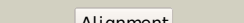
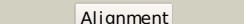
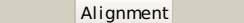
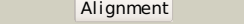
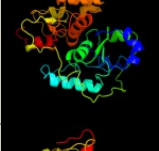
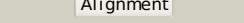
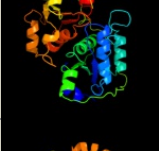
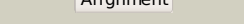
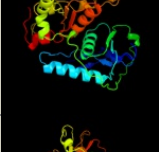
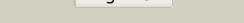
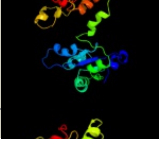


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P31142
Date	Thu Jan 5 11:47:20 GMT 2012
Unique Job ID	ceb3777181587bc2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1urhA_	 Alignment		100.0	98	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: the "rhodanese" fold and catalytic mechanism of 2 3-mercaptopyruvate sulfotransferases: crystal structure of ssea from escherichia coli
2	c3olhA_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
3	c1e0cA_	 Alignment		100.0	28	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
4	c1boiA_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
5	c3aaxB_	 Alignment		100.0	29	PDB header: transferase Chain: B: PDB Molecule: putative thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rv3117) from mycobacterium tuberculosis: monoclinic3 form
6	c3hzuA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase ssea; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase2 cysa3 (rhodanese) from mycobacterium tuberculosis
7	c3ippA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase ynj6; PDBTitle: crystal structure of sulfur-free ynj6
8	c1okgA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
9	c1uarA_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from thermus thermophilus hb8
10	c2eg4B_	 Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: probable thiosulfate sulfurtransferase; PDBTitle: crystal structure of probable thiosulfate sulfurtransferase
11	c1yt8A_	 Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: thiosulfate sulfurtransferase; PDBTitle: crystal structure of thiosulfate sulfurtransferase from pseudomonas2 aeruginosa

12	c3tp9B_	Alignment		100.0	21	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	dlurha1	Alignment		100.0	100	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
14	dlrha1	Alignment		100.0	39	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
15	dluara1	Alignment		99.9	26	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
16	dlokga1	Alignment		99.9	18	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
17	dle0ca1	Alignment		99.9	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
18	dluara2	Alignment		99.9	33	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
19	dlokga2	Alignment		99.9	32	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
20	dle0ca2	Alignment		99.9	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
21	dlrha2	Alignment	not modelled	99.9	31	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
22	dlurha2	Alignment	not modelled	99.9	96	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
23	dlyt8a3	Alignment	not modelled	99.8	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
24	c3d1pA_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: A: PDB Molecule: putative thiosulfate sulfurtransferase yor285w; PDBTitle: atomic resolution structure of uncharacterized protein from2 saccharomyces cerevisiae
25	c3ilmD_	Alignment	not modelled	99.8	31	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
26	dlyt8a1	Alignment	not modelled	99.8	27	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
27	c3nhvE_	Alignment	not modelled	99.8	25	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
28	c2hhgA_	Alignment	not modelled	99.8	22	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

29	c3f4aA_	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase2 of the rhodanese family
30	d1tq1a_	Alignment	not modelled	99.8	28	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
31	d1yt8a4	Alignment	not modelled	99.8	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
32	c3emeA_	Alignment	not modelled	99.8	23	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
33	d1t3ka_	Alignment	not modelled	99.8	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
34	c3gk5A_	Alignment	not modelled	99.8	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
35	d1qxna_	Alignment	not modelled	99.8	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
36	c3i2vA_	Alignment	not modelled	99.7	26	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
37	c3g5jA_	Alignment	not modelled	99.7	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
38	d1gmxa_	Alignment	not modelled	99.7	22	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Single-domain sulfurtransferase
39	d1yt8a2	Alignment	not modelled	99.7	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
40	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 staphylococcus2 saprophyticus subsp. saprophyticus. northeast structural3 genomics target syr101a.
41	c3k9rA_	Alignment	not modelled	99.7	36	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.
42	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
43	c2dcqA_	Alignment	not modelled	99.7	14	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
44	c3icrA_	Alignment	not modelled	99.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
45	c2k0zA_	Alignment	not modelled	99.7	18	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
46	c3ntaA_	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
47	c2j6pF_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: F: PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from leishmania major
48	c2jtqA_	Alignment	not modelled	99.7	18	PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
49	c2vswB_	Alignment	not modelled	99.6	21	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
50	d1whba_	Alignment	not modelled	99.6	17	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
51	d1c25a_	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
52	d1ymka1	Alignment	not modelled	99.6	24	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
53	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
54	d2gwfa1	Alignment	not modelled	99.5	18 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Ubiquitin carboxyl-terminal hydrolase 8, USP8
55	c2uzqE_	Alignment	not modelled	99.5	24 PDB header: hydrolase Chain: E: PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
56	d1hzma_	Alignment	not modelled	99.5	23 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Cell cycle control phosphatase, catalytic domain
57	c3op3A_	Alignment	not modelled	99.5	24 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
58	c3r2uC_	Alignment	not modelled	99.4	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
59	c1wv9B_	Alignment	not modelled	99.1	24 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	96.6	16 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	c2f46A_	Alignment	not modelled	95.8	12 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
62	c3flhC_	Alignment	not modelled	95.8	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
63	d1ywfa1	Alignment	not modelled	95.7	17 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Mycobacterial PtpB-like
64	d1xria_	Alignment	not modelled	94.2	7 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
65	c3rgqA_	Alignment	not modelled	93.0	9 PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
66	d1vhra_	Alignment	not modelled	92.8	9 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
67	c2y96A_	Alignment	not modelled	90.7	17 PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27
68	c2e0tA_	Alignment	not modelled	90.7	16 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
69	c1fpzF_	Alignment	not modelled	90.6	8 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
70	d1ohea2	Alignment	not modelled	90.6	12 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
71	d1fpza_	Alignment	not modelled	90.5	8 Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
72	c2imgA_	Alignment	not modelled	89.9	10 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
73	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
74	c1yn9B_	Alignment	not modelled	89.3	18 PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
75	c1oheaA_	Alignment	not modelled	88.8	13 PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
76	c2gwoC_	Alignment	not modelled	88.6	10 PDB header: hydrolase Chain: C: PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmdp
77	c2i6oA_	Alignment	not modelled	87.0	9 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
78	c2r0bA_	Alignment	not modelled	86.7	16 PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine/tyrosine-interacting protein; PDBTitle: crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein

79	c3nmeA	Alignment	not modelled	86.6	7	PDB header: hydrolase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
80	c2oz5A	Alignment	not modelled	86.2	16	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
81	d1i9sa	Alignment	not modelled	85.7	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
82	d1g4us2	Alignment	not modelled	84.9	21	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
83	d1d5ra2	Alignment	not modelled	84.9	12	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
84	c2c46B	Alignment	not modelled	84.6	16	PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and2 5'-phosphatase
85	d1oywa3	Alignment	not modelled	83.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
86	c2p4dA	Alignment	not modelled	83.0	18	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase; PDBTitle: structure-assisted discovery of variola major h12 phosphatase inhibitors
87	d1mkpa	Alignment	not modelled	82.4	11	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
88	d1fuka	Alignment	not modelled	82.4	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
89	c3s4oB	Alignment	not modelled	81.7	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major
90	c2wgpA	Alignment	not modelled	81.5	16	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 14; PDBTitle: crystal structure of human dual specificity phosphatase 14
91	c2esbA	Alignment	not modelled	81.5	14	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 18; PDBTitle: crystal structure of human dusp18
92	c2oudA	Alignment	not modelled	81.3	21	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
93	c1wrmA	Alignment	not modelled	80.8	16	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 22; PDBTitle: crystal structure of jsp-1
94	c1zzwA	Alignment	not modelled	80.8	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
95	c1yz4A	Alignment	not modelled	80.7	12	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase-like 15 isoform a; PDBTitle: crystal structure of dusp15
96	c2g6zB	Alignment	not modelled	80.2	9	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 5; PDBTitle: crystal structure of human dusp5
97	c2hcmA	Alignment	not modelled	80.1	21	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
98	d1v3aa	Alignment	not modelled	80.0	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
99	c3emuA	Alignment	not modelled	79.8	21	PDB header: hydrolase Chain: A: PDB Molecule: leucine rich repeat and phosphatase domain PDBTitle: crystal structure of a leucine rich repeat and phosphatase2 domain containing protein from entamoeba histolytica
100	c2dg2D	Alignment	not modelled	78.5	21	PDB header: protein binding Chain: D: PDB Molecule: apolipoprotein a-i binding protein; PDBTitle: crystal structure of mouse apolipoprotein a-i binding2 protein
101	d1vi2a1	Alignment	not modelled	77.6	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
102	c2v1xB	Alignment	not modelled	77.5	18	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent dna helicase q1; PDBTitle: crystal structure of human recq-like dna helicase
103	c3i32A	Alignment	not modelled	77.4	17	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

104	c2nz6A_	Alignment	not modelled	76.0	24	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase eta; PDBTitle: crystal structure of the ptpnj inactivating mutant c1239s
105	d1m3ga_	Alignment	not modelled	75.1	11	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
106	c2nt2C_	Alignment	not modelled	74.3	21	PDB header: hydrolase Chain: C: PDB Molecule: protein phosphatase slingshot homolog 2; PDBTitle: crystal structure of slingshot phosphatase 2
107	d1nka4	Alignment	not modelled	74.0	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
108	c3d3jA_	Alignment	not modelled	73.4	26	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
109	d1jzta_	Alignment	not modelled	73.4	22	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
110	d1rxda_	Alignment	not modelled	73.3	24	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
111	c3ohgA_	Alignment	not modelled	73.3	22	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
112	c2j17A_	Alignment	not modelled	73.2	11	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase yil113w; PDBTitle: ptyr bound form of sdp-1
113	d1tyza_	Alignment	not modelled	72.9	12	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
114	c3d3kD_	Alignment	not modelled	71.1	22	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
115	c1npyA_	Alignment	not modelled	70.9	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
116	c1g4wR_	Alignment	not modelled	70.3	21	PDB header: signaling protein Chain: R: PDB Molecule: protein tyrosine phosphatase sptp; PDBTitle: crystal structure of the salmonella tyrosine phosphatase2 and gtpase activating protein sptp
117	d1a1va2	Alignment	not modelled	69.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
118	c3s3fA_	Alignment	not modelled	69.2	18	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
119	c1oywA_	Alignment	not modelled	69.0	16	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase; PDBTitle: structure of the recq catalytic core
120	d1larb1	Alignment	not modelled	68.2	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases