Phyre2

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Description	RVBD2349c_(plcC)_2627182_2628708
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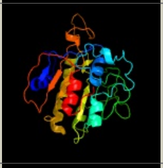
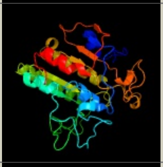
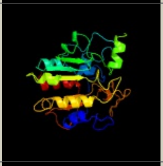
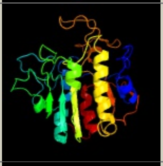
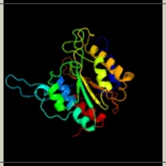
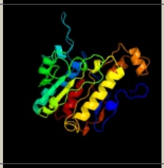
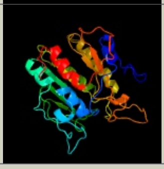
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d1gB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
2	c6hr5A_	Alignment		99.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-l-rhamnosidase/sulfatase (gh78); **PDBTitle:** structure of the s1_25 family sulfatase module of the rhamnosidase2 fa22250 from formosa agariphila
3	d1auka_	Alignment		99.5	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
4	c6b1vB_	Alignment		99.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**iota-carrageenan sulfatase; **PDBTitle:** crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
5	c3lxqB_	Alignment		99.4	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp1736; **PDBTitle:** the crystal structure of a protein in the alkaline phosphatase2 superfamily from vibrio parahaemolyticus to 1.95a
6	c4fdiA_	Alignment		99.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylgalactosamine-6-sulfatase; **PDBTitle:** the molecular basis of mucopolysaccharidosis iv a
7	c6j66B_	Alignment		99.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**chondroitin sulfate/dermatan sulfate 4-o-endosulfatase **PDBTitle:** chondroitin sulfate/dermatan sulfate endolytic 4-o-sulfatase
8	c3ed4A_	Alignment		99.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
9	d1p49a_	Alignment		99.3	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
10	c4mivB_	Alignment		99.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-sulphoglucosamine sulphohydrolase; **PDBTitle:** crystal structure of sulfamidase, crystal form l
11	c6hhmA_	Alignment		99.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of the family s1_7 ulvan-specific sulfatase fa220702 from formosa agariphila

12	c5fqlA_	Alignment		99.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**iduronate-2-sulfatase; **PDBTitle:** insights into hunter syndrome from the structure of iduronate-2-2 sulfatase
13	d1fsua_	Alignment		99.2	20	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
14	c4uopB_	Alignment		99.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipoteichoic acid primase; **PDBTitle:** crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
15	c4uorK_	Alignment		99.2	14	**PDB header:**transferase **Chain:** K: **PDB Molecule:**lipoteichoic acid synthase; **PDBTitle:** structure of lipoteichoic acid synthase ltas from listeria2 monocytogenes in complex with glycerol phosphate
16	c2w8dB_	Alignment		99.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid synthase 2; **PDBTitle:** distinct and essential morphogenic functions for wall- and2 lipo-teichoic acids in bacillus subtilis
17	c2vqrA_	Alignment		99.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase; **PDBTitle:** crystal structure of a phosphonate monoester hydrolase from rhizobium2 leguminosarum: a new member of the alkaline phosphatase superfamily
18	c4ug4H_	Alignment		99.2	15	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**choline sulfatase; **PDBTitle:** crystal structure of a choline sulfatase from sinorhizobium2 melliloti
19	c4upkC_	Alignment		99.1	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**phosphonate monoester hydrolase; **PDBTitle:** phosphonate monoester hydrolase sppmh from silicibacter pomeroyi
20	c5g2vA_	Alignment		99.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylglucosamine-6-sulfatase; **PDBTitle:** structure of bt4656 in complex with its substrate d-glucosamine-2-n,2 6-o-disulfate.
21	c2qzuA_	Alignment	not modelled	99.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of the putative sulfatase yidj from bacteroides2 fragilis. northeast structural genomics consortium target bfr123
22	c4uplC_	Alignment	not modelled	99.1	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**sulfatase family protein; **PDBTitle:** dimeric sulfatase spas2 from silicibacter pomeroyi
23	c4uphA_	Alignment	not modelled	99.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfatase (sulfuric ester hydrolase) protein; **PDBTitle:** crystal structure of phosphonate monoester hydrolase of agrobacterium2 radiobacter
24	c3b5qB_	Alignment	not modelled	99.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of a putative sulfatase (np_810509.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.40 a resolution
25	d1hdha_	Alignment	not modelled	99.0	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
26	c4upiA_	Alignment	not modelled	99.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfatase family protein; **PDBTitle:** dimeric sulfatase spas1 from silicibacter pomeroyi
27	c5i5fA_	Alignment	not modelled	98.9	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein yejm; **PDBTitle:** salmonella global domain 191
28	c2w5tA_	Alignment	not modelled	98.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid **PDBTitle:** structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.

29	c6a82A_	Alignment	not modelled	98.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoethanolamine transferase eptc; **PDBTitle:** crystal structure of the c-terminal periplasmic domain of eceptc from2 escherichia coli
30	c4kayA_	Alignment	not modelled	98.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**yhbx/yhjw/yijp/yjdb family protein; **PDBTitle:** structure of the soluble domain of lipooligosaccharide2 phosphoethanolamine transferase a from neisseria meningitidis -3 complex with zn
31	c5k4pA_	Alignment	not modelled	98.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable phosphatidylethanolamine transferase mcr-1; **PDBTitle:** catalytic domain of mcr-1 phosphoethanolamine transferase
32	c6bneA_	Alignment	not modelled	98.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoethanolamine transferase; **PDBTitle:** crystal structure of the intrinsic colistin resistance enzyme icr(mc)2 from moraxella catarrhalis, catalytic domain, phosphate-bound complex
33	c4tn0C_	Alignment	not modelled	98.6	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**upf0141 protein yjdb; **PDBTitle:** crystal structure of the c-terminal periplasmic domain of2 phosphoethanolamine transferase eptc from campylobacter jejuni
34	d1o98a2	Alignment	not modelled	98.4	11	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
35	c5u9zB_	Alignment	not modelled	98.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoglycerol transferase; **PDBTitle:** phosphoglycerol transferase gach from streptococcus pyogenes
36	c5vemA_	Alignment	not modelled	98.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** human ectonucleotide pyrophosphatase / phosphodiesterase 5 (enpp5,2 npp5)
37	c5egeD_	Alignment	not modelled	98.2	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** structure of enpp6, a choline-specific glycerophosphodiester-2 phosphodiesterase
38	c5fgnA_	Alignment	not modelled	98.0	14	**PDB header:**transferase,hydrolase **Chain:** A: **PDB Molecule:**lipooligosaccharide phosphoethanolamine transferase a; **PDBTitle:** integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
39	c5udyA_	Alignment	not modelled	98.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** human alkaline sphingomyelinase (alk-smase, enpp7, npp7)
40	c4lqyA_	Alignment	not modelled	97.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bis(5'-adenosyl)-triphosphatase enpp4; **PDBTitle:** crystal structure of human enpp4 with amp
41	d2i09a1	Alignment	not modelled	97.7	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
42	c2gsoB_	Alignment	not modelled	97.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide pyrophosphatase/phosphodiesterase in2 complex with vanadate
43	c3m8yC_	Alignment	not modelled	97.6	29	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
44	c3q3qA_	Alignment	not modelled	97.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
45	c2i09A_	Alignment	not modelled	97.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
46	c2zktB_	Alignment	not modelled	96.9	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
47	c4b56A_	Alignment	not modelled	96.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** structure of ectonucleotide pyrophosphatase-phosphodiesterase-12 (npp1)
48	c5gz4A_	Alignment	not modelled	96.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**snake venom phosphodiesterase (pde); **PDBTitle:** crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra)
49	c5gz5A_	Alignment	not modelled	96.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**snake venom phosphodiesterase (pde); **PDBTitle:** crystal structure of snake venom phosphodiesterase (pde) from taiwan2 cobra (naja atra atra) in complex with amp
50	c5kgmA_	Alignment	not modelled	96.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** 2.95a resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form)
51	c5tj3A_	Alignment	not modelled	96.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase pafa; **PDBTitle:** crystal structure of wild type alkaline phosphatase pafa to 1.7a2 resolution

52	c6c02B_	Alignment	not modelled	95.7	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** human ectonucleotide pyrophosphatase / phosphodiesterase 3 (enpp3,2 npp3, cd203c), inactive (t205a), n594s, with alpha,beta-methylene-atp3 (ampcpp)
53	c2xrgA_	Alignment	not modelled	95.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
54	c1o98A_	Alignment	not modelled	95.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
55	c2xr9A_	Alignment	not modelled	94.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
56	c3szzA_	Alignment	not modelled	93.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
57	c4my4A_	Alignment	not modelled	91.8	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
58	c2e76D_	Alignment	not modelled	91.6	16	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
59	c5vpuA_	Alignment	not modelled	91.3	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** crystal structure of 2,3-bisphosphoglycerate-independent2 phosphoglycerate mutase bound to 3-phosphoglycerate, from3 acinetobacter baumannii
60	c3igzB_	Alignment	not modelled	90.7	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
61	d1y6va1	Alignment	not modelled	87.2	11	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
62	d1ei6a_	Alignment	not modelled	84.6	10	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
63	c2w0yB_	Alignment	not modelled	81.4	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
64	c2fynO_	Alignment	not modelled	81.1	22	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
65	c2pq4B_	Alignment	not modelled	70.2	37	**PDB header:**chaperone/oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic nitrate reductase precursor; **PDBTitle:** nmr solution structure of napd in complex with napa1-352 signal peptide
66	c2fyuE_	Alignment	not modelled	69.5	12	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
67	c2iucB_	Alignment	not modelled	68.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic bacterium tab5
68	c2x98A_	Alignment	not modelled	64.5	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
69	c6fo2R_	Alignment	not modelled	61.5	14	**PDB header:**membrane protein **Chain:** R: **PDB Molecule:**cytochrome b-c1 complex subunit rieske, mitochondrial; **PDBTitle:** cryoem structure of bovine cytochrome bc1 with no ligand bound
70	c1p84E_	Alignment	not modelled	61.5	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
71	c3e2dB_	Alignment	not modelled	41.1	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active vibrio sp.2 alkaline phosphatase
72	c3wbhB_	Alignment	not modelled	37.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structural characteristics of alkaline phosphatase from a moderately2 halophilic bacteria halomonas sp.593
73	c6dq3B_	Alignment	not modelled	36.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polysaccharide deacetylase; **PDBTitle:** streptococcus pyogenes deacetylase pdi in complex with acetate
74	d1okta2	Alignment	not modelled	35.3	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
						Fold: Thioredoxin fold

75	d1k0ma2	Alignment	not modelled	31.7	20	**Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
76	c3couA_	Alignment	not modelled	31.4	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 16; **PDBTitle:** crystal structure of human nudix motif 16 (nudt16)
77	c6jcnB_	Alignment	not modelled	28.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dehydrodolichyl diphosphate synthase complex subunit nus1; **PDBTitle:** yeast dehydrodolichyl diphosphate synthase complex subunit nus1
78	c1ew2A_	Alignment	not modelled	26.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase
79	d1zeda1	Alignment	not modelled	26.3	24	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
80	c6acsA_	Alignment	not modelled	24.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ditrans,polycis-undecaprenyl-diphosphate synthase ((2e,6e)- **PDBTitle:** poly-cis-prenyltransferase
81	d2gsra2	Alignment	not modelled	22.4	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
82	c2odiA_	Alignment	not modelled	21.9	29	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**r.bcni; **PDBTitle:** restriction endonuclease bcni-cognate dna substrate complex
83	c2d2rA_	Alignment	not modelled	19.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
84	c6hwhB_	Alignment	not modelled	19.8	22	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
85	c5j43F_	Alignment	not modelled	18.2	44	**PDB header:**toxin **Chain:** F: **PDB Molecule:**trna nuclease cdia; **PDBTitle:** cdia-ct from uropathogenic escherichia coli in complex with cysk
86	d1m0ua2	Alignment	not modelled	17.9	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
87	c4q9mA_	Alignment	not modelled	17.8	23	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**isoprenyl transferase; **PDBTitle:** crystal structure of upps in complex with fpp and an allosteric2 inhibitor
88	c4h8eA_	Alignment	not modelled	17.7	31	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of s. aureus undecaprenyl diphosphate synthase in complex2 with fpp and sulfate
89	c3kvhA_	Alignment	not modelled	16.2	31	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
90	d1f75a_	Alignment	not modelled	15.8	23	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
91	d1v2aa2	Alignment	not modelled	15.7	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
92	c5jx6C_	Alignment	not modelled	15.7	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glucanase; **PDBTitle:** gh6 orpinomyces sp. y102 enzyme
93	d1b5ea_	Alignment	not modelled	14.9	17	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
94	d1g57a_	Alignment	not modelled	14.8	21	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
95	d1dysa_	Alignment	not modelled	14.3	14	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
96	c5v6xB_	Alignment	not modelled	13.8	20	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**pyrrolysine--trna ligase; **PDBTitle:** crystal structure of the trna binding domain of pyrrolysyl-trna2 synthetase mutant (32a ntd) bound to trna(pyl)
97	d1txka2	Alignment	not modelled	13.7	36	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**MdoG-like
98	c5bu6B_	Alignment	not modelled	13.0	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bpsb (pgab), poly-beta-1,6-n-acetyl-d-glucosamine n- **PDBTitle:** structure of bpsb deaceylase domain from bordetella bronchiseptica
99	c1txkA_	Alignment	not modelled	12.7	36	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glucans biosynthesis protein g; **PDBTitle:** crystal structure of escherichia coli opgg