


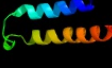

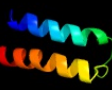





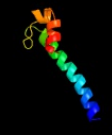
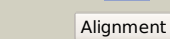

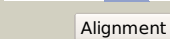

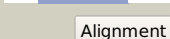

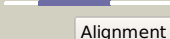

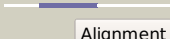



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0095c_(-)_104802_105212
Date	Tue Jul 23 14:50:13 BST 2019
Unique Job ID	401f468160b915b2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5hsbA_</a>	 Alignment		58.8	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase; <b>PDBTitle:</b> andes virus endonuclease
2	<a href="#">c4bgoA_</a>	 Alignment		53.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> efem m75 peptidase; <b>PDBTitle:</b> structural and functional role of the imelysin-like protein2 efem from pseudomonas syringae pv. syringae and3 implications in bacterial iron transport
3	<a href="#">c5tw9D_</a>	 Alignment		38.2	25	<b>PDB header:</b> lipid-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> iron uptake system component efeo; <b>PDBTitle:</b> 1.50 angstrom crystal structure of c-terminal fragment (residues 322-2 384) of iron uptake system component efeo from yersinia pestis.
4	<a href="#">c3at7B_</a>	 Alignment		33.2	22	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> alginate-binding flagellin; <b>PDBTitle:</b> crystal structure of bacterial cell-surface alginate-binding protein2 algp7
5	<a href="#">c3udiA_</a>	 Alignment		31.4	21	<b>PDB header:</b> penicillin-binding protein/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein 1a; <b>PDBTitle:</b> crystal structure of acinetobacter baumannii pbp1a in complex with2 penicillin g
6	<a href="#">c4widA_</a>	 Alignment		28.4	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> rhul123; <b>PDBTitle:</b> crystal structure of the immediate-early 1 protein (ie1) at 2.312 angstrom (tetragonal form after crystal dehydration)
7	<a href="#">c3zljD_</a>	 Alignment		24.9	21	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> D: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
8	<a href="#">c3zljC_</a>	 Alignment		24.9	21	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> dna mismatch repair protein muts; <b>PDBTitle:</b> crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
9	<a href="#">c1kyqC_</a>	 Alignment		20.4	28	<b>PDB header:</b> oxidoreductase, lyase <b>Chain:</b> C: <b>PDB Molecule:</b> siroheme biosynthesis protein met8; <b>PDBTitle:</b> met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
10	<a href="#">c5nz8A_</a>	 Alignment		19.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cellodextrin phosphorylase; <b>PDBTitle:</b> clostridium thermocellum cellodextrin phosphorylase with cellotetraose2 and phosphate bound
11	<a href="#">c6d0gA_</a>	 Alignment		19.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pirin family protein; <b>PDBTitle:</b> 1.78 angstrom resolution crystal structure of quercetin 2,3-2 dioxygenase from acinetobacter baumannii

12	<a href="#">c3ke3A_</a>	Alignment		19.0	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine-pyruvate aminotransferase; <b>PDBTitle:</b> crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
13	<a href="#">c3f5hB_</a>	Alignment		17.3	38	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> type i polyketide synthase pikaiii, type i polyketide <b>PDBTitle:</b> crystal structure of fused docking domains from pikaiii and pikaiv of2 the pikromycin polyketide synthase
14	<a href="#">c3gtzA_</a>	Alignment		15.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative translation initiation inhibitor; <b>PDBTitle:</b> crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
15	<a href="#">d1u2ca2</a>	Alignment		14.4	14	<b>Fold:</b> Dystroglycan, domain 2 <b>Superfamily:</b> Dystroglycan, domain 2 <b>Family:</b> Dystroglycan, domain 2
16	<a href="#">d1j1la_</a>	Alignment		14.2	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Pirin-like
17	<a href="#">c2ak0A_</a>	Alignment		13.6	43	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-conotoxin mii; <b>PDBTitle:</b> structure of cyclic conotoxin mii-7
18	<a href="#">c3iwkB_</a>	Alignment		13.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aminoaldehyde dehydrogenase 1 from pisum sativum2 (psamadh1)
19	<a href="#">c5o8kB_</a>	Alignment		11.9	38	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of mammalian rev7 in complex with rev3 1875-1895
20	<a href="#">d1rcwa_</a>	Alignment		11.7	17	<b>Fold:</b> Heme oxygenase-like <b>Superfamily:</b> Heme oxygenase-like <b>Family:</b> PqqC-like
21	<a href="#">c2yb5F_</a>	Alignment	not modelled	11.7	14	<b>PDB header:</b> translation <b>Chain:</b> F: <b>PDB Molecule:</b> putative fusidic acid resistance protein; <b>PDBTitle:</b> structure of the fusidic acid resistance protein fusc
22	<a href="#">c3u24A_</a>	Alignment	not modelled	11.4	15	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipoprotein; <b>PDBTitle:</b> the structure of a putative lipoprotein of unknown function from2 shewanella oneidensis.
23	<a href="#">c1aq5C_</a>	Alignment	not modelled	11.4	24	<b>PDB header:</b> coiled-coil <b>Chain:</b> C: <b>PDB Molecule:</b> cartilage matrix protein; <b>PDBTitle:</b> high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
24	<a href="#">c1aq5B_</a>	Alignment	not modelled	11.4	24	<b>PDB header:</b> coiled-coil <b>Chain:</b> B: <b>PDB Molecule:</b> cartilage matrix protein; <b>PDBTitle:</b> high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
25	<a href="#">c3jrzA_</a>	Alignment	not modelled	11.3	33	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> ccdb; <b>PDBTitle:</b> ccdvfi-formii-ph5.6
26	<a href="#">c3korD_</a>	Alignment	not modelled	10.7	13	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> possible trp repressor; <b>PDBTitle:</b> crystal structure of a putative trp repressor from staphylococcus2 aureus <b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cell growth inhibitor/plasmid maintenance toxic component <b>Family:</b> CcdB
27	<a href="#">d3vuba_</a>	Alignment	not modelled	10.3	7	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cysteine desulfurase 2, chloroplastic; <b>PDBTitle:</b> crystal structure of nfs2 c384s mutant, the plastidial cysteine2 desulfurase from arabidopsis thaliana
28	<a href="#">c4q76B_</a>	Alignment	not modelled	10.3	12	<b>PDB header:</b> unknown function

29	<a href="#">c5eurC_</a>	Alignment	not modelled	10.1	23	<b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> hypothetical protein sf216 from shigella flexneri 5a m90t
30	<a href="#">c2wwaj_</a>	Alignment	not modelled	10.0	29	<b>PDB header:</b> ribosome <b>Chain:</b> J: <b>PDB Molecule:</b> 60s ribosomal protein l19; <b>PDBTitle:</b> cryo-em structure of idle yeast ssh1 complex bound to the yeast 80s2 ribosome
31	<a href="#">c4fjoD_</a>	Alignment	not modelled	10.0	46	<b>PDB header:</b> transferase/dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of the rev1 ctd-rev3/7-pol kappa rir complex
32	<a href="#">c1hymB_</a>	Alignment	not modelled	9.8	100	<b>PDB header:</b> hydrolase (serine proteinase) <b>Chain:</b> B: <b>PDB Molecule:</b> hydrolyzed cucurbita maxima trypsin inhibitor v; <b>PDBTitle:</b> hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr structure)
33	<a href="#">d2cg4a1</a>	Alignment	not modelled	9.8	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
34	<a href="#">c3soyA_</a>	Alignment	not modelled	9.4	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ntf2-like superfamily protein; <b>PDBTitle:</b> nuclear transport factor 2 (ntf2-like) superfamily protein from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
35	<a href="#">c3abdY_</a>	Alignment	not modelled	9.3	38	<b>PDB header:</b> cell cycle/replication <b>Chain:</b> Y: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal
36	<a href="#">c3abdX_</a>	Alignment	not modelled	9.3	36	<b>PDB header:</b> cell cycle/replication <b>Chain:</b> X: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of human rev7 in complex with a human rev3 fragment in a2 monoclinic crystal
37	<a href="#">c3on4D_</a>	Alignment	not modelled	9.1	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of tetr transcriptional regulator from legionella2 pneumophila
38	<a href="#">c4aoaA_</a>	Alignment	not modelled	9.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phenylalanine aminotransferase; <b>PDBTitle:</b> biochemical properties and crystal structure of a novel2 beta-phenylalanine aminotransferase from variovorax3 paradoxus
39	<a href="#">c5aa6F_</a>	Alignment	not modelled	8.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> vanadium-dependent bromoperoxidase 2; <b>PDBTitle:</b> homohexameric structure of the second vanadate-dependent2 bromoperoxidase (anii) from ascophyllum nodosum
40	<a href="#">c3zeyU_</a>	Alignment	not modelled	8.7	26	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 40s ribosomal protein s25, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
41	<a href="#">c3t0yA_</a>	Alignment	not modelled	8.6	17	<b>PDB header:</b> transcription regulator/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
42	<a href="#">c4gk5C_</a>	Alignment	not modelled	8.3	45	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of human rev3-rev7-rev1-polkappa complex
43	<a href="#">c4gk0C_</a>	Alignment	not modelled	8.3	45	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of human rev3-rev7-rev1 complex
44	<a href="#">c4gk0D_</a>	Alignment	not modelled	8.3	45	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of human rev3-rev7-rev1 complex
45	<a href="#">c4gk5D_</a>	Alignment	not modelled	8.3	45	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of human rev3-rev7-rev1-polkappa complex
46	<a href="#">c2ajwA_</a>	Alignment	not modelled	8.1	38	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-conotoxin mii; <b>PDBTitle:</b> structure of the cyclic conotoxin mii-6
47	<a href="#">c6d0pC_</a>	Alignment	not modelled	8.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pirin family protein; <b>PDBTitle:</b> 1.88 angstrom resolution crystal structure of quercetin 2,3-2 dioxygenase from acinetobacter baumannii
48	<a href="#">c5mk5A_</a>	Alignment	not modelled	7.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bloom syndrome protein; <b>PDBTitle:</b> structures of dhn domain of human blm helicase
49	<a href="#">c6c52A_</a>	Alignment	not modelled	7.9	50	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> cross-alpha amyloid-like structure alphetat; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphetat
50	<a href="#">c6c52C_</a>	Alignment	not modelled	7.9	50	<b>PDB header:</b> de novo protein <b>Chain:</b> C: <b>PDB Molecule:</b> cross-alpha amyloid-like structure alphetat; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphetat
51	<a href="#">c6c52D_</a>	Alignment	not modelled	7.9	50	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> cross-alpha amyloid-like structure alphetat; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphetat
52	<a href="#">c6c52B_</a>	Alignment	not modelled	7.9	50	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> cross-alpha amyloid-like structure alphetat; <b>PDBTitle:</b> cross-alpha amyloid-like structure alphetat
53	<a href="#">c3i3fB_</a>	Alignment	not modelled	7.8	12	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> hypothetical protein from giardia lamblia gl50803_14299
54	<a href="#">c1zb7A_</a>	Alignment	not modelled	7.8	30	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> neurotoxin; <b>PDBTitle:</b> crystal structure of botulinum neurotoxin type g light chain

55	<a href="#">c5x9kA_</a>	Alignment	not modelled	7.7	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> austinol synthesis protein h; <b>PDBTitle:</b> structre of aush from aspergillus nidulans
56	<a href="#">c4eb5B_</a>	Alignment	not modelled	7.7	23	<b>PDB header:</b> transferase/metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> probable cysteine desulfurase 2; <b>PDBTitle:</b> a. fulgidus iscs-iscu complex structure
57	<a href="#">c5mu4A_</a>	Alignment	not modelled	7.7	18	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> tail tubular protein a; <b>PDBTitle:</b> tail tubular protein a of klebsiella pneumoniae bacteriophage kp32
58	<a href="#">c3niqB_</a>	Alignment	not modelled	7.7	21	<b>PDB header:</b> viral protein/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> orf 17; <b>PDBTitle:</b> crystal structure of kaposi's sarcoma-associated herpesvirus protease2 in complex with dimer disruptor
59	<a href="#">c3k12F_</a>	Alignment	not modelled	7.6	5	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> uncharacterized protein a6v7t0; <b>PDBTitle:</b> crystal structure of an uncharacterized protein a6v7t0 from2 pseudomonas aeruginosa
60	<a href="#">d1f6fa_</a>	Alignment	not modelled	7.6	26	<b>Fold:</b> 4-helical cytokines <b>Superfamily:</b> 4-helical cytokines <b>Family:</b> Long-chain cytokines
61	<a href="#">c5gzhA_</a>	Alignment	not modelled	7.5	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-1,2-glucanase; <b>PDBTitle:</b> endo-beta-1,2-glucanase from chitinophaga pinensis - ligand free form
62	<a href="#">c3iz6V_</a>	Alignment	not modelled	7.4	32	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein s25 (s25e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
63	<a href="#">c3izbV_</a>	Alignment	not modelled	7.4	26	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein rps25 (s25e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
64	<a href="#">c2cy8A_</a>	Alignment	not modelled	7.4	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-phenylglycine aminotransferase; <b>PDBTitle:</b> crystal structure of d-phenylglycine aminotransferase (d-phgat) from2 pseudomonas strutzeri st-201
65	<a href="#">c4go1A_</a>	Alignment	not modelled	7.3	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lsrr; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsrr from e.2 coli.
66	<a href="#">c3abeZ_</a>	Alignment	not modelled	7.1	45	<b>PDB header:</b> cell cycle/replication <b>Chain:</b> Z: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of human rev7 in complex with a human rev3 fragment in a2 tetragonal crystal
67	<a href="#">c3vprA_</a>	Alignment	not modelled	6.9	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, tetr family; <b>PDBTitle:</b> crystal structure of a tetr family transcriptional regulator pfmr from2 thermus thermophilus hb8
68	<a href="#">c4adoA_</a>	Alignment	not modelled	6.8	15	<b>PDB header:</b> antibiotic resistance <b>Chain:</b> A: <b>PDB Molecule:</b> far1; <b>PDBTitle:</b> fusidic acid resistance protein fusb
69	<a href="#">c2xgyA_</a>	Alignment	not modelled	6.7	29	<b>PDB header:</b> viral protein/isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> relik capsid n-terminal domain; <b>PDBTitle:</b> complex of rabbit endogenous lentivirus (relik)capsid with2 cyclophilin a
70	<a href="#">c1oheA_</a>	Alignment	not modelled	6.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cdc14b2 phosphatase; <b>PDBTitle:</b> structure of cdc14b phosphatase with a peptide ligand
71	<a href="#">c5n1wA_</a>	Alignment	not modelled	6.6	56	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> xeco2; <b>PDBTitle:</b> structure of xeco2 acetyltransferase domain bound to k105-coa2 conjugate
72	<a href="#">c3rpdB_</a>	Alignment	not modelled	6.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine synthase (b12-independent); <b>PDBTitle:</b> the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.
73	<a href="#">c3lv2A_</a>	Alignment	not modelled	6.5	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate aminotransferase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
74	<a href="#">d1saza1</a>	Alignment	not modelled	6.4	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
75	<a href="#">c1or7A_</a>	Alignment	not modelled	6.4	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-e factor; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
76	<a href="#">c3vu7Z_</a>	Alignment	not modelled	6.4	45	<b>PDB header:</b> replication <b>Chain:</b> Z: <b>PDB Molecule:</b> dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> crystal structure of rev1-rev7-rev3 ternary complex
77	<a href="#">d1jwya1</a>	Alignment	not modelled	6.3	71	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Myosin S1 fragment, N-terminal domain <b>Family:</b> Myosin S1 fragment, N-terminal domain
78	<a href="#">c1t7IA_</a>	Alignment	not modelled	6.3	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of cobalamin-independent methionine synthase from t.2 maritima
79	<a href="#">c3j3aZ_</a>	Alignment	not modelled	6.1	26	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 40s ribosomal protein s25; <b>PDBTitle:</b> structure of the human 40s ribosomal proteins
80	<a href="#">c5xxuZ_</a>	Alignment	not modelled	6.0	16	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> ribosomal protein es25;

						<b>PDBTitle:</b> small subunit of toxoplasma gondii ribosome
81	<a href="#">c1sseA_</a>	Alignment	not modelled	5.9	63	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> ap-1 like transcription factor yap1; <b>PDBTitle:</b> solution structure of the oxidized form of the yap1 redox2 domain
82	<a href="#">c2kdhA_</a>	Alignment	not modelled	5.8	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> troponin c, slow skeletal and cardiac muscles; <b>PDBTitle:</b> the solution structure of human cardiac troponin c in2 complex with the green tea polyphenol; (-)-3 epigallocatechin-3-gallate
83	<a href="#">c4extB_</a>	Alignment	not modelled	5.6	45	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> peptide from dna polymerase zeta catalytic subunit; <b>PDBTitle:</b> structure of polymerase-interacting domain of human rev1 in complex2 with translesional synthesis polymerase zeta
84	<a href="#">c4mxeA_</a>	Alignment	not modelled	5.5	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyltransferase esco1; <b>PDBTitle:</b> human esco1 (eco1/ctf7 ortholog), acetyltransferase domain in complex2 with acetyl-coa
85	<a href="#">c4xi5B_</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> viral protein/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> envelope glycoprotein I; <b>PDBTitle:</b> ghgl of varicella-zoster virus in complex with human neutralizing2 antibodies
86	<a href="#">c5usrG_</a>	Alignment	not modelled	5.4	21	<b>PDB header:</b> transferase <b>Chain:</b> G: <b>PDB Molecule:</b> cysteine desulfurase, mitochondrial; <b>PDBTitle:</b> crystal structure of human nfs1-isd11 in complex with e. coli acyl-2 carrier protein at 3.09 angstroms
87	<a href="#">c6d42A_</a>	Alignment	not modelled	5.1	33	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> intermediate conductance calcium-activated potassium <b>PDBTitle:</b> crystal structure of the kca3.1 c-terminal four-helix bundle (with2 copper)