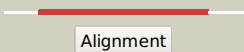

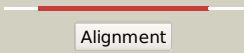

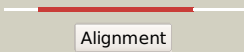

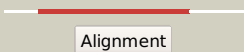

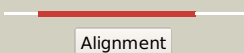

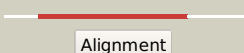

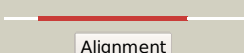

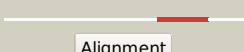

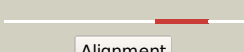

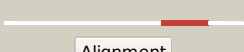

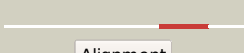



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1739c_(-)_1965962_1967644
Date	Fri Aug 2 13:30:34 BST 2019
Unique Job ID	351842a5653ff8bd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6rtfA_	 Alignment		100.0	25	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 26 member 9,solute carrier family 26 PDBTitle: structure of murine solute carrier 26 family member a9 (slc26a9) anion2 transporter in an intermediate state
2	c5da0A_	 Alignment		100.0	25	PDB header: transport protein Chain: A: PDB Molecule: sulphate transporter; PDBTitle: structure of the the slc26 transporter slc26dg in complex with a2 nanobody
3	c4yzfA_	 Alignment		100.0	15	PDB header: immune system Chain: A: PDB Molecule: band 3 anion transport protein; PDBTitle: crystal structure of the anion exchanger domain of human erythrocyte2 band 3
4	c5sv9B_	 Alignment		100.0	13	PDB header: transport protein Chain: B: PDB Molecule: bor1p boron transporter; PDBTitle: structure of the slc4 transporter bor1p in an inward-facing2 conformation
5	c6caaA_	 Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: electrogenic sodium bicarbonate cotransporter 1; PDBTitle: cryoem structure of human slc4a4 sodium-coupled acid-base transporter2 nbce1
6	c3qe7A_	 Alignment		100.0	16	PDB header: transport protein Chain: A: PDB Molecule: uracil permease; PDBTitle: crystal structure of uracil transporter--uraa
7	c5i6cB_	 Alignment		100.0	12	PDB header: transport protein Chain: B: PDB Molecule: uric acid-xanthine permease; PDBTitle: the structure of the eukaryotic purine/h+ symporter, uapa, in complex2 with xanthine
8	c5ezbB_	 Alignment		99.9	21	PDB header: transport protein Chain: B: PDB Molecule: chicken prestin stas domain,chicken prestin stas domain; PDBTitle: chicken prestin stas domain
9	c3lloA_	 Alignment		99.9	22	PDB header: motor protein Chain: A: PDB Molecule: prestini; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
10	c2klnA_	 Alignment		99.9	100	PDB header: transport protein Chain: A: PDB Molecule: probable sulphate-transport transmembrane protein, cog0659; PDBTitle: solution structure of stas domain of rv1739c from m. tuberculosis
11	c3mglA_	 Alignment		99.8	19	PDB header: transport protein Chain: A: PDB Molecule: sulfate permease family protein; PDBTitle: crystal structure of permease family protein from vibrio cholerae

12	c3oirA_	Alignment		99.8	20	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolfinella2 succinogenes
13	c3ny7A_	Alignment		99.7	20	PDB header: membrane protein Chain: A: PDB Molecule: sulfate transporter; PDBTitle: stas domain of ychm bound to acp
14	c5l25A_	Alignment		99.7	13	PDB header: transport protein Chain: A: PDB Molecule: boron transporter 1; PDBTitle: crystal structure of arabidopsis thaliana bor1
15	c2vy9A_	Alignment		99.5	15	PDB header: gene regulation Chain: A: PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub
16	c3f43A_	Alignment		99.5	19	PDB header: transcription Chain: A: PDB Molecule: putative anti-sigma factor antagonist tm1081; PDBTitle: crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
17	d1th8b_	Alignment		99.5	17	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
18	d1lauza_	Alignment		99.4	14	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
19	c3lklB_	Alignment		99.4	16	PDB header: transport protein Chain: B: PDB Molecule: antisigma-factor antagonist stas; PDBTitle: crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
20	c4hylB_	Alignment		99.4	10	PDB header: transcription regulator Chain: B: PDB Molecule: stage ii sporulation protein; PDBTitle: the crystal structure of an anti-sigma-factor antagonist from2 haliangium ochraceum dsm 14365
21	d1vc1a_	Alignment	not modelled	99.3	16	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
22	c4xs5D_	Alignment	not modelled	99.3	14	PDB header: transport protein Chain: D: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: crystal structure of sulfate transporter/antisigma-factor antagonist2 stas from dyadobacter fermentans dsm 18053
23	c3t6oA_	Alignment	not modelled	99.2	15	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
24	d1h4xa_	Alignment	not modelled	99.1	18	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
25	c6ic4K_	Alignment	not modelled	98.4	14	PDB header: protein transport Chain: K: PDB Molecule: ttg2e; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
26	c3ih9A_	Alignment	not modelled	96.2	14	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
27	d2q3la1	Alignment	not modelled	91.7	11	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
28	c3bezC_	Alignment	not modelled	89.6	10	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals PDB header: unknown function

29	c3bl4B_	Alignment	not modelled	88.5	13	Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
30	c5do7B_	Alignment	not modelled	85.3	17	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
31	c5x7kB_	Alignment	not modelled	85.2	23	PDB header: transport protein Chain: B: PDB Molecule: lipase b; PDBTitle: crystal structure of the nucleotide-binding domain (nbd) of lipb, a2 abc transporter subunit of a type i secretion system
32	c5nj3B_	Alignment	not modelled	84.8	15	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
33	c2r6oB_	Alignment	not modelled	81.4	6	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative diguanylate cyclase/phosphodiesterase (ggdef & eal PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
34	c4ymuJ_	Alignment	not modelled	78.1	10	PDB header: protein binding/transport protein Chain: J: PDB Molecule: abc-type polar amino acid transport system, atpase PDBTitle: crystal structure of an amino acid abc transporter complex with2 arginines and atps
35	c5i6xA_	Alignment	not modelled	78.0	14	PDB header: membrane protein Chain: A: PDB Molecule: sodium-dependent serotonin transporter; PDBTitle: x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
36	c4hluC_	Alignment	not modelled	74.2	14	PDB header: hydrolase Chain: C: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfa-a' heterodimer bound to adp
37	d1mvoa_	Alignment	not modelled	73.3	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
38	c5do7A_	Alignment	not modelled	72.6	18	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family g member 5; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
39	c1yqtA_	Alignment	not modelled	71.3	10	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
40	c5x40A_	Alignment	not modelled	71.1	20	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
41	c4lykB_	Alignment	not modelled	70.6	8	PDB header: hydrolase Chain: B: PDB Molecule: cyclic di-gmp phosphodiesterase yaha; PDBTitle: crystal structure of the eal domain of c-di-gmp specific2 phosphodiesterase yaha in complex with activating cofactor mg++
42	d2nu7b1	Alignment	not modelled	68.9	16	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
43	c3b2nA_	Alignment	not modelled	67.3	13	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
44	c3cu5B_	Alignment	not modelled	66.6	9	PDB header: transcription regulator Chain: B: PDB Molecule: two component transcriptional regulator, arac family; PDBTitle: crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
45	c4rnhA_	Alignment	not modelled	66.1	8	PDB header: transferase, hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora tandem diguanylate cyclase - phosphodiesterase, c-di-gmp2 complex
46	c4rvcA_	Alignment	not modelled	65.8	17	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter
47	c3hvbB_	Alignment	not modelled	62.5	12	PDB header: hydrolase Chain: B: PDB Molecule: protein fimx; PDBTitle: crystal structure of the dual-domain ggdef-eal module of fimx from2 pseudomonas aeruginosa
48	c6amxA_	Alignment	not modelled	61.2	17	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
49	c2q3eH_	Alignment	not modelled	60.9	11	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
50	c5i4cA_	Alignment	not modelled	60.8	6	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: crystal structure of non-phosphorylated receiver domain of the stress2 response regulator rcsb from escherichia coli
51	c3cz5B_	Alignment	not modelled	59.8	12	PDB header: transcription regulator Chain: B: PDB Molecule: two-component response regulator, luxr family; PDBTitle: crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
52	c2pr7A_	Alignment	not modelled	59.7	5	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
						PDB header: transferase

53	c2qvga	Alignment	not modelled	59.2	6	Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
54	c5m3cB	Alignment	not modelled	58.9	7	PDB header: hydrolase Chain: B: PDB Molecule: diguanilate cyclase; PDBTitle: structure of the hybrid domain (ggdef-eal) of pa0575 from pseudomonas2 aeruginosa pao1 at 2.8 ang. with gtp and ca2+ bound to the active3 site of the ggdef domain
55	c5xu1A	Alignment	not modelled	58.8	15	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
56	c5xgdA	Alignment	not modelled	58.6	15	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein pa0861; PDBTitle: crystal structure of the pas-ggdef-eal domain of pa0861 from2 pseudomonas aeruginosa in complex with gtp
57	d1t3va	Alignment	not modelled	58.3	12	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
58	d1jbea	Alignment	not modelled	58.2	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	d1a04a2	Alignment	not modelled	57.9	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
60	c4m48A	Alignment	not modelled	57.7	17	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
61	c3w9sB	Alignment	not modelled	56.7	19	PDB header: signaling protein/antimicrobial protein Chain: B: PDB Molecule: ompr family response regulator in two-component regulatory PDBTitle: crystal structure analysis of the n-terminal receiver domain of2 response regulator pmra
62	d2ooka1	Alignment	not modelled	56.5	19	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
63	d2ayxa1	Alignment	not modelled	56.4	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
64	c4e7pA	Alignment	not modelled	55.7	15	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of receiver domain of putative narl family response2 regulator spr1814 from streptococcus pneumoniae in the presence of3 the phosphoryl analog berylofluoride
65	c4rniA	Alignment	not modelled	55.2	8	PDB header: hydrolase Chain: A: PDB Molecule: motility regulator; PDBTitle: pamora phosphodiesterase domain, apo form
66	c3hv9A	Alignment	not modelled	53.8	12	PDB header: hydrolase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx eal domain from pseudomonas aeruginosa
67	d1dz3a	Alignment	not modelled	53.3	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
68	c2deoA	Alignment	not modelled	53.3	10	PDB header: hydrolase Chain: A: PDB Molecule: 441aa long hypothetical nfed protein; PDBTitle: 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
69	c2pcjB	Alignment	not modelled	53.1	13	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein lold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
70	c5uicA	Alignment	not modelled	52.4	21	PDB header: transcription Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
71	c3rstH	Alignment	not modelled	51.8	13	PDB header: hydrolase Chain: H: PDB Molecule: signal peptide peptidase sppa; PDBTitle: crystal structure of bacillus subtilis signal peptide peptidase a
72	c3gfbB	Alignment	not modelled	51.7	16	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
73	c3kc2A	Alignment	not modelled	51.5	8	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
74	c2d3wB	Alignment	not modelled	51.5	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufcc; PDBTitle: crystal structure of escherichia coli sufcc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
75	c4fokA	Alignment	not modelled	50.9	11	PDB header: protein binding Chain: A: PDB Molecule: fimx; PDBTitle: 1.8 a crystal structure of the fimx eal domain in complex with c-digmp
76	d1b0ua	Alignment	not modelled	49.5	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
77	c4wbsA	Alignment	not modelled	49.3	18	PDB header: transport protein Chain: A: PDB Molecule: abc transporter related; PDBTitle: crystal structure of an abc transporter related protein from2 burkholderia phymatum PDB header: transferase Chain: X: PDB Molecule: uncharacterized protein tm_1570;

78	c3dcmX_	Alignment	not modelled	48.8	4	PDBTitle: crystal structure of the thermotoga maritima spout family rna-2 methyltransferase protein tm1570 in complex with s-adenosyl-l-3 methionine
79	c3pihA_	Alignment	not modelled	48.6	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
80	c2dfwA_	Alignment	not modelled	48.6	12	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
81	c2yz2B_	Alignment	not modelled	47.5	13	PDB header: hydrolase Chain: B: PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system
82	d1p2fa2	Alignment	not modelled	47.0	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
83	c2olkD_	Alignment	not modelled	46.9	8	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
84	c3pfmA_	Alignment	not modelled	46.7	10	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf
85	c3zqjF_	Alignment	not modelled	46.6	13	PDB header: dna binding protein Chain: F: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
86	c6gcsY_	Alignment	not modelled	46.5	14	PDB header: oxidoreductase Chain: Y: PDB Molecule: nuym subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
87	d1l7vc_	Alignment	not modelled	46.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
88	c6c4jA_	Alignment	not modelled	46.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: ligand bound full length hughd with a104l substitution
89	c2a5hC_	Alignment	not modelled	45.9	11	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
90	c4hu4B_	Alignment	not modelled	45.7	12	PDB header: signaling protein,hydrolase Chain: B: PDB Molecule: oxygen sensor protein dosp; PDBTitle: crystal structure of eal domain of the e. coli dosp - dimeric form
91	c4q6jB_	Alignment	not modelled	45.4	12	PDB header: unknown function Chain: B: PDB Molecule: lmo0131 protein; PDBTitle: crystal structure of eal domain protein from listeria monocytogenes2 egd-e
92	c5yrpB_	Alignment	not modelled	45.3	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: sensory box/response regulator; PDBTitle: crystal structure of the eal domain of mycobacterium smegmatis dcpa
93	d2basa1	Alignment	not modelled	44.7	7	Fold: TIM beta/alpha-barrel Superfamily: EAL domain-like Family: EAL domain
94	d1vpla_	Alignment	not modelled	44.6	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
95	c4myrD_	Alignment	not modelled	44.5	16	PDB header: transcription Chain: D: PDB Molecule: cpae2 pilus assembly protein; PDBTitle: crystal structure of a putative cpae2 pilus assembly protein (cpae2)2 from sinorhizobium melloti 1021 at 2.72 a resolution (psi community3 target, shapiro)
96	c2zwmA_	Alignment	not modelled	44.5	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
97	c6m8oA_	Alignment	not modelled	44.0	13	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of the receiver domain of lytr from staphylococcus2 aureus
98	c2nq2C_	Alignment	not modelled	44.0	14	PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter.
99	c2y0dB_	Alignment	not modelled	43.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
100	c5m1tB_	Alignment	not modelled	43.8	9	PDB header: signaling protein Chain: B: PDB Molecule: muqr phosphodiesterase; PDBTitle: pamuqr phosphodiesterase, c-di-gmp complex
101	c4qpiC_	Alignment	not modelled	43.8	13	PDB header: signaling protein/dna binding protein Chain: C: PDB Molecule: cell cycle response regulator ctra; PDBTitle: 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain
102	c4n0pH_	Alignment	not modelled	43.6	14	PDB header: signaling protein Chain: H: PDB Molecule: pilus assembly protein cpae; PDBTitle: crystal structure of a pilus assembly protein cpae (cc_2943) from2 caulobacter crescentus cb15 at 1.75 a resolution (psi community3 target, shapiro) PDB header: signaling protein

103	c4h60A_	Alignment	not modelled	43.4	10	Chain: A; PDB Molecule: chemotaxis protein chey; PDBTitle: high resolution structure of vibrio cholerae chemotaxis protein chey42 crystallized in low ph (4.0) condition
104	d1krwa_	Alignment	not modelled	42.4	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
105	c5x5yB_	Alignment	not modelled	42.4	16	PDB header: membrane protein Chain: B; PDB Molecule: probable atp-binding component of abc transporter; PDBTitle: a membrane protein complex
106	c2jyaA_	Alignment	not modelled	42.2	29	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein atu1810; PDBTitle: nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
107	c2it1B_	Alignment	not modelled	41.9	14	PDB header: transport protein Chain: B; PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
108	c1f2uD_	Alignment	not modelled	41.6	15	PDB header: replication Chain: D; PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
109	c4f48A_	Alignment	not modelled	40.9	12	PDB header: signaling protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: the x-ray structural of fimxal-c-di-gmp-pilz complexes from2 xanthomonas campestris
110	d1vm6a3	Alignment	not modelled	40.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
111	c5lnkc_	Alignment	not modelled	40.2	21	PDB header: oxidoreductase Chain: C; PDB Molecule: PDBTitle: entire ovine respiratory complex i
112	c2qv0A_	Alignment	not modelled	40.0	11	PDB header: transcription Chain: A; PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of protein mrke2 from klebsiella pneumoniae
113	d1yioa2	Alignment	not modelled	39.9	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
114	d1tg6a1	Alignment	not modelled	39.6	13	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
115	c5d3mF_	Alignment	not modelled	39.4	16	PDB header: transport protein Chain: F; PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
116	c3inpA_	Alignment	not modelled	39.3	12	PDB header: isomerase Chain: A; PDB Molecule: d-ribose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribose-phosphate 3-2 epimerase from francisella tularensis.
117	c4y8eA_	Alignment	not modelled	39.0	14	PDB header: metal binding protein Chain: A; PDB Molecule: pa3825 eal; PDBTitle: pa3825-eal ca-apo structure
118	c3s83A_	Alignment	not modelled	38.9	9	PDB header: signaling protein Chain: A; PDB Molecule: ggdef family protein; PDBTitle: eal domain of phosphodiesterase pdea
119	c2yx6C_	Alignment	not modelled	38.7	12	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: hypothetical protein ph0822; PDBTitle: crystal structure of ph0822
120	c4gxtA_	Alignment	not modelled	38.6	19	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: a conserved functionally unknown protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548