Phyre2

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Description	P31447
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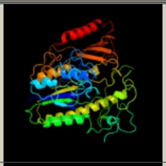
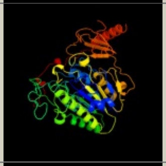
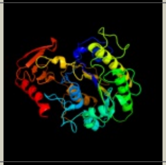
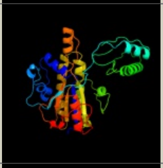
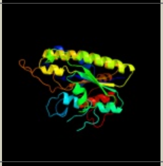
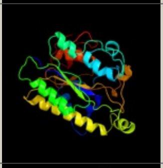
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vqrA_	Alignment		100.0	24	**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
2	c3ed4A_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylsulfatase; **PDBTitle:** crystal structure of putative arylsulfatase from escherichia coli
3	c2qzuA_	Alignment		100.0	26	**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
4	d1hdha_	Alignment		100.0	25	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
5	c3b5qB_	Alignment		100.0	24	**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
6	d1fsua_	Alignment		100.0	22	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
7	d1auka_	Alignment		100.0	22	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
8	d1p49a_	Alignment		100.0	25	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Arylsulfatase
9	c3lxqB_	Alignment		100.0	18	**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
10	c2w8dB_	Alignment		100.0	17	**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
11	c2w5tA_	Alignment		100.0	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.

12	c2zktB_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
13	c3q3qA_	Alignment		100.0	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
14	c2gsoB_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phosphodiesterase-nucleotide pyrophosphatase; **PDBTitle:** structure of xac nucleotide2 pyrophosphatase/phosphodiesterase in complex with vanadate
15	c3m8yC_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
16	d1o98a2	Alignment		100.0	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
17	c2i09A_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
18	c2xr9A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2)
19	c2xrgA_	Alignment		100.0	19	**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
20	d2i09a1	Alignment		100.0	18	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**DeoB catalytic domain-like
21	c3szzA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonoacetate hydrolase; **PDBTitle:** crystal structure of phosphonoacetate hydrolase from sinorhizobium2 meliloti 1021 in complex with acetate
22	d1ei6a_	Alignment	not modelled	100.0	16	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Phosphonoacetate hydrolase
23	c1o98A_	Alignment	not modelled	99.8	18	**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	c2d1gB_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acid phosphatase; **PDBTitle:** structure of francisella tularensis acid phosphatase a (acpa) bound to2 orthovanadate
25	c3igzB_	Alignment	not modelled	99.7	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**cofactor-independent phosphoglycerate mutase; **PDBTitle:** crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
26	c2iucB_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
27	d1y6va1	Alignment	not modelled	99.4	19	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
28	d1k7ha_	Alignment	not modelled	99.4	20	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase

29	c1ew2A_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase
30	d1zeda1	Alignment	not modelled	99.4	14	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
31	c3a52A_	Alignment	not modelled	99.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
32	c2x98A_	Alignment	not modelled	99.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
33	c3e2dB_	Alignment	not modelled	99.1	24	**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	c2w0yB_	Alignment	not modelled	99.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
35	c3iddA_	Alignment	not modelled	95.1	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-bisphosphoglycerate-independent **PDBTitle:** cofactor-independent phosphoglycerate mutase from2 thermoplasma acidophilum dsm 1728
36	d1b4ub_	Alignment	not modelled	67.7	8	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
37	d1jxha_	Alignment	not modelled	45.5	44	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
38	d1j33a_	Alignment	not modelled	25.3	20	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
39	d1xo1a2	Alignment	not modelled	25.3	12	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
40	c2xokG_	Alignment	not modelled	23.8	38	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** refined structure of yeast f1c10 atpase complex to 3 a2 resolution
41	d1fs0g_	Alignment	not modelled	21.3	23	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
42	c2kjzA_	Alignment	not modelled	21.0	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**atc0852; **PDBTitle:** solution nmr structure of protein atc0852 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att2.
43	d1l5oa_	Alignment	not modelled	18.8	30	**Fold:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Superfamily:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) **Family:**Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT)
44	c3owqB_	Alignment	not modelled	18.5	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lin1025 protein; **PDBTitle:** x-ray structure of lin1025 protein from listeria innocua, northeast2 structural genomics consortium target lkr164
45	d1mm0a_	Alignment	not modelled	18.0	29	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Insect defensins
46	c2vyoA_	Alignment	not modelled	17.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitooligosaccharide deacetylase; **PDBTitle:** chitin deacetylase family member from encephalitozoon2 cuniculi
47	c3oaaO_	Alignment	not modelled	17.5	10	**PDB header:**hydrolase/transport protein **Chain:** O: **PDB Molecule:**atp synthase gamma chain; **PDBTitle:** structure of the e.coli f1-atp synthase inhibited by subunit epsilon
48	c2d0jD_	Alignment	not modelled	15.7	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**galactosylgalactosylxylosylprotein 3-beta- **PDBTitle:** crystal structure of human glcat-s apo form
49	d1l6sa_	Alignment	not modelled	15.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
50	d3cu0a1	Alignment	not modelled	14.7	21	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
51	c3anyB_	Alignment	not modelled	14.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ethanolamine ammonia-lyase light chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and (r)-2-amino-1-propanol
52	d2c1ha1	Alignment	not modelled	13.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
53	c3absD_	Alignment	not modelled	13.0	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**ethanolamine ammonia-lyase light chain;

						PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
54	d1gzga_	Alignment	not modelled	12.8	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
55	d1yt3a2	Alignment	not modelled	12.0	15	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains
56	c2r1fB_	Alignment	not modelled	11.6	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**predicted aminodeoxychorismate lyase; **PDBTitle:** crystal structure of predicted aminodeoxychorismate lyase from2 escherichia coli
57	d2iw0a1	Alignment	not modelled	11.6	13	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
58	d1vi7a1	Alignment	not modelled	10.8	5	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
59	c3obkH_	Alignment	not modelled	10.2	19	**PDB header:**lyase **Chain:** H: **PDB Molecule:**delta-aminolevulinic acid dehydratase; **PDBTitle:** crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
60	c2qe7G_	Alignment	not modelled	10.1	31	**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
61	d1cmwa2	Alignment	not modelled	10.1	28	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
62	c2zuuA_	Alignment	not modelled	10.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lacto-n-biose phosphorylase; **PDBTitle:** crystal structure of galacto-n-biose/lacto-n-biose i phosphorylase in2 complex with glcnac
63	d1tfra2	Alignment	not modelled	9.8	28	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
64	c2iw0A_	Alignment	not modelled	9.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
65	d2cvea1	Alignment	not modelled	9.2	10	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
66	d1v7ba2	Alignment	not modelled	8.4	17	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
67	c2pn1A_	Alignment	not modelled	8.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoylphosphate synthase large subunit; **PDBTitle:** crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
68	d2cz4a1	Alignment	not modelled	7.8	15	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
69	d2hrca1	Alignment	not modelled	7.7	38	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
70	d1rkba_	Alignment	not modelled	7.5	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
71	c2edgA_	Alignment	not modelled	7.5	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** solution structure of the gcv_h domain from mouse glycine
72	d2b8ea1	Alignment	not modelled	7.3	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
73	d1onla_	Alignment	not modelled	7.3	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
74	c3bijC_	Alignment	not modelled	7.0	14	**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
75	d1iq0a1	Alignment	not modelled	7.0	35	**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
76	c2cveA_	Alignment	not modelled	6.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
77	d1dxya2	Alignment	not modelled	6.8	18	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
						Fold: Spectrin repeat-like

78	d1w0ba_	Alignment	not modelled	6.8	21	**Superfamily:**Alpha-hemoglobin stabilizing protein AHSP **Family:**Alpha-hemoglobin stabilizing protein AHSP
79	d1v8za1	Alignment	not modelled	6.8	12	**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
80	d1v82a_	Alignment	not modelled	6.8	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**1,3-glucuronyltransferase
81	c1ou5A_	Alignment	not modelled	6.7	8	**PDB header:**translation, transferase **Chain:** A: **PDB Molecule:**trna cca-adding enzyme; **PDBTitle:** crystal structure of human cca-adding enzyme
82	c3dqzB_	Alignment	not modelled	6.6	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-hydroxynitrile lyase-like protein; **PDBTitle:** structure of the hydroxynitrile lyase from arabidopsis2 thaliana
83	c2ihnA_	Alignment	not modelled	6.6	24	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
84	d2fiqa1	Alignment	not modelled	6.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**GatZ-like
85	c3iynR_	Alignment	not modelled	6.4	14	**PDB header:**virus **Chain:** R: **PDB Molecule:**hexon-associated protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
86	d3adka_	Alignment	not modelled	6.4	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
87	d1wmga_	Alignment	not modelled	6.3	17	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
88	d1vela1	Alignment	not modelled	6.3	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
89	c2ka7A_	Alignment	not modelled	6.3	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** nmr solution structure of tm0212 at 40 c
90	d1gm6a_	Alignment	not modelled	6.3	3	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
91	d1exsa_	Alignment	not modelled	6.2	12	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
92	d1szpb1	Alignment	not modelled	6.2	21	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
93	c3aqnA_	Alignment	not modelled	6.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** complex structure of bacterial protein (apo form ii)
94	c2ppvA_	Alignment	not modelled	6.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
95	d3bkjh1	Alignment	not modelled	6.0	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
96	c2v6lI_	Alignment	not modelled	6.0	13	**PDB header:**protein transport **Chain:** I: **PDB Molecule:**mxih; **PDBTitle:** molecular model of a type iii secretion system needle
97	c1vi7A_	Alignment	not modelled	5.9	6	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yigz; **PDBTitle:** crystal structure of an hypothetical protein
98	d2ca5a1	Alignment	not modelled	5.9	13	**Fold:**Long alpha-hairpin **Superfamily:**MxiH-like **Family:**MxiH-like
99	c2r9vA_	Alignment	not modelled	5.8	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution