


Phyre2

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Description	RVBD2918c_glnD_3228264_3230690
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1v4aA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: glutamate-ammonia-ligase adenyllyltransferase; PDBTitle: structure of the n-terminal domain of escherichia coli2 glutamine synthetase adenyllyltransferase
2	c3wfpB_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
3	c3wfpA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
4	c3wfrH_	 Alignment		100.0	24	PDB header: transferase/rna Chain: H: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
5	c3wfsD_	 Alignment		100.0	21	PDB header: transferase/rna Chain: D: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 3
6	c3wfrG_	 Alignment		100.0	23	PDB header: transferase/rna Chain: G: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
7	c3wfrF_	 Alignment		100.0	24	PDB header: transferase/rna Chain: F: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
8	c3wfrE_	 Alignment		100.0	24	PDB header: transferase/rna Chain: E: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
9	c3wfgE_	 Alignment		100.0	22	PDB header: transferase/rna Chain: E: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
10	c3wfsC_	 Alignment		100.0	23	PDB header: transferase/rna Chain: C: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 3
11	c3wfgH_	 Alignment		100.0	22	PDB header: transferase/rna Chain: H: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1

12	c3wfgG_	Alignment		100.0	24	PDB header: transferase/rna Chain: G: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
13	c3wfoB_	Alignment		100.0	23	PDB header: transferase Chain: B: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 1)
14	c3k7dA_	Alignment		100.0	23	PDB header: transferase Chain: A: PDB Molecule: glutamate-ammonia-ligase adenyltransferase; PDBTitle: c-terminal (adenylation) domain of e.coli glutamine synthetase2 adenylyltransferase
15	c3aqaA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: poly(a) polymerase; PDBTitle: complex structure of bacterial protein (apo form ii)
16	d1v4aa2	Alignment		99.9	24	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: GlnE-like domain
17	c1miyB_	Alignment		99.8	15	PDB header: translation, transferase Chain: B: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of bacillus stearotherophilus cca- adding enzyme in2 complex with ctp
18	d1vfga1	Alignment		99.7	14	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like Family: Poly A polymerase C-terminal region-like
19	c1vfgB_	Alignment		99.7	13	PDB header: transferase/rna Chain: B: PDB Molecule: poly a polymerase; PDBTitle: crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
20	c2nyiB_	Alignment		99.7	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
21	c3h37B_	Alignment	not modelled	99.7	17	PDB header: transferase Chain: B: PDB Molecule: trna nucleotidyl transferase-related protein; PDBTitle: the structure of cca-adding enzyme apo form i
22	c1u8sB_	Alignment	not modelled	99.7	10	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
23	d1miwa1	Alignment	not modelled	99.7	16	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like Family: Poly A polymerase C-terminal region-like
24	d1v4aa1	Alignment	not modelled	99.6	18	Fold: Four-helical up-and-down bundle Superfamily: Nucleotidyltransferase substrate binding subunit/domain Family: Glutamine synthase adenylyltransferase GlnE, domain 2
25	c4x4wB_	Alignment	not modelled	99.6	15	PDB header: rna binding protein Chain: B: PDB Molecule: cca trna nucleotidyltransferase 1, mitochondrial; PDBTitle: crystal structure of the full-length human mitochondrial cca-adding2 enzyme
26	c6q52A_	Alignment	not modelled	99.6	15	PDB header: rna binding protein Chain: A: PDB Molecule: cca-adding enzyme; PDBTitle: structure of a psychrophilic cca-adding enzyme in complex with cmpcpp2 at room temperature in chipx microfluidic device
27	c1ou5A_	Alignment	not modelled	99.6	15	PDB header: translation, transferase Chain: A: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of human cca-adding enzyme
28	d1ou5a1	Alignment	not modelled	99.5	16	Fold: Poly A polymerase C-terminal region-like Superfamily: Poly A polymerase C-terminal region-like Family: Poly A polymerase C-terminal region-like

29	d2pq7a1	Alignment	not modelled	98.8	24	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
30	c5ihyB	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of bacillus subtilis semet-yppq
31	d2qgsa1	Alignment	not modelled	98.6	20	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
32	c4n71A	Alignment	not modelled	98.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: predicted hd phosphohydrolase phnz; PDBTitle: x-ray crystal structure of 2-amino-1-hydroxyethylphosphonate-bound2 phnz
33	d3djba1	Alignment	not modelled	98.3	15	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
34	d3b57a1	Alignment	not modelled	98.1	14	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
35	c2f06B	Alignment	not modelled	98.1	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
36	c2q14A	Alignment	not modelled	97.9	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase; PDBTitle: crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
37	c3ibwA	Alignment	not modelled	97.9	12	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp pyrophosphokinase of2 chlorobium tepidum. northeast structural genomics consortium target3 ctr148a
38	c2o08B	Alignment	not modelled	97.8	26	PDB header: hydrolase Chain: B: PDB Molecule: bh1327 protein; PDBTitle: crystal structure of a putative hd superfamily hydrolase (bh1327) from2 bacillus halodurans at 1.90 a resolution
39	c2dqB	Alignment	not modelled	97.8	22	PDB header: hydrolase, dna binding protein Chain: B: PDB Molecule: deoxyguanosinetriphosphate triphosphohydrolase, putative; PDBTitle: crystal structure of dntp triphosphohydrolase from thermus2 thermophilus hb8, which is homologous to dgtp triphosphohydrolase
40	c2ogiA	Alignment	not modelled	97.8	29	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein sag1661; PDBTitle: crystal structure of a putative metal dependent phosphohydrolase2 (sag1661) from streptococcus agalactiae serogroup v at 1.85 a3 resolution
41	d3dtoa1	Alignment	not modelled	97.8	14	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
42	c6npaD	Alignment	not modelled	97.8	26	PDB header: oxidoreductase Chain: D: PDB Molecule: tmbp, (r)-1-hydroxy-2-trimethylaminoethylphosphonate PDBTitle: x-ray crystal structure of tmbp, (r)-1-hydroxy-2-2-trimethylaminoethylphosphonate oxygenase, with (r)-1-hydroxy-2-3-trimethylaminoethylphosphonate
43	c3gw7A	Alignment	not modelled	97.8	13	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein yedj; PDBTitle: crystal structure of a metal-dependent phosphohydrolase with conserved2 hd domain (yedj) from escherichia coli in complex with nickel ions.3 northeast structural genomics consortium target er63
44	d1u8sa2	Alignment	not modelled	97.7	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
45	d2heka1	Alignment	not modelled	97.7	20	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
46	c4bzbB	Alignment	not modelled	97.7	14	PDB header: hydrolase Chain: B: PDB Molecule: deoxynucleoside triphosphate triphosphohydrolase samhd1; PDBTitle: crystal structure of the tetrameric dgtp-bound samhd12 mutant catalytic core
47	c3m5fA	Alignment	not modelled	97.7	20	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent phosphohydrolase; PDBTitle: structure of mj0384, a cas3 protein from methanocaldococcus jannaschii
48	d1u8sa1	Alignment	not modelled	97.6	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
49	c3ccgA	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: A: PDB Molecule: hd superfamily hydrolase; PDBTitle: crystal structure of predicted hd superfamily hydrolase involved in2 nad metabolism (np_347894.1) from clostridium acetobutylicum at 1.503 a resolution
50	d1zpa1	Alignment	not modelled	97.5	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
51	c3skdA	Alignment	not modelled	97.5	24	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein tthb187; PDBTitle: crystal structure of the thermus thermophilus cas3 hd domain in the2 presence of ni2+
52	c4s1cA	Alignment	not modelled	97.4	28	PDB header: hydrolase Chain: A: PDB Molecule: lmo1466 protein; PDBTitle: crystal structure of l. monocytogenes phosphodiesterase pph hd domain

53	c3u1nC	Alignment	not modelled	97.4	18	PDB header: hydrolase Chain: C: PDB Molecule: sam domain and hd domain-containing protein 1; PDBTitle: structure of the catalytic core of human samhd1
54	c5ao4D	Alignment	not modelled	97.3	18	PDB header: hydrolase Chain: D: PDB Molecule: deoxynucleoside triphosphate triphosphohydrolase samhd1; PDBTitle: crystal structure of in vitro phosphorylated human samhd1 (amino acid2 residues 115-626) bound to gtp
55	d1u6za1	Alignment	not modelled	97.3	17	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: Ppx associated domain
56	c6dk9I	Alignment	not modelled	97.3	19	PDB header: lyase Chain: I: PDB Molecule: dna damage-inducible protein; PDBTitle: yeast ddi2 cyanamide hydratase
57	d2pjqa1	Alignment	not modelled	97.3	18	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
58	c3memA	Alignment	not modelled	97.3	20	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein; PDBTitle: crystal structure of a putative signal transduction protein2 (maqu_0641) from marinobacter aquaeolei vt8 at 2.25 a resolution
59	c6brhA	Alignment	not modelled	97.3	19	PDB header: hydrolase Chain: A: PDB Molecule: deoxynucleoside triphosphate triphosphohydrolase samhd1; PDBTitle: the sam domain of mouse samhd1 is critical for its activation and2 regulation
60	c3m1tA	Alignment	not modelled	97.2	18	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphohydrolase; PDBTitle: crystal structure of putative phosphohydrolase (yp_929327.1) from2 shewanella amazonensis sb2b at 1.62 a resolution
61	c2o6iA	Alignment	not modelled	97.2	21	PDB header: hydrolase Chain: A: PDB Molecule: hd domain protein; PDBTitle: structure of an enterococcus faecalis hd domain phosphohydrolase
62	d2o6ia1	Alignment	not modelled	97.2	21	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
63	d1knya2	Alignment	not modelled	97.2	14	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
64	c3hc1A	Alignment	not modelled	97.2	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized hhd domain protein; PDBTitle: crystal structure of hhd domain protein with unknown function2 (np_953345.1) from geobacter sulfurreducens at 1.90 a resolution
65	d1vqra	Alignment	not modelled	97.2	25	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: modified HD domain
66	c4r8zB	Alignment	not modelled	97.1	31	PDB header: hydrolase Chain: B: PDB Molecule: cyclic di-gmp phosphodiesterase; PDBTitle: crystal structure of pa4781 hd-gyp domain from pseudomonas aeruginosa2 at 2.2a resolution showing a bi-metallic ni ion center
67	c3p96A	Alignment	not modelled	97.1	14	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
68	c6iqwA	Alignment	not modelled	97.0	32	PDB header: rna binding protein/rna Chain: A: PDB Molecule: csm1; PDBTitle: cryo-em structure of csm effector complex
69	d2gz4a1	Alignment	not modelled	97.0	19	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
70	c3n0vD	Alignment	not modelled	96.9	10	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
71	c3ljvA	Alignment	not modelled	96.9	19	PDB header: transcription Chain: A: PDB Molecule: mmoq response regulator; PDBTitle: crystal structure of mmoq response regulator (fragment 29-302) from2 methylococcus capsulatus str. bath, northeast structural genomics3 consortium target mcr175m
72	c4q2dA	Alignment	not modelled	96.9	28	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated helicase cas3; PDBTitle: crystal structure of crispr-associated protein in complex with 2'-2 deoxyadenosine 5'-triphosphate
73	c3bg2A	Alignment	not modelled	96.9	28	PDB header: hydrolase Chain: A: PDB Molecule: dgtp triphosphohydrolase; PDBTitle: crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
74	c6ifnA	Alignment	not modelled	96.9	37	PDB header: rna binding protein Chain: A: PDB Molecule: type iii-a crispr-associated protein csm1; PDBTitle: crystal structure of type iii-a crispr csm complex
75	d1vgya3	Alignment	not modelled	96.9	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
76	c2floA	Alignment	not modelled	96.9	17	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
77	c4qqxA	Alignment	not modelled	96.8	26	PDB header: hydrolase/dna Chain: A: PDB Molecule: crispr-associated helicase, cas3 family; PDBTitle: crystal structure of t. fusca cas3-atp

78	c1xozA	Alignment	not modelled	96.8	19	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-specific 3',5'-cyclic phosphodiesterase; PDBTitle: catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil
79	d1tbfa	Alignment	not modelled	96.8	18	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
80	d1sc6a3	Alignment	not modelled	96.7	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
81	c3v94F	Alignment	not modelled	96.7	14	PDB header: hydrolase/hydrolase inhibitor Chain: F: PDB Molecule: cyclic nucleotide specific phosphodiesterase; PDBTitle: tcrpdec1 catalytic domain in complex with inhibitor wyq16
82	c3w7bB	Alignment	not modelled	96.7	14	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
83	c3o1lB	Alignment	not modelled	96.6	16	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
84	c3i7aA	Alignment	not modelled	96.6	22	PDB header: hydrolase Chain: A: PDB Molecule: putative metal-dependent phosphohydrolase; PDBTitle: crystal structure of putative metal-dependent phosphohydrolase2 (yp_926882.1) from shewanella amazonensis sb2b at 2.06 a resolution
85	c3obiC	Alignment	not modelled	96.6	18	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodospseudomonas palustris cga009 at 1.95 a resolution
86	c3louB	Alignment	not modelled	96.5	17	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
87	c2pgsA	Alignment	not modelled	96.5	29	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyguanosinetriphosphate triphosphohydrolase; PDBTitle: crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
88	c4uw2A	Alignment	not modelled	96.4	40	PDB header: immune system Chain: A: PDB Molecule: csm1; PDBTitle: crystal structure of csm1 in t.onnurineus
89	c1knyA	Alignment	not modelled	96.4	23	PDB header: transferase Chain: A: PDB Molecule: kanamycin nucleotidyltransferase; PDBTitle: kanamycin nucleotidyltransferase
90	c3nrB	Alignment	not modelled	96.4	13	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
91	c5z7cA	Alignment	not modelled	96.3	20	PDB header: metal binding protein Chain: A: PDB Molecule: 3'3'-cgamp-specific phosphodiesterase 3; PDBTitle: crystal structure of cyclic gmp-amp specific phosphodiesterases in2 v.cholerae (v-cgap3)
92	c5b7iA	Alignment	not modelled	96.3	32	PDB header: hydrolase/unknown function Chain: A: PDB Molecule: crispr-associated nuclease/helicase cas3 subtype i-f/ypest; PDBTitle: cas3-acrf3 complex
93	c4xdsE	Alignment	not modelled	96.2	22	PDB header: hydrolase/dna Chain: E: PDB Molecule: deoxyguanosinetriphosphate triphosphohydrolase; PDBTitle: deoxyguanosinetriphosphate triphosphohydrolase from escherichia coli2 with nickel
94	c1zklA	Alignment	not modelled	96.1	14	PDB header: hydrolase Chain: A: PDB Molecule: high-affinity camp-specific 3',5'-cyclic nucleotide phosphodiesterases PDBTitle: multiple determinants for inhibitor selectivity of cyclic2 nucleotide phosphodiesterases
95	d1taza	Alignment	not modelled	96.1	20	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
96	c2lvwA	Alignment	not modelled	96.0	15	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme 1 small subunit; PDBTitle: solution nmr studies of the dimeric regulatory subunit ilvn of the2 e.coli acetohydroxyacid synthase i (ahas i)
97	c4mcwA	Alignment	not modelled	95.9	27	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent phosphohydrolase; PDBTitle: metallo-enzyme from p. marina
98	c3ibjB	Alignment	not modelled	95.8	12	PDB header: hydrolase Chain: B: PDB Molecule: cgmp-dependent 3',5'-cyclic phosphodiesterase; PDBTitle: x-ray structure of pde2a
99	d2f06a1	Alignment	not modelled	95.7	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
100	c1xotB	Alignment	not modelled	95.5	14	PDB header: hydrolase Chain: B: PDB Molecule: camp-specific 3',5'-cyclic phosphodiesterase 4b; PDBTitle: catalytic domain of human phosphodiesterase 4b in complex with2 vardenafil Fold: HD-domain/PDEase-like

101	d1f0ja_	Alignment	not modelled	95.5	15	Superfamily: HD-domain/PDEase-like Family: PDEase
102	c3g3nA_	Alignment	not modelled	95.5	12	PDB header: hydrolase Chain: A: PDB Molecule: high affinity camp-specific 3',5'-cyclic PDBTitle: pde7a catalytic domain in complex with 3-(2,6-2 difluorophenyl)-2-(methylthio)quinazolin-4(3h)-one
103	c4cs6A_	Alignment	not modelled	95.4	17	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside adenylyltransferase; PDBTitle: crystal structure of aada - an aminoglycoside adenylyltransferase
104	d2h44a1	Alignment	not modelled	95.4	18	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
105	d1so2a_	Alignment	not modelled	95.4	16	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
106	d2f1fa1	Alignment	not modelled	95.3	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
107	c3hi0B_	Alignment	not modelled	95.3	17	PDB header: hydrolase Chain: B: PDB Molecule: putative exopolyphosphatase; PDBTitle: crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
108	d2f06a2	Alignment	not modelled	95.3	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
109	d2pc6a2	Alignment	not modelled	95.2	20	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
110	d1y2ka1	Alignment	not modelled	95.2	16	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
111	c2rffA_	Alignment	not modelled	95.2	20	PDB header: transferase Chain: A: PDB Molecule: putative nucleotidyltransferase; PDBTitle: crystal structure of a putative nucleotidyltransferase (np_343093.1)2 from sulfobolus solfataricus at 1.40 a resolution
112	d2fgca2	Alignment	not modelled	95.1	18	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
113	c2r8qA_	Alignment	not modelled	95.0	20	PDB header: hydrolase Chain: A: PDB Molecule: class i phosphodiesterase pdeb1; PDBTitle: structure of lmpjdeb1 in complex with ibmx
114	c4i15B_	Alignment	not modelled	95.0	19	PDB header: hydrolase Chain: B: PDB Molecule: class 1 phosphodiesterase pdeb1; PDBTitle: crystal structure of tbrpdeb1
115	c5vydB_	Alignment	not modelled	94.9	22	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase; PDBTitle: crystal structure of phosphodiesterase domain of rhophe fusion protein2 from the choanoflagellate salpingoeca rosetta
116	c5uscB_	Alignment	not modelled	94.9	19	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
117	c3qi4A_	Alignment	not modelled	94.9	13	PDB header: hydrolase Chain: A: PDB Molecule: high affinity cgmp-specific 3',5'-cyclic phosphodiesterase PDBTitle: crystal structure of pde9a(q453e) in complex with ibmx
118	c6dzsD_	Alignment	not modelled	94.8	27	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
119	c2pc6C_	Alignment	not modelled	94.7	21	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
120	c6mzbA_	Alignment	not modelled	94.7	14	PDB header: signaling protein Chain: A: PDB Molecule: rod cgmp-specific 3',5'-cyclic phosphodiesterase subunit PDBTitle: cryo-em structure of phosphodiesterase 6