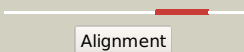

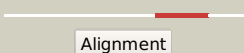

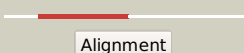


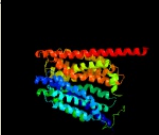




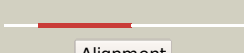

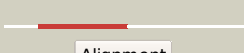









# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3239c_(-)_3614454_3617600
Date	Thu Aug 8 16:20:44 BST 2019
Unique Job ID	4f03de76a6fa1615

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5fyaA_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> patatin-like protein, plpd; <b>PDBTitle:</b> cubic crystal of the native plpd
2	<a href="#">c4akfA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vipd; <b>PDBTitle:</b> crystal structure of vipd from legionella pneumophila
3	<a href="#">c4zp0A_</a>	 Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug transporter mdfa; <b>PDBTitle:</b> crystal structure of e. coli multidrug transporter mdfa in complex2 with deoxycholate
4	<a href="#">d1pw4a_</a>	 Alignment		100.0	14	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
5	<a href="#">c4ldsB_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> bicyclomycin resistance protein tcb; <b>PDBTitle:</b> the inward-facing structure of the glucose transporter from2 staphylococcus epidermidis
6	<a href="#">c6e9oA_</a>	 Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactonate transport; <b>PDBTitle:</b> e. coli d-galactonate:proton symporter mutant e133q in the outward2 substrate-bound form
7	<a href="#">c3wdoA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> mfs transporter; <b>PDBTitle:</b> structure of e. coli yajr transporter
8	<a href="#">c6g9xB_</a>	 Alignment		100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> major facilitator superfamily mfs_1; <b>PDBTitle:</b> crystal structure of a mfs transporter at 2.54 angstrom resolution
9	<a href="#">c3o7pA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose-proton symporter; <b>PDBTitle:</b> crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
10	<a href="#">c6gs7A_</a>	 Alignment		100.0	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide and tripeptide permease a; <b>PDBTitle:</b> crystal structure of peptide transporter dtpa-nanobody in glycine2 buffer
11	<a href="#">c2gfpA_</a>	 Alignment		100.0	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein d; <b>PDBTitle:</b> structure of the multidrug transporter emrd from2 escherichia coli

12	<a href="#">c4qmkB_</a>	Alignment		100.0	27	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> type iii secretion system effector protein exou; <b>PDBTitle:</b> crystal structure of type iii effector protein exou (exou)
13	<a href="#">c6h7dA_</a>	Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar transport protein 10; <b>PDBTitle:</b> crystal structure of a. thaliana sugar transport protein 10 in complex2 with glucose in the outward occluded state
14	<a href="#">c4apsB_</a>	Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> di- or tripeptide h+ symporter; <b>PDBTitle:</b> crystal structure of a pot family peptide transporter in an inward2 open conformation.
15	<a href="#">c4ikyA_</a>	Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-tripeptide abc transporter (permease); <b>PDBTitle:</b> crystal structure of peptide transporter pot (e310q mutant) in complex2 with sulfate
16	<a href="#">c6exsA_</a>	Alignment		100.0	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptide abc transporter permease; <b>PDBTitle:</b> crystal structure of a pot family transporter in complex with2 thioalcohol conjugated peptide.
17	<a href="#">c6ei3A_</a>	Alignment		100.0	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> proton-dependent oligopeptide transporter family protein; <b>PDBTitle:</b> crystal structure of auto inhibited pot family peptide transporter
18	<a href="#">c4cl5B_</a>	Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> nitrate transporter 1.1; <b>PDBTitle:</b> crystal structure of the nitrate transporter nrt1.1 from2 arabidopsis thaliana in complex with nitrate.
19	<a href="#">c3tu3B_</a>	Alignment		100.0	21	<b>PDB header:</b> toxin/toxin chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> exou; <b>PDBTitle:</b> 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
20	<a href="#">c4akxB_</a>	Alignment		100.0	21	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> exou; <b>PDBTitle:</b> structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
21	<a href="#">c4w6vA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> di-/tripeptide transporter; <b>PDBTitle:</b> crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
22	<a href="#">c4ybgB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> rat glut5 with fv in the outward-open form
23	<a href="#">c2xutC_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> proton/peptide symporter family protein; <b>PDBTitle:</b> crystal structure of a proton dependent oligopeptide (pot) family2 transporter.
24	<a href="#">c4q65A_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptide permease d; <b>PDBTitle:</b> structure of the e. coli peptide transporter ybgh
25	<a href="#">c4ppyA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> crystal structure of the human glucose transporter glut1
26	<a href="#">c5c65A_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 2, facilitated glucose transporter <b>PDBTitle:</b> structure of the human glucose transporter glut3 / slc2a3
27	<a href="#">d1oxwa_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> FabD/lysophospholipase-like <b>Superfamily:</b> FabD/lysophospholipase-like <b>Family:</b> Patatin
28	<a href="#">c4gbzA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> d-xylose-proton symporter; <b>PDBTitle:</b> the structure of the mfs (major facilitator superfamily) proton:xylose2 symporter xyle bound to d-glucose <b>PDB header:</b> transport protein

29	<a href="#">c5aynA</a>	Alignment	not modelled	100.0	16	<b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state
30	<a href="#">c4j05A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphate transporter; <b>PDBTitle:</b> crystal structure of a eukaryotic phosphate transporter
31	<a href="#">c4lepB</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> membrane protein, tranport protein <b>Chain:</b> B: <b>PDB Molecule:</b> proton:oligopeptide symporter pot family; <b>PDBTitle:</b> structural insights into substrate recognition in proton dependent2 oligopeptide transporters
32	<a href="#">c6aunB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> pla2g6, ipla2beta; <b>PDBTitle:</b> calcium-independent phospholipase a2 beta
33	<a href="#">c4iu8A</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter (selenomethionine2 derivative)
34	<a href="#">c1pv7B</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lactose permease; <b>PDBTitle:</b> crystal structure of lactose permease with tdg
35	<a href="#">d1pv7a</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
36	<a href="#">c4iu9A</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrite extrusion protein 2; <b>PDBTitle:</b> crystal structure of a membrane transporter
37	<a href="#">c5aymA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> solute carrier family 39 (iron-regulated transporter); <b>PDBTitle:</b> crystal structure of a bacterial homologue of iron transporter2 ferroportin in outward-facing state with soaked iron
38	<a href="#">c4orfA</a>	Alignment	not modelled	99.9	28	<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
39	<a href="#">c4avcA</a>	Alignment	not modelled	99.9	23	<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
40	<a href="#">c5jonA</a>	Alignment	not modelled	99.8	28	<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
41	<a href="#">c4chwB</a>	Alignment	not modelled	99.8	29	<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
42	<a href="#">c4myiA</a>	Alignment	not modelled	99.8	19	<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
43	<a href="#">c3gydA</a>	Alignment	not modelled	99.8	24	<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
44	<a href="#">c3mdpA</a>	Alignment	not modelled	99.7	19	<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
45	<a href="#">c3pvbB</a>	Alignment	not modelled	99.7	29	<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
46	<a href="#">c5t3nB</a>	Alignment	not modelled	99.7	23	<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="#">d2gaua2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
48	<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
49	<a href="#">c2pqqD</a>	Alignment	not modelled	99.7	38	<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)
50	<a href="#">c2byvE</a>	Alignment	not modelled	99.7	28	<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
51	<a href="#">d1cx4a2</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
52	<a href="#">c5u6pA</a>	Alignment	not modelled	99.7	26	<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
53	<a href="#">d1ne6a1</a>	Alignment	not modelled	99.7	27	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like

						<b>Family:</b> cAMP-binding domain
54	<a href="#">c6ob7A_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> equilibrative nucleoside transporter 1; <b>PDBTitle:</b> human equilibrative nucleoside transporter-1, dilazep bound
55	<a href="#">c3j4qC_</a>	Alignment	not modelled	99.7	24	<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
56	<a href="#">c3ogjD_</a>	Alignment	not modelled	99.7	26	<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
57	<a href="#">c2z69A_</a>	Alignment	not modelled	99.7	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
58	<a href="#">d1ne6a2</a>	Alignment	not modelled	99.7	26	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
59	<a href="#">c1o7fA_</a>	Alignment	not modelled	99.6	26	<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
60	<a href="#">c5bv6A_</a>	Alignment	not modelled	99.6	23	<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
61	<a href="#">d1cx4a1</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
62	<a href="#">c3cf6E_</a>	Alignment	not modelled	99.6	28	<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
63	<a href="#">c5c8wB_</a>	Alignment	not modelled	99.6	25	<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
64	<a href="#">c5j3uA_</a>	Alignment	not modelled	99.6	30	<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
65	<a href="#">c3otfA_</a>	Alignment	not modelled	99.6	27	<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
66	<a href="#">c5v4sB_</a>	Alignment	not modelled	99.6	33	<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
67	<a href="#">d1vp6a_</a>	Alignment	not modelled	99.6	29	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
68	<a href="#">c3of1A_</a>	Alignment	not modelled	99.6	30	<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
69	<a href="#">c5v30B_</a>	Alignment	not modelled	99.6	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
70	<a href="#">c3idcB_</a>	Alignment	not modelled	99.6	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
71	<a href="#">c6g52H_</a>	Alignment	not modelled	99.6	25	<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
72	<a href="#">c4m64D_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> melibiose carrier protein; <b>PDBTitle:</b> 3d crystal structure of na+/melibiose symporter of salmonella2 typhimurium
73	<a href="#">c5d1iB_</a>	Alignment	not modelled	99.6	29	<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
74	<a href="#">c5kbfA_</a>	Alignment	not modelled	99.6	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)
75	<a href="#">c5k7IA_</a>	Alignment	not modelled	99.6	23	<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
76	<a href="#">c5h3oA_</a>	Alignment	not modelled	99.6	27	<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
77	<a href="#">d1wgpA_</a>	Alignment	not modelled	99.6	24	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
						<b>PDB header:</b> transport protein

78	<a href="#">c2ptmA</a>	Alignment	not modelled	99.6	23	<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
79	<a href="#">c4dinB</a>	Alignment	not modelled	99.6	29	<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
80	<a href="#">c3dn7A</a>	Alignment	not modelled	99.6	11	<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.
81	<a href="#">c5va1A</a>	Alignment	not modelled	99.6	25	<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
82	<a href="#">c1zybA</a>	Alignment	not modelled	99.6	18	<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
83	<a href="#">c4f8aA</a>	Alignment	not modelled	99.6	24	<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
84	<a href="#">c4kg1A</a>	Alignment	not modelled	99.6	32	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diguanylate cyclase; <b>PDBTitle:</b> cgmp-responsive diguanylate cyclase
85	<a href="#">c4d7sB</a>	Alignment	not modelled	99.6	32	<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
86	<a href="#">c6cjtB</a>	Alignment	not modelled	99.5	33	<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
87	<a href="#">c4ev0A</a>	Alignment	not modelled	99.5	32	<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
88	<a href="#">c3fx3A</a>	Alignment	not modelled	99.5	18	<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
89	<a href="#">d1o7fa2</a>	Alignment	not modelled	99.5	25	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
90	<a href="#">d1q3ea</a>	Alignment	not modelled	99.5	28	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
91	<a href="#">d1o7fa3</a>	Alignment	not modelled	99.5	28	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
92	<a href="#">c6ftfB</a>	Alignment	not modelled	99.5	29	<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
93	<a href="#">c1cx4A</a>	Alignment	not modelled	99.5	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
94	<a href="#">c3e97A</a>	Alignment	not modelled	99.5	26	<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
95	<a href="#">c6hq2A</a>	Alignment	not modelled	99.5	40	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> seal enzyme bd1971; <b>PDBTitle:</b> structure of eal enzyme bd1971 - apo form
96	<a href="#">d3e5ua2</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
97	<a href="#">c3tnqA</a>	Alignment	not modelled	99.5	21	<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
98	<a href="#">d2h6ca2</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
99	<a href="#">d1ft9a2</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> CO-sensing protein CooA, N-terminal domain
100	<a href="#">c4lloE</a>	Alignment	not modelled	99.5	24	<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
101	<a href="#">c3iwzB</a>	Alignment	not modelled	99.5	27	<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



102	<a href="#">c3shrA_</a>	Alignment	not modelled	99.5	26	<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
103	<a href="#">c2d93A_</a>	Alignment	not modelled	99.5	24	<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
104	<a href="#">d2oz6a2</a>	Alignment	not modelled	99.5	31	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
105	<a href="#">c3dv8A_</a>	Alignment	not modelled	99.5	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
106	<a href="#">c3uknC_</a>	Alignment	not modelled	99.5	27	<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/cnbhd of zelk channels in c 2 2 21 space2 group
107	<a href="#">d1o5la1</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
108	<a href="#">c1o5IA_</a>	Alignment	not modelled	99.4	18	<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
109	<a href="#">c5w5aB_</a>	Alignment	not modelled	99.4	22	<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)
110	<a href="#">d2coha2</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
111	<a href="#">c1rgsA_</a>	Alignment	not modelled	99.4	25	<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
112	<a href="#">c2n7gA_</a>	Alignment	not modelled	99.4	24	<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
113	<a href="#">c3d0sA_</a>	Alignment	not modelled	99.4	27	<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
114	<a href="#">d1i5za2</a>	Alignment	not modelled	99.4	29	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
115	<a href="#">c3dkwB_</a>	Alignment	not modelled	99.4	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.
116	<a href="#">c4l11A_</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> agap007709-pa; <b>PDBTitle:</b> structure of the c-linker/cnbhd of agerg channels
117	<a href="#">c4rfaA_</a>	Alignment	not modelled	99.3	12	<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
118	<a href="#">c5e44A_</a>	Alignment	not modelled	99.3	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
119	<a href="#">c2bgcA_</a>	Alignment	not modelled	99.3	9	<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
120	<a href="#">c3kccA_</a>	Alignment	not modelled	99.2	30	<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