

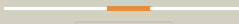

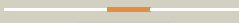
















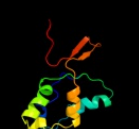
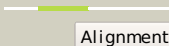

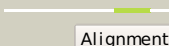

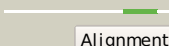
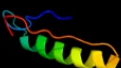
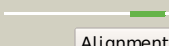

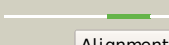

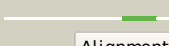



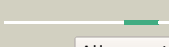
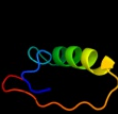

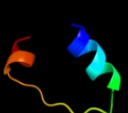
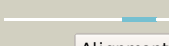

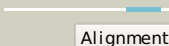
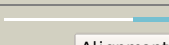

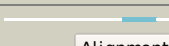

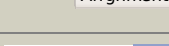


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3c5wc1	 Alignment		88.8	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
2	dljk7a_	 Alignment		87.4	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
3	dls70a_	 Alignment		86.8	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
4	d2p6ba1	 Alignment		86.0	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
5	c2jogA_	 Alignment		85.6	21	PDB header: hydrolase Chain: A: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: structure of the calcineurin-nfat complex
6	c2p6bC_	 Alignment		85.3	21	PDB header: hydrolase/hydrolase regulator Chain: C: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: crystal structure of human calcineurin in complex with2 pvit peptide
7	clauiA_	 Alignment		84.3	23	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine phosphatase 2b; PDBTitle: human calcineurin heterodimer
8	dlauia_	 Alignment		84.3	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
9	c3nx2B_	 Alignment		77.2	15	PDB header: lyase Chain: B: PDB Molecule: ferulic acid decarboxylase; PDBTitle: enterobacter sp. px6-4 ferulic acid decarboxylase in complex with2 substrate analogues
10	c3icfB_	 Alignment		75.8	16	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase t PDBTitle: structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5
11	c2qicA_	 Alignment		68.8	19	PDB header: hydrolase Chain: A: PDB Molecule: diadenosine tetraphosphatase, putative; PDBTitle: crystal structure of a putative diadenosine tetraphosphatase

12	c3nadB_	 Alignment		68.5	25	PDB header: lyase Chain: B: PDB Molecule: ferulate decarboxylase; PDBTitle: crystal structure of phenolic acid decarboxylase from bacillus pumilus2 ui-670
13	dls95a_	 Alignment		63.6	24	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
14	c2zbmA_	 Alignment		58.8	26	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase; PDBTitle: crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
15	d2nxfa1	 Alignment		51.6	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: ADPRibase-Mn-like
16	c1wao4_	 Alignment		51.2	20	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
17	d1ii7a_	 Alignment		50.0	20	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
18	d2qc9a1	 Alignment		47.5	21	Fold: Lipocalins Superfamily: Lipocalins Family: Phenolic acid decarboxylase (PAD)
19	d1uf3a_	 Alignment		47.3	5	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
20	c2dfjA_	 Alignment		47.0	28	PDB header: hydrolase Chain: A: PDB Molecule: diadenosinetetraphosphatase; PDBTitle: crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
21	c2eqxA_	 Alignment	not modelled	37.7	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kelch repeat and btb domain-containing protein 4; PDBTitle: solution structure of the back domain of kelch repeat and2 btb domain-containing protein 4
22	c3av0A_	 Alignment	not modelled	34.2	26	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11-rad50 bound to atp s
23	c2wdfA_	 Alignment	not modelled	32.4	9	PDB header: hydrolase Chain: A: PDB Molecule: sulfur oxidation protein soxb; PDBTitle: termus thermophilus sulfate thiohydrolase soxb
24	c1oidA_	 Alignment	not modelled	32.0	14	PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
25	d1xm7a_	 Alignment	not modelled	31.5	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666
26	c1s3mA_	 Alignment	not modelled	31.0	23	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
27	c3auzA_	 Alignment	not modelled	30.4	26	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese
28	d2z1aa2	 Alignment	not modelled	27.0	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain

29	d1s3la_	Alignment	not modelled	23.2	28	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
30	c2c55A_	Alignment	not modelled	20.5	33	PDB header: viral protein Chain: A: PDB Molecule: protein p6; PDBTitle: solution structure of the human immunodeficiency virus type2 1 p6 protein
31	c2xmoB_	Alignment	not modelled	18.3	22	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
32	c2kknA_	Alignment	not modelled	18.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the motogata maritima protein tm1076:2 northeast structural genomics consortium target vt57
33	d1s04a_	Alignment	not modelled	18.0	20	Fold: PUA domain-like Superfamily: PUA domain-like Family: ProFAR isomerase associated domain
34	c3rl4A_	Alignment	not modelled	17.8	23	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
35	c2la3A_	Alignment	not modelled	16.8	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
36	c2kkrA_	Alignment	not modelled	16.4	18	PDB header: transcription, protein binding Chain: A: PDB Molecule: ataxin-7; PDBTitle: solution structure of sca7 zinc finger domain from human ataxin-72 protein
37	d1qfxa_	Alignment	not modelled	15.1	6	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
38	d1pv8a_	Alignment	not modelled	15.0	48	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
39	c2aklA_	Alignment	not modelled	13.8	47	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
40	d2akka1	Alignment	not modelled	13.4	40	Fold: SH3-like barrel Superfamily: Prokaryotic SH3-related domain Family: PhnA-like
41	d1z2wa1	Alignment	not modelled	13.3	10	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
42	c2i5ha_	Alignment	not modelled	13.3	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1531; PDBTitle: crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
43	d2i5ha1	Alignment	not modelled	13.3	27	Fold: AF1531-like Superfamily: AF1531-like Family: AF1531-like
44	d2akla1	Alignment	not modelled	13.2	47	Fold: SH3-like barrel Superfamily: Prokaryotic SH3-related domain Family: PhnA-like
45	c2dn5A_	Alignment	not modelled	13.2	31	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
46	d1qcsa2	Alignment	not modelled	11.8	32	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
47	d1g5ba_	Alignment	not modelled	11.6	29	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
48	c1xrxD_	Alignment	not modelled	11.5	48	PDB header: replication inhibitor Chain: D: PDB Molecule: sega protein; PDBTitle: crystal structure of a dna-binding protein
49	d1xrxal	Alignment	not modelled	11.5	48	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
50	d1t6la1	Alignment	not modelled	11.5	23	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
51	c1p0oA_	Alignment	not modelled	11.1	63	PDB header: ribosome Chain: A: PDB Molecule: 19-mer peptide from 50s ribosomal protein l1; PDBTitle: hp (2-20) substitution of trp for gln and asp at position2 17 and 19 modification in sds-d25 micelles
52	c3fmtF_	Alignment	not modelled	11.0	55	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein sega; PDBTitle: crystal structure of sega bound to dna
53	c3alxB_	Alignment	not modelled	11.0	28	PDB header: viral protein/membrane protein Chain: B: PDB Molecule: hemagglutinin, cdw150; PDBTitle: crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (mv-h(1482r)-slam(n102h/r108y) fusion)
54	d1xnea_	Alignment	not modelled	10.9	25	Fold: PUA domain-like Superfamily: PUA domain-like Family: ProFAR isomerase associated domain
						PDB header: hydrolase

55	c3c9fB_	Alignment	not modelled	10.4	23	Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from candida albicans sc5314
56	c3zu0A_	Alignment	not modelled	10.4	18	PDB header: hydrolase Chain: A: PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (nadh)
57	d1q60a_	Alignment	not modelled	10.4	38	Fold: GTF2I-like repeat Superfamily: GTF2I-like repeat Family: GTF2I-like repeat
58	c2ftcB_	Alignment	not modelled	9.8	33	PDB header: ribosome Chain: B: PDB Molecule: mitochondrial ribosomal protein l2; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
59	d2p0sa1	Alignment	not modelled	9.4	23	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: PG0945 N-terminal domain-like
60	d2a22a1	Alignment	not modelled	9.3	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
61	c2gfiB_	Alignment	not modelled	9.1	15	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: crystal structure of the phytase from d. castellii at 2.3 a
62	c2dbhA_	Alignment	not modelled	8.9	22	PDB header: signaling protein Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily PDBTitle: solution structure of the carboxyl-terminal card-like2 domain in human tnfr-related death receptor-6
63	d2f9zc1	Alignment	not modelled	8.7	50	Fold: CNF1/YfiH-like putative cysteine hydrolases Superfamily: CNF1/YfiH-like putative cysteine hydrolases Family: CheD-like
64	c3letB_	Alignment	not modelled	8.2	40	PDB header: transferase Chain: B: PDB Molecule: adenosine monophosphate-protein transferase vops; PDBTitle: crystal structure of fic domain containing ampylator, vops
65	c1z8yO_	Alignment	not modelled	8.2	63	PDB header: virus Chain: O: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
66	c1z8yM_	Alignment	not modelled	8.2	63	PDB header: virus Chain: M: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
67	c1z8yK_	Alignment	not modelled	8.2	63	PDB header: virus Chain: K: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
68	c1z8yl_	Alignment	not modelled	8.2	63	PDB header: virus Chain: I: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
69	d1p42a2	Alignment	not modelled	8.0	31	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
70	c2hb0B_	Alignment	not modelled	8.0	36	PDB header: cell adhesion Chain: B: PDB Molecule: cfa/i fimbrial subunit e; PDBTitle: crystal structure of cfae, the adhesive subunit of cfa/i2 fimbria of enterotoxigenic escherichia coli
71	c2vxdA_	Alignment	not modelled	7.9	36	PDB header: nuclear protein Chain: A: PDB Molecule: nucleophosmin; PDBTitle: the structure of the c-terminal domain of nucleophosmin
72	d1su1a_	Alignment	not modelled	7.7	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
73	c1su1A_	Alignment	not modelled	7.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yfce; PDBTitle: structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
74	d1xzwa2	Alignment	not modelled	7.6	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
75	d1c8ba_	Alignment	not modelled	7.5	25	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Germination protease
76	c1t3tA_	Alignment	not modelled	7.5	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
77	c3f83A_	Alignment	not modelled	7.5	36	PDB header: cell adhesion Chain: A: PDB Molecule: fusion of the minor pilin cfae and major pilin cfab; PDBTitle: structure of fusion complex of the minor pilin cfae and major pilin2 cfab of cfa/i pili from etec e. coli
78	c3mmrA_	Alignment	not modelled	7.4	9	PDB header: hydrolase Chain: A: PDB Molecule: arginase; PDBTitle: structure of plasmodium falciparum arginase in complex with abh
79	c2vvxA_	Alignment	not modelled	7.1	13	PDB header: viral protein Chain: A: PDB Molecule: protein a52; PDBTitle: structure of vaccinia virus protein a52
80	c2adlB_	Alignment	not modelled	7.0	46	PDB header: dna binding protein Chain: B: PDB Molecule: ccda; PDBTitle: solution structure of the bacterial antitoxin ccda:2 implications for dna and toxin binding
						PDB header: replication/transferase

81	c1yypA_	Alignment	not modelled	6.8	23	Chain: A: PDB Molecule: dna polymerase processivity factor; PDBTitle: crystal structure of cytomegalovirus ul44 bound to c-terminal peptide2 from cmv ul54
82	c3mcuF_	Alignment	not modelled	6.7	23	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
83	d1cr5a2	Alignment	not modelled	6.6	30	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
84	c2dzqA_	Alignment	not modelled	6.5	31	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
85	c2ed2A_	Alignment	not modelled	6.3	23	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
86	c1rz4A_	Alignment	not modelled	6.3	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit 11; PDBTitle: crystal structure of human eif3k
87	d1bh9b_	Alignment	not modelled	6.2	35	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
88	c2vesA_	Alignment	not modelled	6.1	34	PDB header: hydrolase Chain: A: PDB Molecule: udp-3-o-[3-hydroxymyristoyl] n-acetylglucosamine PDBTitle: crystal structure of lpxc from pseudomonas aeruginosa2 complexed with the potent bb-78485 inhibitor
89	c3ib7A_	Alignment	not modelled	6.1	13	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
90	d1l4zb_	Alignment	not modelled	6.1	78	Fold: beta-Grasp (ubiquitin-like) Superfamily: Staphylokinase/streptokinase Family: Staphylokinase/streptokinase
91	d2awia1	Alignment	not modelled	5.9	44	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: PrgX N-terminal domain-like
92	c2l0eA_	Alignment	not modelled	5.9	29	PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: structural and functional analysis of tm vi of the nhe1 isoform of the2 na+/h+ exchanger
93	c2dp3A_	Alignment	not modelled	5.9	24	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of a double mutant (c202a/a198v) of triosephosphate2 isomerase from giardia lamblia
94	d2j6ba1	Alignment	not modelled	5.9	14	Fold: STIV B116-like Superfamily: STIV B116-like Family: STIV B116-like
95	c3lqkA_	Alignment	not modelled	5.8	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
96	c2dn4A_	Alignment	not modelled	5.7	27	PDB header: transcription Chain: A: PDB Molecule: general transcription factor ii-i; PDBTitle: solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
97	c3lybC_	Alignment	not modelled	5.6	25	PDB header: hydrolase Chain: C: PDB Molecule: putative endoribonuclease; PDBTitle: structure of putative endoribonuclease(kp1_3112) from2 klebsiella pneumoniae
98	c1s1hN_	Alignment	not modelled	5.6	20	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s29-b; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
99	d1wjva1	Alignment	not modelled	5.5	36	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: C2HC finger