Phyre2

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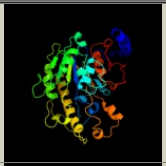
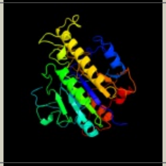
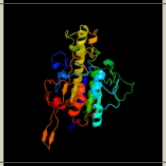
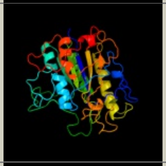
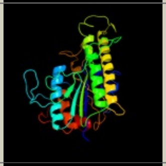
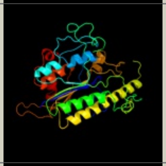
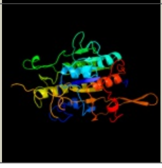
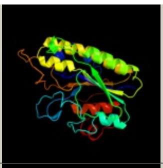
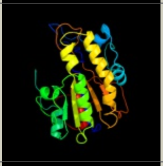
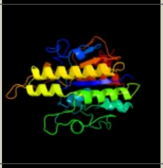
Description	P37661
Date	Thu Jan 5 11:56:34 GMT 2012
Unique Job ID	2032e1476e7bfd1a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w8dB_	Alignment		100.0	13	**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
2	c2w5tA_	Alignment		100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**processed glycerol phosphate lipoteichoic acid **PDBTitle:** structure-based mechanism of lipoteichoic acid synthesis by2 staphylococcus aureus ltas.
3	c3lxqB_	Alignment		100.0	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein vp1736; **PDBTitle:** the crystal structure of a protein in the alkaline2 phosphatase superfamily from vibrio parahaemolyticus to3 1.95a
4	c3ed4A_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
5	d1fsua_	Alignment		100.0	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
6	c2qzuA_	Alignment		100.0	16	**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
7	d1auka_	Alignment		100.0	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
8	c3b5qB_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative sulfatase yidj; **PDBTitle:** crystal structure of a putative sulfatase (np_810509.1)2 from bacteroides thetaiotaomicron vpi-5482 at 2.40 a3 resolution
9	d1hdha_	Alignment		100.0	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
10	c2vqrA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sulfatase; **PDBTitle:** crystal structure of a phosphonate monoester hydrolase2 from rhizobium leguminosarum: a new member of the3 alkaline phosphatase superfamily
11	d1p49a_	Alignment		100.0	13	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase

12	d1o98a2	Alignment		100.0	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
13	d2i09a1	Alignment		100.0	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
14	c2zktB_	Alignment		99.9	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
15	c3m8yC_	Alignment		99.9	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
16	c2gsoB_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
17	c2i09A_	Alignment		99.9	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
18	c3q3qA_	Alignment		99.9	18	**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
19	c3szzA_	Alignment		99.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
20	d1ei6a_	Alignment		99.8	15	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
21	c2xrgA_	Alignment	not modelled	99.8	16	**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
22	c2xr9A_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
23	c1o98A_	Alignment	not modelled	99.7	20	**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
24	c3igzB_	Alignment	not modelled	99.6	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
25	c2iucB_	Alignment	not modelled	99.1	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
26	c2d1gB_	Alignment	not modelled	99.0	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
27	c1ew2A_	Alignment	not modelled	98.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase
28	d1zeda1	Alignment	not modelled	98.8	12	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like

						Family: Alkaline phosphatase
29	d1k7ha_	Alignment	not modelled	98.7	15	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
30	d1y6va1	Alignment	not modelled	98.7	15	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
31	c2w0yB_	Alignment	not modelled	98.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
32	c2x98A_	Alignment	not modelled	98.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
33	c3e2dB_	Alignment	not modelled	98.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
34	c3a52A_	Alignment	not modelled	98.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
35	c3iddA_	Alignment	not modelled	92.1	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
36	c3uoaB_	Alignment	not modelled	70.1	8	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**mucosa-associated lymphoid tissue lymphoma translocation **PDBTitle:** crystal structure of the malt1 paracaspase (p21 form)
37	c3bijC_	Alignment	not modelled	62.8	9	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein gsu0716; **PDBTitle:** crystal structure of protein gsu0716 from geobacter2 sulfurreducens. northeast structural genomics target gsr13
38	d1b4ub_	Alignment	not modelled	60.0	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
39	d1s1qa_	Alignment	not modelled	59.0	21	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
40	c2xmoB_	Alignment	not modelled	45.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
41	d1l5oa_	Alignment	not modelled	24.0	46	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
42	d2hkja2	Alignment	not modelled	19.2	14	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
43	c3t1iC_	Alignment	not modelled	18.2	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
44	c3dufD_	Alignment	not modelled	18.0	13	**PDB header:**oxidoreductase/transferase **Chain:** D: **PDB Molecule:**pyruvate dehydrogenase e1 component subunit beta; **PDBTitle:** snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
45	c1ni4D_	Alignment	not modelled	16.0	6	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**pyruvate dehydrogenase e1 component: beta **PDBTitle:** human pyruvate dehydrogenase
46	d1j33a_	Alignment	not modelled	15.7	36	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
47	d2h6fb1	Alignment	not modelled	12.0	15	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Protein prenyltransferases
48	c2bp7F_	Alignment	not modelled	11.9	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**2-oxoisovalerate dehydrogenase beta subunit; **PDBTitle:** new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
49	c3q7aB_	Alignment	not modelled	11.1	15	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**farnesyltransferase beta subunit; **PDBTitle:** cryptococcus neoformans protein farnesyltransferase in complex with2 fpp and l-778,123
50	d2nxfa1	Alignment	not modelled	11.1	7	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
51	c2xokG_	Alignment	not modelled	10.7	24	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** refined structure of yeast f1c10 atpase complex to 3 a2 resolution
52	d1w85b1	Alignment	not modelled	10.1	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
						PDB header:hydrolase

53	c2pr7A_	Alignment	not modelled	10.1	7	**Chain:** A: **PDB Molecule:**haloacid dehalogenase/epoxide hydrolase family; **PDBTitle:** crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
54	d1pv7a_	Alignment	not modelled	10.0	14	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
55	d1oz9a_	Alignment	not modelled	9.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
56	d1xo1a2	Alignment	not modelled	9.6	8	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
57	c3e37B_	Alignment	not modelled	9.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein farnesyltransferase subunit beta; **PDBTitle:** protein farnesyltransferase complexed with bisubstrate2 ethylenediamine scaffold inhibitor 5
58	d1ma3a_	Alignment	not modelled	9.2	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
59	d1a9xa3	Alignment	not modelled	8.8	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
60	d2pw6a1	Alignment	not modelled	8.7	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
61	c2zbkB_	Alignment	not modelled	8.7	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
62	c3mk7F_	Alignment	not modelled	8.6	5	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
63	c1xaxA_	Alignment	not modelled	8.4	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
64	d1fs0g_	Alignment	not modelled	8.4	16	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
65	d1tfra2	Alignment	not modelled	8.3	17	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
66	d2ozlb1	Alignment	not modelled	8.0	6	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
67	c1cn3F_	Alignment	not modelled	7.9	18	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**fragment of coat protein vp2; **PDBTitle:** interaction of polyomavirus internal protein vp2 with major2 capsid protein vp1 and implications for participation of3 vp2 in viral entry
68	d1xm5a_	Alignment	not modelled	7.9	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
69	c1mx0D_	Alignment	not modelled	7.8	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
70	d1usha2	Alignment	not modelled	7.6	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
71	c2fphX_	Alignment	not modelled	7.5	13	**PDB header:**dna binding protein **Chain:** X: **PDB Molecule:**ylmh; **PDBTitle:** cell division protein ylmh from streptococcus pneumoniae
72	d1umdb1	Alignment	not modelled	7.5	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
73	c2w6jG_	Alignment	not modelled	7.5	33	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
74	d2r7ka1	Alignment	not modelled	7.4	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**PurP N-terminal domain-like
75	d1yc5a1	Alignment	not modelled	7.3	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
76	d1nw9b_	Alignment	not modelled	7.1	10	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
77	d1j3ma_	Alignment	not modelled	7.1	6	**Fold:**TBP-like **Superfamily:**TT1751-like **Family:**TT1751-like
78	c3k35D_	Alignment	not modelled	7.0	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
						PDB header:oxidoreductase

79	c1um9D_	Alignment	not modelled	7.0	13	**Chain:** D: **PDB Molecule:**2-oxo acid dehydrogenase beta subunit; **PDBTitle:** branched-chain 2-oxo acid dehydrogenase (e1) from thermus2 thermophilus hb8 in apo-form
80	d1tvia_	Alignment	not modelled	6.9	25	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Predicted metal-dependent hydrolase
81	c3ib7A_	Alignment	not modelled	6.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
82	d2p0va1	Alignment	not modelled	6.8	32	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
83	c2p0vA_	Alignment	not modelled	6.8	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt3781; **PDBTitle:** crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
84	d1v8za1	Alignment	not modelled	6.7	8	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
85	c3auzA_	Alignment	not modelled	6.5	18	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
86	c3e4cB_	Alignment	not modelled	6.4	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** procaspase-1 zymogen domain crystal strucutre
87	d1uf3a_	Alignment	not modelled	6.4	5	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
88	d1q9ua_	Alignment	not modelled	6.3	13	**Fold:**TBP-like **Superfamily:**TT1751-like **Family:**TT1751-like
89	c2fp3A_	Alignment	not modelled	6.3	17	**PDB header:**hydrolysis/apoptosis **Chain:** A: **PDB Molecule:**caspase nc; **PDBTitle:** crystal structure of the drosophila initiator caspase dronc
90	d1szpb1	Alignment	not modelled	6.2	14	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
91	d1iq0a1	Alignment	not modelled	6.2	27	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
92	c3qfnA_	Alignment	not modelled	6.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
93	c2hy1A_	Alignment	not modelled	6.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
94	d2hy1a1	Alignment	not modelled	6.1	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
95	c2qe7G_	Alignment	not modelled	6.1	22	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
96	d2b8ea1	Alignment	not modelled	6.1	5	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
97	d2axti1	Alignment	not modelled	6.1	17	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein I, PsbI **Family:**PsbI-like
98	d2jdig1	Alignment	not modelled	6.0	33	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
99	c3qspB_	Alignment	not modelled	5.9	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose