

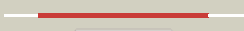





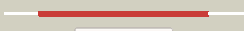















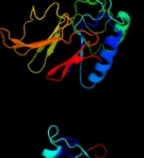
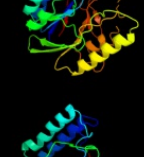


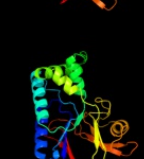

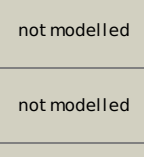


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ib7A_	 Alignment		99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
2	c2xmoB_	 Alignment		99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
3	d2yvta1	 Alignment		99.9	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
4	d3d03a1	 Alignment		99.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
5	c2hy1A_	 Alignment		99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: rv0805; PDBTitle: crystal structure of rv0805
6	d2hy1a1	 Alignment		99.9	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
7	c3av0A_	 Alignment		99.9	17	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11-rad50 bound to atp s
8	d1uf3a_	 Alignment		99.9	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
9	c3auzA_	 Alignment		99.9	17	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese
10	c3qg5D_	 Alignment		99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: mre11; PDBTitle: the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
11	c3tliC_	 Alignment		99.9	16	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations

12	d2nxfal	Alignment		99.8	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: ADPRibase-Mn-like
13	dlsu1a_	Alignment		99.8	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
14	clsu1A_	Alignment		99.8	22	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
15	c2q8uA_	Alignment		99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease, putative; PDBTitle: crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
16	dlii7a_	Alignment		99.8	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
17	dls3la_	Alignment		99.8	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
18	cls3mA_	Alignment		99.8	18	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
19	c3qfnA_	Alignment		99.8	12	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
20	d2a22a1	Alignment		99.8	20	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
21	dlz2wa1	Alignment	not modelled	99.8	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
22	d2qfra2	Alignment	not modelled	99.8	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
23	c3rqzC_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of metallophosphoesterase from spharobacter2 thermophilus
24	d3ck2a1	Alignment	not modelled	99.8	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
25	dlx2wa2	Alignment	not modelled	99.8	10	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
26	dlnnwa_	Alignment	not modelled	99.7	11	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Phosphoesterase-related
27	dlutea_	Alignment	not modelled	99.7	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
28	clqhwA_	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: A: PDB Molecule: protein (purple acid phosphatase); PDBTitle: purple acid phosphatase from rat bone
29	dlqhwa_	Alignment	not modelled	99.7	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases

					Family: Purple acid phosphatase-like
30	d1xm7a_	Alignment	not modelled	99.7	26 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666
31	c2kknA_	Alignment	not modelled	99.7	23 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
32	c1kbpB_	Alignment	not modelled	99.7	13 PDB header: hydrolase (phosphoric monoester) Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: kidney bean purple acid phosphatase
33	c3rl4A_	Alignment	not modelled	99.7	13 PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
34	c1xzwB_	Alignment	not modelled	99.7	14 PDB header: hydrolase Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: sweet potato purple acid phosphatase/phosphate complex
35	d1g5ba_	Alignment	not modelled	99.5	15 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
36	c1oidA_	Alignment	not modelled	99.5	13 PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
37	d1usha2	Alignment	not modelled	99.5	14 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
38	c2zbmA_	Alignment	not modelled	99.3	16 PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase; PDBTitle: crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
39	c3qfkA_	Alignment	not modelled	99.2	13 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate
40	d2z1aa2	Alignment	not modelled	99.1	21 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
41	c3ivdA_	Alignment	not modelled	99.1	16 PDB header: hydrolase Chain: A: PDB Molecule: nucleotidase; PDBTitle: putative 5'-nucleotidase (c4898) from escherichia coli in2 complex with uridine
42	c2z1aA_	Alignment	not modelled	99.1	21 PDB header: hydrolase Chain: A: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
43	d2z06a1	Alignment	not modelled	99.1	15 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
44	c3e0jG_	Alignment	not modelled	99.1	16 PDB header: transferase Chain: G: PDB Molecule: dna polymerase subunit delta-2; PDBTitle: x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
45	c2qjcA_	Alignment	not modelled	99.0	16 PDB header: hydrolase Chain: A: PDB Molecule: diadenosine tetraphosphatase, putative; PDBTitle: crystal structure of a putative diadenosine tetraphosphatase
46	d3c9fa2	Alignment	not modelled	99.0	16 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
47	d3c5wc1	Alignment	not modelled	99.0	8 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
48	d1t70a_	Alignment	not modelled	98.9	16 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
49	c2jogA_	Alignment	not modelled	98.9	8 PDB header: hydrolase Chain: A: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: structure of the calcineurin-nfat complex
50	d1s95a_	Alignment	not modelled	98.9	13 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
51	d1jk7a_	Alignment	not modelled	98.9	12 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
52	d1auia_	Alignment	not modelled	98.8	9 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
53	c1auiA_	Alignment	not modelled	98.8	9 PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine phosphatase 2b; PDBTitle: human calcineurin heterodimer
54	c2p6bC_	Alignment	not modelled	98.8	9 PDB header: hydrolase/hydrolase regulator Chain: C: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: crystal structure of human calcineurin in complex with2 pvvit peptide
55	c3c9fB_	Alignment	not modelled	98.8	16 PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from candida

					albicans sc5314
56	c2wdfA	Alignment	not modelled	98.8	15 PDB header: hydrolase Chain: A: PDB Molecule: sulfur oxidation protein soxb; PDBTitle: termus thermophilus sulfate thiohydrolase soxb
57	d1t71a	Alignment	not modelled	98.8	16 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
58	d2p6ba1	Alignment	not modelled	98.8	9 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
59	c3gveB	Alignment	not modelled	98.8	16 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yfkn protein; PDBTitle: crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
60	c3zu0A	Alignment	not modelled	98.8	16 PDB header: hydrolase Chain: A: PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (nadm)
61	d1s70a	Alignment	not modelled	98.7	11 Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
62	c1wao4	Alignment	not modelled	98.7	10 PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
63	c3icfB	Alignment	not modelled	98.6	11 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
64	c3jyfB	Alignment	not modelled	98.6	16 PDB header: hydrolase Chain: B: PDB Molecule: 2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- PDBTitle: the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
65	c2dfjA	Alignment	not modelled	98.5	25 PDB header: hydrolase Chain: A: PDB Molecule: diadenosinetetraphosphatase; PDBTitle: crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
66	c3floG	Alignment	not modelled	97.6	10 PDB header: transferase Chain: G: PDB Molecule: dna polymerase alpha subunit b; PDBTitle: crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
67	d1o1ya	Alignment	not modelled	80.3	16 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
68	c2issF	Alignment	not modelled	74.2	15 PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
69	c3l7nA	Alignment	not modelled	72.7	21 PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
70	d1ka9h	Alignment	not modelled	69.7	21 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
71	d2qedal	Alignment	not modelled	68.9	7 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
72	c3g23A	Alignment	not modelled	43.2	15 PDB header: hydrolase Chain: A: PDB Molecule: ld-carboxypeptidase a; PDBTitle: crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution
73	d1qh5a	Alignment	not modelled	38.4	19 Fold: Metallo-hydrolase/oxi doreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
74	c3drwA	Alignment	not modelled	37.9	14 PDB header: transferase Chain: A: PDB Molecule: adp-specific phosphofructokinase; PDBTitle: crystal structure of a phosphofructokinase from pyrococcus2 horikoshii ot3 with amp
75	c2h0rD	Alignment	not modelled	35.5	15 PDB header: hydrolase Chain: D: PDB Molecule: nicotinamidase; PDBTitle: structure of the yeast nicotinamidase pnc1p
76	d1u2xa	Alignment	not modelled	33.4	14 Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
77	d1k9vf	Alignment	not modelled	33.2	10 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
78	d1xm8a	Alignment	not modelled	31.2	12 Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
79	d1gc5a	Alignment	not modelled	30.0	13 Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
80	d1l2la	Alignment	not modelled	27.5	13 Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
81	c3aj3A	Alignment	not modelled	23.6	7 PDB header: hydrolase Chain: A: PDB Molecule: 4-pyridoxolactonase; PDBTitle: crystal structure of selenomethionine substituted 4-

						pyridoxolactonase2 from mesorhizobium loti
82	c1b74A_	Alignment	not modelled	22.9	23	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
83	d2a9va1	Alignment	not modelled	22.3	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
84	c2xmpB_	Alignment	not modelled	20.8	12	PDB header: sugar binding protein Chain: B: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
85	d2auna1	Alignment	not modelled	20.7	21	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LD-carboxypeptidase A C-terminal domain-like Family: LD-carboxypeptidase A C-terminal domain-like
86	d2bisa1	Alignment	not modelled	19.4	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
87	c2ywjA_	Alignment	not modelled	17.8	18	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
88	d1ua4a_	Alignment	not modelled	17.6	10	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
89	d1xi8a3	Alignment	not modelled	17.4	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
90	c2h2wA_	Alignment	not modelled	16.8	14	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
91	c1sazA_	Alignment	not modelled	16.5	14	PDB header: transferase Chain: A: PDB Molecule: probable butyrate kinase 2; PDBTitle: membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
92	d1ijta_	Alignment	not modelled	15.7	4	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
93	c2e11B_	Alignment	not modelled	15.5	13	PDB header: hydrolase Chain: B: PDB Molecule: hydrolase; PDBTitle: the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
94	c2i2aA_	Alignment	not modelled	15.4	8	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes
95	c3p4iA_	Alignment	not modelled	14.9	13	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium
96	c2zwrA_	Alignment	not modelled	14.8	19	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase superfamily protein; PDBTitle: crystal structure of ttha1623 from thermus thermophilus hb8
97	d1b74a1	Alignment	not modelled	14.5	24	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
98	d2uubb1	Alignment	not modelled	14.5	24	Fold: Flavodoxin-like Superfamily: Ribosomal protein S2 Family: Ribosomal protein S2
99	d1a3xa2	Alignment	not modelled	14.4	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase