



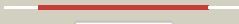









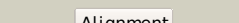

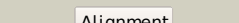



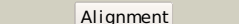



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dfjA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: diadenosinetetraphosphatase; PDBTitle: crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
2	c2qjcA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: diadenosine tetraphosphatase, putative; PDBTitle: crystal structure of a putative diadenosine tetraphosphatase
3	c2zbmA_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase; PDBTitle: crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
4	d1g5ba_	 Alignment		100.0	24	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
5	d1jk7a_	 Alignment		100.0	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
6	d3c5wc1	 Alignment		100.0	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
7	d1s70a_	 Alignment		100.0	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
8	c2jogA_	 Alignment		99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: structure of the calcineurin-nfat complex
9	d1s95a_	 Alignment		99.9	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
10	c1auiA_	 Alignment		99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine phosphatase 2b; PDBTitle: human calcineurin heterodimer
11	d1auiA_	 Alignment		99.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase

12	c2p6bC_	Alignment		99.9	17	PDB header: hydrolase/hydrolase regulator Chain: C: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: crystal structure of human calcineurin in complex with2 pvivit peptide
13	d2p6ba1	Alignment		99.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
14	c3icfB_	Alignment		99.9	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
15	c1wao4_	Alignment		99.9	18	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
16	d1uf3a_	Alignment		99.9	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
17	d1nnwa_	Alignment		99.8	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Phosphoesterase-related
18	c3qfnA_	Alignment		99.8	23	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
19	d1su1a_	Alignment		99.7	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
20	c1su1A_	Alignment		99.7	23	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
21	c3rqzC_	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
22	d2yvta1	Alignment	not modelled	99.5	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
23	c1s3mA_	Alignment	not modelled	99.5	21	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
24	d1s3la_	Alignment	not modelled	99.5	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
25	d2a22a1	Alignment	not modelled	99.4	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
26	c2kknA_	Alignment	not modelled	99.3	21	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
27	d1z2wa1	Alignment	not modelled	99.3	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
28	d3ck2a1	Alignment	not modelled	99.3	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
29	d1xm7a_	Alignment	not modelled	99.2	34	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666

30	c3av0A_	Alignment	not modelled	98.8	29	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11-rad50 bound to atp s
31	d1ii7a_	Alignment	not modelled	98.8	27	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
32	c3auzA_	Alignment	not modelled	98.7	29	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese
33	c3rl4A_	Alignment	not modelled	98.5	28	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
34	c2hy1A_	Alignment	not modelled	98.4	17	PDB header: hydrolase Chain: A: PDB Molecule: rv0805; PDBTitle: crystal structure of rv0805
35	d2hy1a1	Alignment	not modelled	98.4	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
36	c2q8uA_	Alignment	not modelled	98.4	23	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease, putative; PDBTitle: crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
37	d3d03a1	Alignment	not modelled	98.4	25	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
38	c3ib7A_	Alignment	not modelled	98.4	32	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
39	c2xmoB_	Alignment	not modelled	98.4	34	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
40	c3qg5D_	Alignment	not modelled	98.4	30	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
41	d2nxfal	Alignment	not modelled	98.3	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: ADPRibase-Mn-like
42	c3tliC_	Alignment	not modelled	98.2	27	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations
43	d2z1aa2	Alignment	not modelled	98.0	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
44	c2z1aA_	Alignment	not modelled	97.8	20	PDB header: hydrolase Chain: A: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
45	c3qfkA_	Alignment	not modelled	97.8	20	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
46	d1usha2	Alignment	not modelled	97.8	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
47	d1xwa2	Alignment	not modelled	97.7	20	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
48	c3ivdA_	Alignment	not modelled	97.7	14	PDB header: hydrolase Chain: A: PDB Molecule: nucleotidase; PDBTitle: putative 5'-nucleotidase (c4898) from escherichia coli in2 complex with uridine
49	cloidA_	Alignment	not modelled	97.7	22	PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
50	d1utea_	Alignment	not modelled	97.6	25	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
51	c1qhwA_	Alignment	not modelled	97.6	23	PDB header: hydrolase Chain: A: PDB Molecule: protein (purple acid phosphatase); PDBTitle: purple acid phosphatase from rat bone
52	d1qhwa_	Alignment	not modelled	97.6	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
53	c3zu0A_	Alignment	not modelled	97.6	18	PDB header: hydrolase Chain: A: PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (nadr)
54	d1t71a_	Alignment	not modelled	97.5	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
55	d2z06a1	Alignment	not modelled	97.4	26	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
						Fold: Metallo-dependent phosphatases

56	d2qfra2	Alignment	not modelled	97.3	23	Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
57	c3jyfb	Alignment	not modelled	97.3	23	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
58	c3gveB	Alignment	not modelled	97.3	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yfkn protein; PDBTitle: crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
59	d1t70a	Alignment	not modelled	97.2	32	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
60	d3c9fa2	Alignment	not modelled	97.0	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
61	c3c9fB	Alignment	not modelled	96.8	23	PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from candida albicans sc5314
62	c1kbpB	Alignment	not modelled	95.8	25	PDB header: hydrolase (phosphoric monoester) Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: kidney bean purple acid phosphatase
63	c2wdfA	Alignment	not modelled	95.6	23	PDB header: hydrolase Chain: A: PDB Molecule: sulfur oxidation protein soxb; PDBTitle: termus thermophilus sulfate thiohydrolase soxb
64	c1xzwB	Alignment	not modelled	95.3	21	PDB header: hydrolase Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: sweet potato purple acid phosphatase/phosphate complex
65	c3floG	Alignment	not modelled	86.7	13	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
66	c3e0jG	Alignment	not modelled	60.2	27	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
67	d1gg4a1	Alignment	not modelled	43.0	16	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
68	c1y8aA	Alignment	not modelled	34.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein af1437; PDBTitle: structure of gene product af1437 from archaeoglobus fulgidus
69	d1qupa2	Alignment	not modelled	33.2	20	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
70	d1ecfa1	Alignment	not modelled	31.3	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
71	d1ux6a1	Alignment	not modelled	31.2	13	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Thrombospondin C-terminal domain
72	c2rogA	Alignment	not modelled	30.1	19	PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
73	d1gph11	Alignment	not modelled	29.4	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
74	c2issF	Alignment	not modelled	25.7	34	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
75	d1o57a2	Alignment	not modelled	20.3	8	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
76	d1okga1	Alignment	not modelled	18.5	19	Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multidomain sulfurtransferase (rhodanese)
77	d1nbwa2	Alignment	not modelled	17.2	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
78	d1ka9h	Alignment	not modelled	16.3	32	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
79	c1gph1	Alignment	not modelled	16.1	17	PDB header: transferase(glutamine amidotransferase) Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
80	c1m6yA	Alignment	not modelled	14.3	24	PDB header: transferase Chain: A: PDB Molecule: s-adenosyl-methyltransferase mraw; PDBTitle: crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
81	c1urhA	Alignment	not modelled	13.9	8	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: the "rhodanese" fold and catalytic mechanism of2 3-mercaptopyruvate sulfotransferases: crystal structure3 of ssea from

					escherichia coli
82	c2b3yB_	Alignment	not modelled	13.5	30 PDB header: lyase Chain: B: PDB Molecule: iron-responsive element binding protein 1; PDBTitle: structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
83	c1o57A_	Alignment	not modelled	13.4	8 PDB header: dna binding protein Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
84	d1fe0a_	Alignment	not modelled	13.2	17 Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
85	c3mjdB_	Alignment	not modelled	13.0	14 PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
86	d1yt8a4	Alignment	not modelled	12.2	17 Fold: Rhodanese/Cell cycle control phosphatase Superfamily: Rhodanese/Cell cycle control phosphatase Family: Multi domain sulfurtransferase (rhodanese)
87	c1ecjB_	Alignment	not modelled	12.1	17 PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
88	c3n9iA_	Alignment	not modelled	11.8	20 PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
89	c2gamA_	Alignment	not modelled	11.6	27 PDB header: transferase Chain: A: PDB Molecule: beta-1,6-n-acetylglucosaminyltransferase; PDBTitle: x-ray crystal structure of murine leukocyte-type core 2 b1,2 6-n-acetylglucosaminyltransferase (c2gnt-l) in complex3 with galb1,3galnac
90	d2b3ya1	Alignment	not modelled	11.5	31 Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: LeuD-like
91	c3elyA_	Alignment	not modelled	10.4	67 PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: wesselsbron virus methyltransferase in complex with adohcy
92	d1ylea1	Alignment	not modelled	10.2	24 Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: AstA-like
93	c2nz2A_	Alignment	not modelled	9.9	26 PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
94	c2zufA_	Alignment	not modelled	9.7	15 PDB header: ligase/rna Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
95	c2ov6A_	Alignment	not modelled	9.4	38 PDB header: hydrolase Chain: A: PDB Molecule: v-type atp synthase subunit f; PDBTitle: the nmr structure of subunit f of the methanogenic a1ao atp synthase2 and its interaction with the nucleotide-binding subunit b
96	c3rjtA_	Alignment	not modelled	9.2	21 PDB header: hydrolase Chain: A: PDB Molecule: lipolytic protein g-d-s-l family; PDBTitle: crystal structure of lipolytic protein g-d-s-l family from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
97	c2przB_	Alignment	not modelled	9.1	9 PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
98	c2l8bA_	Alignment	not modelled	9.1	17 PDB header: hydrolase Chain: A: PDB Molecule: protein trai; PDBTitle: trai (381-569)
99	c2wnsB_	Alignment	not modelled	9.1	19 PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: human orotate phosphoribosyltransferase (optase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)