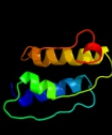
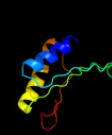
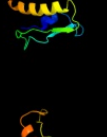
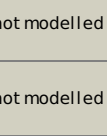
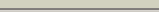
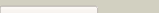


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fm0e_	 Alignment		100.0	100	Fold: alpha/beta-Hammerhead Superfamily: Molybdopter in synthase subunit MoaE Family: Molybdopter in synthase subunit MoaE
2	c2qieA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: molybdopter in-converting factor subunit 2; PDBTitle: staphylococcus aureus molybdopter in synthase in complex2 with precursor z
3	c2omdB_	 Alignment		100.0	29	PDB header: lyase Chain: B: PDB Molecule: molybdopter in-converting factor subunit 2; PDBTitle: crystal structure of molybdopter in converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
4	c3rpfB_	 Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: molybdopter in synthase catalytic subunit; PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopter in-converting2 factor from helicobacter pylori 26695
5	d1nvja_	 Alignment		100.0	100	Fold: alpha/beta-Hammerhead Superfamily: Molybdopter in synthase subunit MoaE Family: Molybdopter in synthase subunit MoaE
6	c2wp4A_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: molybdopter in-converting factor subunit 2 1; PDBTitle: crystal structure of rv3119 from mycobacterium tuberculosis
7	c1v8cA_	 Alignment		98.8	21	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
8	c3upsA_	 Alignment		78.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: iojap-like protein; PDBTitle: crystal structure of iojap-like protein from zymomonas mobilis
9	d2id1a1	 Alignment		61.0	12	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Iojap/YbeB-like
10	d2o5aa1	 Alignment		33.2	15	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Iojap/YbeB-like
11	c2ys6A_	 Alignment		32.4	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus

12	d1n0ua5	Alignment		27.8	24	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
13	d2dy1a5	Alignment		27.4	20	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
14	c1zcoA_	Alignment		21.1	11	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphoheptonate aldolase; PDBTitle: crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
15	d1sq1a_	Alignment		15.4	9	Fold: Chorismate synthase, AroC Superfamily: Chorismate synthase, AroC Family: Chorismate synthase, AroC
16	c2i2xO_	Alignment		13.4	17	PDB header: transferase Chain: O: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
17	d1xmba2	Alignment		13.4	11	Fold: Ferredoxin-like Superfamily: Bacterial exopeptidase dimerisation domain Family: Bacterial exopeptidase dimerisation domain
18	c1zrsB_	Alignment		13.1	16	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: wild-type Id-carboxypeptidase
19	c3lvmB_	Alignment		13.1	17	PDB header: transferase Chain: B: PDB Molecule: cysteine desulfurase; PDBTitle: crystal structure of e.coli iscs
20	c3cb4D_	Alignment		12.6	16	PDB header: translation Chain: D: PDB Molecule: gtp-binding protein lepa; PDBTitle: the crystal structure of lepa
21	c2kouA_	Alignment	not modelled	12.1	13	PDB header: hydrolase Chain: A: PDB Molecule: dicer-like protein 4; PDBTitle: dicer like protein
22	d2od6a1	Alignment	not modelled	10.6	26	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Marine metagenome family DABB1
23	d2k49a2	Alignment	not modelled	10.5	8	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
24	d2dkya1	Alignment	not modelled	9.9	33	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
25	d1p3wa_	Alignment	not modelled	9.7	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
26	d1uwda_	Alignment	not modelled	9.4	12	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
27	d1rpma_	Alignment	not modelled	8.6	17	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
28	c2xd4A_	Alignment	not modelled	8.5	13	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycylamide2 ribonucleotide synthetase
29	c3nizB_	Alignment	not modelled	8.0	21	PDB header: immune system Chain: B: PDB Molecule: microcin immunity protein mccf;

29	c9jz6_	Alignment	not modelled	8.0	41	PDBTitle: crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
30	d2qn6b1	Alignment	not modelled	7.8	26	Fold: Ferredoxin-like Superfamily: eIF-2-alpha, C-terminal domain Family: eIF-2-alpha, C-terminal domain
31	d2k8ea1	Alignment	not modelled	7.6	7	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
32	d2burb1	Alignment	not modelled	7.4	24	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
33	d2k49a1	Alignment	not modelled	7.3	7	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
34	d1dt9a3	Alignment	not modelled	7.3	10	Fold: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Superfamily: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Family: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
35	c3iuuA_	Alignment	not modelled	7.2	15	PDB header: hydrolase Chain: A: PDB Molecule: putative metallopeptidase; PDBTitle: crystal structure of putative metallopeptidase (yp_676511.1) from2 mesorhizobium sp. bnc1 at 2.13 a resolution
36	d1larb1	Alignment	not modelled	7.2	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
37	d2k8ea2	Alignment	not modelled	7.2	7	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
38	d2h80a1	Alignment	not modelled	7.1	21	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain
39	c2bija_	Alignment	not modelled	6.9	16	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)
40	c3okqA_	Alignment	not modelled	6.9	22	PDB header: protein binding Chain: A: PDB Molecule: bud site selection protein 6; PDBTitle: crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
41	d1udsa2	Alignment	not modelled	6.8	17	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
42	d3bida1	Alignment	not modelled	6.8	27	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
43	d2auna2	Alignment	not modelled	6.8	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
44	d2pa2a1	Alignment	not modelled	6.7	15	Fold: alpha/beta-Hammerhead Superfamily: Ribosomal protein L16p/L10e Family: Ribosomal protein L10e
45	c3eggC_	Alignment	not modelled	6.6	40	PDB header: hydrolase Chain: C: PDB Molecule: spinophilin; PDBTitle: crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
46	c2h04A_	Alignment	not modelled	6.5	21	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
47	c3e15D_	Alignment	not modelled	6.4	12	PDB header: hydrolase Chain: D: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: 6-phosphogluconolactonase from plasmodium vivax
48	c1dd3D_	Alignment	not modelled	6.1	24	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
49	c1dd3C_	Alignment	not modelled	6.1	24	PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein l7/l12; PDBTitle: crystal structure of ribosomal protein l12 from thermotoga maritima
50	d1v6ba_	Alignment	not modelled	6.1	40	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
51	d1p15a_	Alignment	not modelled	6.1	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
52	c2i75A_	Alignment	not modelled	6.1	10	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase non-receptor type 4; PDBTitle: crystal structure of human protein tyrosine phosphatase n4 (ptpn4)
53	d2pjua1	Alignment	not modelled	5.9	16	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
54	d2o0ma1	Alignment	not modelled	5.9	21	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like

55	c2o0mA	 Alignment	not modelled	5.9	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, sorc family; PDBTitle: the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
56	c1ceuA	 Alignment	not modelled	5.8	35	PDB header: viral protein Chain: A: PDB Molecule: protein (hiv-1 regulatory protein n-terminal PDBTitle: nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
57	c2pjuD	 Alignment	not modelled	5.8	16	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
58	d2gnoa1	 Alignment	not modelled	5.7	6	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: DNA polymerase III clamp loader subunits, C-terminal domain
59	d1jlna	 Alignment	not modelled	5.6	21	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
60	d1wfga	 Alignment	not modelled	5.4	40	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
61	d1yfoa	 Alignment	not modelled	5.4	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
62	c2k18A	 Alignment	not modelled	5.4	19	PDB header: de novo protein Chain: A: PDB Molecule: or15; PDBTitle: solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
63	c3jrlA	 Alignment	not modelled	5.4	12	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
64	c2qdmA	 Alignment	not modelled	5.4	25	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
65	d2k7ia1	 Alignment	not modelled	5.4	7	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
66	c2k7iB	 Alignment	not modelled	5.4	7	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: upf0339 protein atu0232; PDBTitle: solution nmr structure of protein atu0232 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att3. ontario center for structural proteomics target atc0223.
67	c2b49A	 Alignment	not modelled	5.2	9	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