














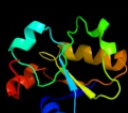






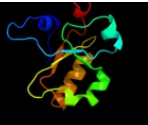






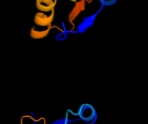



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">dlgmx_</a>	 Alignment		100.0	100	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Single-domain sulfurtransferase
2	<a href="#">c3tp9B_</a>	 Alignment		100.0	32	<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
3	<a href="#">dlyt8a3</a>	 Alignment		99.9	17	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
4	<a href="#">c1yt8A_</a>	 Alignment		99.9	17	<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
5	<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
6	<a href="#">dlyt8a1</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)
7	<a href="#">c3emeA_</a>	 Alignment		99.9	24	<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
8	<a href="#">c3gk5A_</a>	 Alignment		99.9	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized rhodanese-related protein <b>PDBTitle:</b> crystal structure of rhodanese-related protein (tv90868615)2 from thermoplasma volcanium, northeast structural genomics3 consortium target tvr109a
9	<a href="#">c3ilmD_</a>	 Alignment		99.9	21	<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
10	<a href="#">dltqla_</a>	 Alignment		99.9	29	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Single-domain sulfurtransferase
11	<a href="#">c3dlpA_</a>	 Alignment		99.9	18	<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

12	<a href="#">c3fojA</a>	Alignment		99.9	22	<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.
13	<a href="#">c3icrA</a>	Alignment		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
14	<a href="#">d1yt8a4</a>	Alignment		99.9	22	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
15	<a href="#">c3k9rA</a>	Alignment		99.9	21	<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.
16	<a href="#">c1e0cA</a>	Alignment		99.9	23	<b>PDB header:</b> sulfurtransferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfurtransferase; <b>PDBTitle:</b> sulfurtransferase from azotobacter vinelandii
17	<a href="#">c3i2vA</a>	Alignment		99.9	29	<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
18	<a href="#">d1qxna</a>	Alignment		99.9	22	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Single-domain sulfurtransferase
19	<a href="#">c3f4aA</a>	Alignment		99.9	21	<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 phosphatase2 of the rhodanese family
20	<a href="#">d1c25a</a>	Alignment		99.9	19	<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
21	<a href="#">c3nhvE</a>	Alignment	not modelled	99.9	23	<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
22	<a href="#">d1e0ca1</a>	Alignment	not modelled	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)
23	<a href="#">d1t3ka</a>	Alignment	not modelled	99.9	19	<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
24	<a href="#">d1ymka1</a>	Alignment	not modelled	99.9	17	<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
25	<a href="#">c2fsxA</a>	Alignment	not modelled	99.9	26	<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
26	<a href="#">c3aaxB</a>	Alignment	not modelled	99.9	20	<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
27	<a href="#">c2uzqE</a>	Alignment	not modelled	99.9	19	<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
28	<a href="#">d1yt8a2</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
						<b>PDB header:</b> transferase

29	<a href="#">c1urhA_</a>	Alignment	not modelled	99.9	22	<b>Chain:</b> A: <b>PDB Molecule:</b> 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> the "rhodanese" fold and catalytic mechanism of 2 3-mercaptopyruvate sulfurtransferases: crystal structure of ssea from escherichia coli
30	<a href="#">c2j6pF_</a>	Alignment	not modelled	99.9	17	<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
31	<a href="#">c3hzuA_</a>	Alignment	not modelled	99.9	13	<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
32	<a href="#">c1uarA_</a>	Alignment	not modelled	99.9	16	<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
33	<a href="#">d1uara2</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
34	<a href="#">c3ntaA_</a>	Alignment	not modelled	99.9	20	<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 loihica pv-4 nadh-dependent persulfide2 reductase
35	<a href="#">c3g5jA_</a>	Alignment	not modelled	99.9	19	<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
36	<a href="#">d1rhsa1</a>	Alignment	not modelled	99.9	17	<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="#">c1boiA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rhodanese; <b>PDBTitle:</b> n-terminally truncated rhodanese
38	<a href="#">d1urha1</a>	Alignment	not modelled	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)
39	<a href="#">c2dcqA_</a>	Alignment	not modelled	99.9	20	<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
40	<a href="#">c3op3A_</a>	Alignment	not modelled	99.9	17	<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
41	<a href="#">c2k0zA_</a>	Alignment	not modelled	99.8	17	<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
42	<a href="#">c3olhA_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-mercaptopyruvate sulfurtransferase; <b>PDBTitle:</b> human 3-mercaptopyruvate sulfurtransferase
43	<a href="#">c3ippA_</a>	Alignment	not modelled	99.8	17	<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
44	<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)
45	<a href="#">d1e0ca2</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> Multidomain sulfurtransferase (rhodanese)
46	<a href="#">d1rhsa2</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)
47	<a href="#">c2jqtA_</a>	Alignment	not modelled	99.8	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
48	<a href="#">d1okga2</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
49	<a href="#">c2vswB_</a>	Alignment	not modelled	99.8	25	<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 dual2 specificity phosphatase 16
50	<a href="#">d1okga1</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> Multidomain sulfurtransferase (rhodanese)
51	<a href="#">c1wv9B_</a>	Alignment	not modelled	99.8	24	<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
52	<a href="#">c1okgA_</a>	Alignment	not modelled	99.8	23	<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
53	<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

54	<a href="#">d1whba_</a>	Alignment	not modelled	99.8	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
55	<a href="#">c2oucB_</a>	Alignment	not modelled	99.7	16	<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
56	<a href="#">d2gwfa1</a>	Alignment	not modelled	99.7	14	<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
57	<a href="#">d1hzma_</a>	Alignment	not modelled	99.7	22	<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
58	<a href="#">d1urha2</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Rhodanese/Cell cycle control phosphatase <b>Superfamily:</b> Rhodanese/Cell cycle control phosphatase <b>Family:</b> Multidomain sulfurtransferase (rhodanese)
59	<a href="#">c3r2uC_</a>	Alignment	not modelled	99.6	12	<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
60	<a href="#">c3flhC_</a>	Alignment	not modelled	96.7	21	<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 lactobacillus2 plantarum,northeast structural genomics consortium target3 lpr140b
61	<a href="#">d1ywfa1</a>	Alignment	not modelled	87.2	22	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Mycobacterial PtpB-like
62	<a href="#">c3rggA_</a>	Alignment	not modelled	82.4	13	<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
63	<a href="#">c2f46A_</a>	Alignment	not modelled	81.1	19	<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
64	<a href="#">c3gxgA_</a>	Alignment	not modelled	80.5	16	<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
65	<a href="#">d1fpza_</a>	Alignment	not modelled	67.1	12	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
66	<a href="#">d1jl3a_</a>	Alignment	not modelled	62.1	17	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
67	<a href="#">d1jf8a_</a>	Alignment	not modelled	56.6	8	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
68	<a href="#">c2l18A_</a>	Alignment	not modelled	56.3	20	<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
69	<a href="#">d1p8aa_</a>	Alignment	not modelled	56.3	8	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
70	<a href="#">c3rh0A_</a>	Alignment	not modelled	54.2	23	<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
71	<a href="#">d1xria_</a>	Alignment	not modelled	53.5	11	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
72	<a href="#">c2oz5A_</a>	Alignment	not modelled	52.7	22	<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
73	<a href="#">d1dg9a_</a>	Alignment	not modelled	47.6	17	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
74	<a href="#">c3rofA_</a>	Alignment	not modelled	45.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight protein-tyrosine-phosphatase ptpa; <b>PDBTitle:</b> crystal structure of the s. aureus protein tyrosine phosphatase ptpa
75	<a href="#">c2wgpA_</a>	Alignment	not modelled	40.2	10	<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
76	<a href="#">d1a1va2</a>	Alignment	not modelled	39.3	9	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RNA helicase
77	<a href="#">c1fpzF_</a>	Alignment	not modelled	35.5	11	<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 phosphatase2 (kap) with a substitution of the catalytic site cysteine3 (cys140) to a serine
78	<a href="#">c2gi4A_</a>	Alignment	not modelled	35.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> possible phosphotyrosine protein phosphatase; <b>PDBTitle:</b> solution structure of the low molecular weight protein2

						tyrosine phosphatase from campylobacter jejuni.
79	<a href="#">c2i6oA_</a>	Alignment	not modelled	34.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfolobus solfataricus protein tyrosine phosphatase <b>PDBTitle:</b> crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g(p)y-k-n
80	<a href="#">d5pnta_</a>	Alignment	not modelled	33.4	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
81	<a href="#">c3ohgA_</a>	Alignment	not modelled	32.6	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
82	<a href="#">d1d5ra2</a>	Alignment	not modelled	32.4	16	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
83	<a href="#">d1d1qa_</a>	Alignment	not modelled	30.8	8	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
84	<a href="#">d1iiba_</a>	Alignment	not modelled	30.6	13	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Lactose/Cellobiose specific IIB subunit
85	<a href="#">c1tvmA_</a>	Alignment	not modelled	29.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, galactitol-specific iib component; <b>PDBTitle:</b> nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
86	<a href="#">c3nbmA_</a>	Alignment	not modelled	29.3	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.
87	<a href="#">c2fekA_</a>	Alignment	not modelled	29.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight protein-tyrosine-phosphatase <b>PDBTitle:</b> structure of a protein tyrosine phosphatase
88	<a href="#">c2imgA_</a>	Alignment	not modelled	28.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity protein phosphatase 23; <b>PDBTitle:</b> crystal structure of dual specificity protein phosphatase23 from homo sapiens in complex with ligand malate ion
89	<a href="#">c2vxob_</a>	Alignment	not modelled	28.3	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> human gmp synthetase in complex with xmp
90	<a href="#">d1nka4</a>	Alignment	not modelled	27.3	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
91	<a href="#">c3i32A_</a>	Alignment	not modelled	24.9	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
92	<a href="#">c2cwaA_</a>	Alignment	not modelled	23.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight phosphotyrosine protein phosphatase; <b>PDBTitle:</b> crystal structure of tt1001 protein from thermus thermophilus hb8
93	<a href="#">c3jviA_</a>	Alignment	not modelled	21.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine phosphatase; <b>PDBTitle:</b> product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
94	<a href="#">d1zmaa1</a>	Alignment	not modelled	21.5	27	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Thioltransferase
95	<a href="#">c3t38B_</a>	Alignment	not modelled	21.0	21	<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'
96	<a href="#">c1u2pA_</a>	Alignment	not modelled	19.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> low molecular weight protein-tyrosine-phosphatase <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
97	<a href="#">c2l2qa_</a>	Alignment	not modelled	16.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, cellobiose-specific iib component (cela); <b>PDBTitle:</b> solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
98	<a href="#">d1oywa3</a>	Alignment	not modelled	14.5	16	<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
99	<a href="#">d1k92a1</a>	Alignment	not modelled	14.5	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases