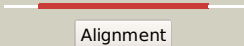

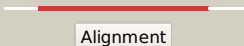

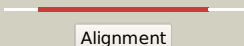





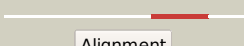

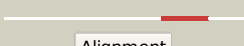


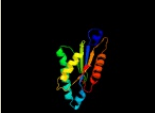






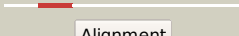

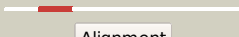











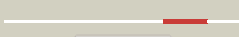


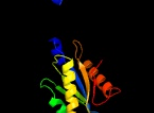
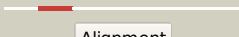
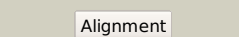

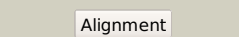
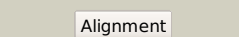
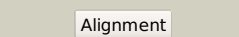
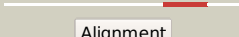
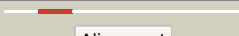


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2823c_(-)_3129354_3131783
Date	Wed Aug 7 12:50:48 BST 2019
Unique Job ID	1462f3a9366f507f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ifnA_	 Alignment		100.0	44	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
2	c6iqwA_	 Alignment		100.0	27	PDB header: rna binding protein/rna Chain: A: PDB Molecule: csm1; PDBTitle: cryo-em structure of csm effector complex
3	c4uw2A_	 Alignment		100.0	29	PDB header: immune system Chain: A: PDB Molecule: csm1; PDBTitle: crystal structure of csm1 in t.onnurineus
4	c4w8yA_	 Alignment		100.0	19	PDB header: rna binding protein Chain: A: PDB Molecule: crispr system cmr subunit cmr2; PDBTitle: structure of full length cmr2 from pyrococcus furiosus (manganese2 bound form)
5	c3ungC_	 Alignment		100.0	20	PDB header: unknown function Chain: C: PDB Molecule: cmr2dhd; PDBTitle: structure of the cmr2 subunit of the crispr rna silencing complex
6	c4uw2C_	 Alignment		100.0	30	PDB header: immune system Chain: C: PDB Molecule: csm1; PDBTitle: crystal structure of csm1 in t.onnurineus
7	c3breA_	 Alignment		98.5	19	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
8	c1w25B_	 Alignment		98.4	20	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
9	c5llxB_	 Alignment		98.4	16	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase (ggdef) domain-containing protein; PDBTitle: bacteriophytochrome activated diguanylyl cyclase from idiomarina2 species a28l with gtp bound
10	c2o08B_	 Alignment		98.4	17	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
11	c3i5aA_	 Alignment		98.4	22	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae

12	c3ccgA_	 Alignment		98.3	26	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
13	c2ogiA_	 Alignment		98.3	20	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
14	c4h54B_	 Alignment		98.2	17	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase ydeh; PDBTitle: crystal structure of the diguanylate cyclase dgcz
15	c4zvB_	 Alignment		98.2	18	PDB header: signaling protein Chain: B: PDB Molecule: diguanylate cyclase dosc; PDBTitle: crystal structure of ggdef domain of the e. coli dosc - form iv
16	c6eibC_	 Alignment		98.2	17	PDB header: transferase Chain: C: PDB Molecule: sensory box/ggdef family protein; PDBTitle: structure of the active ggeef domain of a diguanylate cyclase from2 vibrio cholerae.
17	c4zmuD_	 Alignment		98.1	19	PDB header: lyase Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
18	c6d9mA_	 Alignment		98.1	17	PDB header: hydrolase Chain: A: PDB Molecule: fusion protein of endolysin, response receiver sensor PDBTitle: t4-lysozyme fusion to geobacter ggdef
19	c3ezuA_	 Alignment		98.1	24	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
20	c4iobA_	 Alignment		98.1	14	PDB header: lyase Chain: A: PDB Molecule: diguanylate cyclase tpbb; PDBTitle: crystal structure of the ggdef domain of pa1120 (yfin or tpbb) from2 pseudomonas aeruginosa at 2.7 ang.
21	c4s1cA_	 Alignment	not modelled	98.0	18	PDB header: hydrolase Chain: A: PDB Molecule: lmo1466 protein; PDBTitle: crystal structure of l. monocytogenes phosphodiesterase ppph hd domain
22	c4mCWa_	 Alignment	not modelled	98.0	19	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent phosphohydrolase; PDBTitle: metallo-enzyme from p. marina
23	c3ignA_	 Alignment	not modelled	98.0	16	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of the ggdef domain from marinobacter aquaeolei2 diguanylate cyclase complexed with c-di-gmp - northeast structural3 genomics consortium target mqr89a
24	c3i5bA_	 Alignment	not modelled	97.9	18	PDB header: signaling protein Chain: A: PDB Molecule: wspr response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wspr from2 pseudomonas aeruginosa
25	c3icIA_	 Alignment	not modelled	97.9	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: eal/ggdef domain protein; PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium target mcr174c
26	c3tvkA_	 Alignment	not modelled	97.8	18	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase dgcz; PDBTitle: diguanylate cyclase domain of dgcz
27	c3i5cA_	 Alignment	not modelled	97.8	19	PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein gcn4 and wspr response PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
28	d2pq7a1	 Alignment	not modelled	97.8	29	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like

						Family:HD domain
29	c5ihyB	Alignment	not modelled	97.8	12	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of bacillus subtilis semet-yppq
30	c3mtkA	Alignment	not modelled	97.8	13	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase/phosphodiesterase; PDBTitle: x-ray structure of diguanylate cyclase/phosphodiesterase from 2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
31	c4wxoA	Alignment	not modelled	97.8	13	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: sadc (300-487) from pseudomonas aeruginosa pao1
32	c5z7cA	Alignment	not modelled	97.8	21	PDB header: metal binding protein Chain: A: PDB Molecule: 3'3'-cgamp-specific phosphodiesterase 3; PDBTitle: crystal structure of cyclic gmp-amp specific phosphodiesterases in 2 v.cholerae (v-cgap3)
33	c4r8zB	Alignment	not modelled	97.7	19	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 nickel ion center
34	c4n71A	Alignment	not modelled	97.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: predicted hd phosphohydrolase phnz; PDBTitle: x-ray crystal structure of 2-amino-1-hydroxyethylphosphonate-bound2 phnz
35	c4zmmB	Alignment	not modelled	97.6	18	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: ggdef domain of dcsbis complexed with c-di-gmp
36	c3qyyB	Alignment	not modelled	97.6	19	PDB header: signaling protein/inhibitor Chain: B: PDB Molecule: response regulator; PDBTitle: a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
37	c4ymeA	Alignment	not modelled	97.6	17	PDB header: lyase Chain: A: PDB Molecule: sensory box/ggdef family protein; PDBTitle: crystal structure of a sensory box/ggdef family protein (cc_0091) from 2 caulobacter crescentus cb15 at 1.40 a resolution (psi community3 target, shapiro)
38	c3m1tA	Alignment	not modelled	97.6	25	PDB header: hydrolase Chain: A: PDB Molecule: putative phosphohydrolase; PDBTitle: crystal structure of putative phosphohydrolase (yp_929327.1) from 2 shewanella amazonensis sb2b at 1.62 a resolution
39	d1w25a3	Alignment	not modelled	97.5	14	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
40	c5euhA	Alignment	not modelled	97.5	18	PDB header: membrane protein Chain: A: PDB Molecule: putative ggdef domain membrane protein; PDBTitle: crystal structure of the c-di-gmp-bound ggdef domain of p. fluorescens2 gcbc
41	c3wfrH	Alignment	not modelled	97.5	22	PDB header: transferase/rna Chain: H: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
42	c3hvaA	Alignment	not modelled	97.5	10	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas aeruginosa
43	c3wfrG	Alignment	not modelled	97.5	23	PDB header: transferase/rna Chain: G: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
44	c4urgB	Alignment	not modelled	97.4	14	PDB header: lyase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of ggdef domain from t.maritima (active-like dimer)
45	c3wfpA	Alignment	not modelled	97.4	22	PDB header: transferase Chain: A: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
46	c3wfpB	Alignment	not modelled	97.4	22	PDB header: transferase Chain: B: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 2)
47	c6npaD	Alignment	not modelled	97.4	37	PDB header: oxidoreductase Chain: D: PDB Molecule: tmpb, (r)-1-hydroxy-2-trimethylaminoethylphosphonate PDBTitle: x-ray crystal structure of tmpb, (r)-1-hydroxy-2-2-trimethylaminoethylphosphonate oxygenase, with (r)-1-hydroxy-2-3-trimethylaminoethylphosphonate
48	c3hc1A	Alignment	not modelled	97.3	18	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
49	c3wfrF	Alignment	not modelled	97.1	21	PDB header: transferase/rna Chain: F: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
50	c3gw7A	Alignment	not modelled	97.1	23	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
51	d2qgsa1	Alignment	not modelled	97.1	14	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
52	c3memA	Alignment	not modelled	97.0	16	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

53	c3wfsD	Alignment	not modelled	97.0	20	PDB header: transferase/rna Chain: D: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 3
54	c2qv6D	Alignment	not modelled	97.0	16	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii; PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
55	c3wfrE	Alignment	not modelled	96.9	20	PDB header: transferase/rna Chain: E: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 2
56	c3wfgH	Alignment	not modelled	96.9	20	PDB header: transferase/rna Chain: H: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
57	c3wfgG	Alignment	not modelled	96.9	20	PDB header: transferase/rna Chain: G: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
58	d1vqra	Alignment	not modelled	96.9	13	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: modified HD domain
59	c3wfsC	Alignment	not modelled	96.8	22	PDB header: transferase/rna Chain: C: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 3
60	c3wfgE	Alignment	not modelled	96.8	20	PDB header: transferase/rna Chain: E: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme complex 1
61	c5b7iA	Alignment	not modelled	96.4	24	PDB header: hydrolase/unknown function Chain: A: PDB Molecule: crispr-associated nuclease/helicase cas3 subtype i-f/ypest; PDBTitle: cas3-acrf3 complex
62	c3i7aA	Alignment	not modelled	96.3	7	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
63	c3ljvA	Alignment	not modelled	96.3	14	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
64	c3wfoB	Alignment	not modelled	96.2	25	PDB header: transferase Chain: B: PDB Molecule: poly a polymerase; PDBTitle: trna processing enzyme (apo form 1)
65	d3djba1	Alignment	not modelled	96.1	19	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
66	d2pjqa1	Alignment	not modelled	96.0	16	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
67	c3hvwA	Alignment	not modelled	95.9	15	PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc); PDBTitle: crystal structure of the ggdef domain of the pa2567 protein from2 pseudomonas aeruginosa, northeast structural genomics consortium3 target par365c
68	c3m5fA	Alignment	not modelled	95.9	22	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent phosphohydrolase; PDBTitle: structure of mj0384, a cas3 protein from methanocaldococcus jannaschii
69	c3pjwA	Alignment	not modelled	95.7	18	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
70	c2floA	Alignment	not modelled	95.6	10	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
71	d1u6za1	Alignment	not modelled	95.6	10	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: Ppx associated domain
72	d3b57a1	Alignment	not modelled	95.2	16	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
73	c5xgdA	Alignment	not modelled	95.1	19	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
74	d3dtoa1	Alignment	not modelled	94.9	14	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
75	c4q2dA	Alignment	not modelled	93.8	33	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
76	c4qqxA	Alignment	not modelled	93.3	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: crispr-associated helicase, cas3 family; PDBTitle: crystal structure of t. fusca cas3-atp
77	c5m3cB	Alignment	not modelled	92.6	18	PDB header: hydrolase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: structure of the hybrid domain (ggdef-eal) of pa0575 from pseudomonas2 aeruginosa pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain
78	c3kldA	Alignment	not modelled	92.1	21	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein tthb187;

78	c5skvA	Alignment	not modelled	92.1	41	PDBTitle: crystal structure of the thermus thermophilus cas3 hd domain in the2 presence of ni2+
79	d2heka1	Alignment	not modelled	91.1	15	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
80	c6brhA	Alignment	not modelled	90.8	29	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
81	c3u1nC	Alignment	not modelled	90.2	29	PDB header: hydrolase Chain: C; PDB Molecule: sam domain and hd domain-containing protein 1; PDBTitle: structure of the catalytic core of human samhd1
82	c4bzbB	Alignment	not modelled	90.0	18	PDB header: hydrolase Chain: B; PDB Molecule: deoxynucleoside triphosphate triphosphohydrolase samhd1; PDBTitle: crystal structure of the tetrameric dgtp-bound samhd12 mutant catalytic core
83	c2pgsA	Alignment	not modelled	89.9	22	PDB header: hydrolase Chain: A; PDB Molecule: putative deoxyguanosinetriphosphate triphosphohydrolase; PDBTitle: crystal structure of a putative deoxyguanosinetriphosphate2 triphosphohydrolase from pseudomonas syringae pv. phaseolicola 1448a
84	c3hi0B	Alignment	not modelled	89.7	24	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
85	c2o6iA	Alignment	not modelled	88.6	29	PDB header: hydrolase Chain: A; PDB Molecule: hd domain protein; PDBTitle: structure of an enterococcus faecalis hd domain phosphohydrolase
86	d2o6ia1	Alignment	not modelled	88.6	29	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
87	c5ao4D	Alignment	not modelled	88.1	31	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
88	c2q14A	Alignment	not modelled	87.7	33	PDB header: hydrolase Chain: A; PDB Molecule: phosphohydrolase; PDBTitle: crystal structure of phosphohydrolase (bt4208) from bacteroides2 thetaiotaomicron vpi-5482 at 2.20 a resolution
89	d2fiqa1	Alignment	not modelled	85.8	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: GatZ-like
90	c6dk9I	Alignment	not modelled	85.4	18	PDB header: lyase Chain: I; PDB Molecule: dna damage-inducible protein; PDBTitle: yeast ddi2 cyanamide hydratase
91	c2dqB	Alignment	not modelled	84.7	44	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
92	c3kq5A	Alignment	not modelled	84.7	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical cytosolic protein; PDBTitle: crystal structure of an uncharacterized protein from coxiella burnetii
93	d3bxda1	Alignment	not modelled	74.4	43	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: MioX-like
94	c2huoA	Alignment	not modelled	74.4	43	PDB header: oxidoreductase Chain: A; PDB Molecule: inositol oxygenase; PDBTitle: crystal structure of mouse myo-inositol oxygenase in complex with2 substrate
95	c4rnhA	Alignment	not modelled	72.3	21	PDB header: transferase, hydrolase Chain: A; PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
96	d2ibna1	Alignment	not modelled	71.4	43	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: MioX-like
97	c3j20P	Alignment	not modelled	67.7	24	PDB header: ribosome Chain: P; PDB Molecule: 30s ribosomal protein s14p type z; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
98	c3bg2A	Alignment	not modelled	64.3	45	PDB header: hydrolase Chain: A; PDB Molecule: dgtp triphosphohydrolase; PDBTitle: crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
99	c3jyvN	Alignment	not modelled	62.5	33	PDB header: ribosome Chain: N; PDB Molecule: 40s ribosomal protein s29(a); PDBTitle: structure of the 40s rna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
100	c2xznN	Alignment	not modelled	62.2	24	PDB header: ribosome Chain: N; PDB Molecule: rps29e; 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
101	c2cqzA	Alignment	not modelled	61.0	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: 177aa long hypothetical protein; PDBTitle: crystal structure of ph0347 protein from pyrococcus horikoshii ot3

102	d1hk8a_	Alignment	not modelled	57.7	33	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
103	c1hk8A_	Alignment	not modelled	57.7	33	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity regulation in2 class iii ribonucleotide reductases: nrdd in complex with dgtg
104	c2hr5B_	Alignment	not modelled	54.4	17	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
105	c3zey8_	Alignment	not modelled	53.7	24	PDB header: ribosome Chain: 8: PDB Molecule: ribosomal protein s29, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
106	c2zkqn_	Alignment	not modelled	53.5	22	PDB header: ribosomal protein/rna Chain: N: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
107	c5xxud_	Alignment	not modelled	51.8	27	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein us3; PDBTitle: small subunit of toxoplasma gondii ribosome
108	c1dvbA_	Alignment	not modelled	50.7	13	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
109	c1z1lA_	Alignment	not modelled	50.7	27	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-dependent 3',5'-cyclic phosphodiesterase; PDBTitle: the crystal structure of the phosphodiesterase 2a catalytic2 domain
110	c5xyid_	Alignment	not modelled	49.9	18	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s3, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
111	d3dy8a1	Alignment	not modelled	49.2	13	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
112	c1xotB_	Alignment	not modelled	49.0	27	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
113	c3qi4A_	Alignment	not modelled	48.9	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
114	d1taza_	Alignment	not modelled	48.9	27	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
115	c2ounA_	Alignment	not modelled	48.8	33	PDB header: hydrolase Chain: A: PDB Molecule: camp and camp-inhibited cgmp 3',5'-cyclic PDBTitle: crystal structure of pde10a2 in complex with amp
116	d1so2a_	Alignment	not modelled	48.1	20	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
117	d1y2ka1	Alignment	not modelled	48.1	27	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: PDEase
118	c6az1S_	Alignment	not modelled	48.0	23	PDB header: ribosome/antibiotic Chain: S: PDB Molecule: ribosomal protein s14; PDBTitle: cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
119	c2r8qA_	Alignment	not modelled	47.9	20	PDB header: hydrolase Chain: A: PDB Molecule: class i phosphodiesterase pdeb1; PDBTitle: structure of lmjpdeb1 in complex with ibmx
120	c1xozA_	Alignment	not modelled	47.5	27	PDB header: hydrolase Chain: A: PDB Molecule: cgmp-specific 3',5'-cyclic phosphodiesterase; PDBTitle: catalytic domain of human phosphodiesterase 5a in complex2 with tadalafil