



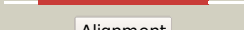

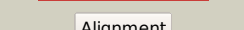

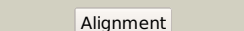




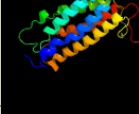
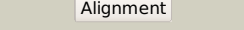

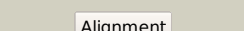

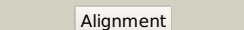


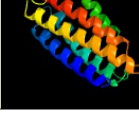


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1314c_(-)_1469677_1470258
Date	Wed Jul 31 22:05:41 BST 2019
Unique Job ID	bc021ec6590e25a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ci1A_</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cobalamin adenosyltransferase pduo-like protein; <b>PDBTitle:</b> structure of the pduo-type atp:co(i)rrinoid adenosyltransferase from2 lactobacillus reuteri complexed with four-coordinate cob(ii)alamin3 and atp
2	<a href="#">c2nt8A_</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cobalamin adenosyltransferase; <b>PDBTitle:</b> atp bound at the active site of a pduo type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri
3	<a href="#">c2zhzC_</a>	 Alignment		100.0	51	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> atp:co(b(i)alamin adenosyltransferase, putative; <b>PDBTitle:</b> crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
4	<a href="#">c2g2dA_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp:cobalamin adenosyltransferase; <b>PDBTitle:</b> crystal structure of a putative pduo-type atp:cobalamin2 adenosyltransferase from mycobacterium tuberculosis
5	<a href="#">c3ke4B_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical cytosolic protein; <b>PDBTitle:</b> crystal structure of a pduo-type atp:co(b(i)alamin adenosyltransferase2 from bacillus cereus
6	<a href="#">d1rtyb_</a>	 Alignment		100.0	40	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Cobalamin adenosyltransferase-like <b>Family:</b> Cobalamin adenosyltransferase
7	<a href="#">c2ah6B_</a>	 Alignment		100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bh1595, unknown conserved protein; <b>PDBTitle:</b> crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution
8	<a href="#">d1rtya_</a>	 Alignment		100.0	42	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Cobalamin adenosyltransferase-like <b>Family:</b> Cobalamin adenosyltransferase
9	<a href="#">c1wozA_</a>	 Alignment		100.0	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 177aa long conserved hypothetical protein (st1454); <b>PDBTitle:</b> crystal structure of uncharacterized protein st1454 from sulfolobus2 tokodaii
10	<a href="#">c1wvtA_</a>	 Alignment		100.0	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein st2180; <b>PDBTitle:</b> crystal structure of uncharacterized protein st2180 from sulfolobus2 tokodaii
11	<a href="#">c1nogA_</a>	 Alignment		100.0	37	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein ta0546; <b>PDBTitle:</b> crystal structure of conserved protein 0546 from thermoplasma2 acidophilum

12	<a href="#">d1noga_</a>	Alignment		100.0	37	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Cobalamin adenosyltransferase-like <b>Family:</b> Cobalamin adenosyltransferase
13	<a href="#">c2idxA_</a>	Alignment		100.0	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cob(i)yrinic acid a,c-diamide adenosyltransferase; <b>PDBTitle:</b> structure of human atp:cobalamin adenosyltransferase bound to atp.
14	<a href="#">c1wy1B_</a>	Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ph0671; <b>PDBTitle:</b> crystal structure of the ph0671 protein from pyrococcus horikoshii ot3
15	<a href="#">c6c9kO_</a>	Alignment		91.8	35	<b>PDB header:</b> de novo protein <b>Chain:</b> Q: <b>PDB Molecule:</b> darpp14 - subunit a with darpin; <b>PDBTitle:</b> single-particle reconstruction of darpp14 - a designed protein scaffold2 displaying ~17kda darpin proteins
16	<a href="#">d1niga_</a>	Alignment		82.4	15	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> Cobalamin adenosyltransferase-like <b>Family:</b> Hypothetical protein Ta1238
17	<a href="#">c5fv8A_</a>	Alignment		55.8	23	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.
18	<a href="#">d1xrsa_</a>	Alignment		50.8	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Cobalamin (vitamin B12)-dependent enzymes <b>Family:</b> D-lysine 5,6-aminomutase alpha subunit, KamD
19	<a href="#">c5fv8B_</a>	Alignment		47.1	21	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> fosw; <b>PDBTitle:</b> structure of cjun-fosw coiled coil complex.
20	<a href="#">d1nu9c2</a>	Alignment		45.5	16	<b>Fold:</b> immunoglobulin/albumin-binding domain-like <b>Superfamily:</b> Staphylocoagulase <b>Family:</b> Staphylocoagulase
21	<a href="#">c3edpB_</a>	Alignment	not modelled	43.3	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lin2111 protein; <b>PDBTitle:</b> the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
22	<a href="#">c6o9gA_</a>	Alignment	not modelled	35.8	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> sesquisabinene b synthase 1; <b>PDBTitle:</b> wild-type sasqs1
23	<a href="#">c6gnyD_</a>	Alignment	not modelled	32.5	42	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> telomere repeats-binding bouquet formation protein 2; <b>PDBTitle:</b> crystal structure of the majin-terb2 heterotetrameric complex
24	<a href="#">c3t6gB_</a>	Alignment	not modelled	32.4	24	<b>PDB header:</b> signaling protein, cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> breast cancer anti-estrogen resistance protein 1; <b>PDBTitle:</b> structure of the complex between nsp3 (shep1) and p130cas
25	<a href="#">c3axjB_</a>	Alignment	not modelled	32.4	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> translin associated factor x, isoform b; <b>PDBTitle:</b> high resolution crystal structure of c3po
26	<a href="#">c6gnxB_</a>	Alignment	not modelled	31.7	42	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> telomere repeats-binding bouquet formation protein 2; <b>PDBTitle:</b> crystal structure of the majin-terb2 heterotetrameric complex -2 selenomethionine derivative
27	<a href="#">c3w8hB_</a>	Alignment	not modelled	25.2	16	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase 25; <b>PDBTitle:</b> crystal structure of ccm3 in complex with the c-terminal regulatory2 domain of stk25
						<b>Fold:</b> Nucleocapsid protein dimerization domain

28	<a href="#">d2giba1</a>	Alignment	not modelled	21.8	17	<b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Coronavirus nucleocapsid protein
29	<a href="#">c3f8mA</a>	Alignment	not modelled	21.4	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gntr-family protein transcriptional regulator; <b>PDBTitle:</b> crystal structure of phnf from mycobacterium smegmatis
30	<a href="#">c3bwgA</a>	Alignment	not modelled	21.2	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator yydk; <b>PDBTitle:</b> the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
31	<a href="#">d1z9ha1</a>	Alignment	not modelled	21.0	17	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
32	<a href="#">c2gzdC</a>	Alignment	not modelled	20.9	29	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> rab11 family-interacting protein 2; <b>PDBTitle:</b> crystal structure of rab11 in complex with rab11-fip2
33	<a href="#">d1yhta1</a>	Alignment	not modelled	19.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-N-acetylhexosaminidase catalytic domain
34	<a href="#">c5a7yA</a>	Alignment	not modelled	19.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> trna (adenine(9)-n1)-methyltransferase; <b>PDBTitle:</b> crystal structure of sulfolobus acidocaldarius trm10 in2 complex with s-adenosylhomocysteine
35	<a href="#">c1n20A</a>	Alignment	not modelled	18.5	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> (+)-bornyl diphosphate synthase; <b>PDBTitle:</b> (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2,2,3-dihydrogeranyl diphosphate
36	<a href="#">c2k6sB</a>	Alignment	not modelled	18.3	29	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> rab11fip2 protein; <b>PDBTitle:</b> structure of rab11-fip2 c-terminal coiled-coil domain
37	<a href="#">c5m4aA</a>	Alignment	not modelled	17.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> neutral trehalase; <b>PDBTitle:</b> neutral trehalase nth1 from saccharomyces cerevisiae in complex with2 trehalose
38	<a href="#">c4gehB</a>	Alignment	not modelled	17.7	15	<b>PDB header:</b> protein binding/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase mst4; <b>PDBTitle:</b> crystal structure of mst4 dimerization domain complex with pdcd10
39	<a href="#">c5oayA</a>	Alignment	not modelled	17.6	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator whib1; <b>PDBTitle:</b> m. tuberculosis [4fe-4s] protein whib1 is a four-helix bundle that2 forms a no-sensitive complex with sigmaa and regulates the major3 virulence factor esx-1
40	<a href="#">c4r1hA</a>	Alignment	not modelled	16.9	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0741 protein; <b>PDBTitle:</b> gntr family transcriptional regulator from listeria monocytogenes
41	<a href="#">d1hywa</a>	Alignment	not modelled	16.5	17	<b>Fold:</b> gpW/XkdW-like <b>Superfamily:</b> Head-to-tail joining protein W, gpW <b>Family:</b> Head-to-tail joining protein W, gpW
42	<a href="#">c2q4dB</a>	Alignment	not modelled	16.3	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> lysine decarboxylase-like protein at5g11950; <b>PDBTitle:</b> ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
43	<a href="#">c4v36B</a>	Alignment	not modelled	16.1	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lysyl-trna-dependent l-ysyl-phosphatidylglycerol synthase; <b>PDBTitle:</b> the structure of l-pgs from bacillus licheniformis
44	<a href="#">c4zs8A</a>	Alignment	not modelled	16.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor dasr; <b>PDBTitle:</b> crystal structure of ligand-free, full length dasr
45	<a href="#">c2j5cB</a>	Alignment	not modelled	15.3	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 1,8-cineole synthase; <b>PDBTitle:</b> rational conversion of substrate and product specificity in a2 monoterpene synthase. structural insights into the molecular basis of3 rapid evolution.
46	<a href="#">c3by6C</a>	Alignment	not modelled	15.3	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> predicted transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator from oenococcus oeni
47	<a href="#">d2cjra1</a>	Alignment	not modelled	14.8	17	<b>Fold:</b> Nucleocapsid protein dimerization domain <b>Superfamily:</b> Nucleocapsid protein dimerization domain <b>Family:</b> Coronavirus nucleocapsid protein
48	<a href="#">d1hw1a1</a>	Alignment	not modelled	14.6	33	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
49	<a href="#">c5c05A</a>	Alignment	not modelled	14.4	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative gamma-terpinene synthase; <b>PDBTitle:</b> crystal structure of gamma-terpinene synthase from thymus vulgaris
50	<a href="#">d1ydha</a>	Alignment	not modelled	14.3	14	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
51	<a href="#">c3e90C</a>	Alignment	not modelled	14.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ns2b cofactor; <b>PDBTitle:</b> west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
52	<a href="#">c4v1ae</a>	Alignment	not modelled	14.1	13	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 22 of 2
53	<a href="#">c2jia</a>	Alignment	not modelled	14.1	21	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> polyprotein;

53	<a href="#">c2jqvA_</a>	Alignment	not modelled	14.1	41	<b>PDBTitle:</b> crystal structure of the west nile virus ns2b-ns3 protease2 complexed with bovine pancreatic trypsin inhibitor <b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> arabinose metabolism transcriptional repressor;
54	<a href="#">c4egzA_</a>	Alignment	not modelled	14.0	15	<b>PDBTitle:</b> crystal structure of arar(dbd) in complex with operator orr3
55	<a href="#">d1a4ia2</a>	Alignment	not modelled	14.0	19	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Tetrahydrofolate dehydrogenase/cyclohydrolase
56	<a href="#">c2vl8A_</a>	Alignment	not modelled	14.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-n-acetylhexosaminidase; <b>PDBTitle:</b> inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
57	<a href="#">c3eetA_</a>	Alignment	not modelled	13.2	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative gntr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative gntr-family transcriptional2 regulator
58	<a href="#">c2krxA_</a>	Alignment	not modelled	12.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> asl3597 protein; <b>PDBTitle:</b> solution nmr structure of asl3597 from nostoc sp. pcc7120. northeast2 structural genomics consortium target id nsr244.
59	<a href="#">c2cnwF_</a>	Alignment	not modelled	12.7	15	<b>PDB header:</b> signal recognition <b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases fff and ftsy
60	<a href="#">c3p5rB_</a>	Alignment	not modelled	12.6	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> taxadiene synthase; <b>PDBTitle:</b> crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
61	<a href="#">d2bl7a1</a>	Alignment	not modelled	12.6	29	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bacteriocin immunity protein-like <b>Family:</b> EntA-Im
62	<a href="#">c5whaF_</a>	Alignment	not modelled	12.5	22	<b>PDB header:</b> protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> miniprotein 225-11; <b>PDBTitle:</b> kras g12v, bound to gdp and miniprotein 225-11
63	<a href="#">c2n5mA_</a>	Alignment	not modelled	12.4	45	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein khnyn; <b>PDBTitle:</b> unveiling the structural determinants of kiaa0323 binding preference2 for nedd8
64	<a href="#">c5uv1A_</a>	Alignment	not modelled	11.9	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> (+)-limonene synthase; <b>PDBTitle:</b> crystal structure of (+)-limonene synthase complexed with 2-2 fluorogeranyl diphosphate
65	<a href="#">c3g4dB_</a>	Alignment	not modelled	11.7	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> (+)-delta-cadinene synthase isozyme xc1; <b>PDBTitle:</b> crystal structure of (+)-delta-cadinene synthase from gossypium2 arboreum and evolutionary divergence of metal binding motifs for3 catalysis
66	<a href="#">d2b7ma1</a>	Alignment	not modelled	10.8	14	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> Cullin repeat-like <b>Family:</b> Exocyst complex component
67	<a href="#">c1zunA_</a>	Alignment	not modelled	10.4	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate adenylyltransferase subunit 2; <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
68	<a href="#">d1jw2a_</a>	Alignment	not modelled	10.3	27	<b>Fold:</b> Open three-helical up-and-down bundle <b>Superfamily:</b> Hemolysin expression modulating protein HHA <b>Family:</b> Hemolysin expression modulating protein HHA
69	<a href="#">c6aqeB_</a>	Alignment	not modelled	10.2	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> molecule a; <b>PDBTitle:</b> crystal structure of ppk2 in complex with mg atp
70	<a href="#">c1hx9A_</a>	Alignment	not modelled	9.5	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-epi-aristolochene synthase; <b>PDBTitle:</b> crystal structure of teas w273s form 1
71	<a href="#">c5zzjC_</a>	Alignment	not modelled	9.5	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> santalene synthase; <b>PDBTitle:</b> crystal structure of a enzyme from santalum album
72	<a href="#">c5i4qB_</a>	Alignment	not modelled	9.5	28	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> contact-dependent inhibitor i; <b>PDBTitle:</b> contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (domains 2 and 3)
73	<a href="#">c5kvrA_</a>	Alignment	not modelled	9.4	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase complex repressor; <b>PDBTitle:</b> x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073
74	<a href="#">c4d0gC_</a>	Alignment	not modelled	9.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> rab11 family-interacting protein 1; <b>PDBTitle:</b> structure of rab14 in complex with rab-coupling protein (rcp)
75	<a href="#">c4bvvB_</a>	Alignment	not modelled	9.2	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoadenosine-phosphosulphate reductase; <b>PDBTitle:</b> structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
76	<a href="#">c2gl7C_</a>	Alignment	not modelled	9.1	55	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> b-cell lymphoma 9 protein; <b>PDBTitle:</b> crystal structure of a beta-catenin/bcl9/tcf4 complex
77	<a href="#">c3sl9D_</a>	Alignment	not modelled	9.1	55	<b>PDB header:</b> signaling protein, protein binding <b>Chain:</b> D: <b>PDB Molecule:</b> b-cell cll/lymphoma 9 protein; <b>PDBTitle:</b> x-ray structure of beta catenin in complex with bcl9
						<b>PDB header:</b> lyase

78	<a href="#">c3saeA</a>	Alignment	not modelled	9.1	14	<b>Chain:</b> A: <b>PDB Molecule:</b> alpha-bisabolene synthase; <b>PDBTitle:</b> structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
79	<a href="#">c4hamA</a>	Alignment	not modelled	9.1	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo2241 protein; <b>PDBTitle:</b> crystal structure of transcriptional antiterminator from listeria2 monocytogenes egd-e
80	<a href="#">d1wjwa</a>	Alignment	not modelled	9.0	21	<b>Fold:</b> TBP-like <b>Superfamily:</b> Phosphoglucomutase, C-terminal domain <b>Family:</b> Phosphoglucomutase, C-terminal domain
81	<a href="#">c3s9vD</a>	Alignment	not modelled	9.0	10	<b>PDB header:</b> lyase, isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> abietadiene synthase, chloroplastic; <b>PDBTitle:</b> abietadiene synthase from abies grandis
82	<a href="#">c2jg0A</a>	Alignment	not modelled	8.8	50	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic trehalase; <b>PDBTitle:</b> family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
83	<a href="#">d2jg0a1</a>	Alignment	not modelled	8.8	50	<b>Fold:</b> alpha/alpha toroid <b>Superfamily:</b> Six-hairpin glycosidases <b>Family:</b> Trehalase-like
84	<a href="#">c4heoA</a>	Alignment	not modelled	8.8	31	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoprotein; <b>PDBTitle:</b> hendra virus phosphoprotein c terminal domain
85	<a href="#">d1czan2</a>	Alignment	not modelled	8.8	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
86	<a href="#">c1unyA</a>	Alignment	not modelled	8.7	29	<b>PDB header:</b> four helix bundle <b>Chain:</b> A: <b>PDB Molecule:</b> general control protein gcn4; <b>PDBTitle:</b> structure based engineering of internal molecular surfaces2 of four helix bundles
87	<a href="#">c3sl9F</a>	Alignment	not modelled	8.7	28	<b>PDB header:</b> signaling protein, protein binding <b>Chain:</b> F: <b>PDB Molecule:</b> b-cell cl/lymphoma 9 protein; <b>PDBTitle:</b> x-ray structure of beta catenin in complex with bc19
88	<a href="#">c3sl9C</a>	Alignment	not modelled	8.7	28	<b>PDB header:</b> signaling protein, protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> b-cell cl/lymphoma 9 protein; <b>PDBTitle:</b> x-ray structure of beta catenin in complex with bc19
89	<a href="#">c6c48D</a>	Alignment	not modelled	8.7	16	<b>PDB header:</b> cell cycle/dna binding <b>Chain:</b> D: <b>PDB Molecule:</b> protein lin-9 homolog; <b>PDBTitle:</b> crystal structure of b-myb-lin9-lin52 complex
90	<a href="#">c6bk4A</a>	Alignment	not modelled	8.7	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> caprin homolog; <b>PDBTitle:</b> crystal structure of the hr-1 domain of drosophila caprin in the2 p212121 space group
91	<a href="#">c1e2xA</a>	Alignment	not modelled	8.6	25	<b>PDB header:</b> transcriptional regulation <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid metabolism regulator protein; <b>PDBTitle:</b> fadr, fatty acid responsive transcription factor from e.2 coli
92	<a href="#">c5he9E</a>	Alignment	not modelled	8.5	71	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> phage inhibitor protein; <b>PDBTitle:</b> bacterial initiation protein in complex with phage inhibitor protein
93	<a href="#">d1am7a</a>	Alignment	not modelled	8.5	13	<b>Fold:</b> Lysozyme-like <b>Superfamily:</b> Lysozyme-like <b>Family:</b> Lambda lysozyme
94	<a href="#">d1weka</a>	Alignment	not modelled	8.5	13	<b>Fold:</b> MCP/YpsA-like <b>Superfamily:</b> MCP/YpsA-like <b>Family:</b> MoCo carrier protein-like
95	<a href="#">c6rdi8</a>	Alignment	not modelled	8.4	20	<b>PDB header:</b> proton transport <b>Chain:</b> 8: <b>PDB Molecule:</b> mitochondrial atp synthase subunit asa8; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 1a,2 monomer-masked refinement
96	<a href="#">c6rdr8</a>	Alignment	not modelled	8.4	20	<b>PDB header:</b> proton transport <b>Chain:</b> 8: <b>PDB Molecule:</b> mitochondrial atp synthase subunit asa8; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 1d,2 monomer-masked refinement
97	<a href="#">c2du9A</a>	Alignment	not modelled	8.4	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> predicted transcriptional regulators; <b>PDBTitle:</b> crystal structure of the transcriptional factor from c.glutamicum
98	<a href="#">d2fgca1</a>	Alignment	not modelled	8.3	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> IlvH-like
99	<a href="#">c3neuA</a>	Alignment	not modelled	8.3	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin1836 protein; <b>PDBTitle:</b> the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262