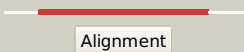

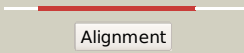

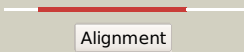
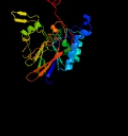
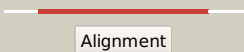

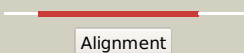

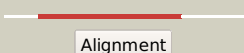

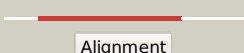





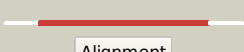

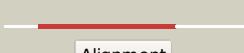












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1277_(-)_1426170_1427423
Date	Wed Jul 31 22:05:37 BST 2019
Unique Job ID	1747d0bcbb692ca1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ltyD_	 Alignment		100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: exonuclease subunit sbcd; PDBTitle: crystal structure of e.coli sbcd at 1.8 a resolution
2	c4fcxB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: dna repair protein rad32; PDBTitle: s.pombe mre11 apoenzym
3	c4ykeA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: mre11; PDBTitle: crystal structure of eukaryotic mre11 catalytic domain from chaetomium2 thermophilum
4	c3qg5D_	 Alignment		100.0	16	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
5	c2q8uA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease, putative; PDBTitle: crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
6	c4fbkB_	 Alignment		100.0	19	PDB header: hydrolase, protein binding Chain: B: PDB Molecule: dna repair and telomere maintenance protein nbs1,dna repair PDBTitle: crystal structure of a covalently fused nbs1-mre11 complex with one2 manganese ion per active site
7	c3t1iC_	 Alignment		100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: double-strand break repair protein mre11a; PDBTitle: crystal structure of human mre11: understanding tumorigenic mutations
8	c3av0A_	 Alignment		100.0	20	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11-rad50 bound to atp s
9	c3auzA_	 Alignment		100.0	21	PDB header: recombination Chain: A: PDB Molecule: dna double-strand break repair protein mre11; PDBTitle: crystal structure of mre11 with manganese
10	d1ii7a_	 Alignment		100.0	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DNA double-strand break repair nuclease
11	c3ib7A_	 Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805

12	d2yvta1	Alignment		99.9	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
13	d3d03a1	Alignment		99.9	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
14	c2xmoB	Alignment		99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: lmo2642 protein; PDBTitle: the crystal structure of lmo2642
15	d1usha2	Alignment		99.9	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
16	d1uf3a	Alignment		99.8	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TT1561-like
17	c3qfnA	Alignment		99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of streptococcal asymmetric ap4a hydrolase and 2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
18	d1s3la	Alignment		99.7	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
19	c1s3mA	Alignment		99.7	16	PDB header: phosphodiesterase Chain: A: PDB Molecule: hypothetical protein mj0936; PDBTitle: structural and functional characterization of a novel 2 archaeal phosphodiesterase
20	c5k8kA	Alignment		99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: udp-2,3-diacylglucosamine hydrolase; PDBTitle: structure of the haemophilus influenzae lpxh-lipid x complex
21	d1utea	Alignment	not modelled	99.7	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
22	d2hy1a1	Alignment	not modelled	99.7	20	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: GpdQ-like
23	c2hy1A	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: rv0805; PDBTitle: crystal structure of rv0805
24	c1qhWA	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: protein (purple acid phosphatase); PDBTitle: purple acid phosphatase from rat bone
25	d1qhwa	Alignment	not modelled	99.7	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
26	c5wlyA	Alignment	not modelled	99.7	17	PDB header: hydrolase Chain: A: PDB Molecule: udp-2,3-diacylglucosamine hydrolase; PDBTitle: e. coli lpxh- 8 mutations
27	d2nxfA1	Alignment	not modelled	99.6	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: ADPRibase-Mn-like
28	c5b4bB	Alignment	not modelled	99.6	17	PDB header: hydrolase Chain: B: PDB Molecule: udp-2,3-diacylglucosamine hydrolase; PDBTitle: crystal structure of lpxh with lipid x in spacegroup c2
29	c5xceB	Alignment	not modelled	99.6	16	PDB header: transport protein Chain: B: PDB Molecule: vacuolar protein sorting-associated protein 29;

						PDBTitle: crystal structure of wild type vps29 from entamoeba histolytica
30	c1su1A_	Alignment	not modelled	99.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yfce; PDBTitle: structural and biochemical characterization of yfce, a phosphoesterase2 from e. coli
31	d1su1a_	Alignment	not modelled	99.5	22	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
32	c6nvoA_	Alignment	not modelled	99.5	23	PDB header: dna binding protein Chain: A: PDB Molecule: nuclease mpe; PDBTitle: crystal structure of pseudomonas putida nuclease mpe
33	d1z2wa1	Alignment	not modelled	99.4	18	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
34	c3rl4A_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase mpped2; PDBTitle: rat metallophosphodiesterase mpped2 g252h mutant
35	c1oidA_	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: A: PDB Molecule: protein usha; PDBTitle: 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
36	c3rqzC_	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
37	d1xm7a_	Alignment	not modelled	99.4	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Hypothetical protein aq 1666
38	d2a22a1	Alignment	not modelled	99.3	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
39	c5w8mD_	Alignment	not modelled	99.3	20	PDB header: endocytosis Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 29; PDBTitle: crystal structure of chaetomium thermophilum vps29
40	d1nnwa_	Alignment	not modelled	99.3	10	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Phosphoesterase-related
41	c3tghA_	Alignment	not modelled	99.3	11	PDB header: cell invasion Chain: A: PDB Molecule: glideosome-associated protein 50; PDBTitle: gap50 the anchor in the inner membrane complex of plasmodium
42	c5ebbA_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: A: PDB Molecule: acid sphingomyelinase-like phosphodiesterase 3a; PDBTitle: structure of human sphingomyelinase phosphodiesterase like 3a2 (smpdl3a) with zn2+
43	d2z1aa2	Alignment	not modelled	99.2	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
44	c5karA_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: A: PDB Molecule: acid sphingomyelinase-like phosphodiesterase 3b; PDBTitle: murine acid sphingomyelinase-like phosphodiesterase 3b (smpdl3b)
45	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
46	c2kknA_	Alignment	not modelled	99.2	16	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
47	c5iheB_	Alignment	not modelled	99.2	14	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ii small subunit; PDBTitle: d-family dna polymerase - dp1 subunit (3'-5' proof-reading2 exonuclease)
48	d1xzw2	Alignment	not modelled	99.1	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
49	c3gveB_	Alignment	not modelled	99.1	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yfkn protein; PDBTitle: crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
50	d2qfra2	Alignment	not modelled	99.1	12	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Purple acid phosphatase-like
51	c3ivdA_	Alignment	not modelled	99.0	14	PDB header: hydrolase Chain: A: PDB Molecule: nucleotidase; PDBTitle: putative 5'-nucleotidase (c4898) from escherichia coli in complex with2 uridine
52	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
53	c3c9fB_	Alignment	not modelled	98.9	16	PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from candida albicans sc5314
54	d3ck2a1	Alignment	not modelled	98.9	17	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: YfcE-like
						PDB header: hydrolase

55	c2z1aA_	Alignment	not modelled	98.9	19	Chain: A: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
56	c5h7wB_	Alignment	not modelled	98.7	15	PDB header: hydrolase Chain: B: PDB Molecule: venom 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from venom of naja atra
57	c3zk4A_	Alignment	not modelled	98.7	10	PDB header: oxidoreductase Chain: A: PDB Molecule: diphosphonucleotide phosphatase 1; PDBTitle: structure of purple acid phosphatase ppd1 isolated from2 yellow lupin (lupinus luteus) seeds
58	c1kbpB_	Alignment	not modelled	98.7	11	PDB header: hydrolase (phosphoric monoester) Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: kidney bean purple acid phosphatase
59	c4h1sB_	Alignment	not modelled	98.6	15	PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of a truncated soluble form of human cd73 with ecto-2 5'-nucleotidase activity
60	c3jyfB_	Alignment	not modelled	98.6	17	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
61	c1xzwB_	Alignment	not modelled	98.5	12	PDB header: hydrolase Chain: B: PDB Molecule: purple acid phosphatase; PDBTitle: sweet potato purple acid phosphatase/phosphate complex
62	c3zu0A_	Alignment	not modelled	98.5	16	PDB header: hydrolase Chain: A: PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (naden)
63	c5ficD_	Alignment	not modelled	98.5	28	PDB header: hydrolase Chain: D: PDB Molecule: sphingomyelin phosphodiesterase; PDBTitle: open form of murine acid sphingomyelinase in presence of lipid
64	c4pehC_	Alignment	not modelled	98.5	19	PDB header: hydrolase/rna Chain: C: PDB Molecule: rna lariat debranching enzyme, putative; PDBTitle: dbr1 in complex with synthetic linear rna
65	d1t71a_	Alignment	not modelled	98.4	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
66	c6hv9B_	Alignment	not modelled	98.2	13	PDB header: dna binding protein Chain: B: PDB Molecule: dna polymerase epsilon subunit b; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
67	c4b2oB_	Alignment	not modelled	98.2	15	PDB header: hydrolase Chain: B: PDB Molecule: yymb phosphodiesterase; PDBTitle: crystal structure of bacillus subtilis yymb, a global2 regulator of late adaptive responses.
68	d1t70a_	Alignment	not modelled	98.1	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: DR1281-like
69	d2z06a1	Alignment	not modelled	98.1	19	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: TTHA0625-like
70	c3e0jG_	Alignment	not modelled	98.0	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
71	c2wdfA_	Alignment	not modelled	97.9	18	PDB header: hydrolase Chain: A: PDB Molecule: sulfur oxidation protein soxb; PDBTitle: thermus thermophilus sulfate thiohydrolase soxb
72	c5vbnE_	Alignment	not modelled	97.9	18	PDB header: transferase Chain: E: PDB Molecule: dna polymerase epsilon subunit 2; PDBTitle: crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit
73	d1g5ba_	Alignment	not modelled	97.7	16	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
74	c4j6oA_	Alignment	not modelled	97.6	24	PDB header: hydrolase Chain: A: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of the phosphatase domain of c. thermocellum2 (bacterial) pnkp
75	c3floG_	Alignment	not modelled	97.3	10	PDB header: transferase Chain: G: PDB Molecule: dna polymerase alpha subunit b; PDBTitle: crystal structure of the carboxyl-terminal domain of yeast dna2 polymerase alpha in complex with its b subunit
76	c4y97E_	Alignment	not modelled	97.2	14	PDB header: transferase Chain: E: PDB Molecule: dna polymerase alpha subunit b; PDBTitle: crystal structure of human pol alpha b-subunit in complex with c-2 terminal domain of catalytic subunit
77	c2qjcA_	Alignment	not modelled	97.1	25	PDB header: hydrolase Chain: A: PDB Molecule: diadenosine tetraphosphatase, putative; PDBTitle: crystal structure of a putative diadenosine tetraphosphatase
78	c2dfjA_	Alignment	not modelled	96.5	22	PDB header: hydrolase Chain: A: PDB Molecule: diadenosinetetraphosphatase; PDBTitle: crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
79	c5vjwA_	Alignment	not modelled	96.4	23	PDB header: hydrolase Chain: A: PDB Molecule: rhizobiales-like phosphatase 2; PDBTitle: arabidopsis thaliana rhizobiales-like phosphatase 2 complexed with2 tungstate
80	c2zbmA_	Alignment	not modelled	96.2	23	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase; PDBTitle: crystal structure of i115m mutant cold-active protein2

						tyrosine phosphatase
81	d1jk7a_	Alignment	not modelled	95.3	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
82	d3c5wc1	Alignment	not modelled	95.1	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
83	c5jpfA_	Alignment	not modelled	94.9	14	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine/threonine-protein phosphatase; PDBTitle: serine/threonine phosphatase z1 (candida albicans) binds to inhibitor2 microcystin-Ir
84	d1s70a_	Alignment	not modelled	94.6	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
85	d1s95a_	Alignment	not modelled	94.1	14	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
86	c2jogA_	Alignment	not modelled	94.0	15	PDB header: hydrolase Chain: A: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha PDBTitle: structure of the calcineurin-nfat complex
87	c5jttA_	Alignment	not modelled	93.7	19	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine-protein phosphatase 5; PDBTitle: crystal structure of a type 5 serine/threonine protein phosphatase2 from arabidopsis thaliana
88	c3icfB_	Alignment	not modelled	93.0	15	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
89	d1auia_	Alignment	not modelled	92.8	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
90	c1auia_	Alignment	not modelled	92.8	15	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine phosphatase 2b; PDBTitle: human calcineurin heterodimer
91	c1wao4_	Alignment	not modelled	92.4	13	PDB header: hydrolase Chain: 4: PDB Molecule: serine/threonine protein phosphatase 5; PDBTitle: pp5 structure
92	c2p6bC_	Alignment	not modelled	92.3	15	PDB header: hydrolase/hydrolase regulator Chain: C: PDB Molecule: calmodulin-dependent calcineurin a subunit alpha isoform; PDBTitle: crystal structure of human calcineurin in complex with pvitit peptide
93	d2p6ba1	Alignment	not modelled	92.3	15	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: Protein serine/threonine phosphatase
94	c4mm1E_	Alignment	not modelled	89.9	15	PDB header: transferase Chain: E: PDB Molecule: geranylgeranylglyceryl phosphate synthase; PDBTitle: gggps from methanothermobacter thermautotrophicus
95	d2vgna3	Alignment	not modelled	88.4	11	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
96	c2yeqA_	Alignment	not modelled	87.5	18	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase d; PDBTitle: structure of phod
97	c3menC_	Alignment	not modelled	86.5	14	PDB header: hydrolase Chain: C: PDB Molecule: acetyl/polyamine aminohydrolase; PDBTitle: crystal structure of acetyl/polyamine aminohydrolase from burkholderia2 pseudomallei, iodide soak
98	d1x52a1	Alignment	not modelled	85.5	9	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
99	c2vqmA_	Alignment	not modelled	84.7	11	PDB header: cell cycle Chain: A: PDB Molecule: dom34; PDBTitle: structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
100	c3obwA_	Alignment	not modelled	84.0	17	PDB header: hydrolase Chain: A: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
101	d1gsoa2	Alignment	not modelled	83.8	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
102	c3mcaB_	Alignment	not modelled	81.2	14	PDB header: translation regulation/hydrolase Chain: B: PDB Molecule: protein dom34; PDBTitle: structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
103	c3agjB_	Alignment	not modelled	79.5	15	PDB header: translation/hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
104	c3agjD_	Alignment	not modelled	79.1	15	PDB header: translation/hydrolase Chain: D: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
105	d1y5ea1	Alignment	not modelled	78.2	19	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
106	c3q9cF_	Alignment	not modelled	78.2	19	PDB header: hydrolase Chain: F: PDB Molecule: acetyl/polyamine amidohydrolase; PDBTitle: crystal structure of h159a apah complexed with n8-acetylspermidine

107	c3bleA_	Alignment	not modelled	77.8	15	PDB header: transferase Chain: A; PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
108	c3o3nB_	Alignment	not modelled	77.8	10	PDB header: lyase Chain: B; PDB Molecule: beta-subunit 2-hydroxyacyl-coa dehydratase; PDBTitle: (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
109	c4il1A_	Alignment	not modelled	76.5	15	PDB header: hydrolase Chain: A; PDB Molecule: calmodulin, calcineurin subunit b type 1, serine/threonine- PDBTitle: crystal structure of the rat calcineurin
110	c3maxB_	Alignment	not modelled	75.9	19	PDB header: hydrolase Chain: B; PDB Molecule: histone deacetylase 2; PDBTitle: crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide
111	d1t64a_	Alignment	not modelled	75.3	20	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC
112	c3ew8A_	Alignment	not modelled	74.7	20	PDB header: hydrolase Chain: A; PDB Molecule: histone deacetylase 8; PDBTitle: crystal structure analysis of human hdac8 d101l variant
113	d1y2ia_	Alignment	not modelled	74.7	25	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
114	c1y2iC_	Alignment	not modelled	74.7	25	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: hypothetical protein s0862; PDBTitle: crystal structure of mcsg target apc27401 from shigella flexneri
115	c3lmaC_	Alignment	not modelled	73.7	17	PDB header: membrane protein Chain: C; PDB Molecule: stage v sporulation protein ad (spovad); PDBTitle: crystal structure of the stage v sporulation protein ad (spovad) from2 bacillus licheniformis. northeast structural genomics consortium3 target bir6.
116	c2ftpA_	Alignment	not modelled	72.9	9	PDB header: lyase Chain: A; PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
117	c3ffsC_	Alignment	not modelled	72.7	15	PDB header: oxidoreductase Chain: C; PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
118	c4a69A_	Alignment	not modelled	72.6	17	PDB header: transcription Chain: A; PDB Molecule: histone deacetylase 3,; PDBTitle: structure of hdac3 bound to corepressor and inositol tetraphosphate
119	d3bula2	Alignment	not modelled	72.4	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
120	d1vr4a1	Alignment	not modelled	71.4	28	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like