










# Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2hhgA_</a>	Alignment		99.9	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rpa3614; <b>PDBTitle:</b> structure of protein of unknown function rpa3614, possible tyrosine2 phosphatase, from rhodopseudomonas palustris cga009
2	<a href="#">d1yt8a1</a>	Alignment		99.9	24	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
3	<a href="#">c3tp9B_</a>	Alignment		99.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> beta-lactamase and rhodanese domain protein; <b>PDBTitle:</b> crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
4	<a href="#">c5ve5C_</a>	Alignment		99.9	26	<b>PDB header:</b> oxidoreductase, transferase <b>Chain:</b> C: <b>PDB Molecule:</b> bbpprf; <b>PDBTitle:</b> crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytofirmans in complex with glutathione
5	<a href="#">d1yt8a3</a>	Alignment		99.9	21	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
6	<a href="#">d1tq1a_</a>	Alignment		99.9	21	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Single-domain sulfurtransferase
7	<a href="#">c1yt8A_</a>	Alignment		99.9	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiosulfate sulfurtransferase; <b>PDBTitle:</b> crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
8	<a href="#">d1qxna_</a>	Alignment		99.9	16	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Single-domain sulfurtransferase
9	<a href="#">c2moiA_</a>	Alignment		99.9	20	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein ygap; <b>PDBTitle:</b> 3d nmr structure of the cytoplasmic rhodanese domain of the inner2 membrane protein ygap from escherichia coli
10	<a href="#">c3ilmD_</a>	Alignment		99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> alr3790 protein; <b>PDBTitle:</b> crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
11	<a href="#">c3emeA_</a>	Alignment		99.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese-like domain protein; <b>PDBTitle:</b> crystal structure of rhodanese-like domain protein from2 staphylococcus aureus

12	<a href="#">c6mxvA</a>	Alignment		99.9	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese-like family protein; <b>PDBTitle:</b> the crystal structure of a rhodanese-like family protein from2 francisella tularensis subsp. tularensis schu s4
13	<a href="#">c3k9rA</a>	Alignment		99.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> alr3790 protein; <b>PDBTitle:</b> x-ray structure of the rhodanese-like domain of the alr3790 protein2 from anabaena sp. northeast structural genomics consortium target3 nsr437c.
14	<a href="#">c3d1pA</a>	Alignment		99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase yor285w; <b>PDBTitle:</b> atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
15	<a href="#">c3aaxB</a>	Alignment		99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
16	<a href="#">c2fsxA</a>	Alignment		99.9	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cog0607: rhodanese-related sulfurtransferase; <b>PDBTitle:</b> crystal structure of rv0390 from m. tuberculosis
17	<a href="#">c3hzuA</a>	Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thiosulfate sulfurtransferase ssea; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
18	<a href="#">c6h98A</a>	Alignment		99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase; <b>PDBTitle:</b> native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola.
19	<a href="#">d1rhsa1</a>	Alignment		99.9	16	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
20	<a href="#">d1uara2</a>	Alignment		99.9	20	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
21	<a href="#">c1uarA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese; <b>PDBTitle:</b> crystal structure of rhodanese from thermus thermophilus hb8
22	<a href="#">c3nhvE</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> bh2092 protein; <b>PDBTitle:</b> crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
23	<a href="#">d1gmxA</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Single-domain sulfurtransferase
24	<a href="#">c3gk5A</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rhodanese-related protein tvg0868615; <b>PDBTitle:</b> crystal structure of rhodanese-related protein (tvg0868615) from2 thermoplasma volcanium, northeast structural genomics consortium3 target tvr109a
25	<a href="#">c1urhA</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> the "rhodanese" fold and catalytic mechanism of2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from escherichia coli
26	<a href="#">c3fojA</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
27	<a href="#">c1boiA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese; <b>PDBTitle:</b> n-terminally truncated rhodanese

28	<a href="#">c6bevB</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> thiosulfate sulfurtransferase/rhodanese-like domain- <b>PDBTitle:</b> human single domain sulfurtransferase tstd1
29	<a href="#">c3i2vA</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylyltransferase and sulfurtransferase mocs3; <b>PDBTitle:</b> crystal structure of human mocs3 rhodanese-like domain
30	<a href="#">c3icrA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a-disulfide reductase; <b>PDBTitle:</b> crystal structure of oxidized bacillus anthracis coadr-rhd
31	<a href="#">d1yt8a4</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
32	<a href="#">c3ippA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiosulfate sulfurtransferase ynje; <b>PDBTitle:</b> crystal structure of sulfur-free ynje
33	<a href="#">d1t3ka</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Cell cycle control phosphatase, catalytic domain
34	<a href="#">d1urha1</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
35	<a href="#">c2dcqA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative protein at4g01050; <b>PDBTitle:</b> fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
36	<a href="#">d1yt8a2</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
37	<a href="#">d1okga1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
38	<a href="#">d1e0ca1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
39	<a href="#">c1e0cA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> sulfurtransferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase; <b>PDBTitle:</b> sulfurtransferase from azotobacter vinelandii
40	<a href="#">d1uara1</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
41	<a href="#">c3olhA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> human 3-mercaptopyruvate sulfurtransferase
42	<a href="#">c4f67A</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0176 protein lpg2838; <b>PDBTitle:</b> three dimensional structure of the double mutant of upf0176 protein2 lpg2838 from legionella pneumophila at the resolution 1.8a, northeast3 structural genomics consortium (nesg) target lgr82
43	<a href="#">c3utnX</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> thiosulfate sulfurtransferase tum1; <b>PDBTitle:</b> crystal structure of tum1 protein from saccharomyces cerevisiae
44	<a href="#">c3ntaA</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> structure of the shewanella loihca pv-4 nadh-dependent persulfide2 reductase
45	<a href="#">d1okga2</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
46	<a href="#">d1e0ca2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
47	<a href="#">c2k0zA</a>	Alignment	not modelled	99.8	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein hp1203; <b>PDBTitle:</b> solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
48	<a href="#">c3f4aA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ygr203w; <b>PDBTitle:</b> structure of ygr203w, a yeast protein tyrosine phosphatase of the2 rhodanese family
49	<a href="#">c1okgA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> possible 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> 3-mercaptopyruvate sulfurtransferase from leishmania major
50	<a href="#">c2eg4B</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable thiosulfate sulfurtransferase; <b>PDBTitle:</b> crystal structure of probable thiosulfate sulfurtransferase
51	<a href="#">c3g5jA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative atp/gtp binding protein; <b>PDBTitle:</b> crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
52	<a href="#">c2jtqA</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phage shock protein e; <b>PDBTitle:</b> rhodanese from e.coli

53	<a href="#">d1rhsa2</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
54	<a href="#">d1c25a_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Cell cycle control phosphatase, catalytic domain
55	<a href="#">d1ymka1</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Cell cycle control phosphatase, catalytic domain
56	<a href="#">c2j6pF_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> sb(v)-as(v) reductase; <b>PDBTitle:</b> structure of as-sb reductase from leishmania major
57	<a href="#">c2uzqE_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> E; <b>PDB Molecule:</b> m-phase inducer phosphatase 2; <b>PDBTitle:</b> protein phosphatase, new crystal form
58	<a href="#">c1wv9B_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> rhodanese homolog tt1651; <b>PDBTitle:</b> crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
59	<a href="#">c3op3A_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> m-phase inducer phosphatase 3; <b>PDBTitle:</b> crystal structure of cell division cycle 25c protein isoform a from2 homo sapiens
60	<a href="#">c3r2uC_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> metallo-beta-lactamase family protein; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
61	<a href="#">d1urha2</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
62	<a href="#">d1whba_</a>	Alignment	not modelled	99.5	10	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Ubiquitin carboxyl-terminal hydrolase 8, USP8
63	<a href="#">c2vswB_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> dual specificity protein phosphatase 16; <b>PDBTitle:</b> the structure of the rhodanese domain of the human dual specificity2 phosphatase 16
64	<a href="#">c2oucB_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> dual specificity protein phosphatase 10; <b>PDBTitle:</b> crystal structure of the map kinase binding domain of mkp5
65	<a href="#">d2gwfa1</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Ubiquitin carboxyl-terminal hydrolase 8, USP8
66	<a href="#">d1hzma_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Cell cycle control phosphatase, catalytic domain
67	<a href="#">c3gxgA_</a>	Alignment	not modelled	94.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative phosphatase (duf442); <b>PDBTitle:</b> crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution
68	<a href="#">d1ywfa1</a>	Alignment	not modelled	94.4	24	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Mycobacterial PtpB-like
69	<a href="#">c2f46A_</a>	Alignment	not modelled	93.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
70	<a href="#">c2oz5A_</a>	Alignment	not modelled	91.5	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> phosphotyrosine protein phosphatase ptpb; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
71	<a href="#">c2i6oA_</a>	Alignment	not modelled	89.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> sulfolobus solfataricus protein tyrosine <b>PDBTitle:</b> crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)j-k-n
72	<a href="#">c4nyhB_</a>	Alignment	not modelled	79.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> rna/rnp complex-1-interacting phosphatase; <b>PDBTitle:</b> orthorhombic crystal form of pir1 dual specificity phosphatase core
73	<a href="#">c3rggA_</a>	Alignment	not modelled	79.3	6	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protein-tyrosine phosphatase mitochondrial 1; <b>PDBTitle:</b> crystal structure of ptpmt1 in complex with pi(5)p
74	<a href="#">c6byfl_</a>	Alignment	not modelled	78.6	9	<b>PDB header:</b> transferase <b>Chain:</b> I; <b>PDB Molecule:</b> tyrosine-protein phosphatase siw14; <b>PDBTitle:</b> crystal structure of the core catalytic domain of pp-ip phosphatase2 siw14 from s. cerevisiae in complex with citrate
75	<a href="#">c3flhC_</a>	Alignment	not modelled	78.0	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> uncharacterized protein lp_1913; <b>PDBTitle:</b> crystal structure of lp_1913 protein from lactobacillus plantarum,2 northeast structural genomics consortium target lpr140b
76	<a href="#">c1oheA_</a>	Alignment	not modelled	71.6	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cdc14b2 phosphatase; <b>PDBTitle:</b> structure of cdc14b phosphatase with a peptide ligand
77	<a href="#">d1ohea2</a>	Alignment	not modelled	70.9	8	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
78	<a href="#">c2imgA_</a>	Alignment	not modelled	70.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dual specificity protein phosphatase 23;

78	<a href="#">c2imgA</a>	Alignment	not modelled	70.3	12	<b>PDBTitle:</b> crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
79	<a href="#">d1xria</a>	Alignment	not modelled	69.9	11	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
80	<a href="#">d1fpza</a>	Alignment	not modelled	62.9	11	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
81	<a href="#">d1nka4</a>	Alignment	not modelled	61.2	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
82	<a href="#">c2m3vA</a>	Alignment	not modelled	60.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> solution structure of tyrosine phosphatase related to biofilm2 formation a (tpba) from pseudomonas aeruginosa
83	<a href="#">d1q15a1</a>	Alignment	not modelled	54.2	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
84	<a href="#">d1j3a</a>	Alignment	not modelled	52.9	14	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
85	<a href="#">c2obnA</a>	Alignment	not modelled	52.9	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a duf1611 family protein (ava_3511) from anaebaena2 variabilis atcc 29413 at 2.30 a resolution
86	<a href="#">c1fpzF</a>	Alignment	not modelled	52.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> cyclin-dependent kinase inhibitor 3; <b>PDBTitle:</b> crystal structure analysis of kinase associated phosphatase (kap) with2 a substitution of the catalytic site cysteine (cys140) to a serine
87	<a href="#">c4cdgA</a>	Alignment	not modelled	52.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bloom syndrome protein; <b>PDBTitle:</b> crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
88	<a href="#">c3i32A</a>	Alignment	not modelled	52.2	22	<b>PDB header:</b> rna binding protein,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> heat resistant rna dependent atpase; <b>PDBTitle:</b> dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
89	<a href="#">c3d3jA</a>	Alignment	not modelled	50.6	5	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
90	<a href="#">d1a1va2</a>	Alignment	not modelled	50.0	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
91	<a href="#">c4jmkA</a>	Alignment	not modelled	48.2	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 8; <b>PDBTitle:</b> structure of dusp8
92	<a href="#">d1oywa3</a>	Alignment	not modelled	46.6	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
93	<a href="#">c6ozdB</a>	Alignment	not modelled	46.3	31	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> putative exported protein; <b>PDBTitle:</b> crystal structure of putative exported protein (bpss2145) from2 burkholderia pseudomallei k96243
94	<a href="#">c3ohgA</a>	Alignment	not modelled	45.1	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein from duf2233 family; <b>PDBTitle:</b> crystal structure of a protein with unknown function from duf22332 family (bacova_00430) from bacteroides ovatus at 1.80 a resolution
95	<a href="#">c2i18A</a>	Alignment	not modelled	42.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> an arsenate reductase in the phosphate binding state
96	<a href="#">c1oywA</a>	Alignment	not modelled	40.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase; <b>PDBTitle:</b> structure of the recq catalytic core
97	<a href="#">c2g6zB</a>	Alignment	not modelled	40.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dual specificity protein phosphatase 5; <b>PDBTitle:</b> crystal structure of human dusp5
98	<a href="#">c4q47A</a>	Alignment	not modelled	40.0	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna helicase recq; <b>PDBTitle:</b> structure of the drrecq catalytic core in complex with adp
99	<a href="#">c2v1xB</a>	Alignment	not modelled	39.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent dna helicase q1; <b>PDBTitle:</b> crystal structure of human recq-like dna helicase
100	<a href="#">c2r0bA</a>	Alignment	not modelled	39.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serine/threonine/tyrosine-interacting protein; <b>PDBTitle:</b> crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
101	<a href="#">c4rkkA</a>	Alignment	not modelled	39.1	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> laforin; <b>PDBTitle:</b> structure of a product bound phosphatase
102	<a href="#">c2wgpA</a>	Alignment	not modelled	38.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 14; <b>PDBTitle:</b> crystal structure of human dual specificity phosphatase 14
103	<a href="#">d1jf8a</a>	Alignment	not modelled	38.3	11	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases

104	<a href="#">d2dw4a2</a>	Alignment	not modelled	35.9	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
105	<a href="#">c3t38B</a>	Alignment	not modelled	35.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
106	<a href="#">c1h83A</a>	Alignment	not modelled	35.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> polyamine oxidase; <b>PDBTitle:</b> structure of polyamine oxidase in complex with2 1,8-diaminooctane
107	<a href="#">c1u24A</a>	Alignment	not modelled	35.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> myo-inositol hexaphosphate phosphohydrolase; <b>PDBTitle:</b> crystal structure of selenomonas ruminantium phytase
108	<a href="#">c2e0tA</a>	Alignment	not modelled	34.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dual specificity phosphatase 26; <b>PDBTitle:</b> crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
109	<a href="#">c5h3kA</a>	Alignment	not modelled	34.2	22	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> slr0280 protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein from synechocystis
110	<a href="#">d1t5la2</a>	Alignment	not modelled	34.1	6	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
111	<a href="#">c1e1cA</a>	Alignment	not modelled	33.4	29	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> methylmalonyl-coa mutase alpha chain; <b>PDBTitle:</b> methylmalonyl-coa mutase h244a mutant
112	<a href="#">c3rh0A</a>	Alignment	not modelled	33.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
113	<a href="#">c3bicA</a>	Alignment	not modelled	32.9	27	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> methylmalonyl-coa mutase, mitochondrial precursor; <b>PDBTitle:</b> crystal structure of human methylmalonyl-coa mutase
114	<a href="#">d1k92a1</a>	Alignment	not modelled	32.7	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
115	<a href="#">c2b9yA</a>	Alignment	not modelled	32.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> putative aminooxidase; <b>PDBTitle:</b> crystal structure of cla-producing fatty acid isomerase2 from p. acnes
116	<a href="#">d1j9ia</a>	Alignment	not modelled	31.5	22	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Terminase gpNU1 subunit domain
117	<a href="#">d1tf5a4</a>	Alignment	not modelled	31.3	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
118	<a href="#">c3nbmA</a>	Alignment	not modelled	31.1	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> pts system, lactose-specific iibc components; <b>PDBTitle:</b> the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
119	<a href="#">d1fuka</a>	Alignment	not modelled	29.5	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Tandem AAA-ATPase domain
120	<a href="#">c3o2sB</a>	Alignment	not modelled	29.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> rna polymerase ii subunit a c-terminal domain phosphatase <b>PDBTitle:</b> crystal structure of the human symplekin-ssu72 complex