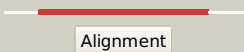

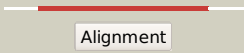



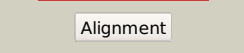

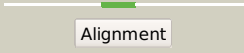
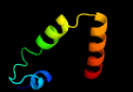
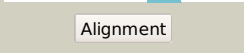

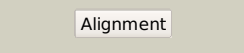
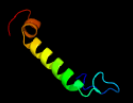
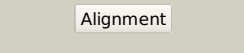

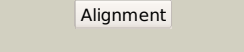



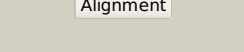



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1029_(kdpA)_1152016_1153731
Date	Wed Jul 31 22:05:10 BST 2019
Unique Job ID	b66d383cd14f6211

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5mrwA_</a>	 Alignment		100.0	51	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> potassium-transporting atpase potassium-binding subunit; <b>PDBTitle:</b> structure of the kdpabc complex
2	<a href="#">c4j7cK_</a>	 Alignment		100.0	15	<b>PDB header:</b> transport protein <b>Chain:</b> K: <b>PDB Molecule:</b> ktr system potassium uptake protein b; <b>PDBTitle:</b> ktrab potassium transporter from bacillus subtilis
3	<a href="#">c3pjzB_</a>	 Alignment		99.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> potassium uptake protein trkh; <b>PDBTitle:</b> crystal structure of the potassium transporter trkh from vibrio2 parahaemolyticus
4	<a href="#">c3pjzA_</a>	 Alignment		99.5	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium uptake protein trkh; <b>PDBTitle:</b> crystal structure of the potassium transporter trkh from vibrio2 parahaemolyticus
5	<a href="#">c6o7ua_</a>	 Alignment		52.4	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo
6	<a href="#">c2ndjA_</a>	 Alignment		39.1	35	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 3; <b>PDBTitle:</b> structural basis for kcne3 and estrogen modulation of the kcnq12 channel
7	<a href="#">c4ev6E_</a>	 Alignment		27.9	24	<b>PDB header:</b> metal transport <b>Chain:</b> E: <b>PDB Molecule:</b> magnesium transport protein cora; <b>PDBTitle:</b> the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
8	<a href="#">d1wmxa_</a>	 Alignment		24.8	38	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 30 carbohydrate binding module, CBM30 (PKD repeat)
9	<a href="#">c6o7xa_</a>	 Alignment		22.0	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar atp synthase catalytic subunit a; <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-v1vo state 3
10	<a href="#">d1wmxb_</a>	 Alignment		21.6	43	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 30 carbohydrate binding module, CBM30 (PKD repeat)
11	<a href="#">c5nhul_</a>	 Alignment		16.0	71	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> agap008004-pa; <b>PDBTitle:</b> human alpha thrombin complexed with anopheles gambiae ce52 anticoagulant

12	<a href="#">c6cfwF_</a>	Alignment		15.6	25	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> monovalent cation/h+ antiporter subunit b; <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase
13	<a href="#">c3ogiC_</a>	Alignment		15.5	60	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative esat-6-like protein 6; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
14	<a href="#">c4gzaA_</a>	Alignment		15.2	60	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> esat-6-like protein 6; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis h37rv esxop2 (rv2346c-rv2347c) complex in space group c2221
15	<a href="#">c2k21A_</a>	Alignment		15.1	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e <b>PDBTitle:</b> nmr structure of human kcne1 in Impg micelles at ph 6.0 and 2 40 degree c
16	<a href="#">c3j47O_</a>	Alignment		14.2	60	<b>PDB header:</b> protein binding <b>Chain:</b> O: <b>PDB Molecule:</b> 26s proteasome regulatory subunit rpn9; <b>PDBTitle:</b> formation of an intricate helical bundle dictates the assembly of the 2 26s proteasome lid
17	<a href="#">c5nhuJ_</a>	Alignment		12.7	71	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> agap008004-pa; <b>PDBTitle:</b> human alpha thrombin complexed with anopheles gambiae ce52 anticoagulant
18	<a href="#">c5n9yB_</a>	Alignment		12.5	20	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> zinc transport protein zntb; <b>PDBTitle:</b> the full-length structure of zntb
19	<a href="#">d1oe8a1</a>	Alignment		11.9	13	<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
20	<a href="#">d1gu3a_</a>	Alignment		11.5	8	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> CBM4/9
21	<a href="#">c5yf4A_</a>	Alignment	not modelled	11.3	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> mob-like protein phocein; <b>PDBTitle:</b> a kinase complex mst4-mob4
22	<a href="#">c5halA_</a>	Alignment	not modelled	11.2	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative beta-lactamase from burkholderia2 vietnamiensis
23	<a href="#">c1ot0A_</a>	Alignment	not modelled	11.0	25	<b>PDB header:</b> antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> 50s ribosomal protein l1; <b>PDBTitle:</b> structure of antimicrobial peptide, hp (2-20) and its2 analogues derived from helicobacter pylori, as determined3 by 1h nmr spectroscopy
24	<a href="#">c1p0jA_</a>	Alignment	not modelled	11.0	25	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 19-mer peptide from 50s ribosomal protein l1; <b>PDBTitle:</b> hp (2-20) substitution asp to trp modification in sds-d252 micelles
25	<a href="#">c5wylB_</a>	Alignment	not modelled	11.0	40	<b>PDB header:</b> ribosomal protein/nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum utp10 n-terminal domain2 in complex with utp17 c-terminal helices
26	<a href="#">c2kk2A_</a>	Alignment	not modelled	10.9	38	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> en-a1; <b>PDBTitle:</b> nmr solution structure of the pheromone en-a1 from euplotes nobilii
27	<a href="#">d1d02a_</a>	Alignment	not modelled	10.7	57	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease MunI
28	<a href="#">c5twvG_</a>	Alignment	not modelled	10.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> atp-sensitive inward rectifier potassium channel 11;

						<b>PDBTitle:</b> cryo-em structure of the pancreatic atp-sensitive k+ channel2 sur1/kir6.2 in the presence of atp and glibenclamide
29	<a href="#">c5wyID_</a>	Alignment	not modelled	10.6	40	<b>PDB header:</b> ribosomal protein/nuclear protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of chaetomium thermophilum utp10 n-terminal domain2 in complex with utp17 c-terminal helices
30	<a href="#">c2v52M_</a>	Alignment	not modelled	10.3	38	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> M: <b>PDB Molecule:</b> mk1/myocardin-like protein 1; <b>PDBTitle:</b> structure of mal-rpel2 complexed to g-actin
31	<a href="#">c2levA_</a>	Alignment	not modelled	10.2	53	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> ler; <b>PDBTitle:</b> structure of the dna complex of the c-terminal domain of ler
32	<a href="#">c1zcdA_</a>	Alignment	not modelled	10.1	21	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> na(+)/h(+) antiporter 1; <b>PDBTitle:</b> crystal structure of the na+/h+ antiporter nhaa
33	<a href="#">c3lw5K_</a>	Alignment	not modelled	9.6	31	<b>PDB header:</b> photosynthesis <b>Chain:</b> K: <b>PDB Molecule:</b> photosystem i reaction center subunit x psak; <b>PDBTitle:</b> improved model of plant photosystem i
34	<a href="#">c2bpgB_</a>	Alignment	not modelled	9.5	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
35	<a href="#">d1kz1a_</a>	Alignment	not modelled	9.5	18	<b>Fold:</b> Lumazine synthase <b>Superfamily:</b> Lumazine synthase <b>Family:</b> Lumazine synthase
36	<a href="#">c2m0qA_</a>	Alignment	not modelled	9.5	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 2; <b>PDBTitle:</b> solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix
37	<a href="#">d1hnra_</a>	Alignment	not modelled	9.4	41	<b>Fold:</b> H-NS histone-like proteins <b>Superfamily:</b> H-NS histone-like proteins <b>Family:</b> H-NS histone-like proteins
38	<a href="#">c5xyvC_</a>	Alignment	not modelled	9.4	26	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> protein deadlock; <b>PDBTitle:</b> crystal structure of drosophila melanogaster rhino chromoshadow domain2 in complex with deadlock n-terminal domain
39	<a href="#">c4p22A_</a>	Alignment	not modelled	9.2	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme 1; <b>PDBTitle:</b> crystal structure of n-terminal fragments of e1
40	<a href="#">c2wscK_</a>	Alignment	not modelled	9.0	38	<b>PDB header:</b> photosynthesis <b>Chain:</b> K: <b>PDB Molecule:</b> photosystem i reaction center subunit psak, chloroplastic; <b>PDBTitle:</b> improved model of plant photosystem i
41	<a href="#">c5zghJ_</a>	Alignment	not modelled	8.9	32	<b>PDB header:</b> photosynthesis <b>Chain:</b> J: <b>PDB Molecule:</b> psaj; <b>PDBTitle:</b> cryo-em structure of the red algal psi-lhcr
42	<a href="#">c3nr1B_</a>	Alignment	not modelled	8.6	36	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein rumgna_01417; <b>PDBTitle:</b> crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
43	<a href="#">d1gvha3</a>	Alignment	not modelled	8.6	24	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Flavo-hemoglobin, C-terminal domain
44	<a href="#">d1nvmb1</a>	Alignment	not modelled	8.5	32	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	<a href="#">d1yova1</a>	Alignment	not modelled	8.3	38	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Ubiquitin activating enzymes (UBA)
46	<a href="#">d1d4oa_</a>	Alignment	not modelled	8.1	67	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
47	<a href="#">c1pt9B_</a>	Alignment	not modelled	8.1	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase, mitochondrial; <b>PDBTitle:</b> crystal structure analysis of the diii component of transhydrogenase2 with a thio-nicotinamide nucleotide analogue
48	<a href="#">d1jb0j_</a>	Alignment	not modelled	8.0	21	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit IX of photosystem I reaction centre, Psaj <b>Family:</b> Subunit IX of photosystem I reaction centre, Psaj
49	<a href="#">c2ks1A_</a>	Alignment	not modelled	8.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
50	<a href="#">c2jwaA_</a>	Alignment	not modelled	8.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> erbb2 transmembrane segment dimer spatial structure
51	<a href="#">d2cnda2</a>	Alignment	not modelled	7.9	10	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
52	<a href="#">c3cmmA_</a>	Alignment	not modelled	7.9	23	<b>PDB header:</b> ligase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1 1; <b>PDBTitle:</b> crystal structure of the uba1-ubiquitin complex
53	<a href="#">d1pnoa_</a>	Alignment	not modelled	7.8	44	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Transhydrogenase domain III (dIII)
						<b>PDB header:</b> plant protein

54	<a href="#">c6igzK_</a>	Alignment	not modelled	7.8	36	<b>Chain:</b> K: <b>PDB Molecule:</b> psak; <b>PDBTitle:</b> structure of psi-lhci
55	<a href="#">c6dc6A_</a>	Alignment	not modelled	7.8	31	<b>PDB header:</b> signaling protein/ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme 1; <b>PDBTitle:</b> crystal structure of human ubiquitin activating enzyme e1 (uba1) in2 complex with ubiquitin
56	<a href="#">c4ky0B_</a>	Alignment	not modelled	7.7	18	<b>PDB header:</b> transport protein, membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> proton/glutamate symporter, sdf family; <b>PDBTitle:</b> crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis
57	<a href="#">c2o01J_</a>	Alignment	not modelled	7.5	32	<b>PDB header:</b> photosynthesis <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem i reaction center subunit ix; <b>PDBTitle:</b> the structure of a plant photosystem i supercomplex at 3.4 angstrom2 resolution
58	<a href="#">c5xtrC_</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> fad-linked sulfhydryl oxidase; <b>PDBTitle:</b> crystal structure of baculoviral sulfhydryl oxidase p33 (r127a, e183a2 mutant)
59	<a href="#">c3j9pD_</a>	Alignment	not modelled	7.3	27	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> maltose-binding periplasmic protein, transient receptor <b>PDBTitle:</b> structure of the trpa1 ion channel determined by electron cryo-2 microscopy
60	<a href="#">c6rdi8_</a>	Alignment	not modelled	7.2	42	<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
61	<a href="#">c6rdr8_</a>	Alignment	not modelled	7.2	42	<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
62	<a href="#">c2bruC_</a>	Alignment	not modelled	7.1	56	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
63	<a href="#">c4gtnA_</a>	Alignment	not modelled	7.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anthranilate phosphoribosyltransferase; <b>PDBTitle:</b> structure of anthranilate phosphoribosyl transferase from2 acinetobacter baylyi
64	<a href="#">d1g3wa2</a>	Alignment	not modelled	7.1	19	<b>Fold:</b> Iron-dependent repressor protein, dimerization domain <b>Superfamily:</b> Iron-dependent repressor protein, dimerization domain <b>Family:</b> Iron-dependent repressor protein, dimerization domain
65	<a href="#">c5h5pA_</a>	Alignment	not modelled	7.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> myelin regulatory factor; <b>PDBTitle:</b> crystal structure of myelin-gene regulatory factor dna binding domain
66	<a href="#">c4ii3A_</a>	Alignment	not modelled	7.0	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1 1; <b>PDBTitle:</b> crystal structure of s. pombe ubiquitin activating enzyme 1 (uba1) in2 complex with ubiquitin and atp/mg
67	<a href="#">c2yf3F_</a>	Alignment	not modelled	6.9	33	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> mazg-like nucleoside triphosphate pyrophosphohydrolase; <b>PDBTitle:</b> crystal structure of dr2231, the mazg-like protein from deinococcus2 radiodurans, complex with manganese
68	<a href="#">c2yn9B_</a>	Alignment	not modelled	6.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> potassium-transporting atpase subunit beta; <b>PDBTitle:</b> cryo-em structure of gastric h+,k+-atpase with bound rubidium
69	<a href="#">d2h8pc1</a>	Alignment	not modelled	6.6	30	<b>Fold:</b> Voltage-gated potassium channels <b>Superfamily:</b> Voltage-gated potassium channels <b>Family:</b> Voltage-gated potassium channels
70	<a href="#">c6ijjK_</a>	Alignment	not modelled	6.4	17	<b>PDB header:</b> membrane protein <b>Chain:</b> K: <b>PDB Molecule:</b> psak; <b>PDBTitle:</b> photosystem i of chlamydomonas reinhardtii
71	<a href="#">c3dxeB_</a>	Alignment	not modelled	6.3	43	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> amyloid beta a4 protein; <b>PDBTitle:</b> crystal structure of the intracellular domain of human app (t668a2 mutant) in complex with fe65-ptb2
72	<a href="#">d1tvca2</a>	Alignment	not modelled	6.2	20	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Aromatic dioxygenase reductase-like
73	<a href="#">d2piaa2</a>	Alignment	not modelled	6.2	15	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Aromatic dioxygenase reductase-like
74	<a href="#">c5mqfT_</a>	Alignment	not modelled	6.2	19	<b>PDB header:</b> splicing <b>Chain:</b> T: <b>PDB Molecule:</b> pre-mrna-splicing factor cwc22 homolog; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
75	<a href="#">c6ijoG_</a>	Alignment	not modelled	6.1	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> psag; <b>PDBTitle:</b> photosystem i of chlamydomonas reinhardtii
76	<a href="#">c3qnqD_</a>	Alignment	not modelled	6.0	15	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
77	<a href="#">d2c7na1</a>	Alignment	not modelled	6.0	30	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> A20-like zinc finger
78	<a href="#">d1usha1</a>	Alignment	not modelled	5.7	17	<b>Fold:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain <b>Superfamily:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain <b>Family:</b> 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal

						domain
79	<a href="#">d2isya2</a>	Alignment	not modelled	5.7	21	<b>Fold:</b> Iron-dependent repressor protein, dimerization domain <b>Superfamily:</b> Iron-dependent repressor protein, dimerization domain <b>Family:</b> Iron-dependent repressor protein, dimerization domain
80	<a href="#">c2zxeB_</a>	Alignment	not modelled	5.7	17	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> na+,k+-atpase beta subunit; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
81	<a href="#">c1nvmB_</a>	Alignment	not modelled	5.7	32	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetaldehyde dehydrogenase (acylating); <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
82	<a href="#">c2epgB_</a>	Alignment	not modelled	5.6	40	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ttha1785; <b>PDBTitle:</b> crystal structure of ttha1785
83	<a href="#">d1qfja2</a>	Alignment	not modelled	5.6	4	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
84	<a href="#">c4ainB_</a>	Alignment	not modelled	5.6	16	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of betp with asymmetric protomers.
85	<a href="#">c2lsjA_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> protein binding/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna repair protein rev1; <b>PDBTitle:</b> solution structure of the mouse rev1 ctd in complex with the rev1-2 interacting region (rir)of pol kappa
86	<a href="#">c5z47A_</a>	Alignment	not modelled	5.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrrolidone-carboxylate peptidase; <b>PDBTitle:</b> crystal structure of pyrrolidone carboxylate peptidase i with2 disordered loop a from deinococcus radiodurans r1
87	<a href="#">c2ot8D_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> heterogeneous nuclear ribonucleoprotein m; <b>PDBTitle:</b> karyopherin beta2/transportin-hnrnp nls complex
88	<a href="#">c4nkpD_</a>	Alignment	not modelled	5.4	18	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> putative extracellular heme-binding protein; <b>PDBTitle:</b> crystal structure of a putative extracellular heme-binding protein2 (despig_02683) from desulfovibrio piger atcc 29098 at 1.24 a3 resolution
89	<a href="#">d1fdra2</a>	Alignment	not modelled	5.3	4	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
90	<a href="#">c4uecB_</a>	Alignment	not modelled	5.3	36	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 4g, isoform a; <b>PDBTitle:</b> complex of d. melanogaster eif4e with eif4g and cap analog
91	<a href="#">d1x7fa1</a>	Alignment	not modelled	5.3	40	<b>Fold:</b> Cyclophilin-like <b>Superfamily:</b> Cyclophilin-like <b>Family:</b> Outer surface protein, C-terminal domain
92	<a href="#">c3mk7F_</a>	Alignment	not modelled	5.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
93	<a href="#">c2c7mA_</a>	Alignment	not modelled	5.2	30	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> rab guanine nucleotide exchange factor 1; <b>PDBTitle:</b> human rabex-5 residues 1-74 in complex with ubiquitin
94	<a href="#">d1krha2</a>	Alignment	not modelled	5.2	12	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Aromatic dioxygenase reductase-like