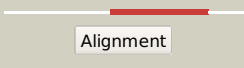

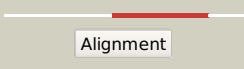

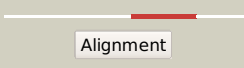

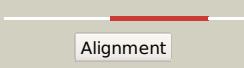

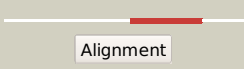

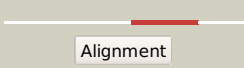
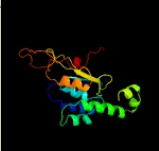
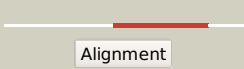

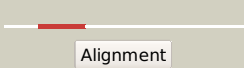

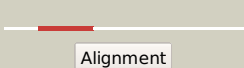

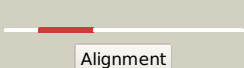

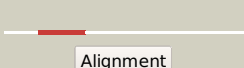








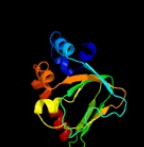



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2565_(-)_2884621_2886372
Date	Wed Aug 7 12:50:20 BST 2019
Unique Job ID	220175d6e89db25f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fyaA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A: PDB Molecule: patatin-like protein, plpd; PDBTitle: cubic crystal of the native plpd
2	c4akfA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: vipd; PDBTitle: crystal structure of vipd from legionella pneumophila
3	c4qmkB_	 Alignment		100.0	29	PDB header: toxin Chain: B: PDB Molecule: type iii secretion system effector protein exou; PDBTitle: crystal structure of type iii effector protein exou (exou)
4	d1oxwa_	 Alignment		100.0	16	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Patatin
5	c3tu3B_	 Alignment		100.0	24	PDB header: toxin/toxin chaperone Chain: B: PDB Molecule: exou; PDBTitle: 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
6	c4akxB_	 Alignment		100.0	23	PDB header: transport protein Chain: B: PDB Molecule: exou; PDBTitle: structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
7	c6aunB_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: pla2g6, ipla2beta; PDBTitle: calcium-independent phospholipase a2 beta
8	c5jonA_	 Alignment		99.9	17	PDB header: transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,potassium/sodium PDBTitle: crystal structure of the unliganded form of hcn2 cnbd
9	c4avcA_	 Alignment		99.9	21	PDB header: transferase Chain: A: PDB Molecule: lysine acetyltransferase; PDBTitle: crystal structure of protein lysine acetyltransferase rv09982 in complex with acetyl coa and camp
10	c4orfA_	 Alignment		99.9	20	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase pat; PDBTitle: camp-binding acyltransferase from mycobacterium smegmatis, mutant r95k
11	c4chwB_	 Alignment		99.9	21	PDB header: transport protein Chain: B: PDB Molecule: cyclic nucleotide-gated potassium channel ml3241; PDBTitle: the electron crystallography structure of the camp-free potassium2 channel ml0k1

12	c3gydA	Alignment		99.9	18	PDB header: dna binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding domain; PDBTitle: crystal structure of a cyclic nucleotide-binding domain (mfla_1926)2 from methylobacillus flagellatus kt at 1.79 a resolution
13	d1zyba2	Alignment		99.9	11	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
14	c2pqqD	Alignment		99.9	29	PDB header: transcription Chain: D: PDB Molecule: putative transcriptional regulator; PDBTitle: structural genomics, the crystal structure of the n-terminal domain of2 a transcriptional regulator from streptomyces coelicolor a3(2)
15	c3mdpA	Alignment		99.8	20	PDB header: nucleotide binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding domain (cnmp-bd) protein; PDBTitle: crystal structure of a putative cyclic nucleotide-binding protein2 (gmet_1532) from geobacter metallireducens gs-15 at 1.90 a resolution
16	c5v30B	Alignment		99.8	19	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the sensor domain of the transcriptional2 regulator hcpr from porphyromonas gingivalis
17	d1cx4a2	Alignment		99.8	16	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
18	d2gaua2	Alignment		99.8	16	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
19	c5t3nB	Alignment		99.8	20	PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase regulatory subunit; PDBTitle: sp-2cl-camps bound to pkar cbd2
20	c4myiA	Alignment		99.8	20	PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase, putative; PDBTitle: crystal structure of pvx_084705
21	c2z69A	Alignment	not modelled	99.8	16	PDB header: transcription regulator Chain: A: PDB Molecule: dnr protein; PDBTitle: crystal structure of the sensor domain of the transcriptional2 regulator dnr from pseudomonas aeruginosa
22	c5u6pA	Alignment	not modelled	99.8	15	PDB header: transport protein Chain: A: PDB Molecule: potassium/sodium hyperpolarization-activated cyclic PDBTitle: structure of the human hcn1 hyperpolarization-activated cyclic2 nucleotide-gated ion channel in complex with camp
23	c5v4sB	Alignment	not modelled	99.8	24	PDB header: transport protein Chain: B: PDB Molecule: transporter, cation channel family / cyclic nucleotide- PDBTitle: cryoem structure of a prokaryotic cyclic nucleotide-gated ion channel
24	c2ptmA	Alignment	not modelled	99.8	17	PDB header: transport protein Chain: A: PDB Molecule: hyperpolarization-activated (ih) channel; PDBTitle: structure and rearrangements in the carboxy-terminal region of spih2 channels
25	d1cx4a1	Alignment	not modelled	99.8	19	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
26	d1ne6a2	Alignment	not modelled	99.8	18	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
27	c5bv6A	Alignment	not modelled	99.8	20	PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase 2; PDBTitle: pkg ii's carboxyl terminal cyclic nucleotide binding domain (cnb-b) in2 a complex with cgmp
28	c4kg1A	Alignment	not modelled	99.8	25	PDB header: lyase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: cgmp-responsive diguanylate cyclase

29	d1vp6a_	Alignment	not modelled	99.8	21	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
30	d1ne6a1	Alignment	not modelled	99.8	20	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
31	c5k7lA_	Alignment	not modelled	99.8	26	PDB header: metal transport/calcium binding protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: single particle cryo-em structure of the voltage-gated k+ channel eag12 bound to the channel inhibitor calmodulin
32	c3dn7A_	Alignment	not modelled	99.8	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cyclic nucleotide binding regulatory protein; PDBTitle: cyclic nucleotide binding regulatory protein from cytophaga2 hutchinsonii.
33	c2byvE_	Alignment	not modelled	99.8	17	PDB header: regulation Chain: E: PDB Molecule: rap guanine nucleotide exchange factor 4; PDBTitle: structure of the camp responsive exchange factor epac2 in2 its auto-inhibited state
34	c3cf6E_	Alignment	not modelled	99.8	26	PDB header: signaling protein/gtp-binding protein Chain: E: PDB Molecule: rap guanine nucleotide exchange factor (gef) 4; PDBTitle: structure of epac2 in complex with cyclic-amp and rap
35	c5h3oA_	Alignment	not modelled	99.8	23	PDB header: transport protein Chain: A: PDB Molecule: cyclic nucleotide-gated cation channel; PDBTitle: structure of a eukaryotic cyclic nucleotide-gated channel
36	c3otfA_	Alignment	not modelled	99.8	17	PDB header: transport protein Chain: A: PDB Molecule: potassium/sodium hyperpolarization-activated cyclic PDBTitle: structural basis for the camp-dependent gating in human hcn4 channel
37	c3pvyB_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase type i-alpha regulatory PDBTitle: crystal structure of (73-244)ria:c holoenzyme of camp-dependent2 protein kinase
38	c3fx3A_	Alignment	not modelled	99.8	17	PDB header: camp-binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: structure of a putative camp-binding regulatory protein from2 silicibacter pomeroyi dss-3
39	c6cjtB_	Alignment	not modelled	99.8	21	PDB header: transport protein Chain: B: PDB Molecule: sthk cyclic nucleotide-gated potassium channel; PDBTitle: structure of the sthk cyclic nucleotide-gated potassium channel in2 complex with cgmp
40	c3j4qC_	Alignment	not modelled	99.8	17	PDB header: transferase Chain: C: PDB Molecule: camp-dependent protein kinase type ii-alpha regulatory PDBTitle: pseudo-atomic model of the akap18-pka complex in a bent conformation2 derived from electron microscopy
41	c5va1A_	Alignment	not modelled	99.8	20	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: cryo-em structure of the human ether-a-go-go related k+ channel
42	c1o7fA_	Alignment	not modelled	99.8	17	PDB header: regulation Chain: A: PDB Molecule: camp-dependent rap1 guanine-nucleotide exchange PDBTitle: crystal structure of the regulatory domain of epac2
43	c3idcB_	Alignment	not modelled	99.8	19	PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase type ii-beta regulatory PDBTitle: crystal structure of (102-265)riib:c holoenzyme of camp-dependent2 protein kinase
44	c4f8aA_	Alignment	not modelled	99.8	26	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: cyclic nucleotide binding-homology domain from mouse eag1 potassium2 channel
45	c4d7sB_	Alignment	not modelled	99.8	20	PDB header: transport protein Chain: B: PDB Molecule: sthk_cnbd_cgmp; PDBTitle: structure of the sthk carboxy-terminal region in complex with cgmp
46	c3ogjD_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: D: PDB Molecule: prkg1 protein; PDBTitle: crystal structure of partial apo (92-227) of cgmp-dependent protein2 kinase
47	c4ev0A_	Alignment	not modelled	99.8	21	PDB header: transcription activator Chain: A: PDB Molecule: transcription regulator, crp family; PDBTitle: crystal structure of thermus thermophilus catabolite activator protein
48	c1zybA_	Alignment	not modelled	99.8	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator, crp family; PDBTitle: crystal structure of transcription regulator from bacteroides2 thetaiotaomicron vpi-5482 at 2.15 a resolution
49	d3e5ua2	Alignment	not modelled	99.8	9	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
50	c5d1iB_	Alignment	not modelled	99.8	29	PDB header: unknown function Chain: B: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: structure of cyclic nucleotide-binding-like protein from brucella2 abortus bv. 1 str. 9-941
51	d1o7fa3	Alignment	not modelled	99.8	23	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
52	c3of1A_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit;

						PDBTitle: crystal structure of bcy1, the yeast regulatory subunit of pka
53	c3e97A_	Alignment	not modelled	99.8	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of transcriptional regulator of crp/fnr family2 (yp_604437.1) from deinococcus geothermalis dsm 11300 at 1.86 a3 resolution
54	c5c8wB_	Alignment	not modelled	99.8	20	PDB header: transferase Chain: B: PDB Molecule: cgmp-dependent protein kinase 2; PDBTitle: pkg ii's amino terminal cyclic nucleotide binding domain (cnb-a) in a2 complex with cgmp
55	c6g52H_	Alignment	not modelled	99.8	21	PDB header: metal transport Chain: H: PDB Molecule: metal transporter cnm4; PDBTitle: crystal structure of the cnmp binding domain of the magnesium2 transporter cnm4
56	d1q3ea_	Alignment	not modelled	99.8	17	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
57	d1o7fa2	Alignment	not modelled	99.7	17	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
58	d1i5za2	Alignment	not modelled	99.7	27	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
59	d2h6ca2	Alignment	not modelled	99.7	12	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
60	c3iwzB_	Alignment	not modelled	99.7	23	PDB header: transcription Chain: B: PDB Molecule: catabolite activation-like protein; PDBTitle: the c-di-gmp responsive global regulator clp links cell-cell signaling2 to virulence gene expression in xanthomonas campestris
61	d1ft9a2	Alignment	not modelled	99.7	16	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: CO-sensing protein CooA, N-terminal domain
62	c6hq2A_	Alignment	not modelled	99.7	22	PDB header: signaling protein Chain: A: PDB Molecule: eal enzyme bd1971; PDBTitle: structure of eal enzyme bd1971 - apo form
63	c3uknC_	Alignment	not modelled	99.7	22	PDB header: transport protein, membrane protein Chain: C: PDB Molecule: novel protein similar to vertebrate potassium voltage-gated PDBTitle: structure of the c-linker/cnbhd of zelk channels in c 2 2 21 space2 group
64	c2n7gA_	Alignment	not modelled	99.7	20	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: structure of the cyclic nucleotide-binding homology domain of the herg2 channel
65	c3dv8A_	Alignment	not modelled	99.7	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of a putative transcriptional regulator of the2 crp/fnr family (eubrec_1222) from eubacterium rectale atcc 33656 at3 2.55 a resolution
66	c4lloE_	Alignment	not modelled	99.7	26	PDB header: transport protein Chain: E: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: structure of the eag domain-cnbdh complex of the mouse eag1 channel
67	d1wgpA_	Alignment	not modelled	99.7	20	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
68	d2oz6a2	Alignment	not modelled	99.7	23	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
69	d1o5la1	Alignment	not modelled	99.7	17	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
70	c1o5IA_	Alignment	not modelled	99.7	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp family; PDBTitle: crystal structure of transcriptional regulator (tm1171) from2 thermotoga maritima at 2.30 a resolution
71	c5kbfA_	Alignment	not modelled	99.7	20	PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit, putative; PDBTitle: camp bound pfpka-r (141-441)
72	c5w5aB_	Alignment	not modelled	99.7	21	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator cmr; PDBTitle: crystal structure of mycobacterium tuberculosis crp-fnr family2 transcription factor cmr (rv1675c)
73	c4dinB_	Alignment	not modelled	99.7	22	PDB header: transferase/transport protein Chain: B: PDB Molecule: camp-dependent protein kinase type i-beta regulatory PDBTitle: novel localization and quaternary structure of the pka ri beta2 holoenzyme
74	c1cx4A_	Alignment	not modelled	99.7	18	PDB header: signaling protein Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit PDBTitle: crystal structure of a deletion mutant of the type ii beta2 regulatory subunit of camp-dependent protein kinase
75	c3d0sA_	Alignment	not modelled	99.7	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: camp receptor protein from m.tuberculosis, camp-free form
76	c6ftfB_	Alignment	not modelled	99.7	21	PDB header: signaling protein Chain: B: PDB Molecule: protein kinase a regulatory subunit, putative; PDBTitle: regulatory subunit of a camp-independent protein kinase a from2 trypanosoma cruzi at 1.09 a resolution

77	c4l11A	Alignment	not modelled	99.7	20	PDB header: metal transport Chain: A: PDB Molecule: agap007709-pa; PDBTitle: structure of the c-linker/cnbhd of agerg channels
78	c3shrA	Alignment	not modelled	99.7	17	PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase 1; PDBTitle: crystal structure of cgmp-dependent protein kinase reveals novel site2 of interchain communication
79	c2d93A	Alignment	not modelled	99.7	18	PDB header: signaling protein Chain: A: PDB Molecule: rap guanine nucleotide exchange factor 6; PDBTitle: solution structure of the ccmp_binding domain of human rap2 guanine nucleotide exchange factor 6
80	d2coha2	Alignment	not modelled	99.6	19	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
81	c5j3uA	Alignment	not modelled	99.6	23	PDB header: transferase Chain: A: PDB Molecule: protein kinase a; PDBTitle: co-crystal structure of the regulatory domain of toxoplasma gondii pka2 with camp
82	c2bgcA	Alignment	not modelled	99.6	7	PDB header: transcription Chain: A: PDB Molecule: prfa; PDBTitle: prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
83	c3dkwB	Alignment	not modelled	99.6	16	PDB header: transcription regulator Chain: B: PDB Molecule: dnr protein; PDBTitle: crystal structure of dnr from pseudomonas aeruginosa.
84	c1rgsA	Alignment	not modelled	99.6	19	PDB header: kinase Chain: A: PDB Molecule: camp dependent protein kinase; PDBTitle: regulatory subunit of camp dependent protein kinase
85	c5e44A	Alignment	not modelled	99.6	22	PDB header: transcription Chain: A: PDB Molecule: fmr regulator; PDBTitle: crystal structure of holo-fmr of a. fischeri
86	c4rfaA	Alignment	not modelled	99.6	12	PDB header: transcription regulator Chain: A: PDB Molecule: lmo0740 protein; PDBTitle: crystal structure of cyclic nucleotide-binding domain containing2 protein from listeria monocytogenes egd-e
87	c3tnqA	Alignment	not modelled	99.6	19	PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase type ii-beta regulatory PDBTitle: structure and allostery of the pka riib tetrameric holoenzyme
88	c3kccA	Alignment	not modelled	99.6	28	PDB header: transcription Chain: A: PDB Molecule: catabolite gene activator; PDBTitle: crystal structure of d138l mutant of catabolite gene activator protein
89	c3e6dA	Alignment	not modelled	99.6	10	PDB header: transcription regulation Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: crystal structure of cprk c200s
90	c1zreB	Alignment	not modelled	99.5	28	PDB header: gene regulation/dna Chain: B: PDB Molecule: catabolite gene activator; PDBTitle: 4 crystal structures of cap-dna with all base-pair substitutions at2 position 6, cap-[6g;17c]icap38 dna
91	c3la2A	Alignment	not modelled	99.5	23	PDB header: transcription Chain: A: PDB Molecule: global nitrogen regulator; PDBTitle: crystal structure of ntca in complex with 2-oxoglutarate
92	c2oz6A	Alignment	not modelled	99.5	23	PDB header: dna binding protein Chain: A: PDB Molecule: virulence factor regulator; PDBTitle: crystal structure of virulence factor regulator from pseudomonas2 aeruginosa in complex with camp
93	c2zdbA	Alignment	not modelled	99.4	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, crp family; PDBTitle: crystal structure of tthb099, a transcriptional regulator crp family2 from thermus thermophilus hb8
94	c2h6bA	Alignment	not modelled	99.4	9	PDB header: dna binding protein Chain: A: PDB Molecule: chlorophenol reduction gene k; PDBTitle: crystal structure of oxidized cprk in complex with o-2 chlorophenolacetic acid
95	c2fmyB	Alignment	not modelled	99.4	15	PDB header: dna binding protein Chain: B: PDB Molecule: carbon monoxide oxidation system transcription regulator PDBTitle: co-dependent transcription factor cooa from carboxydotherrmus2 hydrogenoformans (imidazole-bound form)
96	c2gauA	Alignment	not modelled	99.4	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, crp/fnr family; PDBTitle: crystal structure of transcriptional regulator, crp/fnr family from2 porphyromonas gingivalis (apc80792), structural genomics, mcsg
97	c1ft9A	Alignment	not modelled	99.3	16	PDB header: transcription Chain: A: PDB Molecule: carbon monoxide oxidation system transcription PDBTitle: structure of the reduced (feii) co-sensing protein from r.2 rubrum
98	c2zwcA	Alignment	not modelled	99.3	20	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, fnr/crp family; PDBTitle: crystal structure of ttha1359, a transcriptional regulator,2 crp/fnr family from thermus thermophilus hb8
99	c4i2oA	Alignment	not modelled	99.2	18	PDB header: transcription regulator/dna Chain: A: PDB Molecule: fixk2 protein; PDBTitle: the structure of fixk2 from bradyrhizobium japonicum
100	d1cya2	Alignment	not modelled	99.1	18	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Lysophospholipase
101	c6hq7B	Alignment	not modelled	99.0	22	PDB header: signaling protein Chain: B: PDB Molecule: eal enzyme bd1971; PDBTitle: structure of eal enzyme bd1971 - cgmp bound form
102	c6di3B	Alignment	not modelled	98.8	10	PDB header: transport protein Chain: B: PDB Molecule: metal transporter cnm2;

102	c0uj3B_	Alignment	not modelled	98.8	19	PDBTitle: crystal structure of cnm2 cyclic nucleotide-binding homology domain PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: cytosolic phospholipase a2 delta;
103	c5izrC_	Alignment	not modelled	98.8	18	PDBTitle: human givd cytosolic phospholipase a2 in complex with methyl gamma-2 linolenyl fluorophosphonate inhibitor and terbium chloride PDB header: metal transport Chain: B: PDB Molecule: metal transporter cnm3;
104	c6dfdB_	Alignment	not modelled	98.6	18	PDBTitle: crystal structure of cnm3 cyclic nucleotide-binding homology domain PDB header: hydrolase Chain: B: PDB Molecule: protein (cytosolic phospholipase a2);
105	c1cyjB_	Alignment	not modelled	97.9	20	PDBTitle: human cytosolic phospholipase a2
106	d1mlaa1	Alignment	not modelled	96.1	12	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
107	c5ydmA_	Alignment	not modelled	93.4	27	PDB header: transferase Chain: A: PDB Molecule: pk5; PDBTitle: the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
108	d1yhfa1	Alignment	not modelled	92.6	13	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: TM1287-like
109	c6iytA_	Alignment	not modelled	92.6	29	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: crystal structure of the acyltransferase domain from second module 142 of salinomycin polyketide synthase
110	c5dz6A_	Alignment	not modelled	92.2	11	PDB header: transferase Chain: A: PDB Molecule: polyketide biosynthesis malonyl coa-acyl carrier protein PDBTitle: acyl transferase from bacillaene pks
111	c3im8A_	Alignment	not modelled	92.0	25	PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
112	c4ammA_	Alignment	not modelled	91.9	27	PDB header: transferase Chain: A: PDB Molecule: dyne8; PDBTitle: crystal structure of the acyltransferase domain of the2 iterative polyketide synthase in enediyne biosynthesis3 reveals the molecular basis of substrate specificity
113	c2jfkD_	Alignment	not modelled	91.7	23	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
114	c4rr5A_	Alignment	not modelled	91.6	10	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase
115	c5hw4C_	Alignment	not modelled	91.3	17	PDB header: transferase Chain: C: PDB Molecule: ribosomal rna small subunit methyltransferase i; PDBTitle: crystal structure of escherichia coli 16s rrna methyltransferase rsmi2 in complex with adomet
116	c2ozjB_	Alignment	not modelled	91.1	10	PDB header: unknown function Chain: B: PDB Molecule: cupin 2, conserved barrel; PDBTitle: crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
117	c3ptwA_	Alignment	not modelled	90.9	15	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
118	c3rgiA_	Alignment	not modelled	90.9	15	PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
119	c4qbuA_	Alignment	not modelled	90.8	20	PDB header: transferase Chain: A: PDB Molecule: zmaa; PDBTitle: structure of the acyl transferase domain of zmaa
120	c3tzzA_	Alignment	not modelled	90.7	29	PDB header: transferase Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a