entity
  - disease of mental health
  - disease of metabolism
    - acquired metabolic disease
      - amyloidosis
      - carbohydrate metabolis…
        - glucose metabolism …
          - diabetes mellitus

4 Records Found Page 1 of 1 5 Per Page

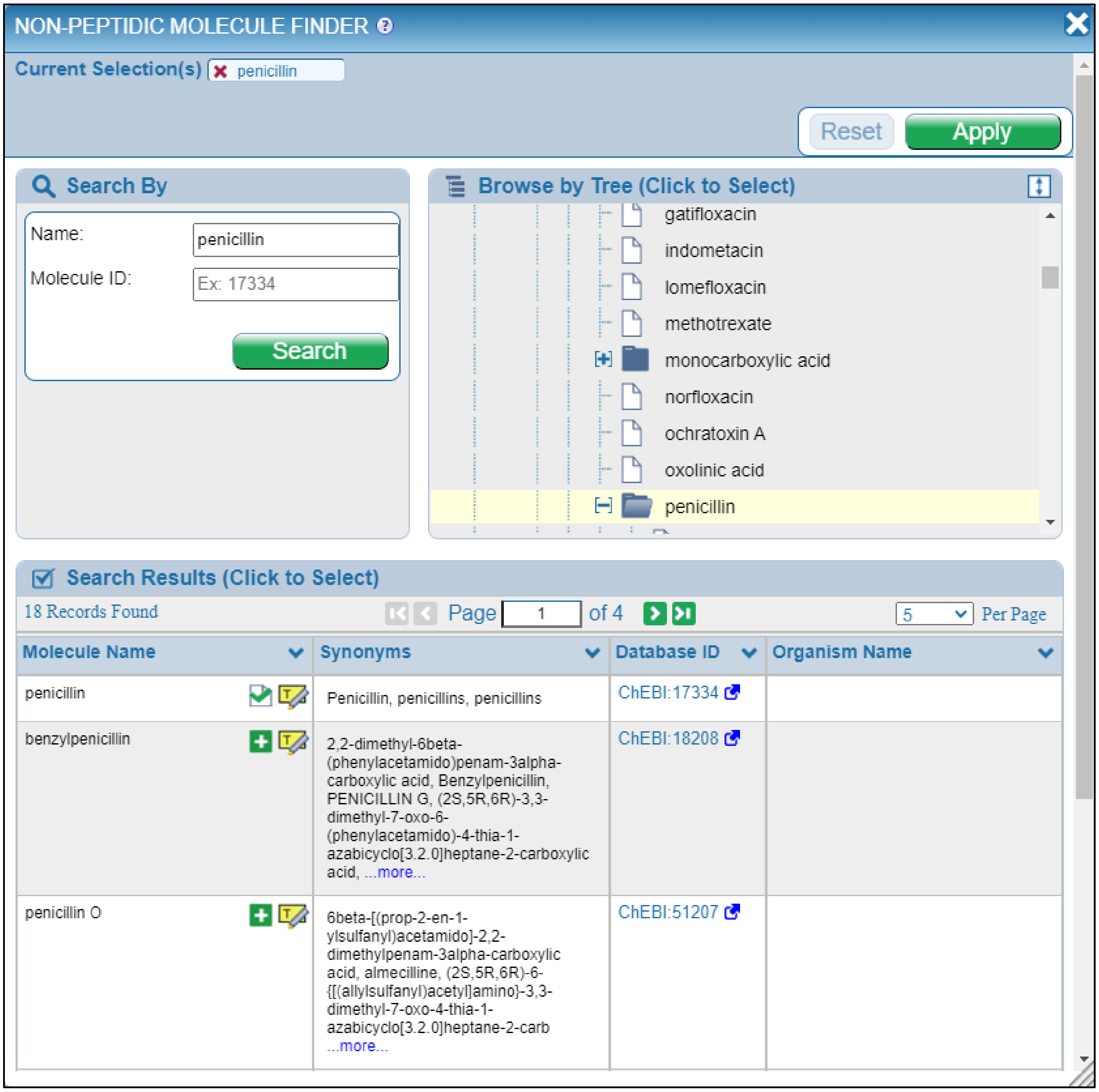
Disease Name	Synonyms	Disease ID
diabetes mellitus ✓		DOID [DOID:9351]
prediabetes syndrome +	prediabetic state, Prediabetes	DOID [DOID:11716]
type 1 diabetes mellitus +	type I diabetes mellitus, insulin-dependent diabetes mellitus, IDDM	DOID [DOID:9744]
type 2 diabetes mellitus +	type 2 diabetes, non-insulin-dependent diabetes mellitus, type II diabetes mellitus, NIDDM	DOID [DOID:9352]

4 Records Found Page 1 of 1 5 Per Page

Figure 2.8 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 2.9.



Current Selection(s): penicillin

Name: penicillin

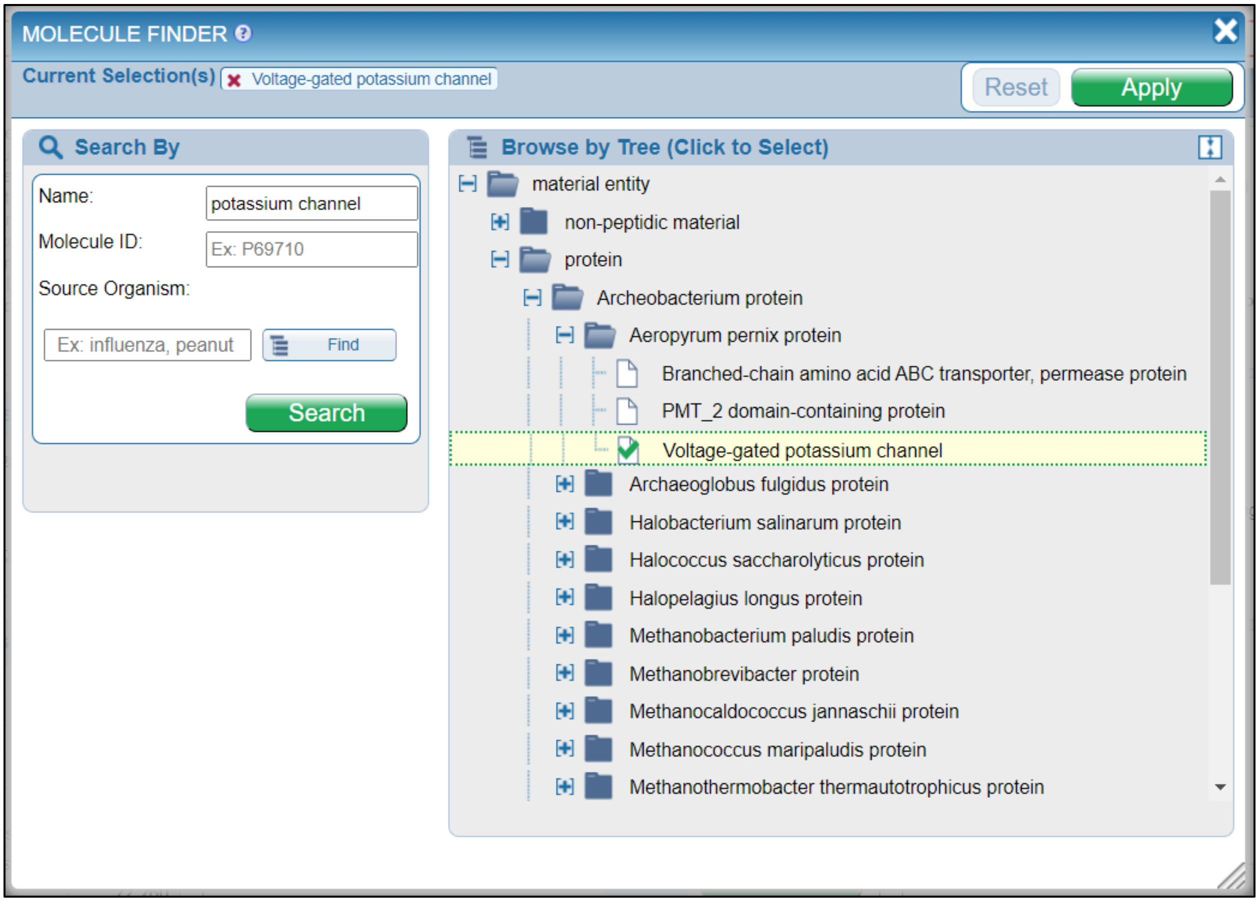
Molecule ID: Ex: 17334

18 Records Found

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

Figure 2.9 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.



Current Selection(s): Voltage-gated potassium channel

Name: potassium channel

Molecule ID: Ex: P69710

Source Organism: Ex: influenza, peanut

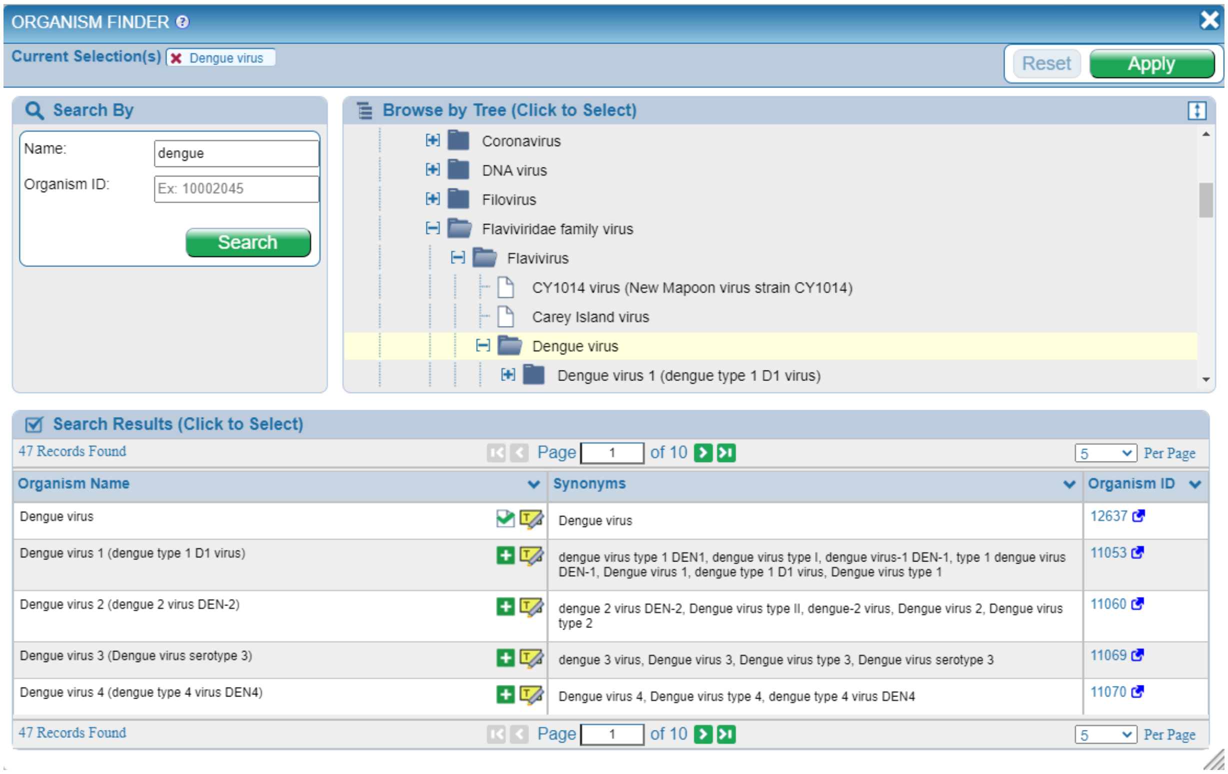
Figure 2.10 An example of the protein branch of the Molecule Finder

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

2.2.4.5 Organism Finder

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

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



Name: dengue

Organism ID: Ex: 10002045

47 Records Found Page 1 of 10 5 Per Page

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

47 Records Found Page 1 of 10 5 Per Page

Figure 2.11 Organism Finder showing a search for dengue with dengue highlighted in the tree

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

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

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

2.3.1 T Cell and B Cell Prediction Tools

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

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

2.3.1.1 T Cell Epitopes - MHC binding prediction

The Analysis Resource provides tools for predicting peptide binding to MHC class I and II molecules. For class I binding predictions, users can select predictions performed with tools derived from ten different methods – IEDB Recommended, artificial neural network (ANN), stabilized matrix method (SMM), SMM with a peptide:MHC binding energy covariance matrix (SMMPMBEC), Scoring matrices derived from combinatorial peptide libraries (Comblib_Sidney2008), Consensus, NetMHCpan, PickPocket, NetMHCcons, and NetMHCstabpan. The Consensus method is derived from the ANN, SMM, and CombLib methods. For class II binding predictions, users can select IEDB Recommended, the Combinatorial Library method, the NN_align, the SMM_align method, a method devised by Sturniolo et al. and used in TEPITOPE, NetMHCIIpan, and a consensus method derived from the NN-align, SMM_align, Sturniolo methods, and the Combinatorial Library. Tutorials and example data are available for both the class I and II tools.

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

2.3.1.1.1 Peptide Binding to MHC Class I Molecules

Users can select from ten different methods for predicting class I epitopes – ANN, SMM, SMMPMBEC, Comblib_Sidney2008, Consensus, NetMHCpan, NetMHCcons, PickPocket, NetMHCstabpan, and IEDB recommended, which are described further below. A check box can be used to show only frequently occurring alleles. This allows the selection of only those alleles that occur in at least 1% of the human population or allele frequency of 1% or higher. However, un-checking the check-box will allow selection of all the alleles and corresponding peptide lengths for a particular species. Users can also upload an allele file instead of entering allele on the page one at a time.

Artificial Neural Network

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

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

Stabilized Matrix Method (SMM)

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

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

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

Scoring matrices derived from combinatorial peptide libraries (Comblib_Sidney2008)

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

Consensus

The Consensus predictor was motivated by an idea that predictions made by consulting "consensus" of individual predictions from multiple predictors may result in improved performance over that of any individual ones. For MHC-I, a work describing an early implementation can be found in Moutaftsi et al. (Nat Biotech 2006). The methods used for Consensus are ANN, SMM, and CombLib_Sidney2008. The Consensus method uses as many of these three component methods as possible, depending on their applicability for the chosen allele and length.

NetMHCpan

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

In 2020, NetMHCpan was updated to version 4.1, as described in Reynisson et al. (Nucleic Acids Res, 2020). The updated version of NetMHCpan differs from its predecessor in two critical aspects: the training data and the machine-learning modeling framework. The training data have been vastly extended by accumulating MHC BA and EL data from the public domain. In particular, EL data were extended to include MA data. The combined dataset used for training of NetMHCpan-4.1 consists of 13,245,212 data points covering 250 distinct MHC class I molecules. The machine learning framework was updated from NNAlign to NNAlign_MA to allow for effective handling of these MA data. In short, the NNAlign framework is a single-allele framework permitting the integration of mixed data types (BA and EL) in the model training, which allows information to be leveraged across the different data types, resulting in a boosted predictive power. NNAlign_MA extends this training framework to allow for the incorporation of EL MA data. This is achieved by iteratively annotating the best single-allele to the MA data during the model training, effectively deconvoluting the MA binding motifs. In 2020, NetMHCpan EL 4.1 became the 'IEDB recommended' method based on benchmarking results.

PickPocket

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

NetMHCcons

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

NetMHCstabpan

NetMHCstabpan was introduced in 2016. It predicts binding stability of peptides to any known MHC molecule using artificial neural networks (ANNs). The method is trained on more than 25,000 quantitative stability data covering 75 different HLA molecules. The user can upload full length MHC protein sequences, and have the server predict MHC restricted peptides from any given protein of interest. Predictions can be made for 8-14 mer peptides, although all non 9mer predictions are made using approximations. Most HLA molecules have a strong preference for binding 9mers. The prediction values are given in half life time in hours values and as %-Rank to a set of 200,000 random natural peptides. The method is described in Rasmussen et al. (Journal of Immunology, 2016).

IEDB Recommended

IEDB recommended is the default prediction method selection. Prior to 2020, IEDB recommended considered all alleles and their corresponding peptide lengths for a particular species. For each allele-length combination, consensus method was used, which includes ANN, SMM, and CombLib. However, as of 2020, NetMHCpan EL 4.1 became the 'IEDB recommended' method based on benchmarking results.

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 considered. A 2009 paper in BMC Bioinformatics by Nielsen and Lund describes the method in detail (PMID: 19765293).

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

In 2020, NetMHCIIpan was updated to version 4.0, as described in Reynisson et al. (Nucleic Acids Res, 2020). The updated version of NetMHCIIpan differs from its predecessor in two critical aspects: the training data and the machine-learning modeling framework. The training data have been vastly extended by accumulating MHC BA and EL data from the public domain. In particular, EL data were extended to include MA data. The combined dataset used for training of NetMHCIIpan-4.0 consists of 4 086 230 data points covering a total of 116 distinct MHC class II molecules. The machine learning framework was updated from NNAlign to NNAlign_MA to allow for effective handling of these MA data. In short, the NNAlign framework is a single-allele framework permitting the integration of mixed data types (BA and EL) in the model training, which allows information to be leveraged across the different data types, resulting in a boosted predictive power. NNAlign_MA extends this training framework to allow for the incorporation of EL MA data. This is achieved by iteratively annotating the best single-allele to the MA data during the model training, effectively deconvoluting the MA binding motifs.

IEDB Recommended

IEDB recommended 2.22 is the default prediction method selection. It considers all alleles and their corresponding peptide lengths for a particular species. For each allele-length combination, consensus method is used, as described above. If none of these methods are available for the allele, NetMHCIIpan is used.

2.3.1.1.3 Tepitool

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

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

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

2.3.1.2 T Cell Epitopes – MHC Processing Prediction

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

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

The proteasomal cleavage predictions evaluate how efficiently a peptide or its N-terminally prolonged precursors can be liberated from its source protein. The TAP transport predictions evaluate how efficiently a peptide or its N-terminal prolonged precursors are transported into the ER by TAP (Peters et al., Immunol, 2003). When this information is taken together and combined with MHC class I binding predictions, the tool yields a prediction of the efficiency with which a peptide is presented on the cell surface. The methods available are ANN, SMM, SMMPMBEC, Comblib_Sidney2008, NetMHCpan, PickPocket, NetMHCcons, and IEDB Recommended, which are described in Section 2.3.1.1.1.

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

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

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

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

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

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

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

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

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

2.3.1.3 T Cell Class I pMHC Immunogenicity Predictor

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

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

2.3.1.4 Deimmunization

The deimmunization tool is attempt to identify immunodominant regions in a given therapeutically important protein, and suggest amino-acid substitutions that create non-immunogenic versions of the proteins. Therefore, we have opted for a two steps process; 1) In the first step, the deimmunization tool will list all the immunogenic regions or peptides based on selected threshold. These peptides will be generated from the protein with 15mer window size and 10mer overlap. 2) In the second step, the user can select one or more peptides listed in the results and final result window will display the non-immunogenic substitution of each selected peptides. The default threshold is 8.5 (which is difference in the median of percentile rank from 26 reference alleles set for MHC class II). In the final result window, the tools will also take care of the fact that non-immunogenic substitution in the immunogenic peptides, should not create new immunogenic site in the neighboring peptides. Therefore, the result window will also display the effect of substitution on the neighboring peptides. This tool is described in Dhanda et al. (Immunology, 2018).

2.3.1.5 CD4 T cell immunogenicity

The server is developed to predict the allele independent CD4 T cell immunogenicity at population level, overcoming complications related to the high level of variability of HLA molecules, potential other factors beyond HLA as well as a frequent lack of HLA typing data. With this tool, users can predict the T cell immunogenicity using 7-allele method (Paul et. al. 2015), immunogenicity method and combined method (IEDB recommended). The combined method predicts the final score that combines the predictions from 7-allele method and immunogenicity method. This tool is described in Dhanda et al. (Front Immunol, 2018).

2.3.1.6 Antigen Expression Based Epitope Likelihood-Function (Axel-F)

AXEL-F incorporates antigen abundance estimates with MHC binding predictions to enhance epitope predictions. This tool is described in Koşaloğlu-Yalçın et al. (iScience, 2020).

2.3.2 TCR Analysis

2.3.2.1 TCRMatch

TCRMatch compares input CDR3b sequences against curated CDR3b sequences in the IEDB to find matches that are predicted to share epitope specificity. Matches are determined by sequence similarity, which is scored using a comprehensive k-mer comparison. This tool is described in Chronister et al. (Front Immunol, 2021).

2.3.3 B Cell Epitope Prediction

2.3.3.1 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.

2.3.3.2 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).

2.3.3.3 ElliPro - Epitope prediction based upon structural protrusion

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

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

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

2.3.4 Structure Tools

2.3.4.1 LYmphocyte Receptor Automated modeling (LYRA)

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

2.3.4.2 Structural Complexes of Epitope Receptor (SCEptRe)

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

2.3.4.3 Docktope

Docktope is a web-based tool, based on the D1-EM-D2 approach, intended to allow the pMHC-I modeling. Some applications allowed from the pMHC-I construction include the study of the pMHC-I tridimensional structure, epitope-MHC-I interaction patterns, cross-reactivity assessment and molecular dynamics studies. The tool allows the user to construct pMHC-I structures for the following alleles: HLA-A*02:01 (9-mer epitopes), HLA-B*27:05 (9-mer epitopes), H2-Db (9-mer/10-mer epitopes) and H2-Kb (8-mer epitopes). The tool is described in detail by Rigo et al. (Scientific Reports, 2015).

2.3.5 Epitope Analysis Tools

2.3.5.1 Population Coverage

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

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

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).

2.3.5.2 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.

2.3.5.3 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.

2.3.5.4 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.

2.3.5.5 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).

2.3.5.6 ImmunomeBrowser

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

2.3.5.7 PepSySco

Given a set of peptide sequences, Peptide Synthesis Score (PepSySco) predicts the likelihood that they can be synthesized successfully. The tool is described in detail by Gutman et al. (ACS Omega, 2022).

2.3.6 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, 11 tools are currently available under the Labs designation:

Prediction LABS Tools	**Analysis LABS Tools**
MHCII-NP	RATE
Deimmunization	ImmunomeBrowser
CD4 T Cell Immunogenicity	PepSySco
LYRA	
SCEptRe	
Docktope	
Axel-F	
TCRMatch	

2.3.7 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:

- Reynisson B, Alvarez B, Paul S, Peters B, Nielsen M. NetMHCpan-4.1 and NetMHCIIpan-4.0: improved predictions of MHC antigen presentation by concurrent motif deconvolution and integration of MS MHC eluted ligand data. Nucleic Acids Res. 2020 Jul 2;48(W1):W449-W454. doi: 10.1093/nar/gkaa379. PMID: 32406916; PMCID: PMC7319546.
- Jurtz V, Paul S, Andreatta M, Marcatili P, Peters B, Nielsen M. NetMHCpan-4.0: Improved Peptide-MHC Class I Interaction Predictions Integrating Eluted Ligand and Peptide Binding Affinity Data. J Immunol. 2017 Nov 1;199(9):3360-3368. doi: 10.4049/jimmunol.1700893. Epub 2017 Oct 4. PMID: 28978689; PMCID: PMC5679736.
- Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M. Automated benchmarking of peptide-MHC class I binding predictions. Bioinformatics. 2015 Jul 1;31(13):2174-81. doi: 10.1093/bioinformatics/btv123. Epub 2015 Feb 25. PMID: 25717196; PMCID: PMC4481849
- Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B. Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. BMC Bioinformatics. 2014 Jul 14;15:241. doi: 10.1186/1471-2105-15-241. PMID: 25017736; PMCID: PMC4111843.
- Kim Y, Sidney J, Pinilla C, Sette A, Peters B. Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior. BMC Bioinformatics. 2009 Nov 30;10:394. PMID: 19948066.

- Peters B, Bui HH, Frankild S, Nielson M, Lundegaard C, Kostem E, Basch D, Lamberth K, Harndahl M, Fleri W, Wilson SS, Sidney J, Lund O, Buus S, Sette A., A community resource benchmarking predictions of peptide binding to MHC-I molecules, PLoS Comput Biol. 2006 Jun 9;2(6):e65. Epub 2006 Jun 9. PMID: 16789818

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

- Reynisson B, Alvarez B, Paul S, Peters B, Nielsen M. NetMHCpan-4.1 and NetMHCIIpan-4.0: improved predictions of MHC antigen presentation by concurrent motif deconvolution and integration of MS MHC eluted ligand data. Nucleic Acids Res. 2020 Jul 2;48(W1):W449-W454. doi: 10.1093/nar/gkaa379. PMID: 32406916; PMCID: PMC7319546.
- Andreatta M, Trolle T, Yan Z, Greenbaum JA, Peters B, Nielsen M. An automated benchmarking platform for MHC class II binding prediction methods. Bioinformatics. 2018 May 1;34(9):1522-1528. doi: 10.1093/bioinformatics/btx820. PMID: 29281002; PMCID: PMC5925780.
- Jensen KK, Andreatta M, Marcatili P, Buus S, Greenbaum JA, Yan Z, Sette A, Peters B, Nielsen M. Improved methods for predicting peptide binding affinity to MHC class II molecules. Immunology. 2018 Jul;154(3):394-406. doi: 10.1111/imm.12889. Epub 2018 Feb 6. PMID: 29315598; PMCID: PMC6002223.
- Wang P, Sidney J, Kim Y, Sette A, Lund O, Nielsen M, Peters B. Peptide binding predictions for HLA DR, DP and DQ molecules. BMC Bioinformatics. 2010 Nov 22;11:568. PMID: 21092157; PMCID: PMC2998531.
- Wang, P., J. Sidney, C. Dow, B. Mothe, A. Sette, B. Peters. (2008). A Systematic Assessment of MHC Class II Peptide Binding Predictions and Evaluation of a Consensus Approach. PLoS Computational Biology 4(4). PMID: 18389056

For the B cell predictions, the references are:

- Kringelum JV, Nielsen M, Padkjær SB, Lund O. Structural analysis of B-cell epitopes in antibody:protein complexes. Mol Immunol. 2013 Jan;53(1-2):24-34. doi: 10.1016/j.molimm.2012.06.001. Epub 2012 Jul 10. PMID: 22784991; PMCID: PMC3461403
- Kringelum JV, Lundegaard C, Lund O, Nielsen M. Reliable B cell epitope predictions: impacts of method development and improved benchmarking. PLoS Comput Biol. 2012;8(12):e1002829. doi: 10.1371/journal.pcbi.1002829. Epub 2012 Dec 27. PMID: 23300419; PMCID: PMC3531324.
- Rubinstein ND, Mayrose I, Martz E, Pupko T. Epitopia: a web-server for predicting B-cell epitopes. BMC Bioinformatics. 2009 Sep 14;10:287. doi: 10.1186/1471-2105-10-287. PMID: 19751513; PMCID: PMC2751785.
- Liang S, Zheng D, Standley DM, Yao B, Zacharias M, Zhang C. EPSVR and EPMeta: prediction of antigenic epitopes using support vector regression and multiple server results. BMC Bioinformatics. 2010 Jul 16;11:381. doi: 10.1186/1471-2105-11-381. PMID: 20637083; PMCID: PMC2910724.
- Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. BMC Struct Biol. 2007 Oct 2;7(1):64. PMID: 17910770

2.3.8 Other Ways to Access Tools

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

The Download tab takes the user to the IEDB Tools Download web page. For users from non-commercial organizations with batch processing needs, the MHC class I and II binding prediction tools, linear B cell epitope prediction tool, ElliPro, the epitope cluster analysis tool, the MHC class I immunogencity 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 and information articles under the Help menu at the top of each web page. This link takes the user to the “How-to Videos” article in the Solutions Center in the Tutorials and Reference Materials folder. Most of the videos are edited versions of live presentations made at the annual IEDB User Workshops. The videos from the 2019 and 2020 events are currently posted for user viewing. An overview of the resource and information regarding the data structure and curation are presented first. The next category addresses the query and reporting features. Videos for all the tools in the Analysis Resource are listed next. Videos for the legacy website have been removed because the legacy site has been retired and can no longer be accessed by users.

2.5 More IEDB

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

2.5.1 Database Export

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

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

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

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

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

2.5.2 Meta-Analyses

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

2.5.3 Citing the IEDB

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

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

2. The journal reference for the IEDB was updated in 2018; and should be cited as:

   Vita R, Mahajan S, Overton JA, Dhanda SK, Martini S, Cantrell JR, Wheeler DK, Sette A, Peters B. The Immune Epitope Database (IEDB): 2018 update. Nucleic Acids Res. 2019 Jan 8;47(D1):D339-D343. doi: 10.1093/nar/gky1006. PMID: 30357391; PMCID: PMC6324067.

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.

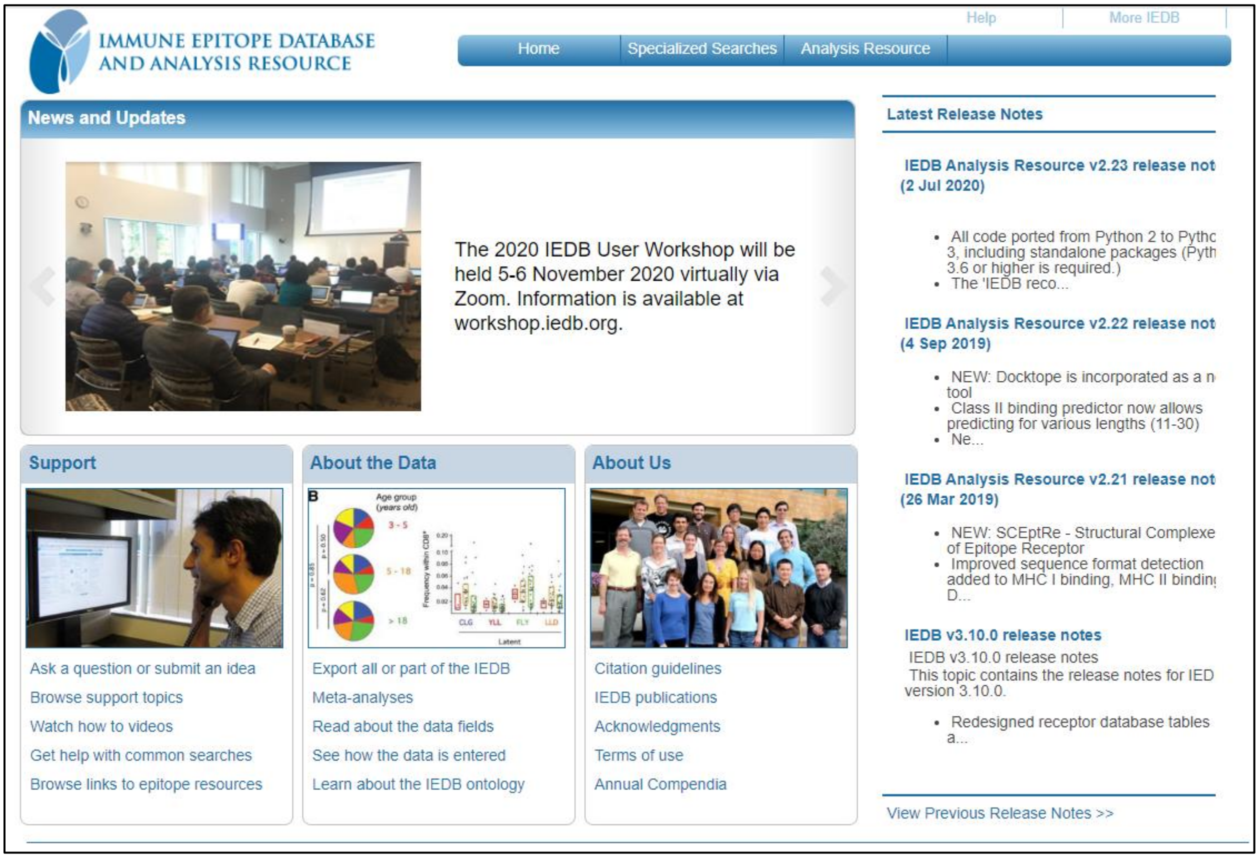
2.5.5 Links to External Sources

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 2020 IEDB User Workshop will be held 5-6 November 2020 virtually via Zoom. Information is available at workshop.iedb.org.

IEDB Analysis Resource v2.23 release not
(2 Jul 2020)

- All code ported from Python 2 to Pythc 3, including standalone packages (Pyth 3.6 or higher is required.)
- The 'IEDB reco...

IEDB Analysis Resource v2.22 release not
(4 Sep 2019)

- NEW: Docktope is incorporated as a n tool
- Class II binding predictor now allows predicting for various lengths (11-30)
- Ne...

IEDB Analysis Resource v2.21 release not
(26 Mar 2019)

- NEW: SCEptRe - Structural Complexe of Epitope Receptor
- Improved sequence format detection added to MHC I binding, MHC II binding D...

IEDB v3.10.0 release notes

IEDB v3.10.0 release notes
This topic contains the release notes for IED version 3.10.0.

- Redesigned receptor database tables a...

Figure 2.12 The Learn More page, accessed from the Welcome message in the upper left corner of the IEDB home page

2.6.1 Support

Each link is briefly described below.

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

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

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

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

2.6.2 About the Data

Each link is briefly described below.

Export all or part of the IEDB
Clicking on this link will bring the user to the Database Export page that is described in Section 2.5.1.

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

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

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

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

2.6.3 About Us

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

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

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

Terms of Use

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

Annual Compendia

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

3 Scientific Publications

This section lists the scientific publications for which the IEDB played a contributory role. The first section lists publications authored by the IEDB contractor team over the past 19 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 2021. This publication list was re-evaluated in December 2021 to ensure that the list was accurate and up to date. As a result of this review, the publication list now contains 177 IEDB sponsored publications (including book chapters) between program inception in 2003 and 31 December 2021. As at the time of preparing this compendium in 2022, we have added the number of citations for that publication in 2021, as well as the cumulative citations from 2003 to 2021.

Publication Year	**Publication Type**	**IEDB Publication**	**2021 Citations**	**Cumulative Citations (2003-2021)**
2021	General	Edwards L, Jackson R, Overton J, Vita R, Blazeska N, Peters B, Sette A. An immunologically friendly classification of non-peptidic ligands. Database (Oxford). 2021 Mar 27;baab014. doi: 10.1093/database/baab014. PubMed PMID: 33772585	0	0
2021	General	Vita R, Zheng J, Jackson R, Dooley D, Overton J, Miller M, Berrios D, Scheuermann R, He Y, McGinty HK, Brochhausen M, Lin A, Jain S, Chibucos M, Judkins J, Giglio M, Feng I, Burns G, Brush M, Peters B, Stoeckert C. Standardization of assay representation in the Ontology for Biomedical Investigations. Database (Oxford). 2021 Jul 9;baab040. doi: 10.1093/database/baab040. PubMed PMID: 34244718	0	0
2021	Tools	Chronister W, Crinklaw A, Mahajan S, Vita R, Kosaloglu-Yalcin Z, Yan Z, Greenbaum J, Jessen L, Nielsen M, Christley S, Cowell L, Sette A, Peters B. TCRMatch: Predicting T-Cell Receptor Specificity Based on Sequence Similarity to Previously Characterized Receptors. Front Immunol. 2021 Mar 11;12:640725. doi: 10.3389/fimmu.2021.640725. PubMed PMID: 33777034	9	9
2021	General	Tarke A, Sidney J, Kidd C, Dan J, Ramirez S, Yu E, Mateus J, da Silva Antunes R, Moore E, Rubiro P, Methot N, Philips E, Mallal S, Frazier A, Rawlings S, Greenbaum J, Peters B, Smith D, Crotty S, Weiskopf D, Grifoni A, Sette A. Comprehensive analysis of T cell immunodominance and immunoprevalence of SARS-CoV-2 epitopes in COVID-19 cases. Cell Rep Med. 2021 Feb 16;2(2):100204. doi: 10.1016/j.xcrm.2021.100204. PubMed PMID: 33521695	130	130
2021	General	Grifoni A, Sidney J, Vita R, Peters B, Crotty S, Weiskopf D, Sette A. SARS-CoV-2 human T cell epitopes: Adaptive immune response against COVID-19. Cell Host Microbe . 2021 Jul 14;29(7):1076-1092. doi: 10.1016/j.chom.2021.05.010. PubMed PMID: 34237248	29	29

2021	Tools	Reardon B, Kosaloglu-Yalcin Z, Paul S, Peters B, Sette A. Allele-Specific Thresholds of Eluted Ligands for T-Cell Epitope Prediction. Mol Cell Proteomics. 2021;20:100122. doi: 10.1016/j.mcpro.2021.100122. PubMed PMID: 34303001	0	0
2021	Tools	Nilsson J, Grifoni A, Tarke A, Sette A, Nielsen M. PopCover-2.0. Improved Selection of Peptide Sets With Optimal HLA and Pathogen Diversity Coverage Front Immunol. 2021 Aug 17;12:728936. doi: 10.3389/fimmu.2021.728936. PubMed PMID: 34484239	2	2
2021	General	Eberhardt C, Kissick H, Patel M, Cardenas M, Prokhnevska N, Obeng R, Nasti T, Griffith C, Im S, Wang X, Shin D, Carrington M, Chen Z, Sidney J, Sette A, Saba N, Wieland A, Ahmed R. Functional HPV-specific PD-1 + stem-like CD8 T cells in head and neck cancer. Nature. 2021 Sep;597(7875):279-284. doi: 10.1038/s41586-021-03862-z. PubMed PMID: 34471285	12	12
2021	Tools	Refsgaard C, Barra C, Peng Z, Ternette N, Nielsen M. NetMHCphosPan - Pan-specific prediction of MHC class I antigen presentation of phosphorylated ligands. Immunoinformatics. 20 April 2021. doi: 10.1016/j.immuno.2021.100005	0	0
2021	Tools	Montemurro A, Schuster V, Povlsen H, Bentzen A, Jurtz V, Chronister W, Crinkloaw A, Hadrup S, Winther O, Peters B, Jessen L, Nielsen M. NetTCR-2.0 enables accurate prediction of TCR-peptide binding by using paired TCRα and β sequence data. Commun Biol. 2021 Sep 10;4(1):1060. doi: 10.1038/s42003-021-02610-3. PubMed PMID: 34508155	0	0
2020	Tools	Paul S, Croft N, Purcell A, Tscharke D, Sette A, Nielsen M, Peters B. Benchmarking predictions of MHC class I restricted T cell epitopes in a comprehensively studied model system. PLoS Comput Biol. 2020 May 26;16(5):e1007757. doi: 10.1371/journal.pcbi.1007757. PubMed PMID: 32453790	13	19
2020	General	Dimou A, Grewe P, Sidney J, Sette A, Norman P, Doebele R. HLA Class I Binding of Mutant EGFR Peptides in NSCLC Is Associated With Improved Survival. J Thorac Oncol. 2021 Jan;16(1):104-112. doi: 10.1016/j.jtho.2020.08.023. PubMed PMID: 32927123	2	2
2020	Tools	Peters B, Nielsen M, Sette A. T Cell Epitope Predictions. Annu Rev Immunol. 2020 Apr 26;38:123-145. doi: 10.1146/annurev-immunol-082119-124838. PubMed PMID: 32045313	24	44
2020	Tools	Reynisson B, Alvarez B, Paul S, Peters B, Nielsen M. NetMHCpan-4.1 and NetMHCIIpan-4.0: improved predictions of MHC antigen presentation by concurrent motif deconvolution and integration of MS MHC eluted ligand data. Nucleic Acids Res. 2020 Jul 2;48(W1):W449-W454. doi: 10.1093/nar/gkaa379. PubMed PMID: 32406916	203	246
2020	Tools	Reynisson B, Barra C, Kaabinejadian S, Hildebrand WH, Peters B, Nielsen M. Improved Prediction of MHC II Antigen Presentation through Integration and Motif Deconvolution of Mass Spectrometry MHC Eluted Ligand Data. J Proteome Res. 2020 Jun 5;19(6):2304-2315. doi: 10.1021/acs.jproteome.9b00874. PubMed PMID: 32308001	60	85

2020	General	Grifoni A, Sidney J, Zhang Y, Scheuerman RH, Peters B, Sette A. A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe. 2020 Apr 8;27(4):671-680.e2. doi: 10.1016/j.chom.2020.03.002. PubMed PMID: 32183941	282	597
2020	General	Salimi N, Edwards L, Foos G, Greenbaum JA, Martini S, Reardon B, Shackelford D, Vita R, Zalman L, Peters B, Sette A. A behind-the-scenes tour of the IEDB curation process: an optimized process empirically integrating automation and human curation efforts. Immunology. 2020 Oct;161(2):139-147. doi: 10.1111/imm.13234. PubMed PMID: 32615639.	0	0
2020	Tools	Kosaloglu-Yacin Z, Sidney J, Chronister W, Peters B, Sette A. Comparison of HLA ligand elution data and binding predictions reveals varying prediction performance for the multiple motifs recognized by HLA-DQ2.5. Immunology. 2021 Feb;162(2):235-247. doi: 10.1111/imm.13279. PubMed PMID: 33064841	0	0
2020	General	Sidne J, Peters B, Sette A. Epitope prediction and identification- adaptive T cell responses in humans. Semin Immunol. 2020 Aug;50:101418. doi: 10.1016/j.smim.2020.101418. PubMed PMID: 33131981	8	8
2020	Tools	Vita R, Overton JA, Dunn P, Cheung K, Kleinstein SH, Sette A, Peters B. A structured model for immune exposures. Database (Oxford). 2020 Jan 1;2020:baaa016. doi: 10.1093/database/baaa016. PubMed PMID: 32283555	1	2
2020	Tools	Sachs A, Moore E, Kosaloglu-Yalcin Z, Peters B, Sidney J, Rosenberg SA, Robbins PF, Sette A. Impact of Cysteine Residues on MHC Binding Predictions and Recognition by Tumor-Reactive T Cells. J Immunol. 2020 Jul 15;205(2):539-549. doi: 10.4049/jimmunol.1901173. PubMed PMID: 32571843	4	4
2020	Tools	Nielsen M, Andreatta M, Peters B, Buus S. Immunoinformatics: Predicting Peptide–MHC Binding. Annual Review of Biomedical Science. 2020 July 3. doi: 10.1146/annurev-biodatasci-021920-100259.	7	10
2020	Tools	Barra C, Ackaert C, Reynisson B, Schockaert J, Jessen LE, Watson M, Jang A, Comtois-Marotte S, Goulet J, Pattijn S, Paramithiotis E, Nielsen M. Immunopeptidomic Data Integration to Artificial Neural Networks Enhances Protein-Drug Immunogenicity Prediction. Front Immunol. 2020 Jun 23;11:1304. doi: 10.3389/fimmu.2020.01304. PubMed PMID: 32655572	4	7
2019	General	Viscaino JA, Kubinok P, Kovalchik K, Ma Q, Duquette J, Mongrain I, Deutsch E, Peters B, Sette A, Sirois I, Caron E. The Human Immunopeptidome Project: A Roadmap to Predict and Treat Immune Diseases. Mol Cell Proteomics. 2020; 19(1): 31-49. doi: 10.1074/mcp.R119.001743. PubMed PMID: 31744855	21	49
2019	Tools	Paul S, Grifoni A, Peters B, Sette A. Major Histocompatibility Complex Binding, Eluted Ligands, and Immunogenicity: Benchmark Testing and Predictions. Front Immunol. 2020 Feb 5;10:3151. doi: 10.3389/fimmu.2019.03151. eCollection 2019. PubMed PMID: 32117208.	3	9

2019	Tools	Dhanda SK, Mahajan S, Paul S, Yan Z, Kim H, Jespersen MC, Jurtz V, Andreatta M, Greenbaum JA, Marcatili P, Sette A, Nielsen M, Peters B. Immune Epitope Database - Analysis Resource (IEDB-AR) in 2019. Nucleic Acids Res. 2019 Jul 2;47(W1):W502-W506. doi: 10.1093/nar/gkz452. PubMed PMID: 31114900	63	106
2019	General	Heide J, Vaughan KC, Sette A, Jacobs T, Schulze Zur Wiesch J. Comprehensive Review of Human Plasmodium falciparum-Specific CD8+ T Cell Epitopes. Front Immunol. 2019 Mar 21;10:397. doi: 10.3389/fimmu.2019.00397. eCollection 2019. PubMed PMID: 30949162	5	13
2019	General	Grifoni A, Mahajan S, Sidney J, Martini S, Scheuerman RH, Peters B, Sette A. A survey of known immune epitopes in the enteroviruses associated with acute flaccid myelitis. Hum Immunol. 2019 Nov;80(11):923-929. doi: 10.1016/j.humimm.2019.08.004. Epub 2019 Aug 23. PubMed PMID: 31451291	1	1
2019	Tools	Mahajan S, Yan Z, Jespersen MC, Jensen KK, Marcatili P, Nielsen M, Sette A, Peters B. Benchmark datasets of immune receptor-epitope structural complexes. BMC Bioinformatics. 2019 Oct 10;20(1):490. doi: 10.1186/s12859-019-3109-6. PubMed PMID: 31601176	2	5
2018	Tools/ Analysis Resource	Andreatta M, Nielsen M. Bioinformatics Tools for the Prediction of T-Cell Epitopes. Methods Mol Biol. 2018; 1785:269-281. doi: 10.1007/978-1-4939-7841-0_18. PubMed PMID: 29714025	3	16
2018	General	Vaughan K, Xu X, Peters B, Sette A. Investigation of outbreak-specific nonsynonymous mutations on Ebolavirus GP in the context of known immune reactivity. J Immunol Res. 2018 Nov 15;2018:1846207. doi: 10.1155/2018/1846207. eCollection 2018. PubMed PMID: 30581874	0	1
2018	General	Vita R, Overton JA, Mungall CJ, Sette A, Peters B. FAIR principles and the IEDB: Short-term improvements and a Long-term vision of OBO-Foundry mediated machine-actionable interoperability. Database (Oxford). 2018 Jan 1;2018. doi: 10.1093/database/bax105. PubMed PMID: 29688354	3	10
2018	General	Vita R, Overton JA, Peters B. Identification of Errors in the IEDB Using Ontologies. Database (Oxford). 2018 Jan 1;2018. doi: 10.1093/database/bay005. PubMed PMID: 29688357	0	0
2018	General	Mahajan S, Vita R, Shackelford D, Lane J, Schulten V, Zarebski L, Jespersen MC, Marcatili P, Nielsen M, Sette A, Peters B. Epitope Specific Antibodies and T Cell Receptors in the Immune Epitope Database. Front Immunol. 2018 Nov 20;9:2688. doi: 10.3389/fimmu.2018.02688. eCollection 2018. PubMed PMID: 30515166	4	17
2018	General	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. 2019 Jan 8;47(D1):D339-D343. doi: 10.1093/nar/gky1006. PubMed PMID: 30357391	332	769

2018	General	Tian Y, da Silva Antunes R, Sidney J, Lindestam Arlehamn CS, Grifoni A, Dhanda SK, Paul S, Peters B, Weiskopf D, Sette A. A Review on T Cell Epitopes Identified Using Prediction and Cell-Mediated Immune Models for Mycobacterium tuberculosis and Bordetella pertussis. Front Immunol. 2018 Nov 29;9:2778. doi: 10.3389/fimmu.2018.02778. eCollection 2018. PubMed PMID: 30555469	9	27
2018	Tools/ Analysis Resource	Dhanda SK, Vaughan K, Schulten V, Grifoni A, Weiskopf D, Sidney J, Peters B, Sette A. Development of a novel clustering tool for linear peptide sequences. Immunology. 2018 Nov;155(3):331-345. doi: 10.1111/imm.12984. Epub 2018 Aug 6. PubMed PMID: 30014462	9	41
2018	Tools/ Analysis Resource	Dhanda SK, Karosiene E, Edwards L, Grifoni A, Paul S, Andreatta M, Weiskopf D, Sidney J, Nielsen M, Peters B, Sette A. Predicting HLA CD4 immunogenicity in human populations. Front Immunol. 2018 Jun 14;9:1369. doi: 10.3389/fimmu.2018.01369. eCollection 2018. PubMed PMID: 29963059	16	53
2018	Tools/ Analysis Resource	Barra C, Alvarez B, Paul S, Sette A, Peters B, Andreatta M, Buus S, Nielsen M. Footprints of antigen processing boost MHC class II natural ligand binding predictions. Genome Med. 2018 Nov 16;10(1):84. doi: 10.1186/s13073-018-0594-6. PubMed PMID: 30446001.	14	44
2018	Tools/ Analysis Resource	Alvarez B, Barra C, Nielsen M, Andreatta M. Computational Tools for the Identification and Interpretation of Sequence Motifs in Immunopeptidomes. Proteomics. 2018 Jun;18(12):e1700252. doi: 10.1002/pmic.201700252. Epub 2018 Feb 26. PubMed PMID: 29327813.	3	25
2018	Tools/ Analysis Resource	Dhanda SK, Vita R, Ha B, Grifoni A, Peters B, Sette A. ImmunomeBrowser: A tool to aggregate and visualize complex and heterogeneous epitopes in reference protein. Bioinformatics. 2018 Nov 15;34(22):3931-3933. doi: 10.1093/bioinformatics/bty463. PubMed PMID: 29878047	3	14
2018	Tools/ Analysis Resource	Jensen KK, Andreatta M, Marcatili P, Buus S, Greenbaum JA, Yan Z, Sette A, Peters B, Nielsen M. Improved methods for predicting peptide binding affinity to MHC class II molecules. Immunology. 2018 Jul;154(3):394-406. doi: 10.1111/imm.12889. Epub 2018 Feb 6. PubMed PMID: 29315598	113	423
2018	Tools/ Analysis Resource	Paul S, Karosiene E, Dhanda SK, Jurtz V, Edwards L, Nielsen M, Sette A, Peters B. Determination of a Predictive Cleavage Motif for Eluted Major Histocompatibility Complex Class II Ligands. Front Immunol. 2018 Aug 6;9:1795. doi: 10.3389/fimmu.2018.01795. eCollection 2018. PubMed PMID: 30127785	9	32
2018	Tools/ Analysis Resource	Carrasco Pro S, Lindestam Arlehamn CS, Dhanda SK, Carpenter C, Lindvall M, Faruqi AA, Santee CA, Renz H, Sidney J, Peters B, Sette A. Microbiota epitope similarity either dampens or enhances the immunogenicity of disease-associated antigenic epitopes. PLoS One. 2018 May 7;13(5):e0196551. doi: 10.1371/journal.pone.0196551. eCollection 2018. PubMed PMID: 29734356	7	20

2017	General	Vita R, Overton JA, Sette A, Peters B. Better living through ontologies at the Immune Epitope Database. Database (Oxford). 2017 Jan 1;2017(1). doi: 10.1093/database/bax014. PubMed PMID: 28365732	0	1
2017	General	Remesh SG, Andreatta M, Ying G, Kaever T, Nielsen M, McMurtrey C, Hildebrand W, Peters B, Zajonc DM. Unconventional peptide Presentation by Major Histocompatibility Complex (MHC) Class I Allele HLA-A*02:01: Breaking Confinement. J Biol Chem. 2017 Mar 31; 292(13):5262-5270. doi:10.1074/jbc.M117.776542. Epub 2017 Feb 8. PubMed PMID: 28179428	3	40
2017	Tools/ Analysis Resource	Fleri W, Paul S, Dhanda SK, Mahajan S, Xu X, Peters B, Sette A. The Immune Epitope Database and Analysis Resource in Epitope Discovery and Synthetic Vaccine Design. Front Immunol. 2017 Mar 14;8:278. doi:10.3389/fimmu.2017.00278. eCollection 2017. Review. PubMed PMID: 28352270; PubMed Central PMCID: PMC5348633.	65	226
2017	Tools/ Analysis Resource	Nielsen M, Andreatta M. NNAlign: a platform to construct and evaluate artificial neural network models of receptor-ligand interactions. Nucleic Acids Res. 2017 April 12. doi:10.1093/nar/gkx276. [Epub ahead of print] PubMed PMID: 28407117.	5	27
2017	Tools/ Analysis Resource	Andreatta M, Alvarez B, Nielsen M. GibbsCluster: unsupervised clustering and alignment of peptide sequences. Nucleic Acids Res. 2017 Apr 12. doi:10.1093/nar/gkx248. [Epub ahead of print] PubMed PMID: 28407089.	23	98
2017	Tools/ Analysis Resource	Jespersen MC, Peters B, Nielsen M, Marcatili P. BepiPred-2.0: improving sequence-based B-cell epitope predictions using conformational epitopes. Nucleic Acids Res. 2017 May 2. doi:10.1093/nar/gkx346. [Epub ahead of print] PubMed PMID: 28472356.	224	709
2017	General	Sidney J, Becart S, Zhou M, Duffy K, Lindvall M, Moore EC, Moore EL, Rao T, Rao N, Nielsen M, Peters B, Sette A. Citrullination only infrequently impacts peptide binding to HLA class II MHC. PLoS One. 2017 May 8;12(5):e0177140. doi:10.1371/journal.pone.0177140. eCollection 2017. PubMed PMID: 28481943; PubMed Central PMCID: PMC5421785	8	33
2017	Tools/ Analysis Resource	Andreatta M, Jurtz VI, Kaever T, Sette A, Peters B, Nielsen M. Machine learning reveals a non-canonical mode of peptide binding to MHC class II molecules. Immunology. 2017 May 24. doi:10.1111/imm.12763. [Epub ahead of print] PubMed PMID: 28542831.	3	15
2017	General	Fleri W, Vaughan K, Salimi N, Vita R, Peters B, Sette A. The Immune Epitope Database: How Data Are Entered and Retrieved. J Immunol Res. 2017; 2017:5974574. doi:10.1155/2017/5974574. Epub 2017 May 29. Review. PubMed PMID: 28634590; PubMed Central PMCID: PMC5467323.	6	16
2017	Tools/ Analysis Resource	Paul S, Arlehamm CSL, Schulten V, Westernberg L, Sidney J, Peters B, Sette A. Experimental validation of the RATE tool for inferring HLA restrictions of T cell epitopes. BMC Immunol. 2017 Jun 21; 18(Suppl 1):20. doi: 10.1186/s12865-017-0204-1. PubMed PMID: 28681704.	0	8

2017	General	Shao W, Pedrioli PGA, Wolski W, Scurtescu C, Schmid E, Vizcano JA, Courcelles M, Schuster H, Kowalewski D, Marino F, Arlehamm CSL, Vaughan K, Peters B, Sette A, Ottenhoff THM, Meijgaarden KE, Nieuwenhuizen N, Kaufmann SHE, Schlapbach R, Castle JC, Nesvizhskii AI, Nielsen M, Deutsch EW, Campbell DS, Moritz RL, Zubarev RA, Ytterberg AJ, Purcell AW, Marcilla M, Paradela A, Wang Q, Costello CE, Ternette N, van Rammensee HG, Thibault P, Perreault C, Bassani-Sterberg M, Aebersold R, Caron E. The SysteMHC Atlas project. Nucleic Acids Res. 2017 Jul 29. doi:10.1093/nar/gkx664. [Epub ahead of print] PubMed PMID: 28985418.	18	109
2017	General	Vaughan K, Xu X, Cron E, Peters B, Sette A. Deciphering the MHC-associated peptidome: a review of naturally processed ligand data. Expert Rev Proteomics. 2017 Sep; 14(9):729-736. doi:10.1080/14789450.2017.1361825. Epub 2017 Aug 11. PubMed PMID: 28756714.	2	22
2017	Tools/ Analysis Resource	Dhanda SK, Grifoni A, Pham J, Vaughan K, Sidney J, Peters B, Sette A. Development of a strategy and computational application to select candidate protein analouges with reduced HLA binding and immunogenicity. Immunology. 2017 Aug 22. doi:10.1111/imm.12816. [Epub ahead of print] PubMed PMID: 28833085.	4	20
2017	Tools/ Analysis Resource	Jurtz VI, Rosenberg Johansen A, Nielsen M, Almagro Armenteros JJ, Nielsen H, Kaae Sonderby C, Winther O, Kaae Sonderby S. An introduction to Deep learning on biological sequence data - Examples and solutions. Bioinformatics. 2017 Aug 23 doi:10.1093/bioinformatics/btx531. [Epub ahead of print] PubMed PMID: 28961695.	27	114
2017	Tools/ Analysis Resource	Jurtz V, Paul S, Andreaata M, Marcatili P, Peters B, Nielsen M. NetMHCpan-4.0: Improved Peptide-MHC Class I Interaction Predictions Integrating Eluted Ligand and Peptide Binding Affinity Data. J Immunol. 2017 Nov 1;199(9):3360-3368. doi:10.4049/jimmunol/1700893. Epub 2017 Oct 4. PubMed PMID: 28978689; PubMed Central PMCID: PMC5679736.	207	827
2017	Tools/ Analysis Resource	Andreatta M, Trolle T, Yan Z, Greenbaum JA, Peters B, Nielsen M. An automated benchmarking platform for MHC class II binding prediction methods. Bioinformatics. 2017 Dec 21. doi:10.1093/bioinformatics/btx820. [Epub ahead of print] PubMed PMID: 29281002.	11	55
2016	Tools/ Analysis Resource	Rasmussen M, Fenoy E, Harndahl M, Kristensen AB, Nielsen IK, Nielsen M, Buus S. Pan-Specific Prediction of Peptide-MHC Class I Complex Stability, a Correlate of T Cell Immunogenicity. J Immunol. 2016 Aug 15;197(4):1517-24. doi: 10.4049/jimmunol.1600582. Epub 2016 Jul 8. PubMed PMID: 27402703.	26	105

2016	General	Bandrowski A, Brinkman R, Brochhausen M, Brush MH, Bug B, Chibucos MC, Clancy K, Courtot M, Derom D, Dumontier M, Fan L, Fostel J, Fragoso G, Gibson F, Gonzalez-Beltran A, Haendel MA, He Y, Heiskanen M, Hernandez-Boussard T, Jensen M, Lin Y, Lister AL, Lord P, Malone J, Manduchi E, McGee M, Morrison N, Overton JA, Parkinson H, Peters B, Rocca-Serra P, Ruttenberg A, Sansone SA, Scheuermann RH, Schober D, Smith B, Soldatova LN, Stoeckert CJ Jr, Taylor CF, Torniai C, Turner JA, Vita R, Whetzel PL, Zheng J. The Ontology for Biomedical Investigations. PLoS One. 2016 Apr 29;11(4):e0154556. doi: 10.1371/journal.pone.0154556. eCollection 2016. PubMed PMID: 27128319	33	214
2016	Tools/ Analysis Resource	Bresciani A, Paul S, Schommer N, Dillon MB, Bancroft T, Greenbaum J, Sette A, Nielsen M, Peters B. T-cell recognition is shaped by epitope sequence conservation in the host proteome and microbiome. Immunology. 2016 May;148(1):34-9. doi: 10.1111/imm.12585. Epub 2016 Feb 8. PubMed PMID: 26789414	4	18
2016	General	Fleri W, Salimi N, Vita R, Peters B, Sette A, Immune Epitope Database and Analysis Resource, Encyclopedia of Immunobiology, Vol. 2, Elsevier Ltd., 20 May 2016, doi:10.1016/B978-0-12-374279-7.06004-5	0	0
2016	Tools/ Analysis Resource	McMurtrey C, Trolle T, Sansom T, Remesh SG, Kaever T, Bardet W, Jackson K, McLeod R, Sette A, Nielsen M, Zajonc DM, Blader IJ, Peters B, Hildebrand W. Toxoplasma gondii peptide ligands open the gate of the HLA class I binding groove. Elife. 2016 Jan 29;5. pii: e12556. doi: 10.7554/eLife.12556. PubMed PMID: 26824387	6	56
2016	Tools/ Analysis Resource	Nielsen M, Andreatta M, NetMHCpan-3.0; improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length data sets. Genome Medicine, March 2016, Mar 30;8(1):33. doi: 10.1186/s13073-016-0288-x. PubMed PMID: 27029192	60	393
2016	Tools/ Analysis Resource	Paul S, Sidney J, Sette A, Peters B. TepiTool: A Pipeline for Computational Prediction of T Cell Epitope Candidates. Curr Protoc Immunol. 2016 Aug 1;114:18.19.1-18.19.24. doi: 10.1002/cpim.12. PubMed PMID: 27479659	28	117
2016	General	Ponomarenko J, Vaughan K, Paul S, Peters B, Sette A, Haeussler M, Maurer-Stroh S, Ebola: an analysis of immunity at the molecular level, 2015 International Workshop on Artificial Immune Systems (AIS), Taormina, 2015, pp. 1-8. doi: 10.1109/AISW.2015.7469230,published online at IEEE Xplore Digital Library, URL: http://ieeexplore.ieee.org/stamp/stamp.jsp?tp=&arnumber=7469230&isnumber=7469223	0	5
2016	Tools/ Analysis Resource	Trolle T, McMurtrey CP, Sidney J, Bardet W, Osborn SC, Kaever T, Sette A, Hildebrand WH, Nielsen M, Peters B. The Length Distribution of Class I-Restricted T Cell Epitopes Is Determined by Both Peptide Supply and MHC Allele-Specific Binding Preference. J Immunol. 2016 Feb 15;196(4):1480-7. doi: 10.4049/jimmunol.1501721. Epub 2016 Jan 18. PubMed PMID: 26783342	16	114

2016	General	Vita R, Overton JA, Seymour E, Sidney J, Kaufman J, Tallmadge RL, Ellis S, Hammond J, Butcher GW, Sette A, Peters B. An ontology for major histocompatibility restriction. J Biomed Semantics. 2016 Jan 11;7:1. doi:10.1186/s13326-016-0045-5. eCollection 2016. PubMed PMID: 26759709	0	4
2016	General	Xu X, Vaughan K, Weiskopf D, Grifoni A, Diamond MS, Sette A, Peters B. Identifying Candidate Targets of Immune Responses in Zika Virus Based on Homology to Epitopes in Other Flavivirus Species. PLoS Curr. 2016 Nov 15;8. pii: ecurrents.outbreaks.9aa2e1fb61b0f632f58a098773008c4b. doi: 10.1371/currents.outbreaks.9aa2e1fb61b0f632f58a098773008c4b. PubMed PMID: 28018746	7	70
2015	General	Cheloha RW, Sullivan JA, Wang T, Sand JM, Sidney J1, Sette A1, Cook ME, Suresh M, Gellman SH. Consequences of periodic α-to-β(3) residue replacement for immunological recognition of peptide epitopes. ACS Chem Biol. 2015 Mar 20;10(3):844-54. doi: 10.1021/cb500888q. Epub 2015 Jan 5. PubMed PMID: 25559929.	1	11
2015	General	Vita R, Vasilevsky N, Bandrowski A, Haendel M, Sette A, Peters B. Reproducibility and Conflicts in Immune Epitope Data. Immunology. 2015 Dec 17. doi: 10.1111/imm.12566. [Epub ahead of print] PubMed PMID: 26678806	0	4
2015	Tools/ Analysis Resource	Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M. “Automated benchmarking of peptide-MHC class I binding predictions”. Bioinformatics. 2015 Feb 25. pii: btv123. [Epub ahead of print] PubMed PMID: 25717196.	13	111
2015	Tools/ Analysis Resource	Sela-Culang, I., 1, Ofran, Y., and Peters, B. “Antibody specific epitope prediction - emergence of a new paradigm”, Current Opinion in Virology, Volume 11, April 2015, Pages 98–102, PMID: 25837466.	5	45
2015	Tools/ Analysis Resource	Paul S, Lindestam Arlehamn CS, Scriba TJ, Dillon MB, Oseroff C, Hinz D, McKinney DM, Carrasco Pro S, Sidney J, Peters B, Sette A. Development and validation of a broad scheme for prediction of HLA class II restricted T cell epitopes. J Immunol Methods. 2015 Jul;422:28-34. doi: 10.1016/j.jim.2015.03.022. Epub 2015 Apr 7. PubMed PMID: 25862607.	24	108
2015	Tools/ Analysis Resource	Paul S, Dillon MB, Lindestam Arlehamn CS, Huang H, Davis MM, McKinney DM, Scriba TJ, Sidney J, Peters B, Sette A. A Population Response Analysis Approach To Assign Class II HLA-Epitope Restrictions. J Immunol. 2015 Jun 15;194(12):6164-76. doi: 10.4049/jimmunol.1403074. Epub 2015 May 6. PubMed PMID: 25948811; PubMed Central PMCID: PMC4458389.	1	25
2015	Tools/ Analysis Resource	Klausen MS, Anderson MV, Jespersen MC, Nielsen M, Marcatili P. LYRA, a webserver for lymphocyte receptor structural modeling. Nucleic Acids Res. 2015 Jul 1;43(W1):W349-W355. Epub 2015 May 24. PubMed PMID: 26007650.	4	41
2015	Tools/ Analysis Resource	Andreatta M, Karosiene E, Rasmussen M, Stryhn A, Buus S, Nielsen M. Accurate pan-specific prediction of peptide-MHC class II binding affinity with improved binding core	24	221

		identification. Immunogenetics. 2015 Sep 29. [Epub ahead of print] PubMed PMID: 26416257.		
2015	Tools/ Analysis Resource	Carrasco Pro S, Sidney J, Paul S, Lindestam Arlehamn C, Weiskopf D, Peters B, Sette A. Automatic Generation of Validated Specific Epitope Sets. J Immunol Res. 2015;2015:763461. doi: 10.1155/2015/763461. Epub 2015 Oct 19. PubMed PMID: 26568965.	13	47
2015	Tools/ Analysis Resource	Andreatta M, Nielsen M. Gapped sequence alignment using artificial neural networks: application to the MHC class I system. Bioinformatics. 2015 Oct 29. pii: btv639. [Epub ahead of print] PubMed PMID: 26515819.	136	716
2015	General	Vaughan K, Ponomarenko J, Peters B, Sette A. Analysis of Human RSV Immunity at the Molecular Level: Learning from the Past and Present. PLoS One. 2015 May 22;10(5):e0127108. doi: 10.1371/journal.pone.0127108. eCollection 2015. PubMed PMID: 26001197 .	0	3
2015	General	Sette A, Paul S, Vaughan K, Peters B. The Use of the Immune Epitope Database to Study Autoimmune Epitope Data Related to Alopecia Areata. J Investig Dermatol Symp Proc. 2015 Nov;17(2):36-41. doi: 10.1038/jidsymp.2015.39. Review. PubMed PMID: 26551944.	1	6
2014	Tools/ Analysis Resource	Hansen AM, Rasmussen M, Svitek N, Harndahl M, Golde WT, Barlow J, Nene V, Buus S, Nielsen M. Characterization of binding specificities of bovine leucocyte class I molecules: impacts for rational epitope discovery. Immunogenetics. 2014 Dec;66(12):705-18. doi: 10.1007/s00251-014-0802-5. Epub 2014 Sep 4. PubMed PMID: 25186069.	1	9
2014	General	Ponomarenko J, Vaughan K, Sette A, Maurer-Stroh S. Conservancy of mAb Epitopes in Ebolavirus Glycoproteins of Previous and 2014 Outbreaks. PLOS Currents Outbreaks. 2014 Nov 3. Edition 1.	0	13
2014	General	Vaughan K, Peters B, Mallone R, von Herrath M, Roep BO, Sette A. Navigating diabetes-related immune epitope data: resources and tools provided by the Immune Epitope Database (IEDB). Immunome Res. 2013;9(1). doi: 10.4172/1745-7580.1000063. PubMed PMID: 25140192; PubMed Central PMCID: PMC4134942	0	6
2014	General	Vaughan K, Seymour E, Peters B, Sette A. Substantial gaps in knowledge of Bordetella pertussis antibody and T cell epitopes relevant for natural immunity and vaccine efficacy. Hum Immunol. 2014 May;75(5):440-451. doi: 10.1016/j.humimm.2014.02.013. Epub 2014 Feb 12. Review. PubMed PMID: 24530743	2	21
2014	Tools/ Analysis Resource	Trolle T, Nielsen M. NetTepi: an integrated method for the prediction of T cell epitopes. Immunogenetics. 2014 May 27. [Epub ahead of print] PubMed PMID: 24863339.	3	39
2014	Tools/ Analysis Resource	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	6	99

2014	General	Vita R, Overton JA, Greenbaum JA, Ponomarenko J, Clark JD, Cantrell JR, Wheeler DK, Gabbard JL, Hix D, Sette A, Peters B. The immune epitope database (IEDB) 3.0. Nucleic Acids Res. 2014 Oct 9. pii: gku938. [Epub ahead of print] PubMed PMID: 25300482.	74	855
2013	General	Kim Y, Yewdell JW, Sette A, Peters B. Positional bias of MHC class I restricted T-cell epitopes in viral antigens is likely due to a bias in conservation. PLoS Comput Biol. 2013 Jan;9(1):e1002884. doi: 10.1371/journal.pcbi.1002884. Epub 2013 Jan 24. PubMed PMID: 23357871; PubMed Central PMCID: PMC3554532.	0	11
2013	General	Vita R, Overton JA, Greenbaum JA, Sette A; OBI consortium, Peters B. Query enhancement through the practical application of ontology: the IEDB and OBI. J Biomed Semantics. 2013 Apr 15;4 Suppl 1:S6. doi: 10.1186/2041-1480-4-S1-S6. Epub 2013 Apr 15. PubMed PMID: 23734660; PubMed Central PMCID: PMC3633001	0	6
2013	Tools/ Analysis Resource	Jessen LE, Hoof I, Lund O, Nielsen M. SigniSite: Identification of residue-level genotype-phenotype correlations in protein multiple sequence alignments. Nucleic Acids Res. 2013 Jul 1;41(Web Server issue):W286-91. doi: 10.1093/nar/gkt497. Epub 2013 Jun 12. PMID: 23761454; PMCID: PMC3692133	3	20
2013	Tools/ Analysis Resource	Jørgensen KW, Rasmussen M, Buus S, Nielsen M. NetMHCstab - predicting stability of peptide:MHC-I complexes; impacts for CTL epitope discovery. Immunology. 2013 Aug 8. doi: 10.1111/imm.12160. PubMed PMID: 23927693; PubMed Central PMCID: PMC3893846	10	112
2013	Tools/ Analysis Resource	Schubert B, Lund O, Nielsen M. Evaluation of peptide selection approaches for epitope-based vaccine design. Tissue Antigens. 2013 Oct;82(4):243-51. doi: 10.1111/tan.12199. PubMed PMID: 24461003.	3	24
2013	Tools/ Analysis Resource	Karosiene E, Rasmussen M, Blicher T, Lund O, Buus S, Nielsen M. NetMHCIIpan-3.0, a common pan-specific MHC class II prediction method including all three human MHC class II isotypes, HLA-DR, HLA-DP and HLA-DQ. Immunogenetics. 2013 Oct;65(10):711-24. doi: 10.1007/s00251-013-0720-y. Epub 2013 Jul 31. PubMed PMID: 23900783	25	218
2013	General	Vaughan K, Peters B, O'Connor KC, Martin R, Sette A. A molecular view of multiple sclerosis and experimental autoimmune encephalitis: What can we learn from the epitope data? J Neuroimmunol. 2013 Dec 12. pii: S0165-5728(13)00340-8. doi: 10.1016/j.jneuroim.2013.12.009. PubMed PMID: 24365494	0	12
2013	Tools/ Analysis Resource	Paul S, Kolla RV, Sidney J, Weiskopf D, Fleri W, Kim Y, Peters B, Sette A. Evaluating the immunogenicity of protein drugs by applying in vitro MHC binding data and the immune epitope database and analysis resource. Clin Dev Immunol. 2013;2013:467852. doi: 10.1155/2013/467852. Epub 2013 Oct 8. PubMed PMID: 24222776; PubMed Central PMCID: PMC3816028	1	44

2013	Tools/ Analysis Resource	Calis JJ, Maybeno M, Greenbaum JA, Weiskopf D, De Silva AD, Sette A, Kesmir C, Peters B. Properties of MHC class I presented peptides that enhance immunogenicity. PLoS Comput Biol. 2013 Oct;9(10):e1003266. doi: 10.1371/journal.pcbi.1003266. Epub 2013 Oct 24. PubMed PMID: 24204222; PubMed Central PMCID: PMC3808449	121	445
2013	Tools/ Analysis Resource	Paul S, Weiskopf D, Angelo MA, Sidney J, Peters B, Sette A. HLA Class I Alleles Are Associated with Peptide-Binding Repertoires of Different Size, Affinity, and Immunogenicity. J Immunol. 2013 Dec 15;191(12):5831-9. doi: 10.4049/jimmunol.1302101. Epub 2013 Nov 4. PubMed PMID: 24190657; PubMed Central PMCID: PMC3872965	25	189
2012	Tools/ Analysis Resource	Lundegaard C, Lund O, Nielsen M. Predictions versus high-throughput experiments in T-cell epitope discovery: competition or synergy? Expert Rev Vaccines. 2012 Jan;11(1):43-54. doi: 10.1586/erv.11.160. PubMed PMID: 22149708.	3	13
2012	Tools/ Analysis Resource	Karosiene E, Lundegaard C, Lund O, Nielsen M. NetMHCcons: a consensus method for the major histocompatibility complex class I predictions. Immunogenetics. 2012 Mar;64(3):177-86. doi: 10.1007/s00251-011-0579-8. Epub 2011 Oct 20. PubMed PMID: 22009319.	37	184
2012	Tools/ Analysis Resource	Kim Y, Ponomarenko J, Zhu Z, Tamang D, Wang P, Greenbaum J, Lundegaard C, Sette A, Lund O, Bourne PE, Nielsen M, Peters B. Immune epitope database analysis resource. Nucleic Acids Res. 2012 Jul;40 (Web Server issue):W525-30. Epub 2012 May 18. PubMed PMID: 22610854.	44	385
2012	General	Kim Y, Vaughan K, Greenbaum J, Peters B, Law M, Sette A. A Meta-Analysis of the Existing Knowledge of Immunoreactivity against Hepatitis C Virus (HCV). PLoS One. 2012;7(5):e38028. Epub 2012 May 31. PubMed PMID: 22675428; PubMed Central PMCID: PMC3364976.	2	17
2012	Tools/ Analysis Resource	Kringelum JV, Nielsen M, Padkjær SB, Lund O. Structural analysis of B-cell epitopes in antibody:protein complexes. Mol Immunol. 2013 Jan;53(1-2):24-34. doi: 10.1016/j.molimm.2012.06.001. Epub 2012 Jul 10. PubMed PMID: 22784991; PubMed Central PMCID: PMC3461403	27	211
2012	General	Salimi N, Fleri W, Peters B, Sette A. The Immune Epitope Database: A Historical Retrospective of the First Decade. Immunology. 2012 Jun 8. doi:10.1111/j.1365-2567.2012.03611.x. [Epub ahead of print] PubMed PMID: 22681406.	1	34
2012	General	Vaughan K, Kim Y, Sette A. A comparison of epitope repertoires associated with myasthenia gravis in humans and nonhuman hosts. Autoimmune Dis. 2012;2012:403915. doi: 10.1155/2012/403915. Epub 2012 Dec 2. PubMed PMID: 23243503; PubMed Central PMCID: PMC3518085.	0	6
2012	General	Vaughan K, Peters B, Larche M, Pomes A, Broide D, Sette A. Strategies to Query and Display Allergy-Derived Epitope Data from the Immune Epitope Database. Int Arch Allergy Immunol. 2012 Nov 21;160(4):334-345. [Epub ahead of print] PubMed PMID: 23172234.	1	10

2011	Tools/ Analysis Resource	Lundegaard C, Lund O, Nielsen M. Prediction of epitopes using neural network based methods. J Immunol Methods. 2011 Nov 30;374(1-2):26-34. doi: 10.1016/j.jim.2010.10.011. Epub 2010 Oct 31. PubMed PMID: 21047511.	6	37
2011	Tools/ Analysis Resource	Wang P, Sidney J, Sette A, Peters B. A computational pipeline to generate MHC binding motifs. Immunome Res. 2011 May;7(2). pii: 3. PubMed PMID: 28747991	0	0
2011	General	Seymour E., Damle R., Sette A., Peters B. (2011). "Cost sensitive hierarchical document classification to triage PubMed abstracts for manual curation." BMC Bioinformatics 12(1): 482. [Epub ahead of print]. PMID: 22182279.	1	10
2011	General	Vaughan K, Greenbaum J, Kim Y, Vita R, Chung J, Peters B, Broide D, Goodman R, Grey H, Sette A. Towards defining molecular determinants recognized by adaptive immunity in allergic disease: an inventory of the available data. J Allergy (Cairo). 2010;2010:628026. Epub 2011 Feb 13. PubMed PMID: 21403821.	1	12
2011	General	Vita R, Peters B, Josephs Z, de Matos P, Ennis M, Turner S, Steinbeck C, Seymour E, Zarebski L, Sette A. (2011). "A Model for Collaborative Curation, The IEDB and ChEBI Curation of Non-peptidic Epitopes." Immunome Res. 2011 Apr 1;7(1):1-8. PubMed PMID: 21897450.	0	2
2010	Tools/ Analysis Resource	Stranzl T, Larsen MV, Lundegaard C, Nielsen M. NetCTLpan: pan-specific MHC class I pathway epitope predictions. Immunogenetics. 2010 Jun;62(6):357-68. doi: 10.1007/s00251-010-0441-4. Epub 2010 Apr 9. PubMed PMID: 20379710.	41	138
2010	General	Oseroff C, Sidney J, Kotturi MF, Kolla R, Alam R, Broide DH, Wasserman SI, Weiskopf D, McKinney DM, Chung JL, Petersen A, Grey H, Peters B, Sette A. Molecular determinants of T cell epitope recognition to the common Timothy grass allergen. PubMed PMID: 20554959.	6	34
2010	General	Sidney J, Steen A, Moore C, Ngo S, Chung J, Peters B, Sette A. Divergent motifs but overlapping binding repertoires of six HLA-DQ molecules frequently expressed in the worldwide human population. J Immunol. 2010 Oct 1;185(7):4189-98. doi: 10.4049/jimmunol.1001006. Epub 2010 Sep 1. PubMed PMID: 20810981.	3	24
2010	General	Sidney J, Steen A, Moore C, Ngo S, Chung J, Peters B, Sette A. Five HLA-DP molecules frequently expressed in the worldwide human population share a common HLA supertypic binding specificity. J Immunol. 2010 Mar 1;184(5):2492-503. doi: 10.4049/jimmunol.0903655. Epub 2010 Feb 5. PubMed PMID: 20139279	6	36
2010	General	Moutaftsi M, Tscharke DC, Vaughan K, Koelle DM, Stern L, Calvo-Calle M, Ennis F, Terajima M, Sutter G, Crotty S, Drexler I, Franchini G, Yewdell JW, Head SR, Blum J, Peters B, Sette A. Uncovering the interplay between CD8, CD4 and antibody responses to complex pathogens. Future Microbiol. 2010 Feb;5(2):221-39. doi: 10.2217/fmb.09.110. PubMed: 20143946	5	28
2010	Tools/ Analysis Resource	Rapin N, Hoof I, Lund O, Nielsen M. The MHC motif viewer: a visualization tool for MHC binding motifs. Curr Protoc Immunol. 2010 Feb;Chapter 18:Unit 18.17. doi: 10.1002/0471142735.im1817s88. PubMed PMID: 20143317	3	14

2010	General	Brinkman RR, Courtot M, Derom D, Fostel JM, He Y, Lord P, Malone J, Parkinson H, Peters B, Rocca-Serra P, Ruttenberg A, Sansone SA, Soldatova LN, Stoeckert CJ Jr, Turner JA, Zheng J; OBI consortium. Modeling biomedical experimental processes with OBI. J Biomed Semantics. 2010 Jun 22;1 Suppl 1:S7. PubMed PMID: 20626927.	6	223
2010	Tools/ Analysis Resource	Kim Y, Sette A, Peters B. Applications for T-cell epitope queries and tools in the Immune Epitope Database and Analysis Resource. J Immunol Methods. 2010 Oct 31. [Epub ahead of print] PubMed PMID: 21047510.	1	47
2010	Tools/ Analysis Resource	Nielsen M, Lund O, Buus S, Lundegaard C. MHC class II epitope predictive algorithms. Immunology. 2010 Jul;130(3):319-28. Epub 2010 Apr 12. Review. PubMed PMID: 20408898;	18	175
2010	General	Ponomarenko J, Papangelopoulos N, Zajonc DM, Peters B, Sette A, Bourne PE. IEDB-3D: structural data within the immune epitope database. Nucleic Acids Res. 2010 Oct 28. [Epub ahead of print] PubMed PMID: 21030437.	2	53
2010	General	Salimi N, Fleri W, Peters B, Sette A. Design and utilization of epitope-based databases and predictive tools. Immunogenetics. 2010 Apr;62(4):185-96. Epub 2010 Mar 6. Review. PubMed PMID: 20213141; PubMed Central PMCID: PMC2843836.	2	36
2010	General	Vaughan K, Greenbaum J, Blythe M, Peters B, Sette A. Meta-analysis of all immune epitope data in the Flavivirus genus: inventory of current immune epitope data status in the context of virus immunity and immunopathology. Viral Immunol. 2010 Jun;23(3):259-84. PubMed PMID: 20565291; PubMed Central PMCID: PMC2942863.	0	50
2010	Tools/ Analysis Resource	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.	68	479
2010	Tools/ Analysis Resource	Zhang H, Wang P, Papangelopoulos N, Xu Y, Sette A, Bourne PE, Lund O, Ponomarenko J, Nielsen M, Peters B. Limitations of Ab initio predictions of peptide binding to MHC class II molecules. PLoS One. 2010 Feb 17;5(2):e9272. PubMed PMID: 20174654; PubMed Central PMCID: PMC2822856.	4	40
2009	Tools/ Analysis Resource	Zhang H, Lundegaard C, Nielsen M. Pan-specific MHC class I predictors: a benchmark of HLA class I pan-specific prediction methods. Bioinformatics. 2009 Jan 1;25(1):83-9. doi: 10.1093/bioinformatics/btn579. Epub 2008 Nov 7. PubMed PMID: 18996943.	4	17
2009	General	Loffredo JT, Sidney J, Bean AT, Beal DR, Bardet W, Wahl A, Hawkins OE, Piaskowski S, Wilson NA, Hildebrand WH, Watkins DI, Sette A. 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. PubMed PMID: 19494300.	1	32
2009	General	Walsh SR, Gillis J, Peters B, Mothé BR, Sidney J, Sette A, Johnson RP. Diverse recognition of conserved orthopoxvirus CD8+ T cell epitopes in vaccinated rhesus macaques. Vaccine. 2009 Aug 6;27(36):4990-5000. doi:	0	1

		10.1016/j.vaccine.2009.05.077. Epub 2009 Jun 14. PubMed PMID: 19531389.		
2009	General	Sette A, Grey H, Oseroff C, Peters B, Moutaftsi M, Crotty S, Assarsson E, Greenbaum J, Kim Y, Kolla R, Tscharke D, Koelle D, Johnson RP, Blum J, Head S, Sidney J. 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. Vaccine. 2009 Dec 30;27 Suppl 6:G21-6. doi: 10.1016/j.vaccine.2009.10.011. PubMed PMID: 20006135.	2	16
2009	General	Davies V, Vaughan K, Damle R, Peters B, Sette A. Classification of the universe of immune epitope literature: representation and knowledge gaps. PLoS One. 2009 Sep 14;4(9):e6948. PubMed PMID: 19774228;	2	13
2009	General	Greenbaum JA, Kotturi MF, Kim Y, Oseroff C, Vaughan K, Salimi N, Vita R, Ponomarenko J, Scheuermann RH, Sette A, Peters B. Pre-existing immunity against swine-origin H1N1 influenza viruses in the general human population. Proc Natl Acad Sci U S A. 2009 Dec 1;106(48):20365-70. Epub 2009 Nov 16. PubMed PMID: 19918065; PubMed Central PMCID: PMC2777968.	9	291
2009	Tools/ Analysis Resource	Hoof I, Peters B, Sidney J, Pedersen LE, Sette A, Lund O, Buus S, Nielsen M, NetMHCpan, a method for MHC class I binding prediction beyond humans. Immunogenetics. 2009 Jan;61(1):1-13. PMID: 19002680.	50	604
2009	Tools/ Analysis Resource	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.	16	135
2009	General	Vaughan K, Blythe M, Greenbaum J, Zhang Q, Peters B, Doolan DL, Sette A, Meta-analysis of immune epitope data for all Plasmodia: overview and applications for malarial immunobiology and vaccine-related issues. Parasite Immunol. 2009 Feb;31(2):78-97. [PMID: 19149776]	1	1
2009	General	Vita R, Zarebski L, Greenbaum JA, Emami H, Hoof I, Salimi N, Damle R, Sette A, Peters B. The Immune Epitope Database 2.0. Nucleic Acids Res. 2009 Nov 11. [Epub ahead of print] PubMed PMID: 19906713.	18	536
2009	Tools/ Analysis Resource	Zhang H, Lund O, Nielsen M. The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: Application to MHC-peptide binding. Bioinformatics. 2009 Mar 17. PMID: 19297351.	24	143
2008	General	Sidney J, Assarsson E, Moore C, Ngo S, Pinilla C, Sette A, Peters B. Quantitative peptide binding motifs for 19 human and mouse MHC class I molecules derived using positional scanning combinatorial peptide libraries. Immunome Res. 2008 Jan 25;4:2. doi: 10.1186/1745-7580-4-2. PubMed PMID: 18221540.	20	156
2008	General	Sidney J, Peters B, Frahm N, Brander C, Sette A. HLA class I supertypes: a revised and updated classification. BMC Immunol. 2008 Jan 22;9:1. doi: 10.1186/1471-2172-9-1. PubMed: 18211710.	49	274

2008	General	Kim M, Taylor J, Sidney J, Mikloska Z, Bodsworth N, Lagios K, Dunckley H, Byth-Wilson K, Denis M, Finlayson R, Khanna R, Sette A, Cunningham AL. Immunodominant epitopes in herpes simplex virus type 2 glycoprotein D are recognized by CD4 lymphocytes from both HSV-1 and HSV-2 seropositive subjects. J Immunol. 2008 Nov 1;181(9):6604-15. PubMed PMID: 18941251.	0	7
2008	Tools/ Analysis Resource	Lundegaard C., K. Lamberth, M. Harndahl, S. Buus, O. Lund, M. Nielsen. (2008). “NetMHC-3.0: accurate web accessible predictions of human, mouse and monkey MHC class I affinities for peptides of length 8-11.” Nucleic Acids Res. 2008 36:W509-12. PMID: 18996943.	65	654
2008	Tools/ Analysis Resource	Nielsen, M., C. Lundegaard, T. Blicher, B. Peters, A. Sette, S. Justesen, S. Buus, O. Lund. (2008). "Quantitative Predictions of Peptide Binding to Any HLA-DR Molecule of Known Sequence: NetMHCIIpan." PLoS Computational Biology 4(7). PMID: 18604266.	16	211
2008	Tools/ Analysis Resource	Ponomarenko J, H. H. Bui, W. Li, N. Fusseder, P. E. Bourne, A. Sette, B. Peters. (2008). “ElliPro: a new structure-based tool for the prediction of antibody epitopes.” BMC Bioinformatics, 9(514). PMID: 19055730.	206	833
2008	Tools/ Analysis Resource	Ponomarenko J. V., M. H. C. van Regenmortel (2008) “B-cell epitope prediction.” Structural Bioinformatics, Ed: Bourne PE, Gu J. Wiley-Liss; 2 edition.	4	63
2008	General	Vita R., B. Peters, A. Sette. (2008). “The Curation Guidelines of the Immune Epitope Database and Analysis Resource.” Cytometry A 73(11): 1066-1070. PMID: 18688821	2	26
2008	Tools/ Analysis Resource	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	68	683
2008	General	Zarebski L. M., K. Vaughan, J. Sidney, B. Peters, H. Grey, K. D. Janda, A. Casadevall, A. Sette. (2008). “Analysis of epitope information related to Bacillus anthracis and Clostridium botulinum.” Expert Rev Vaccines 7(1): 55-74. PMID: 18251694	0	23
2008	Tools/ Analysis Resource	Zhang, Q., P. Wang, et al. (2008). "Immune epitope database analysis resource (IEDB-AR)." Nucleic Acids Research 36: W513-W518. PMID: 18515843	27	266
2007	general	Sidney J, Peters B, Moore C, Pencille TJ, Ngo S, Masterman KA, Asabe S, Pinilla C, Chisari FV, Sette A. Characterization of the peptide-binding specificity of the chimpanzee class I alleles A 0301 and A 0401 using a combinatorial peptide library. Immunogenetics. 2007 Sep;59(9):745-51. Epub 2007 Aug 16. PubMed PMID: 17701407.	0	4
2007	Tools/ Analysis Resource	Beaver JE, Bourne PE, Ponomarenko JV. EpitopeViewer: a Java application for the visualization and analysis of immune epitopes in the Immune Epitope Database and Analysis Resource (IEDB). Immunome Res. 2007 Feb 21;3:3. PMID: 17313688	2	42
2007	General	Blythe MJ, Zhang Q, Vaughan K, de Castro R Jr, Salimi N, Bui HH, Lewinsohn DM, Ernst JD, Peters B, Sette A. An analysis of the epitope knowledge related to Mycobacteria. Immunome Res. 2007 Dec 14;3(1):10. PMID: 18081934	1	54

2007	General	Bui HH, Peters B, Assarsson E, Mbawuike I, Sette A. Ab and T cell epitopes of influenza A virus, knowledge and opportunities. Proc Natl Acad Sci U S A. 2007 Jan 2;104(1):246-51. PMID: 17200302	2	176
2007	Tools/ Analysis Resource	Bui HH, Sidney J, Li W, Fusseder N, Sette A. Development of an epitope conservancy analysis tool to facilitate the design of epitope-based diagnostics and vaccines. BMC Bioinformatics. 2007 Sep 26;8(1):361. PMID: 17897458.	62	318
2007	General	Ernst JD, Lewinsohn DM, Behar S, Blythe M, Schlesinger LS, Kornfeld H, Sette A. Meeting Report: NIH Workshop on the Tuberculosis Immune Epitope Database. Tuberculosis (Edinb). 2007 Dec 6. PMID: 18068490	1	29
2007	Tools/ Analysis Resource	Greenbaum JA, Andersen PH, Blythe M, Bui HH, Cachau RE, Crowe J, Davies M, Kolaskar AS, Lund O, Morrison S, Mumey B, Ofran Y, Pellequer JL, Pinilla C, Ponomarenko JV, Raghava GP, van Regenmortel MH, Roggen EL, Sette A, Schlessinger A, Sollner J, Zand M, Peters B. Towards a consensus on datasets and evaluation metrics for developing B-cell epitope prediction tools. J Mol Recognit. 2007 Mar-Apr;20(2):75-82. PMID: 17205610	13	202
2007	Tools/ Analysis Resource	Lundegaard C, Lund O, Kesmir C, Brunak S, Nielsen M. Modeling the adaptive immune system: predictions and simulations. Bioinformatics. 2007 Dec 15;23(24):3265-75. PMID: 18045832	8	109
2007	Tools/ Analysis Resource	Nielsen M, Lundegaard C, Blicher T, Lamberth K, Harndahl M, Justesen S, Røder G, Peters B, Sette A, Lund O, Buus S. NetMHCpan, a method for quantitative predictions of peptide binding to any HLA-A and -B locus protein of known sequence. PLoS ONE. 2007 Aug 29;2(8):e796. PMID: 17726526	45	461
2007	General	Peters B, Sette A. Integrating epitope data into the emerging web of biomedical knowledge resources. Nat Rev Immunol. 2007 Jun;7(6):485-90. PMID: 17479127	2	51
2007	Tools/ Analysis Resource	Ponomarenko JV, Bourne PE., Antibody-protein interactions: benchmark datasets and prediction tools evaluation. BMC Struct Biol. 2007 Oct 2;7(1):64. PMID: 17910770	13	195
2007	General	Sette A, Peters B., Immune epitope mapping in the post-genomic era: lessons for vaccine development. Curr Opin Immunol. 2007 Feb;19(1):106-10. PMID: 17113275	3	55
2007	General	Wang P, Morgan AA, Zhang Q, Sette A, Peters B. Automating document classification for the Immune Epitope Database. BMC Bioinformatics. 2007 Jul 26;8:269. PMID: 17655769	2	40
2006	Tools/ Analysis Resource	Bui HH, Sidney J, Dinh K, Southwood S, Newman MJ, Sette A. Predicting population coverage of T-cell epitope-based diagnostics and vaccines. BMC Bioinformatics. 2006 Mar 17;7(1):153. PMID: 16545123	97	429
2006	Tools/ Analysis Resource	Peters B, Bui HH, Frankild S, Nielson M, Lundegaard C, Kostem E, Basch D, Lamberth K, Harndahl M, Fleri W, Wilson SS, Sidney J, Lund O, Buus S, Sette A., A community resource benchmarking predictions of peptide binding to MHC-I molecules, PLoS Comput Biol. 2006 Jun 9;2(6):e65. Epub 2006 Jun 9. PMID: 16789818	5	275

2006	General	Salimi N, R. Vita. (2006). "The biocurator: connecting and enhancing scientific data". PLoS Comput Biol 2(10) :e125. PMID: 17069454	3	30
2006	General	Sette, A., H. H. Bui, S. Buus, W. Fleri, R. Kubo, O. Lund, D. Nemazee, J. V. Ponomarenko, M. Sathiamurthy, S. Stewart, S. Way, S. S. Wilson, B. Peters. (2006). “The Immune Epitope Database and Analysis Resource.” Pattern Recognition in Bioinformatics: International Workshop, Hong Kong, China, August 20, 2006 : Procedings, Springer, Jagath C. Rajapakse, Limsoon Wong, Raj Acharya (Eds). ISBN: 3540374469 9783540374466	0	3
2006	General	Vita R, K. Vaughan, L. Zarebski, N. Salimi, W. Fleri , H. Grey, M. Sathiamurthy, J. Mokili, H. H. Bui, P. E. Bourne, J. V. Ponomarenko, R. de Castro Jr, R. K. Chan, J. Sidney, S. S. Wilson, S. Stewart, S. Way, B. Peters, A. Sette. (2006) "Curation of complex, context-dependent immunological data." BMC Bioinformatics. 12(7): 341. PMID: 16836764	1	21
2005	General	Sette A, Sidney J, Bui HH, del Guercio MF, Alexander J, Loffredo J, Watkins DI, Mothé BR. Characterization of the peptide-binding specificity of Mamu-A*11 results in the identification of SIV-derived epitopes and interspecies cross-reactivity. Immunogenetics. 2005 Apr;57(1-2):53-68. Epub 2005 Mar 4. PubMed PMID: 15747117.	0	0
2005	Tools/ Analysis Resource	Peters B, Bui HH, Sidney J, Weng Z, Loffredo JT, Watkins DI, Mothé BR, Sette A. A computational resource for the prediction of peptide binding to Indian rhesus macaque MHC class I molecules. Vaccine. 2005 Nov 1;23(45):5212-24. Epub 2005 Aug 18. PubMed PMID: 16137805.	0	5
2005	Tools/ Analysis Resource	Peters B, Sette A. Generating quantitative models describing the sequence specificity of biological processes with the stabilized matrix method. BMC Bioinformatics. 2005 May 31;6:132. PMID: 15927070	40	461
2005	General	Peters, B., J. Sidney, P. Bourne, H. H. Bui, S. Buus, G. Doh, W. Fleri, M. Kronenberg, R.Kubo, O. Lund, D. Nemazee, J. V. Ponomarenko, M. Sathiamurthy, S. Schoenberger, S. Stewart, P. Surko, S. Way, S. Wilson, A. Sette. (2005). "The design and implementation of the immune epitope database and analysis resource." Immunogenetics 57(5): 326-336. PMID: 15895191	4	80
2005	General	Peters, B., J. Sidney, P. Bourne, H. H. Bui, S. Buus, G. Doh, W. Fleri, M. Kronenberg, R.Kubo, O. Lund, D. Nemazee, J. V. Ponomarenko, M. Sathiamurthy, S. Schoenberger, S. Stewart, P. Surko, S. Way, S. Wilson, A. Sette. (2005). "The Immune Epitope Database and Analysis Resource: From Vision to Blueprint." PLoS Biology 3(3). PMID: 15760272	7	327
2005	General	Sathiamurthy, M., B. Peters, H. H. Bui, J. Sidney, J. Mokili, S. S. Wilson, W. Fleri, D. McGuinness, P. Bourne, A. Sette. (2005). "An ontology for immune epitopes: application to the design of a broad scope database of immune reactivities." Immunome Res 1(2): 1745-7580. PMID: 16305755	0	28
2005	General	Sette, A., W. Fleri, B. Peters, M. Sathiamurthy, H. H. Bui, S. Wilson. (2005). "A Roadmap for the Immunomics of Category A–C Pathogens." Immunity 22(2): 155-161. PMID: 15773067	3	65

2004	General	Sette A. (2004). “The immune epitope database and analysis resource: from vision to blueprint.” Genome Inform Ser Workshop Genome Inform 15(2):299. PMID: 16312048	0	9
2004	General	Loffredo JT, Sidney J, Wojewoda C, Dodds E, Reynolds MR, Napoé G, Mothé BR, O'Connor DH, Wilson NA, Watkins DI, Sette A. 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. J Immunol. 2004 Oct 15;173(8):5064-76. PubMed PMID: 15470050.	0	10
2003	General	Iwai LK, Yoshida M, Sidney J, Shikanai-Yasuda MA, Goldberg AC, Juliano MA, Hammer J, Juliano L, Sette A, Kalil J, Travassos LR, Cunha-Neto E. 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. Mol Med. 2003 Sep-Dec;9(9-12):209-19. PubMed PMID: 15208742.	2	8
In-Text / Informal Citations (data captured from 2012 only)			552	3,073
Total from Publications			**4,432**	**23,602**

3.2 Publications Citing the IEDB in 2021

In 2021, the IEDB or Analysis Resource received a total of 4,432 individual citations (3,880 total citations for IEDB publications and 552 additional inline citations). This includes citations received by each of the 177 papers written by the IEDB team over the past nineteen years. This represents an increase of 374 citations over 3,506 from the previous year (2020). In 2021, the IEDB received 552 in-text citations that did not cite a specific reference, representing an increase of 88 over 464 from 2020.

The formal citation list was compiled by using Google Scholar and the ISI Web of Knowledge to find citations for each one of the 177 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 or Analysis Resource (AR). By reference, the General IEDB (G) papers received 1,229 citations in 2021 and the Analysis Resource (AR) papers received 2,651 citations. Additionally, there were 552 inline citations, which, in total, sums to the expected 4,432 citations for 2021.

4 References

Andreatta M, Karosiene E, Rasmussen M, Stryhn A, Buus S, Nielsen M. Accurate pan-specific prediction of peptide-MHC class II binding affinity with improved binding core identification. Immunogenetics. 2015 Nov;67(11-12):641-50. doi: 10.1007/s00251-015-0873-y. Epub 2015 Sep 29. PubMed PMID: 26416257; PubMed Central PMCID: PMC4637192.

Andreatta M, Nielsen M. Gapped sequence alignment using artificial neural networks: application to the MHC class I system. Bioinformatics. 2016 Feb 15;32(4):511-7. doi: 10.1093/bioinformatics/btv639. Epub 2015 Oct 29. PubMed PMID: 26515819.

Andreatta M, Trolle T, Yan Z, Greenbaum JA, Peters B, Nielsen M. An automated benchmarking platform for MHC class II binding prediction methods. Bioinformatics. 2018 May 1;34(9):1522-1528. doi: 10.1093/bioinformatics/btx820. PMID: 29281002; PMCID: PMC5925780.

Bui HH, Sidney J, Peters B, Sathiamurthy M, Sinichi A, Purton KA, Mothe BR, Chisari FV, Watkins DI, Sette A. Automated generation and evaluation of specific MHC binding predictive tools: ARB matrix applications. Immunogenetics. 2005 Jun;57(5):304-14. Epub 2005 May 3.

Bui HH, Sidney J, Dinh K, Southwood S, Newman MJ, Sette A. Predicting population coverage of T-cell epitope-based diagnostics and vaccines. BMC Bioinformatics. 2006 Mar 17;7(1):153. PMID: 16545123

Bui HH, Sidney J, Li W, Fusseder N, Sette A. Development of an epitope conservancy analysis tool to facilitate the design of epitope-based diagnostics and vaccines. BMC Bioinformatics. 2007 Sep 26;8(1):361. PMID: 17897458

Calis JJ, Maybeno M, Greenbaum JA, Weiskopf D, De Silva AD, Sette A, Keşmir C, Peters B. Properties of MHC class I presented peptides that enhance immunogenicity. PLoS Comput Biol. 2013 Oct;9(10):e1003266. doi:10.1371/journal.pcbi.1003266. Epub 2013 Oct 24. PubMed PMID: 24204222; PubMed Central PMCID: PMC3808449.

Chou P, Fasman G. Prediction of the secondary structure of proteins from their amino acid sequence. Adv Enzymol Relat Areas Mol Biol. 1978:45–148. PMID: 364941

Dhanda SK, Vaughan K, Schulten V, Grifoni A, Weiskopf D, Sidney J, Peters B, Sette A. Development of a novel clustering tool for linear peptide sequences. Immunology. 2018 Nov;155(3):331-345. doi: 10.1111/imm.12984. Epub 2018 Aug 6. PMID: 30014462; PMCID: PMC6187223.

Emini E, Hughes J, Perlow D, Boger J. Induction of hepatitis A virus-neutralizing antibody by a virus specific synthetic peptide. J Virol. 1985;55:836–839. PMID: 2991600

Giguère S, Drouin A, Lacoste A, Marchand M, Corbeil J, Laviolette F. MHC-NP: predicting peptides naturally processed by the MHC. J Immunol Methods. 2013 Dec 31;400-401:30-6. doi: 10.1016/j.jim.2013.10.003. Epub 2013 Oct 18. PubMed PMID: 24144535.

González-Galarza FF, Takeshita LY, Santos EJ, Kempson F, Maia MH, da Silva AL, Teles e Silva AL, Ghattaoraya GS, Alfirevic A, Jones AR, Middleton D. Allele frequency net 2015 update: new features for HLA epitopes, KIR and disease and HLA adverse drug reaction associations. Nucleic Acids Res. 2015 Jan;43(Database issue):D784-8. doi: 10.1093/nar/gku1166. Epub 2014 Nov 20. PubMed PMID: 25414323; PubMed Central PMCID: PMC4383964

Haste Andersen P, Nielsen M, Lund O. Prediction of residues in discontinuous B-cell epitopes using protein 3D structures. Protein Sci. 2006 Nov;15(11):2558-67. Epub 2006 Sep 25. PMID: 17001032

Hoof I, Peters B, Sidney J, Pedersen LE, Sette A, Lund O, Buus S, Nielsen M, NetMHCpan, a method for MHC class I binding prediction beyond humans. Immunogenetics. 2009 Jan;61(1):1-13. PMID: 19002680

Jespersen MC, Peters B, Nielsen M, Marcatili P. BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes. Nucleic Acids Res. 2017 May 2. doi: 10.1093/nar/gkx346. [Epub ahead of print] PubMed PMID: 28472356.

Karosiene E, Lundegaard C, Lund O and Nielsen M. 2012. NetMHCcons: a consensus method for the major histocompatibility complex class I predictions. *Immunogenetics* 64(3):177-186. PMID: 22009319

Karplus PA, Schulz GE. Prediction of chain flexibility in proteins. Naturwissenschaften. 1985. 72:212-213.

Keşmir C, Nussbaum AK, Schild H, Detours V, Brunak S. Prediction of proteasome cleavage motifs by neural networks. Protein Eng. 2002 Apr;15(4):287-96. PMID: 11983929

Kim Y, Ponomarenko J, Zhu Z, Tamang D, Wang P, Greenbaum J, Lundegaard C, Sette A, Lund O, Bourne PE, Nielsen M, Peters B. Immune epitope database analysis resource. Nucleic Acids Res. 2012 Jul;40(Web Server issue):W525-30. doi: 10.1093/nar/gks438. Epub 2012 May 18. PubMed PMID: 22610854; PubMed Central PMCID: PMC3394288

Kim Y, Sidney J, Buus S, Sette A, Nielsen M, Peters B. Dataset size and composition impact the reliability of performance benchmarks for peptide-MHC binding predictions. BMC Bioinformatics. 2014 Jul 14;15:241. doi: 10.1186/1471-2105-15-241. PubMed PMID: 25017736; PubMed Central PMCID: PMC4111843

Kim Y, Sidney J, Pinilla C, Sette A, Peters B. Derivation of an amino acid similarity matrix for peptide: MHC binding and its application as a Bayesian prior. BMC Bioinformatics. 2009 Nov 30;10:394. PMID: 19948066

Kolaskar AS, Tongaonkar PC. A semi-empirical method for prediction of antigenic determinants on protein antigens. FEBS Lett. 1990 Dec 10;276(1-2):172-4. PMID: 1702393

Kringelum JV, Lundegaard C, Lund O, Nielsen M. Reliable B cell epitope predictions: impacts of method development and improved benchmarking. PLoS Comput Biol. 2012;8(12):e1002829. doi: 10.1371/journal.pcbi.1002829. Epub 2012 Dec 27. PubMed PMID: 23300419; PubMed Central PMCID: PMC3531324.

Kringelum JV, Nielsen M, Padkjær SB, Lund O. Structural analysis of B-cell epitopes in antibody:protein complexes. Mol Immunol. 2013 Jan;53(1-2):24-34. doi: 10.1016/j.molimm.2012.06.001. Epub 2012 Jul 10. PubMed PMID: 22784991; PubMed Central PMCID: PMC3461403

Larsen JE, Lund O, Nielsen M. Improved method for predicting linear B-cell epitopes. Immunome Res. 2006 Apr 24;2:2. PMID: 16635264

Larsen MV, Lundegaard C, Lamberth K, Buus S, Brunak S, Lund O, Nielsen M. An integrative approach to CTL epitope prediction: a combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions. Eur J Immunol. 2005 Aug;35(8):2295-303. PMID: 15997466

Liang S, Zheng D, Standley DM, Yao B, Zacharias M, Zhang C. EPSVR and EPMeta: prediction of antigenic epitopes using support vector regression and multiple server results. BMC Bioinformatics. 2010 Jul 16;11:381. doi: 10.1186/1471-2105-11-381. PubMed PMID: 20637083; PubMed Central PMCID: PMC2910724.

Marcatili P, Rosi A, Tramontano A., 2008. PIGS: automatic prediction of antibody structures. Bioinformatics 24(17):1953-4. PMID: 18641403

Moutaftsi M, Peters B, Pasquetto V, Tscharke DC, Sidney J, Bui HH, Grey H, Sette A. A consensus epitope prediction approach identifies the breadth of murine T(CD8+)-cell responses to vaccinia virus. Nat Biotechnol. 2006 Jul;24(7):817-9. PMID: 16767078

Nielsen M, Andreatta M. NNAlign: a platform to construct and evaluate artificial neural network models of receptor-ligand interactions. Nucleic Acids Res. 2017 Apr 12. doi: 10.1093/nar/gkx276. [Epub ahead of print] PubMed PMID: 28407117.

Nielsen M, Andreatta M. NetMHCpan-3.0; improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length datasets. Genome Med. 2016 Mar 30;8(1):33. doi: 10.1186/s13073-016-0288-x. PubMed PMID: 27029192; PubMed Central PMCID: PMC4812631.

Nielsen M, Lundegaard C, Blicher T, Peters B, Sette A, Justesen S, Buus S, and Lund O. 2008. Quantitative predictions of peptide binding to any HLA-DR molecule of known sequence: NetMHCIIpan. PLoS Comput Biol.4(7)e1000107. PMID: 18604266

Nielsen M, Lundegaard C, Lund O. Prediction of MHC class II binding affinity using SMM-align, a novel stabilization matrix alignment method. BMC Bioinformatics. 2007 Jul 4;8:238. PMID: 17608956

Nielsen M, Lundegaard C, Worning P, Lauemoller SL, Lamberth K, Buus S, Brunak S, Lund O., Reliable prediction of T-cell epitopes using neural networks with novel sequence representations, Protein Sci. 2003 May;12(5):1007-17

Parker J, Guo D, Hodges R. New hydrophilicity scale derived from High-Performance Liquid Chromatography peptide retention data: correlation of predicted surface residues with antigenicity and X-ray-derived accessible sites. Biochemistry. 1986;25:5425–5432. PMID: 2430611

Paul S, Arlehamn CSL, Schulten V, Westernberg L, Sidney J, Peters B, Sette A. Experimental validation of the RATE tool for inferring HLA restrictions of T cell epitopes. BMC Immunol. 2017 Jun 21;18(Suppl 1):20. doi: 10.1186/s12865-017-0204-1. PubMed PMID: 28681704.

Paul S, Dillon MB, Lindestam Arlehamn CS, Huang H, Davis MM, McKinney DM, Scriba TJ, Sidney J, Peters B, Sette A. A population response analysis approach to assign class II HLA-epitope restrictions. J Immunol. 2015 Jun 15;194(12):6164-76. doi: 10.4049/jimmunol.1403074. Epub 2015 May 6. PubMed PMID: 25948811; PubMed Central PMCID: PMC4458389.

Paul S, Sidney J, Sette A, Peters B. TepiTool: A Pipeline for Computational Prediction of T Cell Epitope Candidates. Curr Protoc Immunol. 2016 Aug 1;114:18.19.1-18.19.24. doi: 10.1002/cpim.12. PubMed PMID: 27479659; PubMed Central PMCID: PMC4981331.

Peters B, Sidney J, Bourne P, Bui HH, Buus S, Doh G, Fleri W, Kronenberg M, Kubo R, Lund O, Nemazee D, Ponomarenko JV, Sathiamurthy M, Schoenberger S, Stewart S, Surko P, Way S, Wilson S, Sette A. The immune epitope database and analysis resource: from vision to blueprint. PLoS Biol. 2005 Mar;3(3):e91. PMID: 15760272.

Peters B, Sette A., "Generating quantitative models describing the sequence specificity of biological processes with the stabilized matrix method." BMC Bioinformatics 2005 May 31;6(1):132

Peters B, Bulik S, Tampe R, Van Endert PM, Holzhutter HG. Identifying MHC class I epitopes by predicting the TAP transport efficiency of epitope precursors. J Immunol. 2003 Aug 15;171(4):1741-9.

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

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

Rasmussen M, Fenoy E, Harndahl M, Kristensen AB, Nielsen IK, Nielsen M, Buus S. Pan-Specific Prediction of Peptide-MHC Class I Complex Stability, a Correlate of T Cell Immunogenicity. J

Immunol. 2016 Aug 15;197(4):1517-24. doi: 10.4049/jimmunol.1600582. Epub 2016 Jul 8. PubMed PMID: 27402703; PubMed Central PMCID: PMC4976001.

Rubinstein ND, Mayrose I, Martz E, Pupko T. Epitopia: a web-server for predicting B-cell epitopes. BMC Bioinformatics. 2009 Sep 14;10:287. doi: 10.1186/1471-2105-10-287. PubMed PMID: 19751513; PubMed Central PMCID: PMC2751785.

Sidney J, Assarsson E, Moore C, Ngo S, Pinilla C, Sette A, Peters B. Quantitative peptide binding motifs for 19 human and mouse MHC class I molecules derived using positional scanning combinatorial peptide libraries. Immunome Res. 2008 Jan 25;4:2. PMID: 18221540

Stranzl T, Larsen MV, Lundegaard C, Nielsen M. NetCTLpan: pan-specific MHC class I pathway epitope predictions. Immunogenetics. 2010 Jun;62(6):357-68. Epub 2010 Apr 9. PubMed PMID: 20379710; PubMed Central PMCID: PMC2875469

Sturniolo T, Bono E, Ding J, Raddrizzani L, Tuereci O, Sahin U, Braxenthaler M, Gallazzi F, Protti MP, Sinigaglia F, Hammer J. Generation of tissue-specific and promiscuous HLA ligand databases using DNA microarrays and virtual HLA class II matrices. Nat Biotechnol. 1999 Jun;17(6):555-61. PMID: 10385319

Tenzer S, Peters B, Bulik S, Schoor O, Lemmel C, Schatz MM, Kloetzel PM, Rammensee HG, Schild H, Holzhutter HG. Modeling the MHC class I pathway by combining predictions of proteasomal cleavage, TAP transport and MHC class I binding. Cell Mol Life Sci. 2005 May;62(9):1025-37.

Trolle T, Metushi IG, Greenbaum JA, Kim Y, Sidney J, Lund O, Sette A, Peters B, Nielsen M. Automated benchmarking of peptide-MHC class I binding predictions. Bioinformatics. 2015 Jul 1;31(13):2174-81. doi: 10.1093/bioinformatics/btv123. Epub 2015 Feb 25. PubMed PMID: 25717196; PubMed Central PMCID: PMC4481849.

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

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

Wang P, Sidney J, Kim Y, Sette A, Lund O, Nielsen M, Peters B. 2010. Peptide binding predictions for HLA DR, DP and DQ molecules. BMC Bioinformatics. 11:568

Zhang H, Lund O, Nielsen M. The PickPocket method for predicting binding specificities for receptors based on receptor pocket similarities: Application to MHC-peptide binding. Bioinformatics. 2009 Mar 17. PMID: 19297351