

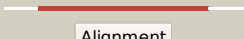

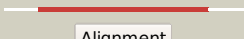



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3676 (- )_4116656_4117330
Date	Fri Aug 9 18:20:36 BST 2019
Unique Job ID	4004f47d62046f07

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3d0sA_</a>	 Alignment		100.0	100	<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
2	<a href="#">c5e44A_</a>	 Alignment		100.0	20	<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
3	<a href="#">c4ev0A_</a>	 Alignment		100.0	33	<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
4	<a href="#">c3fx3A_</a>	 Alignment		100.0	24	<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
5	<a href="#">c1zybA_</a>	 Alignment		100.0	19	<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
6	<a href="#">c3dv8A_</a>	 Alignment		100.0	18	<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
7	<a href="#">c3e97A_</a>	 Alignment		100.0	22	<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
8	<a href="#">c3dkwB_</a>	 Alignment		100.0	26	<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.
9	<a href="#">c5w5aB_</a>	 Alignment		100.0	25	<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)
10	<a href="#">c2gauA_</a>	 Alignment		100.0	27	<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
11	<a href="#">c2h6bA_</a>	 Alignment		100.0	17	<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

12	<a href="#">c2fmyB_</a>	Alignment		100.0	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 coa from carboxythermus2 hydrogenoformans (imidazole-bound form)
13	<a href="#">c2bgcA_</a>	Alignment		100.0	13	<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
14	<a href="#">c3e6dA_</a>	Alignment		100.0	19	<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
15	<a href="#">c3iwzB_</a>	Alignment		100.0	26	<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
16	<a href="#">c2oz6A_</a>	Alignment		100.0	28	<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
17	<a href="#">c3la2A_</a>	Alignment		99.9	26	<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
18	<a href="#">c3kccA_</a>	Alignment		99.9	27	<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
19	<a href="#">c1ft9A_</a>	Alignment		99.9	19	<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
20	<a href="#">c4rfaA_</a>	Alignment		99.9	13	<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
21	<a href="#">c1zreB_</a>	Alignment	not modelled	99.9	27	<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
22	<a href="#">c2zdbA_</a>	Alignment	not modelled	99.9	24	<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
23	<a href="#">c4i2oA_</a>	Alignment	not modelled	99.9	21	<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
24	<a href="#">c2zcwA_</a>	Alignment	not modelled	99.9	25	<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
25	<a href="#">c3gydA_</a>	Alignment	not modelled	99.7	25	<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
26	<a href="#">d1zyba2</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
27	<a href="#">c5v30B_</a>	Alignment	not modelled	99.7	11	<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
28	<a href="#">c2pqqD_</a>	Alignment	not modelled	99.7	47	<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 of2 a transcriptional regulator from streptomyces coelicolor a3(2)
						<b>PDB header:</b> structural genomics, unknown function

29	<a href="#">c3dn7A</a>	Alignment	not modelled	99.7	10	<b>Chain:</b> A: <b>PDB Molecule:</b> cyclic nucleotide binding regulatory protein; <b>PDBTitle:</b> cyclic nucleotide binding regulatory protein from cytophaga2 hutchinsonii.
30	<a href="#">c4avcA</a>	Alignment	not modelled	99.6	28	<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
31	<a href="#">c4orfA</a>	Alignment	not modelled	99.6	29	<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
32	<a href="#">c5jonA</a>	Alignment	not modelled	99.6	23	<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
33	<a href="#">c5bv6A</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-dependent protein kinase 2; <b>PDBTitle:</b> pkg ii's carboxyl terminal cyclic nucleotide binding domain (cnb-b) in2 a complex with cgmp
34	<a href="#">d1cx4a2</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
35	<a href="#">d1ne6a2</a>	Alignment	not modelled	99.6	25	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
36	<a href="#">c4chwB</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cyclic nucleotide-gated potassium channel ml13241; <b>PDBTitle:</b> the electron crystallography structure of the camp-free potassium2 channel ml0k1
37	<a href="#">c2z69A</a>	Alignment	not modelled	99.6	23	<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
38	<a href="#">c3mdpA</a>	Alignment	not modelled	99.6	22	<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
39	<a href="#">d1cx4a1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
40	<a href="#">d3e5ua2</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
41	<a href="#">c5t3nB</a>	Alignment	not modelled	99.6	20	<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
42	<a href="#">d2gaua2</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
43	<a href="#">c3idcB</a>	Alignment	not modelled	99.5	21	<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
44	<a href="#">d1vp6a</a>	Alignment	not modelled	99.5	27	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
45	<a href="#">c5v4sB</a>	Alignment	not modelled	99.5	23	<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
46	<a href="#">c5d1iB</a>	Alignment	not modelled	99.5	23	<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
47	<a href="#">c5u6pA</a>	Alignment	not modelled	99.5	22	<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
48	<a href="#">d2h6ca2</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
49	<a href="#">c4f8aA</a>	Alignment	not modelled	99.5	16	<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
50	<a href="#">d1ne6a1</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
51	<a href="#">d1i5za2</a>	Alignment	not modelled	99.5	24	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
52	<a href="#">c2n7gA</a>	Alignment	not modelled	99.5	20	<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
						<b>Fold:</b> Double-stranded beta-helix

53	<a href="#">d2oz6a2</a>	Alignment	not modelled	99.5	26	<b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
54	<a href="#">c1o5IA</a>	Alignment	not modelled	99.5	15	<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) from <i>Thermotoga maritima</i> at 2.30 Å resolution
55	<a href="#">d1o5la1</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
56	<a href="#">c3j4qC</a>	Alignment	not modelled	99.5	17	<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
57	<a href="#">c5c8wB</a>	Alignment	not modelled	99.5	23	<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
58	<a href="#">c4kg1A</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> cgmp-responsive diguanylate cyclase
59	<a href="#">c3otfA</a>	Alignment	not modelled	99.4	22	<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
60	<a href="#">c2ptmA</a>	Alignment	not modelled	99.4	21	<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
61	<a href="#">c3ogjD</a>	Alignment	not modelled	99.4	25	<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
62	<a href="#">c6cjtB</a>	Alignment	not modelled	99.4	22	<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
63	<a href="#">c5h3oA</a>	Alignment	not modelled	99.4	24	<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
64	<a href="#">d1wgpA</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
65	<a href="#">c4d7sB</a>	Alignment	not modelled	99.4	24	<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
66	<a href="#">c5k7IA</a>	Alignment	not modelled	99.4	20	<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
67	<a href="#">d1q3ea</a>	Alignment	not modelled	99.4	25	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
68	<a href="#">c3pvbB</a>	Alignment	not modelled	99.4	25	<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
69	<a href="#">d1ft9a2</a>	Alignment	not modelled	99.4	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
70	<a href="#">d2h6ca1</a>	Alignment	not modelled	99.4	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
71	<a href="#">c5va1A</a>	Alignment	not modelled	99.4	23	<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
72	<a href="#">c2byvE</a>	Alignment	not modelled	99.4	17	<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
73	<a href="#">d1o7fa2</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
74	<a href="#">d2gaua1</a>	Alignment	not modelled	99.4	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
75	<a href="#">d2coha1</a>	Alignment	not modelled	99.4	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
76	<a href="#">d2bgca1</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
77	<a href="#">c1o7fA</a>	Alignment	not modelled	99.4	17	<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
						<b>PDB header:</b> transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> potassium voltage-gated channel

78	<a href="#">c4lloE_</a>	Alignment	not modelled	99.4	20	subfamily h member 1; <b>PDBTitle:</b> structure of the eag domain-cnbdh complex of the mouse eag1 channel
79	<a href="#">c4myiA_</a>	Alignment	not modelled	99.4	20	<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
80	<a href="#">c1cx4A_</a>	Alignment	not modelled	99.4	18	<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
81	<a href="#">c5kbfA_</a>	Alignment	not modelled	99.3	22	<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)
82	<a href="#">d1o7fa3</a>	Alignment	not modelled	99.3	20	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
83	<a href="#">d3e5ua1</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
84	<a href="#">d1ft9a1</a>	Alignment	not modelled	99.3	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
85	<a href="#">c3uknC_</a>	Alignment	not modelled	99.3	17	<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/cnbdh of zek channels in c 2 2 21 space2 group
86	<a href="#">c4dinB_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transferase/transport protein <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
87	<a href="#">c6hq2A_</a>	Alignment	not modelled	99.2	33	<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
88	<a href="#">c4l11A_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> agap007709-pa; <b>PDBTitle:</b> structure of the c-linker/cnbdh of agerg channels
89	<a href="#">c3cf6E_</a>	Alignment	not modelled	99.2	21	<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
90	<a href="#">c3tnqA_</a>	Alignment	not modelled	99.2	19	<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
91	<a href="#">c3of1A_</a>	Alignment	not modelled	99.2	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
92	<a href="#">c1rgsA_</a>	Alignment	not modelled	99.2	21	<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
93	<a href="#">c5j3uA_</a>	Alignment	not modelled	99.2	22	<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
94	<a href="#">d2coha2</a>	Alignment	not modelled	99.2	25	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
95	<a href="#">c3shrA_</a>	Alignment	not modelled	99.2	24	<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
96	<a href="#">c6ftfB_</a>	Alignment	not modelled	99.1	22	<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
97	<a href="#">c2d93A_</a>	Alignment	not modelled	99.1	15	<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 cnmp_binding domain of human rap2 guanine nucleotide exchange factor 6
98	<a href="#">d2oz6a1</a>	Alignment	not modelled	99.1	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
99	<a href="#">d1i5za1</a>	Alignment	not modelled	99.0	35	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
100	<a href="#">c6g52H_</a>	Alignment	not modelled	99.0	16	<b>PDB header:</b> metal transport <b>Chain:</b> H: <b>PDB Molecule:</b> metal transporter cnm4; <b>PDBTitle:</b> crystal structure of the cnmp binding domain of the magnesium2 transporter cnm4
101	<a href="#">c6hq7B_</a>	Alignment	not modelled	98.1	31	<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
102	<a href="#">d1zyba1</a>	Alignment	not modelled	97.9	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> CAP C-terminal domain-like
						<b>PDB header:</b> transport protein

103	<a href="#">c6dj3B_</a>	Alignment	not modelled	97.3	17	<b>Chain:</b> B: <b>PDB Molecule:</b> metal transporter cnm2; <b>PDBTitle:</b> crystal structure of cnm2 cyclic nucleotide-binding homology domain
104	<a href="#">c2x4hA_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein sso2273; <b>PDBTitle:</b> crystal structure of the hypothetical protein sso2273 from <i>Sulfolobus solfataricus</i>
105	<a href="#">c2w48D_</a>	Alignment	not modelled	97.2	29	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from <i>Klebsiella pneumoniae</i>
106	<a href="#">c4go1A_</a>	Alignment	not modelled	97.1	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lsrr; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsrr from <i>E. coli</i> .
107	<a href="#">c1f5tA_</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> diphtheria toxin repressor (c102d mutant) complexed with nickel and dtxr consensus binding sequence
108	<a href="#">c2h09A_</a>	Alignment	not modelled	97.1	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> crystal structure of diphtheria toxin repressor like protein2 from <i>E. coli</i>
109	<a href="#">c2it0A_</a>	Alignment	not modelled	97.0	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent repressor ider; <b>PDBTitle:</b> crystal structure of a two-domain ider-dna complex crystal2 form ii
110	<a href="#">c5zc2B_</a>	Alignment	not modelled	97.0	9	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> p-hydroxyphenylacetate 3-hydroxylase, reductase component; <b>PDBTitle:</b> acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
111	<a href="#">c4q77B_</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator rot; <b>PDBTitle:</b> crystal structure of rot, a global regulator of virulence genes in <i>Staphylococcus aureus</i>
112	<a href="#">c1g3wA_</a>	Alignment	not modelled	96.9	20	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> diphtheria toxin repressor; <b>PDBTitle:</b> cd-cys102ser dtxr
113	<a href="#">d2d1ha1</a>	Alignment	not modelled	96.9	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
114	<a href="#">c4o6jA_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-dependent transcription repressor related protein; <b>PDBTitle:</b> crystal structure of <i>T. acidophilum</i> ider
115	<a href="#">d2fxaa1</a>	Alignment	not modelled	96.8	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
116	<a href="#">c5cviB_</a>	Alignment	not modelled	96.8	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> slor; <b>PDBTitle:</b> structure of the manganese regulator slor
117	<a href="#">d1g3wa1</a>	Alignment	not modelled	96.8	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Iron-dependent repressor protein
118	<a href="#">c5yhxH_</a>	Alignment	not modelled	96.8	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> H: <b>PDB Molecule:</b> zinc transport transcriptional regulator; <b>PDBTitle:</b> structure of <i>Lactococcus lactis</i> zitri, wild type
119	<a href="#">d3ctaa1</a>	Alignment	not modelled	96.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> MarR-like transcriptional regulators
120	<a href="#">c4nb5D_</a>	Alignment	not modelled	96.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> crystal structure of a transcriptional regulator