Phyre2

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Description	P18956
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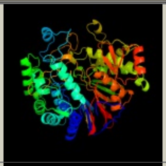
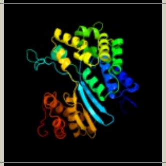
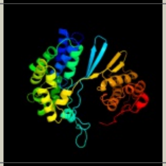
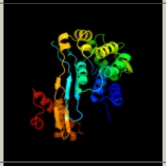
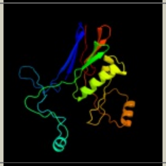
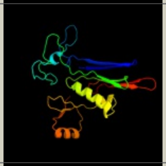
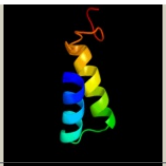
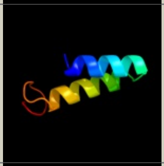
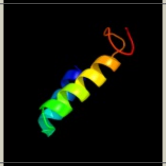
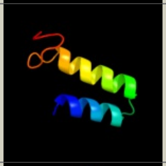
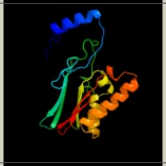
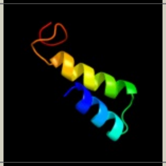
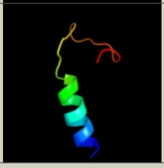
Unique Job ID	acd5409637bd2c84

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2nlza1	Alignment		100.0	31	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Gamma-glutamyltranspeptidase-like
2	c2e0wA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli
3	d2i3oa1	Alignment		100.0	24	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Gamma-glutamyltranspeptidase-like
4	c2z8jA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of escherichia coli gamma-2 glutamyltranspeptidase in complex with azaserine prepared3 in the dark
5	c2v36A_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gamma-glutamyltranspeptidase large chain; **PDBTitle:** crystal structure of gamma-glutamyl transferase from2 bacillus subtilis
6	c2qm6C_	Alignment		100.0	49	**PDB header:**transferase **Chain:** C: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of helicobacter pylori gamma-glutamyltranspeptidase2 in complex with glutamate
7	c3g9kD_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**capsule biosynthesis protein capd; **PDBTitle:** crystal structure of bacillus anthracis transpeptidase enzyme capd
8	c2e0yB_	Alignment		100.0	96	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of the samarium derivative of mature gamma-2 glutamyltranspeptidase from escherichia coli
9	c2nqoB_	Alignment		100.0	58	**PDB header:**transferase **Chain:** B: **PDB Molecule:**gamma-glutamyltranspeptidase; **PDBTitle:** crystal structure of helicobacter pylori gamma-glutamyltranspeptidase
10	c2v36D_	Alignment		100.0	42	**PDB header:**transferase **Chain:** D: **PDB Molecule:**gamma-glutamyltranspeptidase small chain; **PDBTitle:** crystal structure of gamma-glutamyl transferase from2 bacillus subtilis
11	c3ga9S_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** S: **PDB Molecule:**capsule biosynthesis protein capd; **PDBTitle:** crystal structure of bacillus anthracis transpeptidase enzyme capd,2 crystal form ii

12	c1apyA_	Alignment		94.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartylglucosaminidase; **PDBTitle:** human aspartylglucosaminidase
13	c1t3mA_	Alignment		94.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
14	c2gezE_	Alignment		94.4	23	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
15	c2zakB_	Alignment		93.4	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase precursor; **PDBTitle:** orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
16	c1p4vA_	Alignment		92.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n(4)-(beta-n-acetylglucosaminyl)-l-asparaginase **PDBTitle:** crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
17	c2gacA_	Alignment		92.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosylasparaginase; **PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
18	c2a8lB_	Alignment		92.2	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**threonine aspartase 1; **PDBTitle:** crystal structure of human taspase1 (t234a mutant)
19	c1apzB_	Alignment		85.9	19	**PDB header:**complex (hydrolase/peptide) **Chain:** B: **PDB Molecule:**aspartylglucosaminidase; **PDBTitle:** human aspartylglucosaminidase complex with reaction product
20	c3cuqA_	Alignment		85.6	45	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
21	c2zmeA_	Alignment	not modelled	85.4	45	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
22	c1u5tA_	Alignment	not modelled	84.8	28	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
23	d1u5ta1	Alignment	not modelled	78.9	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
24	c1w7pD_	Alignment	not modelled	72.5	33	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**vps36p, ylr417w; **PDBTitle:** the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
25	c1u5tB_	Alignment	not modelled	69.7	37	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**defective in vacuolar protein sorting; vps36p; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
26	c2zmeB_	Alignment	not modelled	69.2	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein-sorting-associated protein 36; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
27	d1jq5a_	Alignment	not modelled	64.7	23	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
28	c1t3mD_	Alignment	not modelled	62.1	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli

29	c1jn9B_	Alignment	not modelled	62.1	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of putative asparaginase encoded by escherichia coli ybik2 gene
30	c1t3mB_	Alignment	not modelled	62.1	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
31	c2zalD_	Alignment	not modelled	58.9	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
32	c2gacD_	Alignment	not modelled	55.0	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glycosylasparaginase; **PDBTitle:** t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
33	c2gezF_	Alignment	not modelled	53.6	21	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**l-asparaginase beta subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
34	c1k2xB_	Alignment	not modelled	51.1	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
35	c1k2xD_	Alignment	not modelled	51.1	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
36	c1jn9D_	Alignment	not modelled	51.1	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of putative asparaginase encoded by escherichia coli ybik2 gene
37	c2zalB_	Alignment	not modelled	48.3	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
38	c3rf7A_	Alignment	not modelled	31.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
39	c2wl8D_	Alignment	not modelled	31.2	19	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**peroxisomal biogenesis factor 19; **PDBTitle:** x-ray crystal structure of pex19p
40	d2fi0a1	Alignment	not modelled	28.9	19	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
41	d1u2ka_	Alignment	not modelled	26.3	11	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
42	c3bt3B_	Alignment	not modelled	25.4	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase-related enzyme, arac type; **PDBTitle:** crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans
43	c3h7hA_	Alignment	not modelled	24.1	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
44	c3gxqB_	Alignment	not modelled	23.9	50	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**putative regulator of transfer genes arta; **PDBTitle:** structure of arta and dna complex
45	d1o2da_	Alignment	not modelled	23.7	27	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
46	d2ccaa1	Alignment	not modelled	23.3	15	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
47	c1udsA_	Alignment	not modelled	21.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of the trna processing enzyme rnase ph r126a mutant2 from aquifex aeolicus
48	d1oj7a_	Alignment	not modelled	20.8	20	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
49	c2kmvA_	Alignment	not modelled	20.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the nucleotide binding domain of the2 human menkes protein in the atp-free form
50	c3hkmB_	Alignment	not modelled	19.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**os03g0854200 protein; **PDBTitle:** crystal structure of rice(oryza sativa) rrp46
51	d1u5tb1	Alignment	not modelled	19.4	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
52	c2qntA_	Alignment	not modelled	19.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1872; **PDBTitle:** crystal structure of protein of unknown function from agrobacterium2 tumefaciens str. c58
53	d2nn6f1	Alignment	not modelled	17.6	33	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
54	d1r6la1	Alignment	not modelled	17.2	11	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
						PDB header:hydrolase/transferase

55	c2nn6D_	Alignment	not modelled	16.9	21	**Chain:** D: **PDB Molecule:**exosome complex exonuclease rrp46; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
56	d2nn6b1	Alignment	not modelled	16.6	22	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
57	c3b4tC_	Alignment	not modelled	16.4	32	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of mycobacterium tuberculosis rnase ph, the2 mycobacterium tuberculosis structural genomics consortium target3 rv1340
58	d1udsa1	Alignment	not modelled	16.1	17	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
59	d2nn6a1	Alignment	not modelled	15.9	33	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
60	d1a0da_	Alignment	not modelled	15.7	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
61	d2nn6e1	Alignment	not modelled	15.6	39	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
62	d1vlja_	Alignment	not modelled	15.6	25	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
63	d2je6b1	Alignment	not modelled	15.6	11	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
64	c1u2jC_	Alignment	not modelled	15.6	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxidase/catalase hpi; **PDBTitle:** crystal structure of the c-terminal domain from the2 catalase-peroxidase katg of escherichia coli (p21 21 21)
65	c2rk9B_	Alignment	not modelled	14.8	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** the crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase superfamily member from vibrio splendidus 12b01
66	d2ba0g1	Alignment	not modelled	13.9	33	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
67	c3itwA_	Alignment	not modelled	13.8	26	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**protein tiox; **PDBTitle:** crystal structure of tiox from micromonospora sp. ml1
68	d2nn6d1	Alignment	not modelled	13.5	6	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
69	c2wnrB_	Alignment	not modelled	13.3	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable exosome complex exonuclease 1; **PDBTitle:** the structure of methanothermobacter thermautotrophicus2 exosome core assembly
70	d1kq3a_	Alignment	not modelled	12.4	20	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
71	c2nn6F_	Alignment	not modelled	12.1	33	**PDB header:**hydrolase/transferase **Chain:** F: **PDB Molecule:**exosome component 6; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
72	d1ny9a_	Alignment	not modelled	12.1	11	**Fold:**Antibiotic binding domain of TipA-like multidrug resistance regulators **Superfamily:**Antibiotic binding domain of TipA-like multidrug resistance regulators **Family:**Antibiotic binding domain of TipA-like multidrug resistance regulators
73	c1ny9A_	Alignment	not modelled	12.1	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional activator tipa-s; **PDBTitle:** antibiotic binding domain of a tipa-class multidrug2 resistance transcriptional regulator
74	c2e5yA_	Alignment	not modelled	11.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase epsilon chain; **PDBTitle:** epsilon subunit and atp complex of f1f0-atp synthase from2 the thermophilic bacillus ps3
75	c2wp8B_	Alignment	not modelled	11.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exosome complex component ski6; **PDBTitle:** yeast rrp44 nuclease
76	d1mwva1	Alignment	not modelled	11.6	9	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
77	c2qz5A_	Alignment	not modelled	11.2	19	**PDB header:**signaling protein, lipid binding protein **Chain:** A: **PDB Molecule:**axin interactor, dorsalization associated **PDBTitle:** crystal structure of the c-terminal domain of aida
78	c3epzA_	Alignment	not modelled	11.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 1; **PDBTitle:** structure of the replication foci-targeting sequence of human dna2 cytosine methyltransferase dnmt1
79	d2qalk1	Alignment	not modelled	11.0	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
80	c2br2G_	Alignment	not modelled	10.9	39	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**exosome complex exonuclease 2;

						PDBTitle: rnase ph core of the archaeal exosome
81	d1oysa1	Alignment	not modelled	10.9	11	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
82	c2zkqk_	Alignment	not modelled	10.9	22	**PDB header:**ribosomal protein/rna **Chain:** K: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
83	c3dd6A_	Alignment	not modelled	10.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribonuclease ph; **PDBTitle:** crystal structure of rph, an exoribonuclease from bacillus2 anthracis at 1.7 a resolution
84	d2je6a1	Alignment	not modelled	10.5	39	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Ribonuclease PH domain 1-like
85	c2koyA_	Alignment	not modelled	10.5	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper-transporting atpase 2; **PDBTitle:** structure of the e1064a mutant of the n-domain of wilson disease2 associated protein
86	d1huwa_	Alignment	not modelled	10.4	15	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
87	c3bvkC_	Alignment	not modelled	10.3	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**ferritin; **PDBTitle:** structural basis for the iron uptake mechanism of helicobacter pylori2 ferritin
88	d1ub2a1	Alignment	not modelled	10.0	12	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
89	c2arfA_	Alignment	not modelled	9.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wilson disease atpase; **PDBTitle:** solution structure of the wilson atpase n-domain in the2 presence of atp
90	d2i09a2	Alignment	not modelled	9.9	20	**Fold:**DeoB insert domain-like **Superfamily:**DeoB insert domain-like **Family:**DeoB insert domain-like
91	d1v74a_	Alignment	not modelled	9.5	12	**Fold:**Colicin D/E5 nuclease domain **Superfamily:**Colicin D/E5 nuclease domain **Family:**Colicin D nuclease domain
92	c3bfjK_	Alignment	not modelled	9.4	18	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
93	d3bzka1	Alignment	not modelled	9.4	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
94	d1itka1	Alignment	not modelled	9.4	12	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
95	c2rq7A_	Alignment	not modelled	9.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase epsilon chain; **PDBTitle:** solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1
96	c2rbbB_	Alignment	not modelled	9.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxalase/bleomycin resistance protein/dioxygenase; **PDBTitle:** crystal structure of a glyoxalase/bleomycin resistance2 protein/dioxygenase family enzyme from burkholderia phytofirmans psjn
97	c2oudA_	Alignment	not modelled	9.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the catalytic domain of human mkp5
98	c2czhB_	Alignment	not modelled	9.0	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inositol monophosphatase 2; **PDBTitle:** crystal structure of human myo-inositol monophosphatase 22 (impa2) with phosphate ion (orthorhombic form)
99	d1ub2a2	Alignment	not modelled	8.9	15	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG