Phyre2

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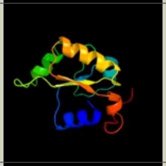
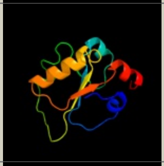
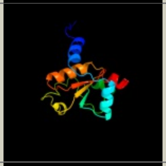
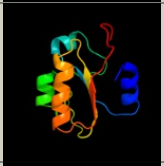
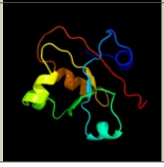
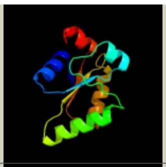
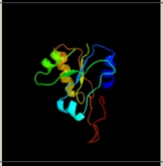
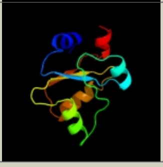
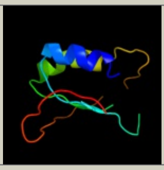
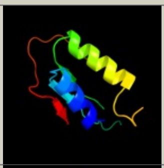
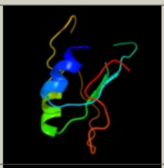
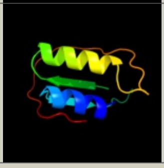
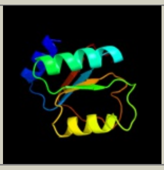
Detailed template information

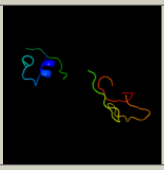
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j6pF_	Alignment		99.9	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**sb(v)-as(v) reductase; **PDBTitle:** structure of as-sb reductase from leishmania major
2	c3i2vA_	Alignment		99.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase and sulfurtransferase mocs3; **PDBTitle:** crystal structure of human mocs3 rhodanese-like domain
3	c3tp9B_	Alignment		99.8	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase and rhodanese domain protein; **PDBTitle:** crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
4	d1c25a_	Alignment		99.8	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
5	c3d1pA_	Alignment		99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase yor285w; **PDBTitle:** atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
6	c3f4aA_	Alignment		99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ygr203w; **PDBTitle:** structure of ygr203w, a yeast protein tyrosine phosphatase2 of the rhodanese family
7	c2hhgA_	Alignment		99.8	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rpa3614; **PDBTitle:** structure of protein of unknown function rpa3614, possible tyrosine2 phosphatase, from rhodopseudomonas palustris cga009
8	d1yt8a4	Alignment		99.8	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
9	d1yt8a1	Alignment		99.8	21	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
10	c3ilmD_	Alignment		99.8	23	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**alr3790 protein; **PDBTitle:** crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
11	c3fojA_	Alignment		99.8	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of ssp1007 from staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.

12	d1gmxa_	Alignment		99.8	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
13	c3icrA_	Alignment		99.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
14	d1ymka1	Alignment		99.8	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
15	c1yt8A_	Alignment		99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
16	c2dcqA_	Alignment		99.8	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative protein at4g01050; **PDBTitle:** fully automated nmr structure determination of the2 rhodanese homology domain at4g01050(175-295) from3 arabidopsis thaliana
17	c2fsxA_	Alignment		99.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cog0607: rhodanese-related sulfurtransferase; **PDBTitle:** crystal structure of rv0390 from m. tuberculosis
18	d1yt8a2	Alignment		99.8	18	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
19	d1qxna_	Alignment		99.8	19	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
20	c1e0cA_	Alignment		99.8	20	**PDB header:**sulfurtransferase **Chain:** A: **PDB Molecule:**sulfurtransferase; **PDBTitle:** sulfurtransferase from azotobacter vinelandii
21	c3emeA_	Alignment	not modelled	99.7	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**rhodanese-like domain protein; **PDBTitle:** crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
22	c3aaxB_	Alignment	not modelled	99.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
23	c3gk5A_	Alignment	not modelled	99.7	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized rhodanese-related protein **PDBTitle:** crystal structure of rhodanese-related protein (tvg0868615)2 from thermoplasma volcanium, northeast structural genomics3 consortium target tvr109a
24	c1urhA_	Alignment	not modelled	99.7	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** the "rhodanese" fold and catalytic mechanism of2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from escherichia coli
25	d1yt8a3	Alignment	not modelled	99.7	15	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
26	c3op3A_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**m-phase inducer phosphatase 3; **PDBTitle:** crystal structure of cell division cycle 25c protein isoform a from2 homo sapiens
27	d1tq1a_	Alignment	not modelled	99.7	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
						PDB header:transferase

28	c3hzuA_	Alignment	not modelled	99.7	20	**Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase ssea; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
29	c3g5jA_	Alignment	not modelled	99.7	27	**PDB header:**nucleotide binding protein **Chain:** A: **PDB Molecule:**putative atp/gtp binding protein; **PDBTitle:** crystal structure of n-terminal domain of putative atp/gtp binding2 protein from clostridium difficile 630
30	c2uzqE_	Alignment	not modelled	99.7	21	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**m-phase inducer phosphatase 2; **PDBTitle:** protein phosphatase, new crystal form
31	c3k9rA_	Alignment	not modelled	99.7	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**alr3790 protein; **PDBTitle:** x-ray structure of the rhodanese-like domain of the alr3790 protein2 from anabaena sp. northeast structural genomics consortium target3 nsr437c.
32	c3ntaA_	Alignment	not modelled	99.7	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
33	d1e0ca1	Alignment	not modelled	99.7	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
34	d1uara2	Alignment	not modelled	99.7	28	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
35	c1uarA_	Alignment	not modelled	99.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8
36	c1boiA_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** n-terminally truncated rhodanese
37	c3ippA_	Alignment	not modelled	99.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
38	d1t3ka_	Alignment	not modelled	99.7	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
39	c3olhA_	Alignment	not modelled	99.7	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
40	c2jtqA_	Alignment	not modelled	99.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phage shock protein e; **PDBTitle:** rhodanese from e.coli
41	d1rhsa1	Alignment	not modelled	99.7	15	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
42	c1wv9B_	Alignment	not modelled	99.6	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**rhodanese homolog tt1651; **PDBTitle:** crystal structure of rhodanese homolog tt1651 from an2 extremely thermophilic bacterium thermus thermophilus hb8
43	c3nhvE_	Alignment	not modelled	99.6	26	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**bh2092 protein; **PDBTitle:** crystal structure of bh2092 protein from bacillus halodurans,2 northeast structural genomics consortium target bhr228f
44	c2k0zA_	Alignment	not modelled	99.6	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp1203; **PDBTitle:** solution nmr structure of protein hp1203 from helicobacter pylori2 26695. northeast structural genomics consortium (nesg) target3 pt1/ontario center for structural proteomics target hp1203
45	d1urha1	Alignment	not modelled	99.6	24	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
46	d1e0ca2	Alignment	not modelled	99.6	24	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
47	d1okga2	Alignment	not modelled	99.6	21	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
48	d1rhsa2	Alignment	not modelled	99.6	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
49	d1uara1	Alignment	not modelled	99.6	24	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
50	c2vswB_	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 16; **PDBTitle:** the structure of the rhodanese domain of the human dual2 specificity phosphatase 16
51	c3r2uC_	Alignment	not modelled	99.4	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallo-beta-lactamase family protein; **PDBTitle:** 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
52	d1urha2	Alignment	not modelled	99.4	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
53	d1okga1	Alignment	not modelled	99.4	19	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase

						Family: Multidomain sulfurtransferase (rhodanese)
54	c2oucB_	Alignment	not modelled	99.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the map kinase binding domain of mkp5
55	d2gwfa1	Alignment	not modelled	99.4	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Ubiquitin carboxyl-terminal hydrolase 8, USP8
56	c2eg4B_	Alignment	not modelled	99.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase
57	d1whba_	Alignment	not modelled	99.4	15	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Ubiquitin carboxyl-terminal hydrolase 8, USP8
58	c1okgA_	Alignment	not modelled	99.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
59	d1hzma_	Alignment	not modelled	99.3	19	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
60	d1urra_	Alignment		95.8	15	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
61	c3flhC_	Alignment	not modelled	95.7	24	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein lp_1913; **PDBTitle:** crystal structure of lp_1913 protein from lactobacillus2 plantarum,northeast structural genomics consortium target3 lpr140b
62	c2gv1A_	Alignment		95.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** nmr solution structure of the acylphosphatase from2 eschaerichia coli
63	d1d5ra2	Alignment	not modelled	95.5	10	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
64	d2acya_	Alignment		95.5	15	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
65	c3br8A_	Alignment		94.9	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis
66	c3rgqA_	Alignment	not modelled	94.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine phosphatase mitochondrial 1; **PDBTitle:** crystal structure of ptpmt1 in complex with pi(5)p
67	d1apsa_	Alignment		94.4	12	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
68	d1ulra_	Alignment		94.4	14	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
69	c3gxgA_	Alignment	not modelled	94.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phosphatase (duf442); **PDBTitle:** crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution
70	d1w2ia_	Alignment	not modelled	94.1	18	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
71	c2f46A_	Alignment	not modelled	94.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
72	c2bjeA_	Alignment	not modelled	94.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylphosphatase; **PDBTitle:** acylphosphatase from sulfolobus solfataricus. monclinic p212 space group
						PDB header:hydrolase, membrane protein

73	c3awfC_	Alignment	not modelled	93.8	18	**Chain:** C: **PDB Molecule:**voltage-sensor containing phosphatase; **PDBTitle:** crystal structure of pten-like domain of ci-vsp (236-576)
74	c2imgA_	Alignment	not modelled	93.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 23; **PDBTitle:** crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
75	d1xria_	Alignment	not modelled	92.9	11	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
76	c1d5rA_	Alignment	not modelled	92.0	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoinositide phosphotase pten; **PDBTitle:** crystal structure of the pten tumor suppressor
77	c1yn9B_	Alignment	not modelled	88.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polynucleotide 5'-phosphatase; **PDBTitle:** crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
78	d1ywfa1	Alignment	not modelled	87.7	16	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Mycobacterial PtpB-like
79	c3rz2B_	Alignment	not modelled	87.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein tyrosine phosphatase type iva 1; **PDBTitle:** crystal of prl-1 complexed with peptide
80	c1fpzF_	Alignment	not modelled	87.1	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cyclin-dependent kinase inhibitor 3; **PDBTitle:** crystal structure analysis of kinase associated phosphatase2 (kap) with a substitution of the catalytic site cysteine3 (cys140) to a serine
81	d1rxda_	Alignment	not modelled	86.4	11	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
82	d1jl3a_	Alignment	not modelled	82.4	29	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
83	d1oywa3	Alignment	not modelled	81.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
84	d1fpza_	Alignment	not modelled	80.7	13	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
85	c3n0aA_	Alignment	not modelled	80.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase auxilin; **PDBTitle:** crystal structure of auxilin (40-400)
86	c3t38B_	Alignment	not modelled	79.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
87	c2c46B_	Alignment	not modelled	78.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** crystal structure of the human rna guanylyltransferase and2 5'-phosphatase
88	c3i32A_	Alignment		77.4	7	**PDB header:**rna binding protein,hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
89	c2l18A_	Alignment	not modelled	77.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
90	c2vxoB_	Alignment	not modelled	75.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
91	d1fuka_	Alignment	not modelled	75.0	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
92	d1a1va2	Alignment	not modelled	74.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
93	d1y4oa1	Alignment	not modelled	73.8	18	**Fold:**Profilin-like **Superfamily:**Roadblock/LC7 domain **Family:**Roadblock/LC7 domain
94	c1oheA_	Alignment	not modelled	73.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cdc14b2 phosphatase; **PDBTitle:** structure of cdc14b phosphatase with a peptide ligand
95	d1jf8a_	Alignment	not modelled	72.7	26	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
96	c2i6oA_	Alignment	not modelled	72.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfolobus solfataricus protein tyrosine **PDBTitle:** crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
97	d1yrxa1	Alignment	not modelled	64.9	11	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**BLUF domain
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine-

98	c3rofA_	Alignment	not modelled	63.7	18	phosphatase ptpa; **PDBTitle:** crystal structure of the s. aureus protein tyrosine phosphatase ptpa
99	c1dvpA_	Alignment		63.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
100	d1ni5a1	Alignment	not modelled	63.2	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
101	c1yz4A_	Alignment	not modelled	62.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase-like 15 isoform a; **PDBTitle:** crystal structure of dusp15
102	c2hcmA_	Alignment	not modelled	62.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural genomics3 consortium
103	c1k97A_	Alignment	not modelled	62.2	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
104	c3ptwA_	Alignment	not modelled	61.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
105	c2f55C_	Alignment	not modelled	60.2	17	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**polyprotein; **PDBTitle:** two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
106	c1oywA_	Alignment	not modelled	59.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase; **PDBTitle:** structure of the recq catalytic core
107	c2jgnB_	Alignment	not modelled	58.2	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase ddx3x; **PDBTitle:** ddx3 helicase domain
108	d1gxua_	Alignment	not modelled	58.2	22	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
109	c2v1xB_	Alignment	not modelled	58.1	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase q1; **PDBTitle:** crystal structure of human recq-like dna helicase
110	d1m3ga_	Alignment	not modelled	58.0	10	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
111	c1wrmA_	Alignment	not modelled	58.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 22; **PDBTitle:** crystal structure of jsp-1
112	d1v3aa_	Alignment	not modelled	57.9	13	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
113	d2g2ja1	Alignment	not modelled	57.6	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
114	c2fekA_	Alignment	not modelled	57.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** structure of a protein tyrosine phosphatase
115	c2gi4A_	Alignment	not modelled	57.5	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
116	c2wmyH_	Alignment	not modelled	56.6	21	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**putative acid phosphatase wzb; **PDBTitle:** crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
117	c2oz5A_	Alignment	not modelled	55.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phosphotyrosine protein phosphatase ptpb; **PDBTitle:** crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
118	d2j0sa2	Alignment	not modelled	54.3	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
119	d1y1la_	Alignment	not modelled	54.2	22	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
120	c2cwdA_	Alignment	not modelled	53.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8