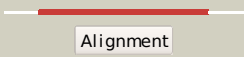

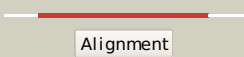

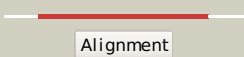

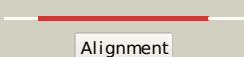

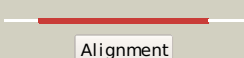

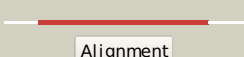

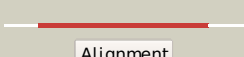

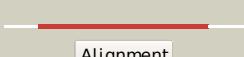

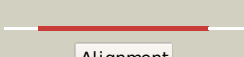

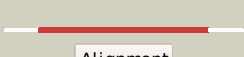













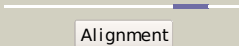

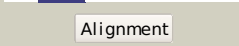
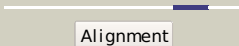

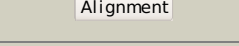
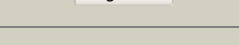
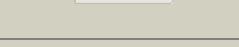
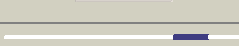

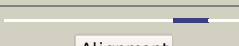


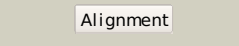
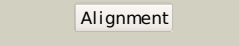
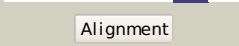




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1g5ba_	 Alignment		100.0	45	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
2	c2qjcA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: diadenosine tetraphosphatase, putative; PDBTitle: crystal structure of a putative diadenosine tetraphosphatase
3	c2dfjA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: diadenosine tetraphosphatase; PDBTitle: crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
4	c2zbmA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase; PDBTitle: crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
5	d1jk7a_	 Alignment		100.0	21	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
6	d3c5wc1	 Alignment		99.9	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
7	d1s95a_	 Alignment		99.9	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
8	d1s70a_	 Alignment		99.9	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
9	d1nnwa_	 Alignment		99.9	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Phosphoesterase-related
10	c3icfB_	 Alignment		99.9	20	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	c1wao4_	 Alignment		99.9	23	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure

12	c2jogA_	Alignment		99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: structure of the calcineurin-nfat complex
13	c1auiA_	Alignment		99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine phosphatase 2b; PDBTitle: human calcineurin heterodimer
14	d1auiA_	Alignment		99.9	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
15	c2p6bC_	Alignment		99.9	22	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
16	d2p6ba1	Alignment		99.9	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
17	c3rqzC_	Alignment		99.9	19	PDB header: hydrolase Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of metallophosphoesterase from sphaeobacter2 thermophilus
18	d1uf3a_	Alignment		99.9	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
19	c3qfnA_	Alignment		99.9	18	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	d1su1a_	Alignment		99.9	28	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
21	c1su1A_	Alignment	not modelled	99.9	28	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
22	d3ck2a1	Alignment	not modelled	99.8	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
23	c2kknA_	Alignment	not modelled	99.8	18	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
24	d2a22a1	Alignment	not modelled	99.8	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
25	d2yvta1	Alignment	not modelled	99.8	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
26	c1s3mA_	Alignment	not modelled	99.8	17	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel2 archaeal phosphodiesterase
27	d1s3la_	Alignment	not modelled	99.8	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
28	d1z2wa1	Alignment	not modelled	99.7	25	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
29	c2su0A_	Alignment	not modelled	99.5	21	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein

29	c3avvA	Alignment	not modelled	99.3	21	mre11; PDBTitle: crystal structure of mre11-rad50 bound to atp s
30	d1xm7a	Alignment	not modelled	99.5	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666
31	c3auzA	Alignment	not modelled	99.4	19	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese
32	c3ib7A	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
33	d1ii7a	Alignment	not modelled	99.3	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
34	d2hy1a1	Alignment	not modelled	99.3	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
35	c2hy1A	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: A: PDB Molecule: rv0805; PDBTitle: crystal structure of rv0805
36	d3d03a1	Alignment	not modelled	99.3	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
37	c3rl4A	Alignment	not modelled	99.2	22	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
38	c2q8uA	Alignment	not modelled	99.1	17	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease, putative; PDBTitle: crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
39	c3qg5D	Alignment	not modelled	99.1	22	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
40	c2xmoB	Alignment	not modelled	98.9	18	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
41	c3tliC	Alignment	not modelled	98.8	23	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations
42	c3qfkA	Alignment	not modelled	98.8	22	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
43	c1oidA	Alignment	not modelled	98.8	16	PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
44	d2nxfal	Alignment	not modelled	98.7	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: ADPRibase-Mn-like
45	d1xzwaz	Alignment	not modelled	98.7	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
46	c3ivdA	Alignment	not modelled	98.6	18	PDB header: hydrolase Chain: A: PDB Molecule: nucleotidase; PDBTitle: putative 5'-nucleotidase (c4898) from escherichia coli in2 complex with uridine
47	d1ushaz	Alignment	not modelled	98.5	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
48	d2qfra2	Alignment	not modelled	98.5	13	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
49	d1qhwaz	Alignment	not modelled	98.5	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
50	c1qhwA	Alignment	not modelled	98.5	15	PDB header: hydrolase Chain: A: PDB Molecule: protein (purple acid phosphatase); PDBTitle: purple acid phosphatase from rat bone
51	d1uteaz	Alignment	not modelled	98.4	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
52	c2wdfA	Alignment	not modelled	98.2	16	PDB header: hydrolase Chain: A: PDB Molecule: sulfur oxidation protein soxb; PDBTitle: termus thermophilus sulfate thiohydrolase soxb
53	c3jyfb	Alignment	not modelled	98.2	21	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
54	c3gveB	Alignment	not modelled	98.1	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yfkn protein; PDBTitle: crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
						PDB header: hydrolase

55	c2z1aA	Alignment	not modelled	98.1	15	Chain: A: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
56	d2z1aa2	Alignment	not modelled	98.0	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
57	c1xzwB	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: sweet potato purple acid phosphatase/phosphate complex
58	c3zu0A	Alignment	not modelled	97.8	18	PDB header: hydrolase Chain: A: PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (nadr)
59	c1kpbB	Alignment	not modelled	97.7	15	PDB header: hydrolase (phosphoric monoester) Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: kidney bean purple acid phosphatase
60	d3c9fa2	Alignment	not modelled	97.0	23	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
61	c3c9fB	Alignment	not modelled	95.0	29	PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from candida albicans sc5314
62	d1t71a	Alignment	not modelled	94.5	24	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
63	c3e0jG	Alignment	not modelled	94.4	7	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
64	d2z06a1	Alignment	not modelled	94.4	27	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
65	d1t70a	Alignment	not modelled	93.6	26	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
66	c3floG	Alignment	not modelled	76.7	24	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	d1gg4a1	Alignment	not modelled	35.7	16	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
68	d1ylea1	Alignment	not modelled	24.8	35	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: AstA-like
69	c3nh8A	Alignment	not modelled	22.9	20	PDB header: hydrolase Chain: A: PDB Molecule: aspartoacylase-2; PDBTitle: crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine
70	c2qj8B	Alignment	not modelled	21.4	21	PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
71	c3cdxB	Alignment	not modelled	19.3	16	PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
72	c2el7A	Alignment	not modelled	17.3	23	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
73	d1j1ua	Alignment	not modelled	17.0	27	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
74	c3n9iA	Alignment	not modelled	16.9	20	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
75	d2i3ca1	Alignment	not modelled	15.8	20	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like
76	c2cybA	Alignment	not modelled	15.7	20	PDB header: ligase Chain: A: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
77	c3hp7A	Alignment	not modelled	15.3	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hemolysin, putative; PDBTitle: putative hemolysin from streptococcus thermophilus.
78	c2dlcX	Alignment	not modelled	14.6	17	PDB header: ligase/trna Chain: X: PDB Molecule: tyrosyl-trna synthetase, cytoplasmic; PDBTitle: crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
79	c3prhB	Alignment	not modelled	14.0	17	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase val144pro mutant from b. subtilis
80	d1i6la	Alignment	not modelled	13.0	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain

81	c3na6A		not modelled	12.8	24	PDB header: hydrolase Chain: A: PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
82	d1ddza2		not modelled	12.7	17	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
83	d1ux6a1		not modelled	11.0	23	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Thrombospondin C-terminal domain
84	c3fmcC		not modelled	9.9	13	PDB header: hydrolase Chain: C: PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
85	d1ddza1		not modelled	9.7	17	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
86	d1i6pa		not modelled	9.4	25	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
87	d1ekja		not modelled	9.0	25	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
88	d2gu2a1		not modelled	8.7	20	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like
89	c2w3nA		not modelled	8.6	17	PDB header: lyase Chain: A: PDB Molecule: carbonic anhydrase 2; PDBTitle: structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
90	c2a8cE		not modelled	8.5	33	PDB header: lyase Chain: E: PDB Molecule: carbonic anhydrase 2; PDBTitle: haemophilus influenzae beta-carbonic anhydrase
91	c3ucoB		not modelled	8.4	17	PDB header: lyase/lyase inhibitor Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: coccomyxa beta-carbonic anhydrase in complex with iodide
92	d1g8pa		not modelled	8.2	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
93	c1ylkA		not modelled	8.0	8	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein rv1284/mt1322; PDBTitle: crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
94	c3eyxB		not modelled	7.8	33	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase; PDBTitle: crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
95	c3ts3D		not modelled	7.7	20	PDB header: viral protein Chain: D: PDB Molecule: capsid polyprotein; PDBTitle: crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
96	d1g5ca		not modelled	7.7	25	Fold: Resolvase-like Superfamily: beta-carbonic anhydrase, cab Family: beta-carbonic anhydrase, cab
97	c2a5vB		not modelled	7.6	17	PDB header: lyase Chain: B: PDB Molecule: carbonic anhydrase (carbonate dehydratase) (carbonic PDBTitle: crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
98	c3ujcA		not modelled	7.3	36	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine n-methyltransferase; PDBTitle: phosphoethanolamine methyltransferase mutant (h132a) from plasmodium2 falciparum in complex with phosphocholine
99	c2gnoA		not modelled	7.2	19	PDB header: replication Chain: A: PDB Molecule: dna polymerase iii, gamma subunit-related protein; PDBTitle: crystal structure of a dna polymerase iii, gamma subunit-related2 protein (tm0771) from thermotoga maritima msb8 at 2.00 a resolution