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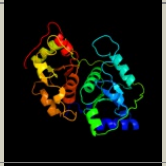
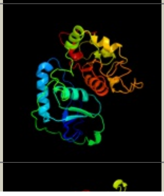
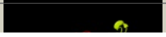
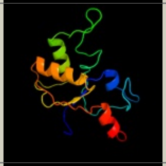
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ippA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase ynje; **PDBTitle:** crystal structure of sulfur-free ynje
2	c1okgA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**possible 3-mercaptopyruvate sulfurtransferase; **PDBTitle:** 3-mercaptopyruvate sulfurtransferase from leishmania major
3	c1yt8A_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
4	c3hzuA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiosulfate sulfurtransferase ssea; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
5	c1boiA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** n-terminally truncated rhodanese
6	c3aaxB_	Alignment		100.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
7	c1uarA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** crystal structure of rhodanese from thermus thermophilus hb8
8	c3olhA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-mercaptopyruvate sulfurtransferase; **PDBTitle:** human 3-mercaptopyruvate sulfurtransferase
9	c1e0cA_	Alignment		100.0	22	**PDB header:**sulfurtransferase **Chain:** A: **PDB Molecule:**sulfurtransferase; **PDBTitle:** sulfurtransferase from azotobacter vinelandii
10	c1urhA_	Alignment		100.0	23	**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
11	c2eg4B_	Alignment		100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiosulfate sulfurtransferase; **PDBTitle:** crystal structure of probable thiosulfate sulfurtransferase
						

12	c3tp9B_	Alignment		100.0	22	**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
13	d1uara2	Alignment		99.9	27	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
14	d1rhsa2	Alignment		99.9	24	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
15	d1rhsa1	Alignment		99.9	30	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
16	d1okga2	Alignment		99.9	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
17	d1urha1	Alignment		99.9	26	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
18	d1e0ca2	Alignment		99.9	24	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
19	d1okga1	Alignment		99.9	18	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
20	d1uara1	Alignment		99.9	31	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
21	d1e0ca1	Alignment	not modelled	99.9	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
22	d1urha2	Alignment	not modelled	99.9	19	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
23	d1yt8a1	Alignment	not modelled	99.8	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
24	c3d1pA_	Alignment	not modelled	99.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative thiosulfate sulfurtransferase yor285w; **PDBTitle:** atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
25	d1yt8a3	Alignment	not modelled	99.8	28	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
26	c3ilmD_	Alignment	not modelled	99.8	18	**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
27	d1tq1a_	Alignment	not modelled	99.7	18	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
28	c2hhgA_	Alignment	not modelled	99.7	23	**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
						PDB header:structural genomics, unknown function

29	c3emeA_	Alignment	not modelled	99.7	16	**Chain:** A: **PDB Molecule:**rhodanese-like domain protein; **PDBTitle:** crystal structure of rhodanese-like domain protein from2 staphylococcus aureus
30	c3nhvE_	Alignment	not modelled	99.7	22	**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
31	c3gk5A_	Alignment	not modelled	99.7	18	**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
32	d1qxna_	Alignment	not modelled	99.7	22	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
33	d1yt8a4	Alignment	not modelled	99.7	20	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
34	c2fsxA_	Alignment	not modelled	99.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cog0607: rhodanese-related sulfurtransferase; **PDBTitle:** crystal structure of rv0390 from m. tuberculosis
35	c3i2vA_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase and sulfurtransferase mocs3; **PDBTitle:** crystal structure of human mocs3 rhodanese-like domain
36	c3k9rA_	Alignment	not modelled	99.7	20	**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.
37	d1gmxa_	Alignment	not modelled	99.7	17	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Single-domain sulfurtransferase
38	c3fojA_	Alignment	not modelled	99.7	20	**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.
39	c2dcqA_	Alignment	not modelled	99.6	13	**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
40	c2k0zA_	Alignment	not modelled	99.6	20	**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
41	d1yt8a2	Alignment	not modelled	99.6	23	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
42	d1t3ka_	Alignment	not modelled	99.6	16	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
43	c3g5jA_	Alignment	not modelled	99.6	17	**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
44	c3icrA_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
45	c3f4aA_	Alignment	not modelled	99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ygr203w; **PDBTitle:** structure of ygr203w, a yeast protein tyrosine phosphatase2 of the rhodanese family
46	c2jtqA_	Alignment	not modelled	99.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phage shock protein e; **PDBTitle:** rhodanese from e.coli
47	c3ntaA_	Alignment	not modelled	99.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
48	d1whba_	Alignment	not modelled	99.5	12	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Ubiquitin carboxyl-terminal hydrolase 8, USP8
49	c2j6pF_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**sb(v)-as(v) reductase; **PDBTitle:** structure of as-sb reductase from leishmania major
50	d1c25a_	Alignment	not modelled	99.5	14	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
51	d1ymka1	Alignment	not modelled	99.5	14	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
52	c3r2uC_	Alignment	not modelled	99.5	22	**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
53	c2vswB_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 16;

53	c2vswB_	Alignment	not modelled	99.4	19	**PDBTitle:** the structure of the rhodanese domain of the human dual2 specificity phosphatase 16
54	c3op3A_	Alignment	not modelled	99.4	17	**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
55	d1hzma_	Alignment	not modelled	99.4	14	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Cell cycle control phosphatase, catalytic domain
56	c2uzqE_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**m-phase inducer phosphatase 2; **PDBTitle:** protein phosphatase, new crystal form
57	d2gwfa1	Alignment	not modelled	99.3	17	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Ubiquitin carboxyl-terminal hydrolase 8, USP8
58	c2oucB_	Alignment	not modelled	99.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the map kinase binding domain of mkp5
59	c1wv9B_	Alignment	not modelled	99.1	19	**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
60	c3gxgA_	Alignment	not modelled	94.4	15	**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
61	c3flhC_	Alignment	not modelled	94.2	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	c2f46A_	Alignment	not modelled	89.6	26	**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
63	d1npya1	Alignment	not modelled	89.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
64	d1ywfa1	Alignment	not modelled	89.2	17	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Mycobacterial PtpB-like
65	c1npyA_	Alignment	not modelled	78.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical shikimate 5-dehydrogenase-like **PDBTitle:** structure of shikimate 5-dehydrogenase-like protein hi0607
66	d1xria_	Alignment	not modelled	77.2	15	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
67	d1p15a_	Alignment	not modelled	75.7	15	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
68	c2nz2A_	Alignment	not modelled	71.8	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
69	c2dg2D_	Alignment	not modelled	71.4	24	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**apolipoprotein a-i binding protein; **PDBTitle:** crystal structure of mouse apolipoprotein a-i binding2 protein
70	c2b9yA_	Alignment	not modelled	71.4	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aminooxidase; **PDBTitle:** crystal structure of cla-producing fatty acid isomerase2 from p. acnes
71	c2i6oA_	Alignment	not modelled	70.1	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
72	c3tozA_	Alignment	not modelled	68.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
73	c2nz6A_	Alignment	not modelled	67.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**receptor-type tyrosine-protein phosphatase eta; **PDBTitle:** crystal structure of the ptprj inactivating mutant c1239s
74	c1u24A_	Alignment	not modelled	65.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**myo-inositol hexaphosphate phosphohydrolase; **PDBTitle:** crystal structure of selenomonas ruminantium phytase
75	d1nkta4	Alignment	not modelled	64.9	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
76	c2imgA_	Alignment	not modelled	64.5	17	**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
77	d1vi2a1	Alignment	not modelled	64.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
78	c3djeA_	Alignment	not modelled	64.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fructosyl amine: oxygen oxidoreductase; **PDBTitle:** crystal structure of the deglycating enzyme

						fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
79	d1fpra_	Alignment	not modelled	61.3	7	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
80	d1xhoa_	Alignment	not modelled	60.9	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
81	c2oz5A_	Alignment	not modelled	60.5	13	**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
82	c3d3jA_	Alignment	not modelled	60.1	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
83	d1lara1	Alignment	not modelled	59.7	22	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
84	c1vl2C_	Alignment	not modelled	59.4	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
85	c3s4oB_	Alignment	not modelled	58.3	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein tyrosine phosphatase-like protein; **PDBTitle:** protein tyrosine phosphatase (putative) from leishmania major
86	c3s3fA_	Alignment	not modelled	57.0	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase 10d; **PDBTitle:** crystal structure of the catalytic domain of ptp10d from drosophila2 melanogaster with a small molecule inhibitor vanadate
87	c2c7sA_	Alignment	not modelled	56.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**receptor-type tyrosine-protein phosphatase kappa; **PDBTitle:** crystal structure of human protein tyrosine phosphatase2 kappa at 1.95a resolution
88	d1larb1	Alignment	not modelled	56.8	22	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
89	c3g7sA_	Alignment	not modelled	56.7	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**long-chain-fatty-acid--coa ligase (fadd-1); **PDBTitle:** crystal structure of a long-chain-fatty-acid-coa ligase2 (fadd1) from archaeoglobus fulgidus
90	d1rxda_	Alignment	not modelled	56.3	11	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
91	c3bnuA_	Alignment	not modelled	56.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyamine oxidase fms1; **PDBTitle:** crystal structure of polyamine oxidase fms1 from2 saccharomyces cerevisiae in complex with bis-(3s,3's)-3 methylated spermine
92	c3d3kD_	Alignment	not modelled	55.5	12	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
93	c3ohgA_	Alignment	not modelled	55.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein from duf2233 family; **PDBTitle:** crystal structure of a protein with unknown function from duf22332 family (bacova_00430) from bacteroides ovatus at 1.80 a resolution
94	c3ivrA_	Alignment	not modelled	55.2	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative long-chain-fatty-acid coa ligase; **PDBTitle:** crystal structure of putative long-chain-fatty-acid coa ligase from2 rhodopseudomonas palustris cga009
95	c3u62A_	Alignment	not modelled	55.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from thermotoga maritima
96	c3rz2B_	Alignment	not modelled	54.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein tyrosine phosphatase type iva 1; **PDBTitle:** crystal of prl-1 complexed with peptide
97	c1xhoB_	Alignment	not modelled	54.6	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**chorismate mutase; **PDBTitle:** chorismate mutase from clostridium thermocellum cth-682
98	c1w2wA_	Alignment	not modelled	54.5	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits
99	c2qcjB_	Alignment	not modelled	53.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type **PDBTitle:** native structure of lyp
100	c2b49A_	Alignment	not modelled	53.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase, non-receptor type 3; **PDBTitle:** crystal structure of the catalytic domain of protein tyrosine2 phosphatase, non-receptor type 3
101	c2hy3A_	Alignment	not modelled	53.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**receptor-type tyrosine-protein phosphatase gamma; **PDBTitle:** crystal structure of the human tyrosine receptor phosphate gamma in2 complex with vanadate

102	c3t38B_	Alignment	not modelled	53.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**arsenate reductase; **PDBTitle:** corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
103	c3etcB_	Alignment	not modelled	52.9	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**amp-binding protein; **PDBTitle:** 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
104	c3i36A_	Alignment	not modelled	52.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**vascular protein tyrosine phosphatase 1; **PDBTitle:** crystal structure of rat protein tyrosine phosphatase eta catalytic2 domain
105	c2qdmA_	Alignment	not modelled	52.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type 7; **PDBTitle:** crystal structure of the heptp catalytic domain c270s/d236a/q314a2 mutant
106	c1z3iX_	Alignment	not modelled	52.1	16	**PDB header:**recombination/dna binding **Chain:** X: **PDB Molecule:**similar to rad54-like; **PDBTitle:** structure of the swi2/snf2 chromatin remodeling domain of eukaryotic2 rad54
107	c1amuB_	Alignment	not modelled	51.9	24	**PDB header:**peptide synthetase **Chain:** B: **PDB Molecule:**gramicidin synthetase 1; **PDBTitle:** phenylalanine activating domain of gramicidin synthetase 12 in a complex with amp and phenylalanine
108	c3o8qB_	Alignment	not modelled	51.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase i alpha; **PDBTitle:** 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
109	c2qepA_	Alignment	not modelled	51.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**receptor-type tyrosine-protein phosphatase n2; **PDBTitle:** crystal structure of the d1 domain of ptprn2 (ia2beta)
110	d1jzta_	Alignment	not modelled	50.5	26	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
111	c2pa5A_	Alignment	not modelled	50.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type 9; **PDBTitle:** crystal structure of human protein tyrosine phosphatase ptpn9
112	d1fuka_	Alignment	not modelled	50.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
113	c2bzlA_	Alignment	not modelled	49.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase, non-receptor type **PDBTitle:** crystal structure of the human protein tyrosine phosphatase2 n14 at 1.65 a resolution
114	d1vl2a1	Alignment	not modelled	49.5	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
115	d1rpma_	Alignment	not modelled	49.4	14	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Higher-molecular-weight phosphotyrosine protein phosphatases
116	d1amua_	Alignment	not modelled	49.2	24	**Fold:**Acetyl-CoA synthetase-like **Superfamily:**Acetyl-CoA synthetase-like **Family:**Acetyl-CoA synthetase-like
117	c2j17A_	Alignment	not modelled	49.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase yil113w; **PDBTitle:** ptyr bound form of sdp-1
118	d1ohea2	Alignment	not modelled	48.9	13	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
119	c3i32A_	Alignment	not modelled	48.7	8	**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
120	c3o82A_	Alignment	not modelled	48.6	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**peptide arylation enzyme; **PDBTitle:** structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine