







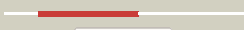






























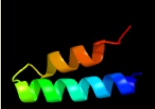

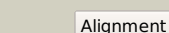








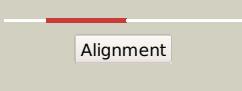
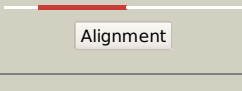
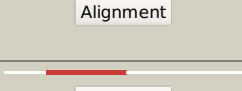
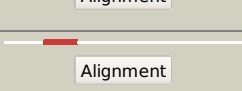
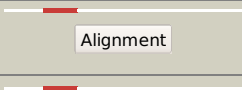
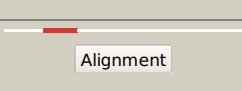
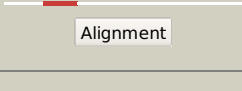
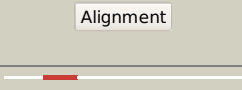
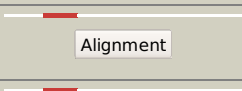
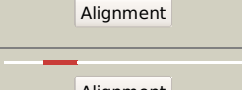
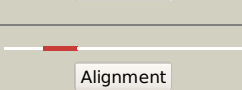
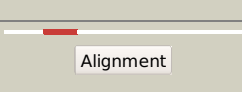
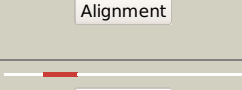
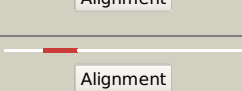
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2344c_(dgt)_2622467_2623762
Date	Mon Aug 5 13:25:49 BST 2019
Unique Job ID	7ce96df01cede2a1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4xdsE_	 Alignment		100.0	25	PDB header: hydrolase/dna Chain: E: PDB Molecule: deoxyguanosinetriphosphate triphosphohydrolase; PDBTitle: deoxyguanosinetriphosphate triphosphohydrolase from escherichia coli2 with nickel
2	c3bg2A_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: dgtp triphosphohydrolase; PDBTitle: crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
3	c2pgsA_	 Alignment		100.0	31	PDB header: hydrolase Chain: A: PDB Molecule: putative deoxyguanosinetriphosphate triphosphohydrolase; PDBTitle: crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
4	c2dqbB_	 Alignment		100.0	34	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
5	d2heka1	 Alignment		100.0	17	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
6	c5ao4D_	 Alignment		100.0	15	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
7	c2q14A_	 Alignment		99.7	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphohydrolase; PDBTitle: crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
8	d2o6ia1	 Alignment		99.7	33	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
9	c2o6iA_	 Alignment		99.7	33	PDB header: hydrolase Chain: A: PDB Molecule: hd domain protein; PDBTitle: structure of an enterococcus faecalis hd domain phosphohydrolase
10	c3u1nC_	 Alignment		99.7	26	PDB header: hydrolase Chain: C: PDB Molecule: sam domain and hd domain-containing protein 1; PDBTitle: structure of the catalytic core of human samhd1
11	c4bzbB_	 Alignment		99.7	24	PDB header: hydrolase Chain: B: PDB Molecule: deoxynucleoside triphosphate triphosphohydrolase samhd1; PDBTitle: crystal structure of the tetrameric dgtp-bound samhd12 mutant catalytic core

12	c6brhA	 Alignment		99.5	26	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
13	c4s1cA	 Alignment		99.2	15	PDB header: hydrolase Chain: A: PDB Molecule: lmo1466 protein; PDBTitle: crystal structure of l. monocytogenes phosphodiesterase pph hd domain
14	c5ihyB	 Alignment		98.6	25	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of bacillus subtilis semet-ypgq
15	c3gw7A	 Alignment		98.6	16	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
16	c2o08B	 Alignment		98.4	18	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
17	d2pq7a1	 Alignment		98.3	19	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
18	c3ccgA	 Alignment		98.3	23	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
19	d2qgsa1	 Alignment		98.3	18	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
20	c2ogiA	 Alignment		98.1	33	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
21	c3m1tA	 Alignment	not modelled	97.8	20	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
22	d3djba1	 Alignment	not modelled	97.7	17	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
23	d3b57a1	 Alignment	not modelled	97.6	28	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
24	d2pjqa1	 Alignment	not modelled	97.5	21	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
25	c6npaD	 Alignment	not modelled	97.5	29	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
26	d3dtoa1	 Alignment	not modelled	97.4	19	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
27	c5z7cA	 Alignment	not modelled	97.3	16	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)
28	c4n71A	 Alignment	not modelled	96.9	42	PDB header: oxidoreductase Chain: A: PDB Molecule: predicted hd phosphohydrolase phnz; PDBTitle: x-ray crystal structure of 2-amino-1-hydroxyethylphosphonate-bound2 phnz

29	c3hc1A	 Alignment	not modelled	96.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized hdod domain protein; PDBTitle: crystal structure of hdod domain protein with unknown function2 (np_953345.1) from geobacter sulfurreducens at 1.90 a resolution
30	c3memA	 Alignment	not modelled	96.2	19	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
31	c3i7aA	 Alignment	not modelled	95.9	17	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
32	c3skdA	 Alignment	not modelled	95.5	29	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+
33	c4r8zB	 Alignment	not modelled	95.1	33	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
34	d1vqra	 Alignment	not modelled	95.0	14	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: modified HD domain
35	c4mcwA	 Alignment	not modelled	94.9	42	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent phosphohydrolase; PDBTitle: metallo-enzyme from p. marina
36	d3dy8a1	 Alignment	not modelled	94.7	31	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
37	c3qi4A	 Alignment	not modelled	94.5	31	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
38	c2r8gA	 Alignment	not modelled	94.5	25	PDB header: hydrolase Chain: A: PDB Molecule: class i phosphodiesterase pdeb1; PDBTitle: structure of lmpdeb1 in complex with ibmx
39	d1ynba1	 Alignment	not modelled	94.4	27	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
40	c2o8hA	 Alignment	not modelled	94.4	24	PDB header: hydrolase Chain: A: PDB Molecule: phosphodiesterase-10a; PDBTitle: crystal structure of the catalytic domain of rat phosphodiesterase 10a
41	c1xozA	 Alignment	not modelled	94.4	33	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-specific 3',5'-cyclic phosphodiesterase; PDBTitle: catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil
42	d1tbfA	 Alignment	not modelled	94.4	33	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
43	c4i15B	 Alignment	not modelled	94.3	25	PDB header: hydrolase Chain: B: PDB Molecule: class 1 phosphodiesterase pdeb1; PDBTitle: crystal structure of tbrpdeb1
44	d1y2ka1	 Alignment	not modelled	94.2	28	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
45	c2ounA	 Alignment	not modelled	94.2	25	PDB header: hydrolase Chain: A: PDB Molecule: camp and camp-inhibited cgmp 3',5'-cyclic PDBTitle: crystal structure of pde10a2 in complex with amp
46	c2cqzA	 Alignment	not modelled	94.2	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 177aa long hypothetical protein; PDBTitle: crystal structure of ph0347 protein from pyrococcus horikoshii ot3
47	c1z1lA	 Alignment	not modelled	94.1	19	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-dependent 3',5'-cyclic phosphodiesterase; PDBTitle: the crystal structure of the phosphodiesterase 2a catalytic2 domain
48	d2h44a1	 Alignment	not modelled	94.1	29	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
49	d1f0ja	 Alignment	not modelled	94.0	32	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
50	c1xotB	Alignment	not modelled	93.9	33	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
51	c3ibjB	Alignment	not modelled	93.7	19	PDB header: hydrolase Chain: B: PDB Molecule: cgmp-dependent 3',5'-cyclic phosphodiesterase; PDBTitle: x-ray structure of pde2a
52	c5vydB	Alignment	not modelled	93.6	22	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase; PDBTitle: crystal structure of phosphodiesterase domain of rhopde fusion protein2 from the choanoflagellate salpingoeca rosetta
53	c3bjcA	Alignment	not modelled	93.5	29	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-specific 3',5'-cyclic phosphodiesterase;

						PDBTitle: crystal structure of the pde5a catalytic domain in complex2 with a novel inhibitor
54	c3v94F_	Alignment	not modelled	93.5	25	PDB header: hydrolase/hydrolase inhibitor Chain: F: PDB Molecule: cyclic nucleotide specific phosphodiesterase; PDBTitle: tcrpdec1 catalytic domain in complex with inhibitor wyq16
55	c3mzoA_	Alignment	not modelled	93.4	21	PDB header: hydrolase Chain: A: PDB Molecule: lin2634 protein; PDBTitle: crystal structure of a hd-domain phosphohydrolase (lin2634) from <i>Listeria innocua</i> at 1.98 Å resolution
56	c6ezuA_	Alignment	not modelled	93.4	33	PDB header: hydrolase Chain: A: PDB Molecule: phosphodiesterase; PDBTitle: schistosoma mansoni phosphodiesterase 4a
57	c6cpuA_	Alignment	not modelled	93.3	36	PDB header: hydrolase Chain: A: PDB Molecule: phosphodiesterase; PDBTitle: crystal structure of yeast capde2
58	c3ecmA_	Alignment	not modelled	93.3	28	PDB header: hydrolase Chain: A: PDB Molecule: high affinity camp-specific and ibmx-insensitive PDBTitle: crystal structure of the unliganded pde8a catalytic domain
59	d2paga1	Alignment	not modelled	93.1	27	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
60	c3ljvA_	Alignment	not modelled	93.0	17	PDB header: transcription Chain: A: PDB Molecule: mmoq response regulator; PDBTitle: crystal structure of mmoq response regulator (fragment 29-302) from <i>Methylococcus capsulatus</i> str. bath, northeast structural genomics3 consortium target mcr175m
61	c1zkaA_	Alignment	not modelled	92.8	28	PDB header: hydrolase Chain: A: PDB Molecule: high-affinity camp-specific 3',5'-cyclic PDBTitle: multiple determinants for inhibitor selectivity of cyclic2 nucleotide phosphodiesterases
62	c6mzbA_	Alignment	not modelled	92.8	26	PDB header: signaling protein Chain: A: PDB Molecule: rod cgmp-specific 3',5'-cyclic phosphodiesterase subunit PDBTitle: cryo-em structure of phosphodiesterase 6
63	c3g3nA_	Alignment	not modelled	92.7	28	PDB header: hydrolase Chain: A: PDB Molecule: high affinity camp-specific 3',5'-cyclic PDBTitle: pde7a catalytic domain in complex with 3-(2,6-difluorophenyl)-2-(methylthio)quinazolin-4(3h)-one
64	c4x0fA_	Alignment	not modelled	92.5	33	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: camp-specific 3',5'-cyclic phosphodiesterase 4b; PDBTitle: crystal structure of crosslink stabilized long-form pde4b in complex2 with (r)-(-)-rolipram
65	c3g45B_	Alignment	not modelled	92.4	33	PDB header: hydrolase Chain: B: PDB Molecule: camp-specific 3',5'-cyclic phosphodiesterase 4b; PDBTitle: crystal structure of human phosphodiesterase 4b with regulatory domain2 and d155988
66	c6dk9I_	Alignment	not modelled	92.3	31	PDB header: lyase Chain: I: PDB Molecule: dna damage-inducible protein; PDBTitle: yeast ddi2 cyanamide hydratase
67	c3kq5A_	Alignment	not modelled	91.4	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical cytosolic protein; PDBTitle: crystal structure of an uncharacterized protein from <i>Coxiella burnetii</i>
68	d1taza_	Alignment	not modelled	91.1	22	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
69	d1so2a_	Alignment	not modelled	91.0	31	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
70	c5tkaA_	Alignment	not modelled	90.8	26	PDB header: metal binding protein Chain: A: PDB Molecule: oxsa protein; PDBTitle: structure of the hd-domain phosphohydrolase oxsa
71	d1xx7a_	Alignment	not modelled	90.7	33	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
72	c4q2dA_	Alignment	not modelled	90.4	27	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	c4qqxA_	Alignment	not modelled	89.2	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: crispr-associated helicase, cas3 family; PDBTitle: crystal structure of <i>T. fusca</i> cas3-atp
74	c4yf1D_	Alignment	not modelled	88.9	46	PDB header: hydrolase Chain: D: PDB Molecule: lmo0812 protein; PDBTitle: 1.85 Å crystal structure of lmo0812 from <i>Listeria monocytogenes</i> 2 egd-e
75	c3kh1B_	Alignment	not modelled	88.6	27	PDB header: hydrolase Chain: B: PDB Molecule: predicted metal-dependent phosphohydrolase; PDBTitle: crystal structure of predicted metal-dependent phosphohydrolase2 (zp_00055740.2) from <i>Magnetospirillum magnetotacticum</i> ms-1 at 1.37 Å resolution
76	c2floA_	Alignment	not modelled	86.3	13	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from <i>E. coli</i> o157:h7
77	d1u6za1	Alignment	not modelled	86.2	15	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: Ppx associated domain
						PDB header: immune system Chain: A: PDB Molecule: hd domain-containing protein 2;

78	c4dmbA_	Alignment	not modelled	86.0	19	PDBTitle: x-ray structure of human hepatitis c virus ns5a-transactivated protein2 2 at the resolution 1.9a, northeast structural genomics consortium3 (nesg) target hr6723
79	c3wfrH_	Alignment	not modelled	85.4	34	PDB header: transferase/rna Chain: H: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
80	c3hi0B_	Alignment	not modelled	84.7	26	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
81	c3wfrE_	Alignment	not modelled	84.2	28	PDB header: transferase/rna Chain: E: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
82	c3wfpB_	Alignment	not modelled	83.7	34	PDB header: transferase Chain: B: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
83	c5xnxB_	Alignment	not modelled	83.0	45	PDB header: hydrolase, transferase Chain: B: PDB Molecule: bifunctional (p)ppgpp synthase/hydrolase rela; PDBTitle: crystallographic structure of the enzymatically active n-terminal2 domain of the rel protein from mycobacterium tuberculosis
84	c3wfpA_	Alignment	not modelled	82.4	34	PDB header: transferase Chain: A: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
85	d1vj7a1	Alignment	not modelled	80.5	34	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
86	c3wfgH_	Alignment	not modelled	78.6	34	PDB header: transferase/rna Chain: H: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
87	c5yoxB_	Alignment	not modelled	73.2	16	PDB header: lyase Chain: B: PDB Molecule: hd domain-containing protein ygl101w; PDBTitle: hd domain-containing protein ygk1(ygl101w)
88	c3wfoB_	Alignment	not modelled	72.4	22	PDB header: transferase Chain: B: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 1)
89	c3wfgG_	Alignment	not modelled	71.1	34	PDB header: transferase/rna Chain: G: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
90	d2gz4a1	Alignment	not modelled	70.9	30	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
91	c1vj7B_	Alignment	not modelled	69.3	34	PDB header: hydrolase, transferase Chain: B: PDB Molecule: bifunctional rela/spot; PDBTitle: crystal structure of the bifunctional catalytic fragment of relseq,2 the rela/spot homolog from streptococcus equisimilis.
92	c3nqwB_	Alignment	not modelled	68.5	29	PDB header: hydrolase Chain: B: PDB Molecule: cg11900; PDBTitle: a metazoan ortholog of spot hydrolyzes pppp and plays a role in2 starvation responses
93	c3wfrF_	Alignment	not modelled	65.3	32	PDB header: transferase/rna Chain: F: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
94	c3m5fA_	Alignment	not modelled	58.0	30	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent phosphohydrolase; PDBTitle: structure of mj0384, a cas3 protein from methanocaldococcus jannaschii
95	c3wfsC_	Alignment	not modelled	54.4	18	PDB header: transferase/rna Chain: C: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 3
96	d1dwka1	Alignment	not modelled	53.1	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
97	c3nr1A_	Alignment	not modelled	50.0	32	PDB header: hydrolase Chain: A: PDB Molecule: hd domain-containing protein 3; PDBTitle: a metazoan ortholog of spot hydrolyzes pppp and plays a role in2 starvation responses
98	c2iv1J_	Alignment	not modelled	49.4	21	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
99	c3aqnA_	Alignment	not modelled	44.6	9	PDB header: transferase Chain: A: PDB Molecule: poly(a) polymerase; PDBTitle: complex structure of bacterial protein (apo form ii)
100	d2ar0a1	Alignment	not modelled	42.1	43	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like
101	c2zxqA_	Alignment	not modelled	40.6	56	PDB header: hydrolase Chain: A: PDB Molecule: endo-alpha-n-acetylgalactosaminidase; PDBTitle: crystal structure of endo-alpha-n-acetylgalactosaminidase2 from bifidobacterium longum (engbf)
102	c5b7iA_	Alignment	not modelled	38.9	58	PDB header: hydrolase/unknown function Chain: A: PDB Molecule: crispr-associated nuclease/helicase cas3 subtype i-f/ypest; PDBTitle: cas3-acrf3 complex
103	c3eccA_	Alignment	not modelled	37.8	44	PDB header: hydrolase Chain: A: PDB Molecule: endo-alpha-n-acetylgalactosaminidase; PDBTitle: endo-alpha-n-acetylgalactosaminidase from streptococcus pneumoniae:2 semet structure
						Fold: S-adenosyl-L-methionine-dependent methyltransferases

104	d2okca1	Alignment	not modelled	37.3	43	Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like
105	c6iqwA_	Alignment	not modelled	36.8	67	PDB header: rna binding protein/rna Chain: A: PDB Molecule: csm1; PDBTitle: cryo-em structure of csm effector complex
106	c3khkA_	Alignment	not modelled	36.7	29	PDB header: dna binding protein Chain: A: PDB Molecule: type i restriction-modification system methylation subunit; PDBTitle: crystal structure of type-i restriction-modification system2 methylation subunit (mm_0429) from methanosarchina mazei.
107	d2ap9a1	Alignment	not modelled	36.5	24	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
108	c1g38A_	Alignment	not modelled	35.9	71	PDB header: transferase/dna Chain: A: PDB Molecule: modification methylase taqi; PDBTitle: adenine-specific methyltransferase m. taqi i/dna complex
109	d2f8la1	Alignment	not modelled	35.0	43	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like
110	c4uw2A_	Alignment	not modelled	34.3	67	PDB header: immune system Chain: A: PDB Molecule: csm1; PDBTitle: crystal structure of csm1 in t.onnurineus
111	c3lkdB_	Alignment	not modelled	33.5	43	PDB header: transferase Chain: B: PDB Molecule: type i restriction-modification system methyltransferase PDBTitle: crystal structure of the type i restriction-modification system2 methyltransferase subunit from streptococcus thermophilus, northeast3 structural genomics consortium target sur80
112	c3ufbA_	Alignment	not modelled	33.0	43	PDB header: transferase Chain: A: PDB Molecule: type i restriction-modification system methyltransferase PDBTitle: crystal structure of a modification subunit of a putative type i2 restriction enzyme from vibrio vulnificus yj016
113	c1aqjB_	Alignment	not modelled	32.5	23	PDB header: methyltransferase Chain: B: PDB Molecule: adenine-n6-dna-methyltransferase taqi; PDBTitle: structure of adenine-n6-dna-methyltransferase taqi
114	c6ifnA_	Alignment	not modelled	31.3	45	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
115	c5ybbA_	Alignment	not modelled	31.0	43	PDB header: dna binding protein/dna Chain: A: PDB Molecule: type i restriction-modification system methyltransferase PDBTitle: structural basis underlying complex assembly and conformational2 transition of the type i r-m system
116	c3ldgA_	Alignment	not modelled	27.0	36	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein smu.472; PDBTitle: crystal structure of smu.472, a putative methyltransferase complexed2 with sah
117	c3v8vB_	Alignment	not modelled	26.5	37	PDB header: transferase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase i; PDBTitle: crystal structure of bifunctional methyltransferase ycbY (rlmK) from2 escherichia coli, sam binding
118	d2ovra1	Alignment	not modelled	25.7	12	Fold: Skp1 dimerisation domain-like Superfamily: Skp1 dimerisation domain-like Family: Skp1 dimerisation domain-like
119	c2xzn3_	Alignment	not modelled	25.6	12	PDB header: ribosome Chain: 3: PDB Molecule: rps7e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
120	c3f5tA_	Alignment	not modelled	25.6	27	PDB header: viral protein Chain: A: PDB Molecule: nonstructural protein 1; PDBTitle: x-ray structure of h5n1 ns1