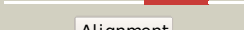
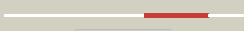


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P76093
Date	Thu Jan 5 12:18:48 GMT 2012
Unique Job ID	1406464c6d20e820

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j17A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase yil113w; PDBTitle: ptyr bound form of sdp-1
2	c2esbA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 18; PDBTitle: crystal structure of human dusp18
3	c2oudA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
4	c2p4dA_	 Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase; PDBTitle: structure-assisted discovery of variola major h12 phosphatase inhibitors
5	c2hcmA_	 Alignment		100.0	22	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
6	c3rggA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
7	c2wgpA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 14; PDBTitle: crystal structure of human dual specificity phosphatase 14
8	c2nt2C_	 Alignment		100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: protein phosphatase slingshot homolog 2; PDBTitle: crystal structure of slingshot phosphatase 2
9	c1zzwA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of catalytic domain of human map kinase2 phosphatase 5
10	c1yz4A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase-like 15 isoform a; PDBTitle: crystal structure of dusp15
11	c2gwoC_	 Alignment		100.0	23	PDB header: hydrolase Chain: C: PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmdp

12	c2r0bA_	Alignment		100.0	21	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
13	d1mkpa_	Alignment		100.0	21	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
14	c2g6zB_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 5; PDBTitle: crystal structure of human dusp5
15	c1wrmA_	Alignment		100.0	23	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 22; PDBTitle: crystal structure of jsp-1
16	c3emuA_	Alignment		100.0	16	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
17	c2imgA_	Alignment		100.0	23	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
18	d1m3ga_	Alignment		100.0	23	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
19	d1vhra_	Alignment		100.0	26	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
20	c2y96A_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27
21	c3nmeA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
22	c2e0tA_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 26; PDBTitle: crystal structure analysis of kinase associated phosphatase2 26, ms0830 from homo sapiens
23	d1ohea2	Alignment	not modelled	99.9	15	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
24	c1fpzF_	Alignment	not modelled	99.9	19	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
25	c2i6oA_	Alignment	not modelled	99.9	24	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
26	c3s4oB_	Alignment	not modelled	99.9	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major
27	d1fpza_	Alignment	not modelled	99.9	19	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
28	c1ohea_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand

29	c2c46B	Alignment	not modelled	99.9	15	PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and 2' 5'-phosphatase
30	d1d5ra2	Alignment	not modelled	99.9	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
31	c1yn9B	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
32	c3awfC	Alignment	not modelled	99.9	22	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: voltage-sensor containing phosphatase; PDBTitle: crystal structure of pten-like domain of ci-vsp (236-576)
33	d1i9sa	Alignment	not modelled	99.9	15	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
34	d1rxda	Alignment	not modelled	99.8	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
35	d1v3aa	Alignment	not modelled	99.8	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
36	c3gxgA	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphatase (duf442); PDBTitle: crystal structure of putative phosphatase (duf442) (yp_001181608.1)2 from shewanella putrefaciens cn-32 at 1.60 a resolution
37	c1d5rA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphoinositide phosphatase pten; PDBTitle: crystal structure of the pten tumor suppressor
38	c3n0aA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase auxilin; PDBTitle: crystal structure of auxilin (40-400)
39	d1xria	Alignment	not modelled	99.8	15	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
40	c3rz2B	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: protein tyrosine phosphatase type iva 1; PDBTitle: crystal of prl-1 complexed with peptide
41	c2f46A	Alignment	not modelled	99.7	13	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
42	c1g4wR	Alignment	not modelled	99.4	14	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
43	d1g4us2	Alignment	not modelled	99.3	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
44	c2akcC	Alignment		99.2	17	PDB header: hydrolase Chain: C: PDB Molecule: class a nonspecific acid phosphatase phon; PDBTitle: crystal structure of tungstate complex of the phon protein2 from s. typhimurium
45	c1u24A	Alignment	not modelled	99.1	17	PDB header: hydrolase Chain: A: PDB Molecule: myo-inositol hexaphosphate phosphohydrolase; PDBTitle: crystal structure of selenomonas ruminantium phytase
46	d1lyva	Alignment	not modelled	99.1	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
47	c2b49A	Alignment	not modelled	99.1	24	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
48	d1ywfa1	Alignment	not modelled	99.1	23	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Mycobacterial PtpB-like
49	d1lara1	Alignment	not modelled	99.1	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
50	c2shpA	Alignment	not modelled	99.0	22	PDB header: tyrosine phosphatase Chain: A: PDB Molecule: shp-2; PDBTitle: tyrosine phosphatase shp-2
51	d1larb1	Alignment	not modelled	99.0	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
52	c2b3oA	Alignment	not modelled	99.0	20	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase, non-receptor type PDBTitle: crystal structure of human tyrosine phosphatase shp-1

53	d1d2ta_	Alignment		99.0	17	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Type 2 phosphatidic acid phosphatase, PAP2
54	c2pa5A_	Alignment	not modelled	99.0	19	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase non-receptor type 9; PDBTitle: crystal structure of human protein tyrosine phosphatase ptpn9
55	c2qepA_	Alignment	not modelled	99.0	20	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase n2; PDBTitle: crystal structure of the d1 domain of ptpn2 (ia2beta)
56	c3ps5A_	Alignment	not modelled	99.0	19	PDB header: hydrolase, signaling protein Chain: A: PDB Molecule: tyrosine-protein phosphatase non-receptor type 6; PDBTitle: crystal structure of the full-length human protein tyrosine2 phosphatase shp-1
57	d1wcha_	Alignment	not modelled	99.0	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
58	c2bz1A_	Alignment	not modelled	99.0	17	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
59	c1larB_	Alignment	not modelled	99.0	16	PDB header: hydrolase Chain: B: PDB Molecule: protein (lar); PDBTitle: crystal structure of the tandem phosphatase domains of rtp2 lar
60	c3s3fA_	Alignment	not modelled	99.0	20	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
61	c2nz6A_	Alignment	not modelled	99.0	21	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase eta; PDBTitle: crystal structure of the ptpnj inactivating mutant c1239s
62	c2i75A_	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase non-receptor type 4; PDBTitle: crystal structure of human protein tyrosine phosphatase n4 (ptpn4)
63	c2bijA_	Alignment	not modelled	98.9	19	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase, non-receptor type 5; PDBTitle: crystal structure of the human protein tyrosine phosphatase2 ptpn5 (step, striatum enriched enriched phosphatase)
64	c2jjdA_	Alignment	not modelled	98.9	20	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase epsilon; PDBTitle: protein tyrosine phosphatase, receptor type, e isoform
65	c2g59B_	Alignment	not modelled	98.9	20	PDB header: hydrolase Chain: B: PDB Molecule: receptor-type tyrosine-protein phosphatase o; PDBTitle: crystal structure of the catalytic domain of protein2 tyrosine phosphatase from homo sapiens
66	c3m4uB_	Alignment	not modelled	98.9	20	PDB header: hydrolase Chain: B: PDB Molecule: tyrosine specific protein phosphatase, putative; PDBTitle: crystal structure of trypanosoma brucei protein tyrosine phosphatase2 tbtp1
67	d1rpma_	Alignment	not modelled	98.9	20	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
68	d2pt0a1	Alignment	not modelled	98.9	12	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Myo-inositol hexaphosphate phosphohydrolase (phytase) PhyA
69	c2oc3A_	Alignment	not modelled	98.9	19	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase non-receptor type PDBTitle: crystal structure of the catalytic domain of human protein2 tyrosine phosphatase non-receptor type 18
70	d1lara2	Alignment	not modelled	98.9	19	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
71	d1jlna_	Alignment	not modelled	98.9	25	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
72	c2qdmA_	Alignment	not modelled	98.9	20	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
73	c2qcjB_	Alignment	not modelled	98.9	23	PDB header: hydrolase Chain: B: PDB Molecule: tyrosine-protein phosphatase non-receptor type PDBTitle: native structure of lyp
74	c3jrlA_	Alignment	not modelled	98.9	19	PDB header: hydrolase Chain: A: PDB Molecule: oncogenic tyrosine phosphatase shp2; PDBTitle: crystal structure of the oncogenic tyrosine phosphatase shp2 complexed2 with a salicylic acid-based small molecule inhibitor
						PDB header: hydrolase

75	c1yguA	Alignment	not modelled	98.9	14	Chain: A: PDB Molecule: leukocyte common antigen; PDBTitle: crystal structure of the tandem phosphatase domains of rtp2 cd45 with a tyr peptide
76	c2h04A	Alignment	not modelled	98.9	22	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase, receptor type, b,; PDBTitle: structural studies of protein tyrosine phosphatase beta2 catalytic domain in complex with inhibitors
77	d2shpa1	Alignment	not modelled	98.9	22	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
78	c1l8ka	Alignment	not modelled	98.9	17	PDB header: hydrolase Chain: A: PDB Molecule: t-cell protein-tyrosine phosphatase; PDBTitle: t cell protein-tyrosine phosphatase structure
79	d1l8ka	Alignment	not modelled	98.9	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
80	c3i36A	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: A: PDB Molecule: vascular protein tyrosine phosphatase 1; PDBTitle: crystal structure of rat protein tyrosine phosphatase eta catalytic2 domain
81	c2c7sA	Alignment	not modelled	98.9	18	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
82	d1yfoa	Alignment	not modelled	98.9	24	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
83	c2nlkA	Alignment	not modelled	98.8	17	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase, receptor type, g variant PDBTitle: crystal structure of d1 and d2 catalytic domains of human protein2 tyrosine phosphatase gamma (d1+d2 ptprg)
84	c2vexA	Alignment	not modelled	98.8	21	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase non-receptor type 1; PDBTitle: crystal strucutre of protein tyrosine phosphatase 1b in2 complex with an isothiazolidinone-containing inhibitor
85	c3f41B	Alignment	not modelled	98.8	11	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: structure of the tandemly repeated protein tyrosine2 phosphatase like phytase from mitsuokella multacida
86	d1fpra	Alignment	not modelled	98.8	20	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
87	d2f71a1	Alignment	not modelled	98.8	22	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
88	c2hy3A	Alignment	not modelled	98.8	25	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
89	d1p15a	Alignment	not modelled	98.7	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
90	c2oz5A	Alignment	not modelled	98.5	23	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 oms
91	d1ohea1	Alignment	not modelled	98.1	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
92	d1zsqa2	Alignment	not modelled	93.3	26	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Myotubularin-like phosphatases
93	d1qi9a	Alignment	not modelled	93.1	23	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Haloperoxidase (bromoperoxidase)
94	c1lw3A	Alignment	not modelled	93.0	26	PDB header: hydrolase Chain: A: PDB Molecule: myotubularin-related protein 2; PDBTitle: crystal structure of myotubularin-related protein 22 complexed with phosphate
95	c1zsqa	Alignment	not modelled	92.5	26	PDB header: hydrolase Chain: A: PDB Molecule: myotubularin-related protein 2; PDBTitle: crystal structure of mtnr2 in complex with2 phosphatidylinositol 3-phosphate
96	c2yf0A	Alignment	not modelled	91.8	35	PDB header: hydrolase Chain: A: PDB Molecule: myotubularin-related protein 6; PDBTitle: human myotubularin related protein 6 (mtnr6)
97	c2j6pF	Alignment	not modelled	87.6	19	PDB header: oxidoreductase Chain: F: PDB Molecule: sb(v)-as(v) reductase; PDBTitle: structure of as-sb reductase from leishmania major
98	d1em8a	Alignment	not modelled	83.8	10	Fold: DNA polymerase III chi subunit Superfamily: DNA polymerase III chi subunit Family: DNA polymerase III chi subunit
99	c3olhA	Alignment	not modelled	78.0	12	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase;

						PDBTitle: human 3-mercaptopyruvate sulfurtransferase
100	d1vnsa_	Alignment	not modelled	76.5	22	Fold: Acid phosphatase/Vanadium-dependent haloperoxidase Superfamily: Acid phosphatase/Vanadium-dependent haloperoxidase Family: Chloroperoxidase PDB header: transferase Chain: A: PDB Molecule: adenyllyltransferase and sulfurtransferase mocs3; PDBTitle: crystal structure of human mocs3 rhodanese-like domain
101	c3i2vA_	Alignment	not modelled	73.8	17	PDB header: haloperoxidase Chain: A: PDB Molecule: vanadium chloroperoxidase; PDBTitle: chloroperoxidase from the fungus curvularia inaequalis:2 mutant h404a
102	c1vngA_	Alignment	not modelled	73.3	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
103	c1wv9B_	Alignment	not modelled	62.3	31	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
104	c3k35D_	Alignment	not modelled	55.8	28	Fold: DHH phosphoesterases Superfamily: DHH phosphoesterases Family: Exonuclease RecJ
105	d1ir6a_	Alignment	not modelled	55.7	30	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease recj; PDBTitle: crystal structure of exonuclease recj bound to manganese
106	c1ir6A_	Alignment	not modelled	55.7	30	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
107	d1tk9a_	Alignment	not modelled	55.0	21	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
108	d1vpea_	Alignment	not modelled	53.2	29	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
109	d16pka_	Alignment	not modelled	52.8	27	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
110	d1phpa_	Alignment	not modelled	51.2	27	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
111	c2vy9A_	Alignment	not modelled	48.2	6	PDB header: gene regulation Chain: A: PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub
112	c1zmrA_	Alignment	not modelled	48.2	24	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of the e. coli phosphoglycerate kinase
113	c1e0cA_	Alignment	not modelled	46.3	18	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
114	d1t5oa_	Alignment	not modelled	46.3	25	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: IF2B-like
115	c3f4aA_	Alignment	not modelled	45.3	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ygr203w; PDBTitle: structure of ygr203w, a yeast protein tyrosine phosphatase2 of the rhodanese family
116	c2cunA_	Alignment	not modelled	45.0	17	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase; PDBTitle: crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
117	c1boiA_	Alignment	not modelled	43.6	19	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
118	d1x92a_	Alignment	not modelled	43.5	21	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
119	d1qpga_	Alignment	not modelled	42.5	20	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
120	c1w2wA_	Alignment	not modelled	42.2	21	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