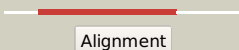

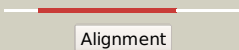

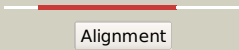

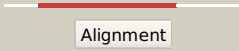

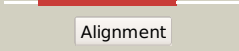

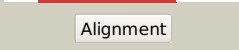

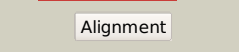

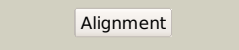

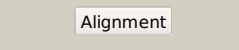



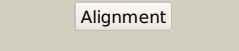



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0104 (-)_122314_123828
Date	Tue Jul 23 14:50:14 BST 2019
Unique Job ID	ae6e22c5cc8f4791

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5hm8C_	 Alignment		100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.
2	c3dhyC_	 Alignment		100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
3	c5v96A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
4	c3oneA_	 Alignment		100.0	18	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
5	c1v8bA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
6	c3n58D_	 Alignment		100.0	21	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
7	c3d64A_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
8	c6aphA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
9	c6f3oC_	 Alignment		100.0	20	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
10	c3x2fa_	 Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
11	c3gvpB_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3

12	c1d4fD_	Alignment		100.0	17	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
13	d1li4a2	Alignment		100.0	16	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
14	d1v8ba2	Alignment		100.0	17	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: S-adenosylhomocystein hydrolase
15	d1li4a1	Alignment		99.9	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
16	d1v8ba1	Alignment		99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
17	c4orfA_	Alignment		99.8	31	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase pat; PDBTitle: camp-binding acyltransferase from mycobacterium smegmatis, mutant r95k
18	c4avcA_	Alignment		99.8	31	PDB header: transferase Chain: A: PDB Molecule: lysine acetyltransferase; PDBTitle: crystal structure of protein lysine acetyltransferase rv09982 in complex with acetyl coa and camp
19	c5jonA_	Alignment		99.8	24	PDB header: transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,potassium/sodium PDBTitle: crystal structure of the unliganded form of hcn2 cnbd
20	c4chwB_	Alignment		99.8	28	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
21	c4myiA_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase, putative; PDBTitle: crystal structure of pvx_084705
22	c5u6pA_	Alignment	not modelled	99.8	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
23	c5h3oA_	Alignment	not modelled	99.7	22	PDB header: transport protein Chain: A: PDB Molecule: cyclic nucleotide-gated cation channel; PDBTitle: structure of a eukaryotic cyclic nucleotide-gated channel
24	d1ne6a1	Alignment	not modelled	99.7	28	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
25	c2byvE_	Alignment	not modelled	99.7	26	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
26	c3j4qC_	Alignment	not modelled	99.7	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
27	c5k7lA_	Alignment	not modelled	99.7	21	PDB header: metal transport/calcium binding protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: single particle cryo-em structure of the voltage-gated k+ channel eag12 bound to the channel inhibitor calmodulin
						PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel

28	c5va1A	Alignment	not modelled	99.7	21	subfamily h member 2; PDBTitle: cryo-em structure of the human ether-a-go-go related k+ channel
29	c3gydA	Alignment	not modelled	99.7	18	PDB header: dna binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding domain; PDBTitle: crystal structure of a cyclic nucleotide-binding domain (mf1a_1926)2 from methylobacillus flagellatus kt at 1.79 a resolution
30	c6g52H	Alignment	not modelled	99.7	16	PDB header: metal transport Chain: H: PDB Molecule: metal transporter cnm4; PDBTitle: crystal structure of the cnmp binding domain of the magnesium2 transporter cnm4
31	c3otfA	Alignment	not modelled	99.7	26	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
32	c3pvbB	Alignment	not modelled	99.7	27	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
33	c4dinB	Alignment	not modelled	99.7	31	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
34	c5t3nB	Alignment	not modelled	99.7	26	PDB header: transferase Chain: B: PDB Molecule: camp-dependent protein kinase regulatory subunit; PDBTitle: sp-2cl-camps bound to pkar cbd2
35	c5v4sB	Alignment	not modelled	99.7	27	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
36	d1zyba2	Alignment	not modelled	99.7	15	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
37	c3dn7A	Alignment	not modelled	99.7	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cyclic nucleotide binding regulatory protein; PDBTitle: cyclic nucleotide binding regulatory protein from cytophaga2 hutchesonii.
38	c5bv6A	Alignment	not modelled	99.6	20	PDB header: transferase Chain: A: PDB Molecule: cgmp-dependent protein kinase 2; PDBTitle: pkg ii's carboxyl terminal cyclic nucleotide binding domain (cnb-b) in2 a complex with cgmp
39	d1cx4a2	Alignment	not modelled	99.6	24	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
40	d2gaua2	Alignment	not modelled	99.6	17	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
41	c3cf6E	Alignment	not modelled	99.6	23	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
42	c2ptmA	Alignment	not modelled	99.6	23	PDB header: transport protein Chain: A: PDB Molecule: hyperpolarization-activated (ih) channel; PDBTitle: structure and rearrangements in the carboxy-terminal region of spih2 channels
43	c2pqqD	Alignment	not modelled	99.6	18	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)
44	d1cx4a1	Alignment	not modelled	99.6	24	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
45	c1o7fA	Alignment	not modelled	99.6	28	PDB header: regulation Chain: A: PDB Molecule: camp-dependent rap1 guanine-nucleotide exchange PDBTitle: crystal structure of the regulatory domain of epac2
46	c3ogjD	Alignment	not modelled	99.6	21	PDB header: transferase Chain: D: PDB Molecule: prkg1 protein; PDBTitle: crystal structure of partial apo (92-227) of cgmp-dependent protein2 kinase
47	c5c8wB	Alignment	not modelled	99.6	25	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
48	c3mdpA	Alignment	not modelled	99.6	15	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
49	c6cjtB	Alignment	not modelled	99.6	23	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
50	d1q3ea	Alignment	not modelled	99.6	24	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
51	d3e5ua2	Alignment	not modelled	99.6	14	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
						PDB header: transferase

52	c5kbfA_	Alignment	not modelled	99.6	24	Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit, putative; PDBTitle: camp bound pfpka-r (141-441)
53	c3idcB_	Alignment	not modelled	99.6	24	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
54	c3shrA_	Alignment	not modelled	99.6	29	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
55	c2z69A_	Alignment	not modelled	99.6	22	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
56	d1o5la1	Alignment	not modelled	99.6	15	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
57	c1o5IA_	Alignment	not modelled	99.6	15	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
58	d1ne6a2	Alignment	not modelled	99.6	29	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
59	c3of1A_	Alignment	not modelled	99.6	26	PDB header: transferase Chain: A: PDB Molecule: camp-dependent protein kinase regulatory subunit; PDBTitle: crystal structure of bcy1, the yeast regulatory subunit of pka
60	d2h6ca2	Alignment	not modelled	99.6	12	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
61	c4d7sB_	Alignment	not modelled	99.6	23	PDB header: transport protein Chain: B: PDB Molecule: sthk_cnbd_cgmp; PDBTitle: structure of the sthk carboxy-terminal region in complex with cgmp
62	c4f8aA_	Alignment	not modelled	99.6	21	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
63	c5v30B_	Alignment	not modelled	99.6	18	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the sensor domain of the transcriptional2 regulator hcpr from porphyromonas gingivalis
64	d1ft9a2	Alignment	not modelled	99.6	20	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: CO-sensing protein CooA, N-terminal domain
65	c4lloE_	Alignment	not modelled	99.6	21	PDB header: transport protein Chain: E: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: structure of the eag domain-cnbd complex of the mouse eag1 channel
66	d1wgpa_	Alignment	not modelled	99.6	21	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
67	d2coha2	Alignment	not modelled	99.5	20	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
68	c6ftfB_	Alignment	not modelled	99.5	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
69	d1vp6a_	Alignment	not modelled	99.5	28	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
70	d1o7fa3	Alignment	not modelled	99.5	24	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
71	d2oz6a2	Alignment	not modelled	99.5	24	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
72	c4kg1A_	Alignment	not modelled	99.5	24	PDB header: lyase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: cgmp-responsive diguanylate cyclase
73	c2bgcA_	Alignment	not modelled	99.5	7	PDB header: transcription Chain: A: PDB Molecule: prfa; PDBTitle: prfa-g145s, a constitutive active mutant of the2 transcriptional regulator in l.monocytogenes
74	c3uknC_	Alignment	not modelled	99.5	25	PDB header: transport protein, membrane protein Chain: C: PDB Molecule: novel protein similar to vertebrate potassium voltage-gated PDBTitle: structure of the c-linker/cnbd of zelk channels in c 2 2 21 space2 group
75	d1i5za2	Alignment	not modelled	99.5	25	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
76	c3iwzB_	Alignment	not modelled	99.5	19	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 PDB header: oxidoreductase

77	c1wwkA	Alignment	not modelled	99.5	17	Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
78	c5d1iB	Alignment	not modelled	99.5	24	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
79	c1cx4A	Alignment	not modelled	99.5	25	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
80	c3fx3A	Alignment	not modelled	99.5	17	PDB header: camp-binding protein Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: structure of a putative camp-binding regulatory protein from 2 silicibacter pomeroyi dss-3
81	c4rfaA	Alignment	not modelled	99.5	11	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
82	c3tnqA	Alignment	not modelled	99.5	29	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
83	d1o7fa2	Alignment	not modelled	99.5	26	Fold: Double-stranded beta-helix Superfamily: cAMP-binding domain-like Family: cAMP-binding domain
84	c2n7gA	Alignment	not modelled	99.5	21	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: structure of the cyclic nucleotide-binding homology domain of the herg2 channel
85	c1zybA	Alignment	not modelled	99.5	14	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
86	c2g76A	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
87	c1gdhA	Alignment	not modelled	99.5	18	PDB header: oxidoreductase(choh (d)-nad(p)+ (a)) Chain: A: PDB Molecule: d-glycerate dehydrogenase; PDBTitle: crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
88	c1rgsA	Alignment	not modelled	99.5	30	PDB header: kinase Chain: A: PDB Molecule: camp dependent protein kinase; PDBTitle: regulatory subunit of camp dependent protein kinase
89	c3d4oA	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
90	c2eklA	Alignment	not modelled	99.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfobolus tokodaii
91	c4ev0A	Alignment	not modelled	99.5	22	PDB header: transcription activator Chain: A: PDB Molecule: transcription regulator, crp family; PDBTitle: crystal structure of thermus thermophilus catabolite activator protein
92	c2d93A	Alignment	not modelled	99.4	16	PDB header: signaling protein Chain: A: PDB Molecule: rap guanine nucleotide exchange factor 6; PDBTitle: solution structure of the cnmp_binding domain of human rap2 guanine nucleotide exchange factor 6
93	c5j3uA	Alignment	not modelled	99.4	27	PDB header: transferase Chain: A: PDB Molecule: protein kinase a; PDBTitle: co-crystal structure of the regulatory domain of toxoplasma gondii pka2 with camp
94	c4l11A	Alignment	not modelled	99.4	21	PDB header: metal transport Chain: A: PDB Molecule: agap007709-pa; PDBTitle: structure of the c-linker/cnbhd of agerg channels
95	c3e97A	Alignment	not modelled	99.4	16	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
96	c3dv8A	Alignment	not modelled	99.4	18	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
97	c4e5kC	Alignment	not modelled	99.4	16	PDB header: oxidoreductase Chain: C: PDB Molecule: phosphite dehydrogenase (thermostable variant); PDBTitle: thermostable phosphite dehydrogenase in complex with nad and sulfite
98	c2dbqA	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
99	c6ih2B	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphite dehydrogenase; PDBTitle: crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
100	c2rirA	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
101	c2zdbA	Alignment	not modelled	99.3	19	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
102	c4njmA	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
103	c2cukC	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
104	c3kccA	Alignment	not modelled	99.3	25	PDB header: transcription Chain: A: PDB Molecule: catabolite gene activator; PDBTitle: crystal structure of d138l mutant of catabolite gene activator protein
105	c3la2A	Alignment	not modelled	99.3	18	PDB header: transcription Chain: A: PDB Molecule: global nitrogen regulator; PDBTitle: crystal structure of ntca in complex with 2-oxoglutarate
106	c3d0sA	Alignment	not modelled	99.3	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: camp receptor protein from m.tuberculosis, camp-free form
107	c1zreB	Alignment	not modelled	99.3	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
108	c3evtA	Alignment	not modelled	99.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
109	d1a4ia1	Alignment	not modelled	99.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
110	c5w5aB	Alignment	not modelled	99.3	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)
111	c3bazA	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coles blumei in2 complex with nadp+
112	c2w2kB	Alignment	not modelled	99.3	11	PDB header: oxidoreductase Chain: B: PDB Molecule: d-mandelate dehydrogenase; PDBTitle: crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
113	c1j4aA	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
114	c3k5pA	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
115	d2naca1	Alignment	not modelled	99.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
116	d1ygya1	Alignment	not modelled	99.2	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
117	c3e6dA	Alignment	not modelled	99.2	13	PDB header: transcription regulation Chain: A: PDB Molecule: cyclic nucleotide-binding protein; PDBTitle: crystal structure of cprk c200s
118	c5tx7A	Alignment	not modelled	99.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase family PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from desulfovibrio vulgaris
119	c1ybaC	Alignment	not modelled	99.2	22	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
120	d1dxya1	Alignment	not modelled	99.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain