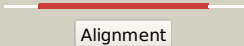

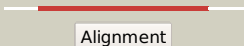

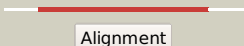







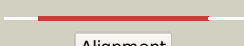











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3077 (-)_3439538_3441349
Date	Thu Aug 8 16:20:25 BST 2019
Unique Job ID	d0fe952f55312e59

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4uplC_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfatase family protein; <b>PDBTitle:</b> dimeric sulfatase spas2 from silicibacter pomeroyi
2	<a href="#">c4upiA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfatase family protein; <b>PDBTitle:</b> dimeric sulfatase spas1 from silicibacter pomeroyi
3	<a href="#">c4uphA_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfatase (sulfuric ester hydrolase) protein; <b>PDBTitle:</b> crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
4	<a href="#">c4upkC_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphonate monoester hydrolase; <b>PDBTitle:</b> phosphonate monoester hydrolase sppmh from silicibacter pomeroyi
5	<a href="#">c2vqrA_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sulfatase; <b>PDBTitle:</b> crystal structure of a phosphonate monoester hydrolase from rhizobium2 leguminosarum: a new member of the alkaline phosphatase superfamily
6	<a href="#">c4ug4H_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> choline sulfatase; <b>PDBTitle:</b> crystal structure of a choline sulfatase from sinorhizobium2 melliloti
7	<a href="#">d1hdha_</a>	 Alignment		100.0	18	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Arylsulfatase
8	<a href="#">c4fdiA_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylgalactosamine-6-sulfatase; <b>PDBTitle:</b> the molecular basis of mucopolysaccharidosis iv a
9	<a href="#">c5fqIA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> iduronate-2-sulfatase; <b>PDBTitle:</b> insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
10	<a href="#">c6hbmA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> arylsulfatase; <b>PDBTitle:</b> crystal structure of the family s1_7 ulvan-specific sulfatase fa220702 from formosa agariphila
11	<a href="#">c3ed4A_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arylsulfatase; <b>PDBTitle:</b> crystal structure of putative arylsulfatase from escherichia coli

12	<a href="#">c2qzuA_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sulfatase yidj; <b>PDBTitle:</b> crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
13	<a href="#">d1p49a_</a>	Alignment		100.0	22	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Arylsulfatase
14	<a href="#">d1auka_</a>	Alignment		100.0	22	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Arylsulfatase
15	<a href="#">d1fsua_</a>	Alignment		100.0	17	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Arylsulfatase
16	<a href="#">c3b5qB_</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sulfatase yidj; <b>PDBTitle:</b> crystal structure of a putative sulfatase (np_810509.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.40 Å resolution
17	<a href="#">c6b1vB_</a>	Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> iota-carrageenan sulfatase; <b>PDBTitle:</b> crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
18	<a href="#">c4mivB_</a>	Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-sulphoglucosamine sulphohydrolase; <b>PDBTitle:</b> crystal structure of sulfamidase, crystal form I
19	<a href="#">c5g2vA_</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine-6-sulfatase; <b>PDBTitle:</b> structure of bt4656 in complex with its substrate d-glucosamine-2-n,2 6-o-disulfate.
20	<a href="#">c6j66B_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> chondroitin sulfate/dermatan sulfate 4-o-endosulfatase <b>PDBTitle:</b> chondroitin sulfate/dermatan sulfate endolytic 4-o-sulfatase
21	<a href="#">c6hr5A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-l-rhamnosidase/sulfatase (gh78); <b>PDBTitle:</b> structure of the s1_25 family sulfatase module of the rhamnosidase2 fa22250 from formosa agariphila
22	<a href="#">c4uopB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipoteichoic acid primase; <b>PDBTitle:</b> crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
23	<a href="#">c3lxqB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein vp1736; <b>PDBTitle:</b> the crystal structure of a protein in the alkaline phosphatase2 superfamily from vibrio parahaemolyticus to 1.95Å
24	<a href="#">c2w8dB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> processed glycerol phosphate lipoteichoic acid synthase 2; <b>PDBTitle:</b> distinct and essential morphogenic functions for wall-and2 lipo-teichoic acids in bacillus subtilis
25	<a href="#">c2w5tA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> processed glycerol phosphate lipoteichoic acid <b>PDBTitle:</b> structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
26	<a href="#">c5i5fA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein yejm; <b>PDBTitle:</b> salmonella global domain 191
27	<a href="#">c4uorK_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> K: <b>PDB Molecule:</b> lipoteichoic acid synthase; <b>PDBTitle:</b> structure of lipoteichoic acid synthase ltas from listeria2 monocytogenes in complex with glycerol phosphate
28	<a href="#">c5k4pA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable phosphatidylethanolamine transferase mcr-1; <b>PDBTitle:</b> catalytic domain of mcr-1 phosphoethanolamine

						transferase
29	<a href="#">c6bneA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine transferase; <b>PDBTitle:</b> crystal structure of the intrinsic colistin resistance enzyme icr(mc)2 from moraxella catarrhalis, catalytic domain, phosphate-bound complex
30	<a href="#">c2zktB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> structure of ph0037 protein from pyrococcus horikoshii
31	<a href="#">c4kayA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> yhbxb/yhjw/yjip/yjdb family protein; <b>PDBTitle:</b> structure of the soluble domain of lipooligosaccharide2 phosphoethanolamine transferase a from neisseria meningitidis -3 complex with zn
32	<a href="#">c6a82A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoethanolamine transferase eptc; <b>PDBTitle:</b> crystal structure of the c-terminal periplasmic domain of eceptc from2 escherichia coli
33	<a href="#">c3m8yC_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphopentomutase; <b>PDBTitle:</b> phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
34	<a href="#">c4tn0C_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> upf0141 protein yjdb; <b>PDBTitle:</b> crystal structure of the c-terminal periplasmic domain of2 phosphoethanolamine transferase eptc from campylobacter jejuni
35	<a href="#">c5tj3A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline phosphatase pafa; <b>PDBTitle:</b> crystal structure of wild type alkaline phosphatase pafa to 1.7a2 resolution
36	<a href="#">c3q3qA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
37	<a href="#">c5udyA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> human alkaline sphingomyelinase (alk-smase, enpp7, npp7)
38	<a href="#">c4lqyA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bis(5'-adenosyl)-triphosphatase enpp4; <b>PDBTitle:</b> crystal structure of human enpp4 with amp
39	<a href="#">c2gsoB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphodiesterase-nucleotide pyrophosphatase; <b>PDBTitle:</b> structure of xac nucleotide pyrophosphatase/phosphodiesterase in2 complex with vanadate
40	<a href="#">c2i09A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopentomutase; <b>PDBTitle:</b> crystal structure of putative phosphopentomutase from streptococcus2 mutans
41	<a href="#">c5vemA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> human ectonucleotide pyrophosphatase / phosphodiesterase 5 (enpp5,2 npp5)
42	<a href="#">d1o98a2</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
43	<a href="#">c5egeD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> structure of enpp6, a choline-specific glycerophosphodiester-2 phosphodiesterase
44	<a href="#">c5u9zB_</a>	Alignment	not modelled	100.0	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglycerol transferase; <b>PDBTitle:</b> phosphoglycerol transferase gach from streptococcus pyogenes
45	<a href="#">c3szzA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonoacetate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
46	<a href="#">c5fgnA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipooligosaccharide phosphoethanolamine transferase a; <b>PDBTitle:</b> integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
47	<a href="#">d2i09a1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> DeoB catalytic domain-like
48	<a href="#">d1ei6a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Phosphonoacetate hydrolase
49	<a href="#">c2xrgA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
50	<a href="#">c6c02B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> human ectonucleotide pyrophosphatase / phosphodiesterase 3 (enpp3,2 npp3, cd203c), inactive (t205a), n594s, with alpha,beta-methylene-atp3 (ampcpp)
51	<a href="#">c2xr9A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> crystal structure of autotaxin (enpp2)

52	<a href="#">c5gz4A_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> snake venom phosphodiesterase (pde); <b>PDBTitle:</b> crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra)
53	<a href="#">c5gz5A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> snake venom phosphodiesterase (pde); <b>PDBTitle:</b> crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra) in complex with amp
54	<a href="#">c4b56A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ectonucleotide pyrophosphatase/phosphodiesterase family <b>PDBTitle:</b> structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
55	<a href="#">c1o98A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent <b>PDBTitle:</b> 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
56	<a href="#">c5kgmA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> 2.95a resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form)
57	<a href="#">c4my4A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
58	<a href="#">c2d1gB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acid phosphatase; <b>PDBTitle:</b> structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
59	<a href="#">c3igzB_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> cofactor-independent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
60	<a href="#">c5vpuA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent phosphoglycerate <b>PDBTitle:</b> crystal structure of 2,3-bisphosphoglycerate-independent2 phosphoglycerate mutase bound to 3-phosphoglycerate, from3 acinetobacter baumannii
61	<a href="#">c2iucB_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> structure of alkaline phosphatase from the antarctic bacterium tab5
62	<a href="#">d1y6va1</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Alkaline phosphatase
63	<a href="#">c1ew2A_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatase; <b>PDBTitle:</b> crystal structure of a human phosphatase
64	<a href="#">d1zeda1</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Alkaline phosphatase
65	<a href="#">d1k7ha_</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> Alkaline phosphatase-like <b>Superfamily:</b> Alkaline phosphatase-like <b>Family:</b> Alkaline phosphatase
66	<a href="#">c2x98A_</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> h.salinarum alkaline phosphatase
67	<a href="#">c2w0yB_</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> h.salinarum alkaline phosphatase
68	<a href="#">c3a52A_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cold-active alkaline phosphatase; <b>PDBTitle:</b> crystal structure of cold-active alkaline phosphatase from2 psychrophile shewanella sp.
69	<a href="#">c3e2dB_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> the 1.4 a crystal structure of the large and cold-active vibrio sp.2 alkaline phosphatase
70	<a href="#">c3wbhB_</a>	Alignment	not modelled	98.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alkaline phosphatase; <b>PDBTitle:</b> structural characteristics of alkaline phosphatase from a moderately2 halophilic bacteria halomonas sp.593
71	<a href="#">c5oltA_</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cellulose biosynthesis protein bcs9; <b>PDBTitle:</b> crystal structure of the extramembrane domain of the cellulose2 biosynthetic protein bcs9 from salmonella typhimurium
72	<a href="#">c3iddA_</a>	Alignment	not modelled	95.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-independent <b>PDBTitle:</b> cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
73	<a href="#">d1b4ub_</a>	Alignment	not modelled	67.3	13	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> LigB-like <b>Family:</b> LigB-like
74	<a href="#">d1xo1a2</a>	Alignment	not modelled	57.1	12	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
75	<a href="#">c4awaA_</a>	Alignment	not modelled	43.0	20	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> legumain; <b>PDBTitle:</b> crystal structure of active legumain in complex with yvad-cmk2 at ph 5.0
76	<a href="#">d2c1ha1</a>	Alignment	not modelled	37.8	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinatase dehydratase, ALAD (porphobilinogen

						synthase)
77	<a href="#">d1gzga_</a>	Alignment	not modelled	37.3	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinic acid dehydratase, ALAD (porphobilinogen synthase)
78	<a href="#">d1l6sa_</a>	Alignment	not modelled	35.5	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinic acid dehydratase, ALAD (porphobilinogen synthase)
79	<a href="#">c3wrbB_</a>	Alignment	not modelled	34.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gallate dioxygenase; <b>PDBTitle:</b> crystal structure of the anaerobic h124f desb-gallate complex
80	<a href="#">d1cmwa2</a>	Alignment	not modelled	34.2	23	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
81	<a href="#">c5lzlH_</a>	Alignment	not modelled	34.0	26	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> delta-aminolevulinic acid dehydratase; <b>PDBTitle:</b> pyrobaculum calidifontis 5-aminolaevulinic acid dehydratase
82	<a href="#">c6fkiq_</a>	Alignment	not modelled	33.4	18	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase subunit c, chloroplastic; <b>PDBTitle:</b> chloroplast f1fo conformation 3
83	<a href="#">c3obkH_</a>	Alignment	not modelled	32.9	19	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> delta-aminolevulinic acid dehydratase; <b>PDBTitle:</b> crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
84	<a href="#">d1j33a_</a>	Alignment	not modelled	32.2	23	<b>Fold:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) <b>Superfamily:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) <b>Family:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
85	<a href="#">c4hdnB_</a>	Alignment	not modelled	31.9	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> arsb; <b>PDBTitle:</b> crystal structure of arsb in the substrate-free state.
86	<a href="#">c5lqxG_</a>	Alignment	not modelled	27.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase gamma subunit; <b>PDBTitle:</b> structure of f-atpase from pichia angusta, state3
87	<a href="#">d1tfra2</a>	Alignment	not modelled	27.4	27	<b>Fold:</b> PIN domain-like <b>Superfamily:</b> PIN domain-like <b>Family:</b> 5' to 3' exonuclease catalytic domain
88	<a href="#">c1mm0A_</a>	Alignment	not modelled	27.3	29	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> termicin; <b>PDBTitle:</b> solution structure of termicin, an antimicrobial peptide2 from the termite pseudacanthotermes spiniger
89	<a href="#">d1mm0a_</a>	Alignment	not modelled	27.3	29	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Scorpion toxin-like <b>Family:</b> Insect defensins
90	<a href="#">c4r29D_</a>	Alignment	not modelled	25.8	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of bacterial cysteine methyltransferase effector2 nlee
91	<a href="#">c4fguB_</a>	Alignment	not modelled	25.4	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> legumain; <b>PDBTitle:</b> crystal structure of prolegumain
92	<a href="#">c3dqzB_</a>	Alignment	not modelled	23.7	9	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-hydroxynitrile lyase-like protein; <b>PDBTitle:</b> structure of the hydroxynitrile lyase from arabidopsis thaliana
93	<a href="#">c2ihnA_</a>	Alignment	not modelled	23.6	23	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ribonuclease h; <b>PDBTitle:</b> co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
94	<a href="#">c5zwlG_</a>	Alignment	not modelled	23.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase gamma chain; <b>PDBTitle:</b> crystal structure of the gamma - epsilon complex of photosynthetic2 cyanobacterial f1-atpase
95	<a href="#">d3cu0a1</a>	Alignment	not modelled	23.3	13	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> 1,3-glucuronyltransferase
96	<a href="#">c4hdnA_</a>	Alignment	not modelled	23.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> arsa; <b>PDBTitle:</b> crystal structure of arsa in the substrate-free state.
97	<a href="#">c5h0iB_</a>	Alignment	not modelled	23.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> asparaginyl endopeptidase; <b>PDBTitle:</b> name to be released when published
98	<a href="#">c1ou5A_</a>	Alignment	not modelled	22.6	12	<b>PDB header:</b> translation, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna cca-adding enzyme; <b>PDBTitle:</b> crystal structure of human cca-adding enzyme
99	<a href="#">d1l5oa_</a>	Alignment	not modelled	22.6	60	<b>Fold:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) <b>Superfamily:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) <b>Family:</b> Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
100	<a href="#">d1fs0g_</a>	Alignment	not modelled	22.6	44	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> ATP synthase (F1-ATPase), gamma subunit <b>Family:</b> ATP synthase (F1-ATPase), gamma subunit
101	<a href="#">c6b5fB_</a>	Alignment	not modelled	22.5	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nicotinate-nucleotide--dimethylbenzimidazole <b>PDBTitle:</b> crystal structure of nicotinate mononucleotide-5,6-2 dimethylbenzimidazole phosphoribosyltransferase cobt from

					yersinia3 enterocolitica
102	<a href="#">c5zbiB_</a>	Alignment	not modelled	22.3	25 <b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> peptide asparaginyl ligase; <b>PDBTitle:</b> crystal structure of asparaginyl endopeptidases from viola canadensis
103	<a href="#">c2xokG_</a>	Alignment	not modelled	21.6	44 <b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> atp synthase subunit gamma, mitochondrial; <b>PDBTitle:</b> refined structure of yeast f1c10 atpase complex to 3 a resolution
104	<a href="#">c30aaO_</a>	Alignment	not modelled	20.5	22 <b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> O: <b>PDB Molecule:</b> atp synthase gamma chain; <b>PDBTitle:</b> structure of the e.coli f1-atp synthase inhibited by subunit epsilon