


























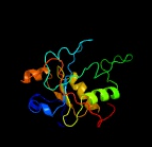





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2291_(sseB)_2563184_2564038
Date	Mon Aug 5 13:25:43 BST 2019
Unique Job ID	d273ba0ee722d951

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3aaxB_	 Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
2	c3ippA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynje; PDBTitle: crystal structure of sulfur-free ynje
3	c6h98A_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: native crystal structure of anaerobic ergothioneine biosynthesis2 enzyme from chlorobium limicola.
4	c1okgA_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
5	c3hzuA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase ssea2 (rhodanese) from mycobacterium tuberculosis
6	c1boiA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
7	c1uarA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
8	c1e0cA_	 Alignment		100.0	25	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
9	c3olhA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
10	c3utnX_	 Alignment		100.0	23	PDB header: transferase Chain: X: PDB Molecule: thiosulfate sulfurtransferase tum1; PDBTitle: crystal structure of tum1 protein from saccharomyces cerevisiae
11	c1urhA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: the "rhodanese" fold and catalytic mechanism of 2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from escherichia coli

12	c6mxvA	Alignment		100.0	18	PDB header: unknown function Chain: A: PDB Molecule: rhodanese-like family protein; PDBTitle: the crystal structure of a rhodanese-like family protein from2 francisella tularensis subsp. tularensis schu s4
13	c1yt8A	Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa
14	c2eg4B	Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
15	c3tp9B	Alignment		100.0	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
16	d1urha1	Alignment		100.0	32	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
17	d1okga1	Alignment		99.9	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
18	d1rha1	Alignment		99.9	30	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
19	d1uara2	Alignment		99.9	30	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
20	d1uara1	Alignment		99.9	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
21	d1e0ca1	Alignment	not modelled	99.9	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
22	d1okga2	Alignment	not modelled	99.9	31	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
23	d1e0ca2	Alignment	not modelled	99.9	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
24	d1rha2	Alignment	not modelled	99.9	26	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
25	d1yt8a1	Alignment	not modelled	99.8	32	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
26	d1urha2	Alignment	not modelled	99.8	33	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
27	d1yt8a3	Alignment	not modelled	99.8	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
28	c3ilmD	Alignment	not modelled	99.8	34	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 PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase

29	c3d1pA	Alignment	not modelled	99.8	19	yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from <i>Saccharomyces cerevisiae</i>
30	c2hhgA	Alignment	not modelled	99.8	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa3614; PDBTitle: structure of protein of unknown function rpa3614, possible tyrosine 2-phosphatase, from <i>Rhodospirillum rubrum</i>
31	c2moiA	Alignment	not modelled	99.8	23	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3D NMR structure of the cytoplasmic rhodanese domain of the inner 2-membrane protein ygap from <i>Escherichia coli</i>
32	c3nhvE	Alignment	not modelled	99.8	26	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: bh2092 protein; PDBTitle: crystal structure of bh2092 protein from <i>Bacillus halodurans</i> , 2-northeast structural genomics consortium target bhr228f
33	c5ve5C	Alignment	not modelled	99.8	36	PDB header: oxidoreductase, transferase Chain: C: PDB Molecule: bpprf; PDBTitle: crystal structure of persulfide dioxygenase rhodanese fusion protein 2 with rhodanese domain inactivating mutation (c314s) from <i>Burkholderia</i> 3-phytofirmans in complex with glutathione
34	c6bevB	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: thiosulfate sulfurtransferase/rhodanese-like domain PDBTitle: human single domain sulfurtransferase tstd1
35	d1yt8a4	Alignment	not modelled	99.8	29	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
36	c3emeA	Alignment	not modelled	99.8	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: rhodanese-like domain protein; PDBTitle: crystal structure of rhodanese-like domain protein from <i>Staphylococcus aureus</i>
37	d1tq1a	Alignment	not modelled	99.8	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
38	d1qxna	Alignment	not modelled	99.8	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
39	c3i2vA	Alignment	not modelled	99.8	22	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
40	c3f4aA	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase of the 2-rhodanese family
41	d1yt8a2	Alignment	not modelled	99.8	35	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
42	c2fsxA	Alignment	not modelled	99.7	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cog0607: rhodanese-related sulfurtransferase; PDBTitle: crystal structure of rv0390 from <i>M. tuberculosis</i>
43	c3fojA	Alignment	not modelled	99.7	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ssp1007 from <i>Staphylococcus</i> 2-saprophyticus subsp. saprophyticus. northeast structural 3-genomics target syr101a.
44	d1t3ka	Alignment	not modelled	99.7	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
45	c3g5iA	Alignment	not modelled	99.7	21	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 binding 2-protein from <i>Clostridium difficile</i> 630
46	c3gk5A	Alignment	not modelled	99.7	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized rhodanese-related protein tvg0868615; PDBTitle: crystal structure of rhodanese-related protein (tvg0868615) from <i>Thermoplasma volcanium</i> , northeast structural genomics consortium 3-target tvr109a
47	c3k9rA	Alignment	not modelled	99.7	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: alr3790 protein; PDBTitle: x-ray structure of the rhodanese-like domain of the alr3790 protein 2 from <i>Anabaena</i> sp. northeast structural genomics consortium target3 nsr437c.
48	c2dcqA	Alignment	not modelled	99.7	12	PDB header: unknown function Chain: A: PDB Molecule: putative protein at4g01050; PDBTitle: fully automated nmr structure determination of the 2-rhodanese homology domain at4g01050(175-295) from <i>Arabidopsis thaliana</i>
49	d1gmxA	Alignment	not modelled	99.7	29	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
50	c2j6pF	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: F: PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from <i>Leishmania major</i>
51	c4f67A	Alignment	not modelled	99.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0176 protein lpg2838; PDBTitle: three-dimensional structure of the double mutant of upf0176 protein 2 lpg2838 from <i>Legionella pneumophila</i> at the resolution 1.8 Å, northeast 3-structural genomics consortium (nesg) target lgr82
52	c2jtqA	Alignment	not modelled	99.7	28	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from <i>E. coli</i>

53	d1whba_	Alignment	not modelled	99.6	20	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
54	d1c25a_	Alignment	not modelled	99.6	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
55	c3ntaA_	Alignment	not modelled	99.6	26	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
56	c2k0zA_	Alignment	not modelled	99.6	16	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
57	c3icrA_	Alignment	not modelled	99.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
58	c2vswB_	Alignment	not modelled	99.6	16	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 16; PDBTitle: the structure of the rhodanese domain of the human dual specificity2 phosphatase 16
59	d1ymka1	Alignment	not modelled	99.6	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
60	c2uzqE_	Alignment	not modelled	99.5	21	PDB header: hydrolase Chain: E: PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
61	c3op3A_	Alignment	not modelled	99.5	20	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
62	d2gwfa1	Alignment	not modelled	99.5	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
63	c2oucB_	Alignment	not modelled	99.5	22	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the map kinase binding domain of mkp5
64	d1hzma_	Alignment	not modelled	99.5	21	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
65	c3r2uC_	Alignment	not modelled	99.3	20	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
66	c1wv9B_	Alignment	not modelled	99.1	30	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
67	c3gxxA_	Alignment	not modelled	95.7	11	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
68	c2f46A_	Alignment	not modelled	95.4	11	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
69	d1ywfa1	Alignment	not modelled	94.2	20	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Mycobacterial PtpB-like
70	c3flhC_	Alignment	not modelled	94.0	22	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein lp_1913; PDBTitle: crystal structure of lp_1913 protein from lactobacillus plantarum,2 northeast structural genomics consortium target lpr140b
71	d1tyza_	Alignment	not modelled	91.9	17	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
72	c6byfl_	Alignment	not modelled	90.6	10	PDB header: transferase Chain: I: PDB Molecule: tyrosine-protein phosphatase siw14; PDBTitle: crystal structure of the core catalytic domain of pp-ip phosphatase2 siw14 from s. cerevisiae in complex with citrate
73	c2imgA_	Alignment	not modelled	90.2	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
74	d1ohea2	Alignment	not modelled	88.9	12	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
75	c2dg2D_	Alignment	not modelled	88.2	15	PDB header: protein binding Chain: D: PDB Molecule: apolipoprotein a-i binding protein; PDBTitle: crystal structure of mouse apolipoprotein a-i binding protein
76	c2i6oA_	Alignment	not modelled	87.9	12	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
77	d1xria_	Alignment	not modelled	87.6	9	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like

78	c5cd1B	Alignment	not modelled	87.6	17	PDB header: transferase/rna non-catalytic Chain: B: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase PDBTitle: structure of an asymmetric tetramer of human trna m1a582 methyltransferase in a complex with sah and trna3lys
79	c3rggA	Alignment	not modelled	87.0	9	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
80	c4nx8A	Alignment	not modelled	85.7	7	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase 2; PDBTitle: structure of a ptp-like phytase from bdellovibrio bacteriovorus
81	d1f2da	Alignment	not modelled	84.9	14	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
82	d1vhra	Alignment	not modelled	84.2	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
83	c1fpzF	Alignment	not modelled	83.6	9	PDB header: hydrolase Chain: F: PDB Molecule: cyclin-dependent kinase inhibitor 3; PDBTitle: crystal structure analysis of kinase associated phosphatase (kap) with2 a substitution of the catalytic site cysteine (cys140) to a serine
84	d1oywa3	Alignment	not modelled	83.3	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
85	c1yn9B	Alignment	not modelled	82.7	16	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
86	c4tvvA	Alignment	not modelled	82.7	13	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine phosphatase ii superfamily protein; PDBTitle: crystal structure of lppa from legionella pneumophila
87	d1fuka	Alignment	not modelled	82.6	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
88	c1oheA	Alignment	not modelled	82.1	12	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
89	c3d3jA	Alignment	not modelled	81.7	21	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
90	d1npya1	Alignment	not modelled	81.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
91	d1nkta4	Alignment	not modelled	81.2	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
92	c4rkkA	Alignment	not modelled	81.2	23	PDB header: hydrolase Chain: A: PDB Molecule: laforin; PDBTitle: structure of a product bound phosphatase
93	d1fpza	Alignment	not modelled	80.0	10	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
94	c4cdgA	Alignment	not modelled	79.4	18	PDB header: hydrolase Chain: A: PDB Molecule: bloom syndrome protein; PDBTitle: crystal structure of the bloom's syndrome helicase blm in complex with2 nanobody
95	c3i32A	Alignment	not modelled	79.3	21	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
96	d1jzta	Alignment	not modelled	78.9	23	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
97	d1i9sa	Alignment	not modelled	78.6	7	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
98	c2m3vA	Alignment	not modelled	78.6	19	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of tyrosine phosphatase related to biofilm2 formation a (tpba) from pseudomonas aeruginosa
99	c2v1xB	Alignment	not modelled	78.5	18	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase q1; PDBTitle: crystal structure of human recq-like dna helicase
100	c3d3kD	Alignment	not modelled	77.2	21	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
101	c2oz5A	Alignment	not modelled	77.1	25	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
102	c3s4oB	Alignment	not modelled	75.3	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major
						PDB header: dna binding protein

103	c4q47A_	Alignment	not modelled	74.9	24	Chain: A: PDB Molecule: dna helicase recq; PDBTitle: structure of the drrecq catalytic core in complex with adp
104	d1p15a_	Alignment	not modelled	74.7	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
105	d1rxda_	Alignment	not modelled	74.5	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
106	d1a1va2	Alignment	not modelled	74.5	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
107	c2e0tA_	Alignment	not modelled	73.5	17	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 26; PDBTitle: crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
108	c1oywA_	Alignment	not modelled	73.2	21	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of the recq catalytic core
109	c4ki9A_	Alignment	not modelled	72.9	16	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 12; PDBTitle: crystal structure of the catalytic domain of human dusp12 at 2.0 a2 resolution
110	c2ax3A_	Alignment	not modelled	72.3	19	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tm0922; PDBTitle: crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
111	c5xw4A_	Alignment	not modelled	72.0	19	PDB header: cell cycle Chain: A: PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
112	d1d5ra2	Alignment	not modelled	71.5	12	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
113	d1t5la2	Alignment	not modelled	70.6	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
114	c3vs9F_	Alignment	not modelled	70.1	17	PDB header: transferase Chain: F: PDB Molecule: type iii polyketide synthase; PDBTitle: crystal structure of type iii pks arcs mutant
115	c6i28A_	Alignment	not modelled	69.4	15	PDB header: viral protein Chain: A: PDB Molecule: orf98 ptp-2; PDBTitle: crystal structure of cydia pomonella ptp-2 phosphatase
116	d1iiba_	Alignment	not modelled	69.3	8	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
117	d2ax3a2	Alignment	not modelled	68.9	19	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
118	c1zzwA_	Alignment	not modelled	68.8	21	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of catalytic domain of human map kinase2 phosphatase 5
119	c5ccbB_	Alignment	not modelled	68.6	18	PDB header: transferase/rna Chain: B: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase non-catalytic PDBTitle: crystal structure of human m1a58 methyltransferase in a complex with2 trna3lys and sah
120	d1mkpa_	Alignment	not modelled	68.5	9	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like