
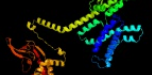
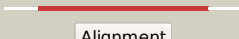

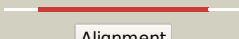


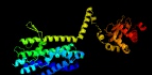



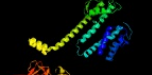





















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2434c (-) _2729125_2730570
Date	Wed Aug 7 12:50:05 BST 2019
Unique Job ID	8131600b3fd246c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5k7IA_</a>	 Alignment		100.0	13	<b>PDB header:</b> metal transport/calcium binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 1; <b>PDBTitle:</b> single particle cryo-em structure of the voltage-gated k+ channel eag12 bound to the channel inhibitor calmodulin
2	<a href="#">c5va1A_</a>	 Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 2; <b>PDBTitle:</b> cryo-em structure of the human ether-a-go-go related k+ channel
3	<a href="#">c5h3oA_</a>	 Alignment		100.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> cyclic nucleotide-gated cation channel; <b>PDBTitle:</b> structure of a eukaryotic cyclic nucleotide-gated channel
4	<a href="#">c5u6pA_</a>	 Alignment		100.0	10	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> potassium/sodium hyperpolarization-activated cyclic <b>PDBTitle:</b> structure of the human hcn1 hyperpolarization-activated cyclic2 nucleotide-gated ion channel in complex with camp
5	<a href="#">c6cjtB_</a>	 Alignment		99.9	18	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> sthk cyclic nucleotide-gated potassium channel; <b>PDBTitle:</b> structure of the sthk cyclic nucleotide-gated potassium channel in2 complex with cgmp
6	<a href="#">c5v4sB_</a>	 Alignment		99.9	14	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> transporter, cation channel family / cyclic nucleotide- <b>PDBTitle:</b> cryoem structure of a prokaryotic cyclic nucleotide-gated ion channel
7	<a href="#">c2vv5D_</a>	 Alignment		99.9	15	<b>PDB header:</b> membrane protein <b>Chain:</b> D; <b>PDB Molecule:</b> small-conductance mechanosensitive channel; <b>PDBTitle:</b> the open structure of msccs
8	<a href="#">c4hw9E_</a>	 Alignment		99.9	13	<b>PDB header:</b> membrane protein <b>Chain:</b> E; <b>PDB Molecule:</b> mechanosensitive channel msccs; <b>PDBTitle:</b> crystal structure of helicobacter pylori msccs (closed state)
9	<a href="#">c3t9nG_</a>	 Alignment		99.9	19	<b>PDB header:</b> membrane protein <b>Chain:</b> G; <b>PDB Molecule:</b> small-conductance mechanosensitive channel; <b>PDBTitle:</b> crystal structure of a membrane protein
10	<a href="#">c4chwB_</a>	 Alignment		99.9	17	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> cyclic nucleotide-gated potassium channel mll3241; <b>PDBTitle:</b> the electron crystallography structure of the camp-free potassium2 channel mlok1
11	<a href="#">c5jonA_</a>	 Alignment		99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> maltose-binding periplasmic protein,potassium/sodium <b>PDBTitle:</b> crystal structure of the unliganded form of hcn2 cnbd

12	<a href="#">c3gydA</a>	Alignment		99.9	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide-binding domain; <b>PDBTitle:</b> crystal structure of a cyclic nucleotide-binding domain (mfla_1926)2 from methylobacillus flagellatus kt at 1.79 a resolution
13	<a href="#">c4avcA</a>	Alignment		99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine acetyltransferase; <b>PDBTitle:</b> crystal structure of protein lysine acetyltransferase rv09982 in complex with acetyl coa and camp
14	<a href="#">c2ptmA</a>	Alignment		99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> hyperpolarization-activated (ih) channel; <b>PDBTitle:</b> structure and rearrangements in the carboxy-terminal region of spih2 channels
15	<a href="#">c4orfA</a>	Alignment		99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyltransferase pat; <b>PDBTitle:</b> camp-binding acyltransferase from mycobacterium smegmatis, mutant r95k
16	<a href="#">c4d7sB</a>	Alignment		99.9	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sthk_cnbd_cgmp; <b>PDBTitle:</b> structure of the sthK carboxy-terminal region in complex with cgmp
17	<a href="#">d1zyba2</a>	Alignment		99.9	11	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
18	<a href="#">c3otfA</a>	Alignment		99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium/sodium hyperpolarization-activated cyclic <b>PDBTitle:</b> structural basis for the camp-dependent gating in human hcn4 channel
19	<a href="#">c2pqqD</a>	Alignment		99.9	22	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structural genomics, the crystal structure of the n-terminal domain of f2 a transcriptional regulator from streptomyces coelicolor a3(2)
20	<a href="#">c5v30B</a>	Alignment		99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of the sensor domain of the transcriptional2 regulator hcpr from porphyromonas gingivalis
21	<a href="#">d1q3ea</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
22	<a href="#">c3uknC</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> novel protein similar to vertebrate potassium voltage-gated <b>PDBTitle:</b> structure of the c-linker/cnbd of zek channels in c 2 2 21 space2 group
23	<a href="#">c3dn7A</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide binding regulatory protein; <b>PDBTitle:</b> cyclic nucleotide binding regulatory protein from cytophaga2 hutchinsonii.
24	<a href="#">c5y4oA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> low conductance mechanosensitive channel ynai; <b>PDBTitle:</b> cryo-em structure of mscs channel, ynai
25	<a href="#">d3e5ua2</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
26	<a href="#">c4l11A</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> agap007709-pa; <b>PDBTitle:</b> structure of the c-linker/cnbd of agerg channels
27	<a href="#">c4ev0A</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator, crp family; <b>PDBTitle:</b> crystal structure of thermus thermophilus catabolite activator protein
28	<a href="#">d2oz6a2</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain

29	<a href="#">d1i5za2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
30	<a href="#">c5bv6A</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> camp-dependent protein kinase 2; <b>PDBTitle:</b> pkg ii's carboxyl terminal cyclic nucleotide binding domain (cnb-b) in2 a complex with cgmp
31	<a href="#">c3iwzB</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> catabolite activation-like protein; <b>PDBTitle:</b> the c-di-gmp responsive global regulator clp links cell-cell signaling2 to virulence gene expression in xanthomonas campestris
32	<a href="#">c3fx3A</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> camp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide-binding protein; <b>PDBTitle:</b> structure of a putative camp-binding regulatory protein from2 silicibacter pomeroyi dss-3
33	<a href="#">d1cx4a2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
34	<a href="#">c1zybA</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcription regulator, crp family; <b>PDBTitle:</b> crystal structure of transcription regulator from bacteroides2 thetaiotaomicron vpi-5482 at 2.15 a resolution
35	<a href="#">c3dv8A</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp/fnr family; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator of the2 crp/fnr family (eubrec_1222) from eubacterium rectale atcc 33656 at3 2.55 a resolution
36	<a href="#">c3mdpA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide-binding domain (cnmp-bd) protein; <b>PDBTitle:</b> crystal structure of a putative cyclic nucleotide-binding protein2 (gmet_1532) from geobacter metallireducens gs-15 at 1.90 a resolution
37	<a href="#">c4lloE</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 1; <b>PDBTitle:</b> structure of the eag domain-cnbd complex of the mouse eag1 channel
38	<a href="#">d2h6ca2</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
39	<a href="#">d1ft9a2</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> CO-sensing protein CooA, N-terminal domain
40	<a href="#">d2gaua2</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
41	<a href="#">d1cx4a1</a>	Alignment	not modelled	99.8	11	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
42	<a href="#">c4f8aA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 1; <b>PDBTitle:</b> cyclic nucleotide binding-homology domain from mouse eag1 potassium2 channel
43	<a href="#">d1o5la1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
44	<a href="#">c1o5IA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp family; <b>PDBTitle:</b> crystal structure of transcriptional regulator (tm1171) from2 thermotoga maritima at 2.30 a resolution
45	<a href="#">d1ne6a2</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
46	<a href="#">c5t3nB</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> camp-dependent protein kinase regulatory subunit; <b>PDBTitle:</b> sp-2cl-camps bound to pkar cbd2
47	<a href="#">c1o7fA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> regulation <b>Chain:</b> A: <b>PDB Molecule:</b> camp-dependent rap1 guanine-nucleotide exchange <b>PDBTitle:</b> crystal structure of the regulatory domain of epac2
48	<a href="#">c4kg1A</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> cgmp-responsive diguanylate cyclase
49	<a href="#">c2z69A</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> dnr protein; <b>PDBTitle:</b> crystal structure of the sensor domain of the transcriptional2 regulator dnr from pseudomonas aeruginosa
50	<a href="#">d1o7fa2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
51	<a href="#">c2byvE</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> regulation <b>Chain:</b> E: <b>PDB Molecule:</b> rap guanine nucleotide exchange factor 4; <b>PDBTitle:</b> structure of the camp responsive exchange factor epac2 in2 its auto-inhibited state
52	<a href="#">d1ne6a1</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
53	<a href="#">c2bgcA</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> prfa; <b>PDBTitle:</b> prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
						<b>Fold:</b> Double-stranded beta-helix

54	<a href="#">d1vp6a_</a>	Alignment	not modelled	99.7	21	<b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
55	<a href="#">d1wgp_a</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
56	<a href="#">c3e97A_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp/fnr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator of crp/fnr family2 (yp_604437.1) from deinococcus geothermalis dsm 11300 at 1.86 a3 resolution
57	<a href="#">c3j4qC_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> camp-dependent protein kinase type ii-alpha regulatory <b>PDBTitle:</b> pseudo-atomic model of the akap18-pka complex in a bent conformation2 derived from electron microscopy
58	<a href="#">c3idcB_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> camp-dependent protein kinase type ii-beta regulatory <b>PDBTitle:</b> crystal structure of (102-265)riib:c holoenzyme of camp-dependent2 protein kinase
59	<a href="#">c5e44A_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fnr regulator; <b>PDBTitle:</b> crystal structure of holo-fnr of a. fischeri
60	<a href="#">c3d0sA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> camp receptor protein from m.tuberculosis, camp-free form
61	<a href="#">c5d1iB_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic nucleotide-binding protein; <b>PDBTitle:</b> structure of cyclic nucleotide-binding-like protein from brucella2 abortus bv. 1 str. 9-941
62	<a href="#">c2n7gA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily h member 2; <b>PDBTitle:</b> structure of the cyclic nucleotide-binding homology domain of the herg2 channel
63	<a href="#">c4myiA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-dependent protein kinase, putative; <b>PDBTitle:</b> crystal structure of pvx_084705
64	<a href="#">c3kccA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> catabolite gene activator; <b>PDBTitle:</b> crystal structure of d138l mutant of catabolite gene activator protein
65	<a href="#">c3pvbB_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> camp-dependent protein kinase type i-alpha regulatory <b>PDBTitle:</b> crystal structure of (73-244)ria:c holoenzyme of camp-dependent2 protein kinase
66	<a href="#">d2coha2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
67	<a href="#">c6hq2A_</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> eal enzyme bd1971; <b>PDBTitle:</b> structure of eal enzyme bd1971 - apo form
68	<a href="#">c3ogjD_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> prkg1 protein; <b>PDBTitle:</b> crystal structure of partial apo (92-227) of cgmp-dependent protein2 kinase
69	<a href="#">c1zreB_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> B: <b>PDB Molecule:</b> catabolite gene activator; <b>PDBTitle:</b> 4 crystal structures of cap-dna with all base-pair substitutions at2 position 6, cap-[6g;17c]icap38 dna
70	<a href="#">c4rfaA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0740 protein; <b>PDBTitle:</b> crystal structure of cyclic nucleotide-binding domain containing2 protein from listeria monocytogenes egd-e
71	<a href="#">c5c8wB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cgmp-dependent protein kinase 2; <b>PDBTitle:</b> pkg ii's amino terminal cyclic nucleotide binding domain (cnb-a) in a2 complex with cgmp
72	<a href="#">d1o7fa3</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
73	<a href="#">c5w5aB_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator cmr; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis crp-fnr family2 transcription factor cmr (rv1675c)
74	<a href="#">c3cf6E_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> signaling protein/gtp-binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> rap guanine nucleotide exchange factor (gef) 4; <b>PDBTitle:</b> structure of epac2 in complex with cyclic-amp and rap
75	<a href="#">c3e6dA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide-binding protein; <b>PDBTitle:</b> crystal structure of cprk c200s
76	<a href="#">c3dkwB_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> dnr protein; <b>PDBTitle:</b> crystal structure of dnr from pseudomonas aeruginosa.
77	<a href="#">c6ftfB_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein kinase a regulatory subunit, putative; <b>PDBTitle:</b> regulatory subunit of a camp-independent protein kinase a from2 trypanosoma cruzi at 1.09 a resolution
78	<a href="#">c2oz6A_</a>	Alignment	not modelled	99.6	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence factor regulator; <b>PDBTitle:</b> crystal structure of virulence factor regulator from pseudomonas2 aeruginosa in complex with camp <b>PDB header:</b> transferase/transport protein

79	<a href="#">c4dinB_</a>	Alignment	not modelled	99.6	15	<b>Chain:</b> B: <b>PDB Molecule:</b> camp-dependent protein kinase type i-beta regulatory <b>PDBTitle:</b> novel localization and quaternary structure of the pka ri beta2 holoenzyme
80	<a href="#">c6g52H_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> metal transport <b>Chain:</b> H: <b>PDB Molecule:</b> metal transporter cnm4; <b>PDBTitle:</b> crystal structure of the cnm4 binding domain of the magnesium2 transporter cnm4
81	<a href="#">c3of1A_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> camp-dependent protein kinase regulatory subunit; <b>PDBTitle:</b> crystal structure of bcy1, the yeast regulatory subunit of pka
82	<a href="#">c3la2A_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> global nitrogen regulator; <b>PDBTitle:</b> crystal structure of ntca in complex with 2-oxoglutarate
83	<a href="#">c2h6bA_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chlorophenol reduction gene k; <b>PDBTitle:</b> crystal structure of oxidized cprk in complex with o-2 chlorophenolacetic acid
84	<a href="#">c1cx4A_</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> camp-dependent protein kinase regulatory subunit <b>PDBTitle:</b> crystal structure of a deletion mutant of the type ii beta2 regulatory subunit of camp-dependent protein kinase
85	<a href="#">c3shrA_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-dependent protein kinase 1; <b>PDBTitle:</b> crystal structure of cgmp-dependent protein kinase reveals novel site2 of interchain communication
86	<a href="#">c2zdbA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp family; <b>PDBTitle:</b> crystal structure of tthb099, a transcriptional regulator crp family2 from thermus thermophilus hb8
87	<a href="#">c5kbfA_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> camp-dependent protein kinase regulatory subunit, putative; <b>PDBTitle:</b> camp bound pfpka-r (141-441)
88	<a href="#">c5j3uA_</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase a; <b>PDBTitle:</b> co-crystal structure of the regulatory domain of toxoplasma gondii pka2 with camp
89	<a href="#">c2d93A_</a>	Alignment	not modelled	99.5	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rap guanine nucleotide exchange factor 6; <b>PDBTitle:</b> solution structure of the cnm4_binding domain of human rap2 guanine nucleotide exchange factor 6
90	<a href="#">c2zcwA_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, fnr/crp family; <b>PDBTitle:</b> crystal structure of ttha1359, a transcriptional regulator,2 crp/fnr family from thermus thermophilus hb8
91	<a href="#">c1rgsA_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> kinase <b>Chain:</b> A: <b>PDB Molecule:</b> camp dependent protein kinase; <b>PDBTitle:</b> regulatory subunit of camp dependent protein kinase
92	<a href="#">c3tnqA_</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> camp-dependent protein kinase type ii-beta regulatory <b>PDBTitle:</b> structure and allostery of the pka riib tetrameric holoenzyme
93	<a href="#">c2fmyB_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> carbon monoxide oxidation system transcription regulator <b>PDBTitle:</b> co-dependent transcription factor cooa from carboxydothermus2 hydrogenoformans (imidazole-bound form)
94	<a href="#">c4i2oA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> fixk2 protein; <b>PDBTitle:</b> the structure of fixk2 from bradyrhizobium japonicum
95	<a href="#">c1ft9A_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> carbon monoxide oxidation system transcription <b>PDBTitle:</b> structure of the reduced (feii) co-sensing protein from r.2 rubrum
96	<a href="#">c2gauA_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, crp/fnr family; <b>PDBTitle:</b> crystal structure of transcriptional regulator, crp/fnr family from2 porphyromonas gingivalis (apc80792), structural genomics, mcsg
97	<a href="#">c6hq7B_</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> eal enzyme bd1971; <b>PDBTitle:</b> structure of eal enzyme bd1971 - cgmp bound form
98	<a href="#">d2vv5a1</a>	Alignment	not modelled	98.8	22	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Mechanosensitive channel protein MscS (YggB), middle domain
99	<a href="#">c6dj3B_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> metal transporter cnm2; <b>PDBTitle:</b> crystal structure of cnm2 cyclic nucleotide-binding homology domain
100	<a href="#">d2vv5a2</a>	Alignment	not modelled	98.3	9	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain <b>Family:</b> Mechanosensitive channel protein MscS (YggB), C-terminal domain
101	<a href="#">c6dfdB_</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> metal transporter cnm3; <b>PDBTitle:</b> crystal structure of cnm3 cyclic nucleotide-binding homology domain
102	<a href="#">d2vv5a3</a>	Alignment	not modelled	96.9	18	<b>Fold:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region <b>Superfamily:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region <b>Family:</b> Mechanosensitive channel protein MscS (YggB), transmembrane region

						transmembrane region
103	<a href="#">c2ozjB_</a>	Alignment	not modelled	95.9	17	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel; <b>PDBTitle:</b> crystal structure of a cupin superfamily protein (dsy2733) from2 desulfotobacterium hafniense dcb-2 at 1.60 a resolution
104	<a href="#">d1yhfa1</a>	Alignment	not modelled	95.6	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1287-like
105	<a href="#">c5vmsA_</a>	Alignment	not modelled	95.5	8	<b>PDB header:</b> transport protein, calcium binding prote <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily kqt member 1; <b>PDBTitle:</b> cryoem structure of xenopus kcnq1 channel
106	<a href="#">c3fjsC_</a>	Alignment	not modelled	94.0	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein with rmlc-like cupin fold; <b>PDBTitle:</b> crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
107	<a href="#">c2q30C_</a>	Alignment	not modelled	94.0	17	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
108	<a href="#">c2i45C_</a>	Alignment	not modelled	92.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of protein nmb1881 from neisseria meningitidis
109	<a href="#">c5j4fB_</a>	Alignment	not modelled	92.8	12	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the n-terminally his6-tagged hp0902, an2 uncharacterized protein from helicobacter pylori 26695
110	<a href="#">c3d82A_</a>	Alignment	not modelled	92.6	19	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of a cupin-2 domain containing protein (sfri_3543)2 from shewanella frigidimarina ncimb 400 at 2.05 a resolution
111	<a href="#">c2d40C_</a>	Alignment	not modelled	92.4	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative gentisate 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of z3393 from escherichia coli o157:h7
112	<a href="#">d2d40a1</a>	Alignment	not modelled	92.0	9	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Gentisate 1,2-dioxygenase-like
113	<a href="#">d1fxza2</a>	Alignment	not modelled	91.7	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
114	<a href="#">c2pfwB_</a>	Alignment	not modelled	91.5	16	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
115	<a href="#">c5tj6A_</a>	Alignment	not modelled	91.4	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> high conductance calcium-activated potassium channel; <b>PDBTitle:</b> ca2+ bound aplysia slo1
116	<a href="#">c1cauB_</a>	Alignment	not modelled	91.0	15	<b>PDB header:</b> seed storage protein <b>Chain:</b> B: <b>PDB Molecule:</b> canavalin; <b>PDBTitle:</b> determination of three crystal structures of canavalin by molecular2 replacement
117	<a href="#">c3rnsA_</a>	Alignment	not modelled	90.3	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> cupin 2 conserved barrel domain protein from leptotrichia buccalis
118	<a href="#">c3ibmB_</a>	Alignment	not modelled	89.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of cupin 2 domain-containing protein hha1_0468 from2 halorhodospira halophila
119	<a href="#">d1uika2</a>	Alignment	not modelled	89.6	10	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
120	<a href="#">c5j7mB_</a>	Alignment	not modelled	89.4	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of cupin 2 conserved barrel domain protein from2 kribbella flavida dsm 17836