Phyre2

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Description	RVBD3728_(-)_4175051_4178248
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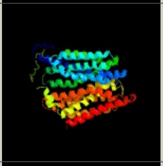
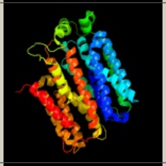
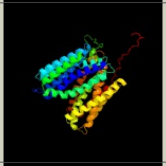
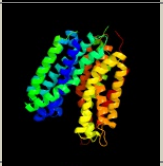
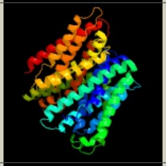
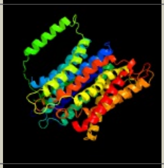
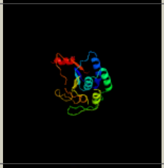
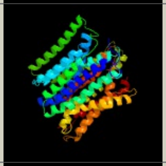
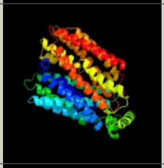
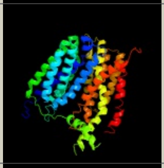
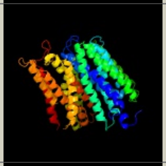
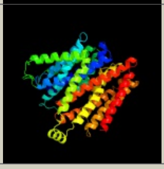
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fyaA_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**patatin-like protein, plpd; **PDBTitle:** cubic crystal of the native plpd
2	c4akfA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vipd; **PDBTitle:** crystal structure of vipd from legionella pneumophila
3	c4zp0A_	Alignment		100.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**multidrug transporter mdfa; **PDBTitle:** crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
4	d1pw4a_	Alignment		100.0	13	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
5	c4ldsB_	Alignment		100.0	16	**PDB header:**transport protein, membrane protein **Chain:** B: **PDB Molecule:**bicyclomycin resistance protein tcab; **PDBTitle:** the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
6	c3wdoA_	Alignment		100.0	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mfs transporter; **PDBTitle:** structure of e. coli yajr transporter
7	c6e9oA_	Alignment		100.0	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**d-galactonate transport; **PDBTitle:** e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
8	c6g9xB_	Alignment		100.0	18	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**major facilitator superfamily mfs_1; **PDBTitle:** crystal structure of a mfs transporter at 2.54 angstroem resolution
9	c2gfpA_	Alignment		100.0	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
10	c6gs7A_	Alignment		100.0	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dipeptide and tripeptide permease a; **PDBTitle:** crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
11	c4apsB_	Alignment		100.0	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**di-or tripeptide h+ symporter; **PDBTitle:** crystal structure of a pot family peptide transporter in an inward2 open conformation.

12	c3o7pA_	Alignment		100.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
13	c4ikyA_	Alignment		100.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**di-tripeptide abc transporter (permease); **PDBTitle:** crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
14	c4qmkB_	Alignment		100.0	28	**PDB header:**toxin **Chain:** B: **PDB Molecule:**type iii secretion system effector protein exou; **PDBTitle:** crystal structure of type iii effector protein exou (exou)
15	c6exsA_	Alignment		100.0	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**peptide abc transporter permease; **PDBTitle:** crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
16	c6ei3A_	Alignment		100.0	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**proton-dependent oligopeptide transporter family protein; **PDBTitle:** crystal structure of auto inhibited pot family peptide transporter
17	c6h7dA_	Alignment		100.0	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sugar transport protein 10; **PDBTitle:** crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
18	c4cl5B_	Alignment		100.0	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**nitrate transporter 1.1; **PDBTitle:** crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
19	c4w6vA_	Alignment		100.0	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**di-/tripeptide transporter; **PDBTitle:** crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
20	c4q65A_	Alignment		100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**dipeptide permease d; **PDBTitle:** structure of the e. coli peptide transporter ybgh
21	c4akxB_	Alignment	not modelled	100.0	21	**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
22	c2xutC_	Alignment	not modelled	100.0	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
23	c3tu3B_	Alignment	not modelled	100.0	18	**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
24	c4ybqB_	Alignment	not modelled	100.0	14	**PDB header:**transport protein/immune system **Chain:** B: **PDB Molecule:**solute carrier family 2, facilitated glucose transporter **PDBTitle:** rat glut5 with fv in the outward-open form
25	c4pypA_	Alignment	not modelled	100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute carrier family 2, facilitated glucose transporter **PDBTitle:** crystal structure of the human glucose transporter glut1
26	c5c65A_	Alignment	not modelled	100.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute carrier family 2, facilitated glucose transporter **PDBTitle:** structure of the human glucose transporter glut3 / slc2a3
27	d1oxwa_	Alignment	not modelled	100.0	19	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Patatin
28	c4gbzA_	Alignment	not modelled	100.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**d-xylose-proton symporter; **PDBTitle:** the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose

29	c4j05A_	Alignment	not modelled	100.0	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**phosphate transporter; **PDBTitle:** crystal structure of a eukaryotic phosphate transporter
30	c4lepB_	Alignment	not modelled	100.0	12	**PDB header:**membrane protein, tranport protein **Chain:** B: **PDB Molecule:**proton:oligopeptide symporter pot family; **PDBTitle:** structural insights into substrate recognition in proton dependent2 oligopeptide transporters
31	c5aynA_	Alignment	not modelled	100.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute carrier family 39 (iron-regulated transporter); **PDBTitle:** crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
32	c4iu8A_	Alignment	not modelled	99.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrite extrusion protein 2; **PDBTitle:** crystal structure of a membrane transporter (selenomethionine2 derivative)
33	c1pv7B_	Alignment	not modelled	99.9	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**lactose permease; **PDBTitle:** crystal structure of lactose permease with tdg
34	d1pv7a_	Alignment	not modelled	99.9	14	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
35	c4iu9A_	Alignment	not modelled	99.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nitrite extrusion protein 2; **PDBTitle:** crystal structure of a membrane transporter
36	c6aunB_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pla2g6, ipla2beta; **PDBTitle:** calcium-independent phospholipase a2 beta
37	c5aymA_	Alignment	not modelled	99.9	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**solute carrier family 39 (iron-regulated transporter); **PDBTitle:** crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
38	c4orfA_	Alignment	not modelled	99.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase pat; **PDBTitle:** camp-binding acyltransferase from mycobacterium smegmatis, mutant r95k
39	c4avcA_	Alignment	not modelled	99.7	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
40	c5jonA_	Alignment	not modelled	99.6	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**maltose-binding periplasmic protein,potassium/sodium **PDBTitle:** crystal structure of the unliganded form of hcn2 cnbd
41	c6ob7A_	Alignment	not modelled	99.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**equilibrative nucleoside transporter 1; **PDBTitle:** human equilibrative nucleoside transporter-1, dilazep bound
42	c4m64D_	Alignment	not modelled	99.6	9	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**melibiose carrier protein; **PDBTitle:** 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
43	c6hq2A_	Alignment	not modelled	99.6	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**eal enzyme bd1971; **PDBTitle:** structure of eal enzyme bd1971 - apo form
44	c4chwB_	Alignment	not modelled	99.6	24	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cyclic nucleotide-gated potassium channel mll3241; **PDBTitle:** the electron crystallography structure of the camp-free potassium2 channel mlok1
45	c3gydA_	Alignment	not modelled	99.6	20	**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
46	c4myiA_	Alignment	not modelled	99.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cgmp-dependent protein kinase, putative; **PDBTitle:** crystal structure of pvx_084705
47	c6g52H_	Alignment	not modelled	99.5	23	**PDB header:**metal transport **Chain:** H: **PDB Molecule:**metal transporter cnnm4; **PDBTitle:** crystal structure of the cnmp binding domain of the magnesium2 transporter cnnm4
48	c3j4qC_	Alignment	not modelled	99.5	22	**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
49	c2pqqD_	Alignment	not modelled	99.5	26	**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)
50	d2h6ca2	Alignment	not modelled	99.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
51	d1ft9a2	Alignment	not modelled	99.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**CO-sensing protein CooA, N-terminal domain
52	c2byvE_	Alignment	not modelled	99.5	31	**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
53	c4rfaA_	Alignment	not modelled	99.5	9	**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

54	d2coha2	Alignment	not modelled	99.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
55	d1ne6a2	Alignment	not modelled	99.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
56	c4dinB_	Alignment	not modelled	99.4	20	**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
57	d2oz6a2	Alignment	not modelled	99.4	27	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
58	d2gaua2	Alignment	not modelled	99.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
59	c1o5lA_	Alignment	not modelled	99.4	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
60	d1o5la1	Alignment	not modelled	99.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
61	d3e5ua2	Alignment	not modelled	99.4	12	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
62	c3of1A_	Alignment	not modelled	99.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**camp-dependent protein kinase regulatory subunit; **PDBTitle:** crystal structure of bcy1, the yeast regulatory subunit of pka
63	d1zyba2	Alignment	not modelled	99.4	12	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
64	d1cx4a1	Alignment	not modelled	99.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
65	d1cx4a2	Alignment	not modelled	99.4	20	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
66	c5v30B_	Alignment	not modelled	99.4	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
67	c5v4sB_	Alignment	not modelled	99.4	26	**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
68	c3idcB_	Alignment	not modelled	99.4	20	**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
69	c1o7fA_	Alignment	not modelled	99.4	31	**PDB header:**regulation **Chain:** A: **PDB Molecule:**camp-dependent rap1 guanine-nucleotide exchange **PDBTitle:** crystal structure of the regulatory domain of epac2
70	c5bv6A_	Alignment	not modelled	99.4	18	**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
71	c6ftfB_	Alignment	not modelled	99.4	20	**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
72	c3mdpA_	Alignment	not modelled	99.4	17	**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
73	c3iwzB_	Alignment	not modelled	99.4	22	**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
74	c3pvbB_	Alignment	not modelled	99.4	24	**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
75	c3dn7A_	Alignment	not modelled	99.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cyclic nucleotide binding regulatory protein; **PDBTitle:** cyclic nucleotide binding regulatory protein from cytophaga2 hutchinsonii.
76	c5d1iB_	Alignment	not modelled	99.3	22	**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
77	d1i5za2	Alignment	not modelled	99.3	24	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
						PDB header:transport protein

78	c5h3oA_	Alignment	not modelled	99.3	28	**Chain:** A: **PDB Molecule:**cyclic nucleotide-gated cation channel; **PDBTitle:** structure of a eukaryotic cyclic nucleotide-gated channel
79	c3shrA_	Alignment	not modelled	99.3	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
80	c3cf6E_	Alignment	not modelled	99.3	25	**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
81	c3tnqA_	Alignment	not modelled	99.3	22	**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
82	c1cx4A_	Alignment	not modelled	99.3	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
83	c5u6pA_	Alignment	not modelled	99.3	23	**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
84	c5kbfA_	Alignment	not modelled	99.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**camp-dependent protein kinase regulatory subunit, putative; **PDBTitle:** camp bound pfpka-r (141-441)
85	c5j3uA_	Alignment	not modelled	99.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase a; **PDBTitle:** co-crystal structure of the regulatory domain of toxoplasma gondii pka2 with camp
86	c4ev0A_	Alignment	not modelled	99.3	32	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**transcription regulator, crp family; **PDBTitle:** crystal structure of thermus thermophilus catabolite activator protein
87	d1vp6a_	Alignment	not modelled	99.3	25	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
88	c5t3nB_	Alignment	not modelled	99.3	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**camp-dependent protein kinase regulatory subunit; **PDBTitle:** sp-2cl-camps bound to pkar cbd2
89	c1rgsA_	Alignment	not modelled	99.3	19	**PDB header:**kinase **Chain:** A: **PDB Molecule:**camp dependent protein kinase; **PDBTitle:** regulatory subunit of camp dependent protein kinase
90	c6cjtB_	Alignment	not modelled	99.3	28	**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
91	c4kg1A_	Alignment	not modelled	99.3	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diguanylate cyclase; **PDBTitle:** cgmp-responsive diguanylate cyclase
92	d1ne6a1	Alignment	not modelled	99.3	24	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
93	c2ptmA_	Alignment	not modelled	99.3	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hyperpolarization-activated (ih) channel; **PDBTitle:** structure and rearrangements in the carboxy-terminal region of spih2 channels
94	c3ogjD_	Alignment	not modelled	99.2	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**prkg1 protein; **PDBTitle:** crystal structure of partial apo (92-227) of cgmp-dependent protein2 kinase
95	c2bgcA_	Alignment	not modelled	99.2	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prfa; **PDBTitle:** prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
96	d1wgpa_	Alignment	not modelled	99.2	19	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
97	c2z69A_	Alignment	not modelled	99.2	21	**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
98	c3fx3A_	Alignment	not modelled	99.2	18	**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
99	c4d7sB_	Alignment	not modelled	99.2	27	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sthk_cnbd_cgmp; **PDBTitle:** structure of the sthk carboxy-terminal region in complex with cgmp
100	c1zybA_	Alignment	not modelled	99.2	12	**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
101	c5c8wB_	Alignment	not modelled	99.2	23	**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
102	c3otfA_	Alignment	not modelled	99.2	23	**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
						PDB header:metal transport/calcium binding protein

103	c5k7lA_	Alignment	not modelled	99.2	30	**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
104	c3dv8A_	Alignment	not modelled	99.2	14	**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
105	d1o7fa2	Alignment	not modelled	99.2	27	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
106	c3e97A_	Alignment	not modelled	99.2	27	**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
107	c5va1A_	Alignment	not modelled	99.1	27	**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
108	c5w5aB_	Alignment	not modelled	99.1	22	**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)
109	c3kccA_	Alignment	not modelled	99.1	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**catabolite gene activator; **PDBTitle:** crystal structure of d138l mutant of catabolite gene activator protein
110	c3d0sA_	Alignment	not modelled	99.1	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** camp receptor protein from m.tuberculosis, camp-free form
111	d1q3ea_	Alignment	not modelled	99.1	22	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
112	c3la2A_	Alignment	not modelled	99.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**global nitrogen regulator; **PDBTitle:** crystal structure of ntca in complex with 2-oxoglutarate
113	c2zdbA_	Alignment	not modelled	99.1	10	**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
114	c1zreB_	Alignment	not modelled	99.0	25	**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
115	c3uknC_	Alignment	not modelled	99.0	23	**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
116	c4f8aA_	Alignment	not modelled	99.0	31	**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
117	c3e6dA_	Alignment	not modelled	99.0	11	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**cyclic nucleotide-binding protein; **PDBTitle:** crystal structure of cprk c200s
118	d1o7fa3	Alignment	not modelled	99.0	28	**Fold:**Double-stranded beta-helix **Superfamily:**cAMP-binding domain-like **Family:**cAMP-binding domain
119	c6hq7B_	Alignment	not modelled	99.0	30	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**eal enzyme bd1971; **PDBTitle:** structure of eal enzyme bd1971 - cgmp bound form
120	d1cjya2	Alignment	not modelled	99.0	20	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Lysophospholipase