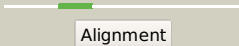





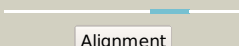

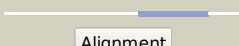
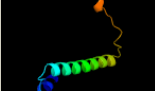
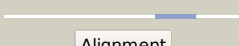

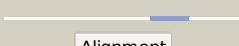

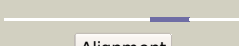




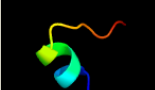




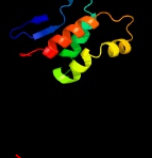

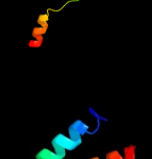
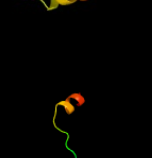
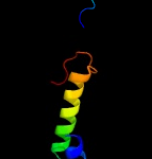

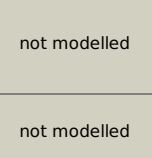


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0612 (-)_706327_706932
Date	Fri Jul 26 01:50:17 BST 2019
Unique Job ID	31c021c75d331838

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5h7yB_	 Alignment		56.3	67	PDB header: hydrolase inhibitor/peptide Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: structure of immunity protein tplei of t6ss from pseudomonas2 aeruginosa complexed with "I" peptide
2	c5nj8D_	 Alignment		38.9	15	PDB header: transcription Chain: D; PDB Molecule: aryl hydrocarbon receptor nuclear translocator; PDBTitle: structural basis for aryl hydrocarbon receptor mediated gene2 activation
3	c3o0yC_	 Alignment		38.0	21	PDB header: lipid binding protein Chain: C; PDB Molecule: lipoprotein; PDBTitle: the crystal structure of the putative lipoprotein from colwellia2 psychrerythraea
4	d2gy9t1	 Alignment		31.3	17	Fold: Spectrin repeat-like Superfamily: Ribosomal protein S20 Family: Ribosomal protein S20
5	c2rfpA_	 Alignment		28.1	17	PDB header: hydrolase Chain: A; PDB Molecule: putative ntp pyrophosphohydrolase; PDBTitle: crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
6	c6oqqA_	 Alignment		25.1	33	PDB header: transferase Chain: A; PDB Molecule: legionella pneumophila sidj; PDBTitle: legionella pneumophila sidj/saccharomyces cerevisiae calmodulin2 complex
7	c5o5tT_	 Alignment		21.3	14	PDB header: ribosome Chain: T; PDB Molecule: 30s ribosomal protein s20; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis
8	d2uubt1	 Alignment		19.7	20	Fold: Spectrin repeat-like Superfamily: Ribosomal protein S20 Family: Ribosomal protein S20
9	c4j8cA_	 Alignment		19.5	36	PDB header: chaperone Chain: A; PDB Molecule: hsc70-interacting protein; PDBTitle: crystal structure of the dimerization domain of hsc70-interacting2 protein
10	c4j8cB_	 Alignment		19.5	36	PDB header: chaperone Chain: B; PDB Molecule: hsc70-interacting protein; PDBTitle: crystal structure of the dimerization domain of hsc70-interacting2 protein
11	d1pbya1	 Alignment		18.9	19	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2

12	c2choA	Alignment		18.6	17	PDB header: hydrolase Chain: A: PDB Molecule: glucosaminidase; PDBTitle: bacteroides thetaiotaomicron hexosaminidase with o-2 glcnacase activity
13	c4uy5A	Alignment		14.8	28	PDB header: transferase Chain: A: PDB Molecule: histidine-specific methyltransferase egttd; PDBTitle: crystal structure of histidine-specific methyltransferase egttd from2 mycobacterium smegmatis
14	c4eqyC	Alignment		14.1	24	PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: crystal structure of acyl-[acyl-carrier-protein]-udp-n-2 acetylglucosamine o-acyltransferase from burkholderia thailandensis
15	c3eukL	Alignment		13.4	36	PDB header: cell cycle Chain: L: PDB Molecule: chromosome partition protein muke; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head domain)-2 atpgammas complex, asymmetric dimer
16	c4e18B	Alignment		13.2	39	PDB header: cell adhesion Chain: B: PDB Molecule: catenin alpha-1; PDBTitle: alpha-e-catenin is an autoinhibited molecule that co-activates2 vinculin
17	d1ya0a1	Alignment		12.6	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
18	c2voyB	Alignment		12.6	14	PDB header: hydrolase Chain: B: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
19	c3hjcA	Alignment		11.5	18	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 83-1; PDBTitle: crystal structure of the carboxy-terminal domain of hsp90 from2 leishmania major, lmjf33.0312
20	d1sf8a	Alignment		11.3	29	Fold: HSP90 C-terminal domain Superfamily: HSP90 C-terminal domain Family: HSP90 C-terminal domain
21	c4bqqB	Alignment	not modelled	11.3	21	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: protein crystal structure of the n-terminal and recombinase domains of2 the streptomyces temperate phage serine recombinase, fc31 integrase.
22	d1dxsa	Alignment	not modelled	11.3	29	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
23	c4tvxT	Alignment	not modelled	11.1	21	PDB header: PDB COMPND:
24	c2I9uA	Alignment	not modelled	10.8	100	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
25	c2I9uB	Alignment	not modelled	10.8	100	PDB header: membrane protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: spatial structure of dimeric erbb3 transmembrane domain
26	d1jmxal	Alignment	not modelled	10.7	14	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
27	c6agbH	Alignment	not modelled	10.7	21	PDB header: hydrolase/rna Chain: H: PDB Molecule: ribonucleases p/mrp protein subunit pop8; PDBTitle: cryo-em structure of yeast ribonuclease p
28	c5ah1A	Alignment	not modelled	10.4	24	PDB header: hydrolase Chain: A: PDB Molecule: triacylglycerol lipase; PDBTitle: structure of esta from clostridium botulinum

29	c2k8dA	Alignment	not modelled	10.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: peptide methionine sulfoxide reductase msrb; PDBTitle: solution structure of a zinc-binding methionine sulfoxide reductase
30	d1ewna	Alignment	not modelled	10.2	36	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: 3-methyladenine DNA glycosylase (AAG, ANPG, MPG)
31	c4oe4A	Alignment	not modelled	10.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase, PDBTitle: crystal structure of yeast ald4a1 complexed with nad+
32	c3mlpA	Alignment	not modelled	10.2	29	PDB header: transcription/dna Chain: A: PDB Molecule: transcription factor coe1; PDBTitle: early b-cell factor 1 (ebf1) bound to dna
33	d1x6ma	Alignment	not modelled	9.8	20	Fold: Mss4-like Superfamily: Mss4-like Family: Glutathione-dependent formaldehyde-activating enzyme, Gfa
34	c2dajA	Alignment	not modelled	9.7	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kiaa0977 protein; PDBTitle: solution structure of the novel identified ubiquitin-like2 domain in the human cobl-like 1 protein
35	d1tuwa	Alignment	not modelled	9.6	35	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Polyketide synthesis cyclase
36	c5m73H	Alignment	not modelled	9.5	43	PDB header: rna binding protein Chain: H: PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp s domain with srp72 rna-binding domain
37	c5i85A	Alignment	not modelled	9.5	33	PDB header: signaling protein Chain: A: PDB Molecule: zinc finger hit domain-containing protein 3; PDBTitle: solution structure of the complex between human znhit3 and nupif12 proteins
38	c6gwjD	Alignment	not modelled	9.5	33	PDB header: rna binding protein Chain: D: PDB Molecule: ekc/keops complex subunit gon7; PDBTitle: protein complex
39	c3hcbB	Alignment	not modelled	9.4	24	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase; PDBTitle: structure of msrb from xanthomonas campestris (oxidized2 form)
40	c5yx5B	Alignment	not modelled	9.4	19	PDB header: replication Chain: B: PDB Molecule: 49 protein; PDBTitle: crystal structure of viral parp1 interacting protein in murine2 gammaherpesvirus 68
41	c1vdfB	Alignment	not modelled	9.4	20	PDB header: extracellular matrix protein Chain: B: PDB Molecule: cartilage oligomeric matrix protein; PDBTitle: assembly domain of cartilage oligomeric matrix protein
42	d1l1da	Alignment	not modelled	9.4	24	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
43	c3s7yX	Alignment	not modelled	9.3	30	PDB header: transferase Chain: X: PDB Molecule: n-acetylglutamate kinase / n-acetylglutamate synthase; PDBTitle: crystal structure of mmnags in space group p3121 at 4.3 a resolution
44	c2kaoA	Alignment	not modelled	9.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b1; PDBTitle: structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
45	c5m73D	Alignment	not modelled	9.1	43	PDB header: rna binding protein Chain: D: PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp s domain with srp72 rna-binding domain
46	c5zwo9	Alignment	not modelled	9.0	14	PDB header: splicing Chain: 9: PDB Molecule: pre-mrna-splicing factor spp381; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
47	c3cezA	Alignment	not modelled	9.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase; PDBTitle: crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
48	c2l1uA	Alignment	not modelled	8.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine-r-sulfoxide reductase b2, mitochondrial; PDBTitle: structure-functional analysis of mammalian msrb2 protein
49	d1g8qa	Alignment	not modelled	8.7	26	Fold: Tetraspanin Superfamily: Tetraspanin Family: Tetraspanin
50	d2ey4c1	Alignment	not modelled	8.5	36	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Gar1-like SnoRNP
51	d1yt3a2	Alignment	not modelled	8.5	13	Fold: SAM domain-like Superfamily: HRDC-like Family: RNase D C-terminal domains
52	d3gata	Alignment	not modelled	8.4	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
53	c6nhwB	Alignment	not modelled	8.3	64	PDB header: immune system Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
						PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor receptor

54	c6nhwA_	Alignment	not modelled	8.3	64	superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
55	c2hvyB_	Alignment	not modelled	8.1	36	PDB header: isomerase/biosynthetic protein/rna Chain: B: PDB Molecule: small nucleolar rnp similar to gar1; PDBTitle: crystal structure of an h/aca box rnp from pyrococcus furiosus
56	d1xm0a1	Alignment	not modelled	8.1	24	Fold: Mss4-like Superfamily: Mss4-like Family: SelR domain
57	c6nhwC_	Alignment	not modelled	8.1	64	PDB header: immune system Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
58	d2euca1	Alignment	not modelled	8.1	44	Fold: YfmB-like Superfamily: YfmB-like Family: YfmB-like
59	c5yudA_	Alignment	not modelled	8.0	31	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: flagellin derivative in complex with the nlr protein naip5
60	c5fa9B_	Alignment	not modelled	8.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra; PDBTitle: bifunctional methionine sulfoxide reductase ab (msrab) from treponema2 denticola
61	c6ijfA_	Alignment	not modelled	7.7	40	PDB header: antitoxin Chain: A: PDB Molecule: tai4; PDBTitle: crystal structure of the type vi effector-immunity complex (tae4-tai4)2 from agrobacterium tumefaciens
62	d2cuqa1	Alignment	not modelled	7.7	31	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
63	c2rn5B_	Alignment	not modelled	7.6	31	PDB header: hormone Chain: B: PDB Molecule: insulin; PDBTitle: humal insulin mutant b31lys-b32arg
64	c1loiA_	Alignment	not modelled	7.6	30	PDB header: hydrolase Chain: A: PDB Molecule: cyclic 3',5'-amp specific phosphodiesterase rd1; PDBTitle: n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
65	c3bpiD_	Alignment	not modelled	7.6	17	PDB header: translation Chain: D: PDB Molecule: eukaryotic translation initiation factor 3 subunit j; PDBTitle: crystal structure of human translation initiation factor 3, subunit 12 alpha
66	c2eapA_	Alignment	not modelled	7.6	20	PDB header: signaling protein Chain: A: PDB Molecule: lymphocyte cytosolic protein 2; PDBTitle: solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
67	c2kz3A_	Alignment	not modelled	7.6	15	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein rad51l3; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
68	c4um2A_	Alignment	not modelled	7.5	14	PDB header: telomerase-binding protein Chain: A: PDB Molecule: telomerase-binding protein est1a; PDBTitle: crystal structure of the tpr domain of smg6
69	c3e0mB_	Alignment	not modelled	7.5	24	PDB header: oxidoreductase Chain: B: PDB Molecule: peptide methionine sulfoxide reductase msra/msrb PDBTitle: crystal structure of fusion protein of msra and msrb
70	c2lkqA_	Alignment	not modelled	7.4	70	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
71	d1z21a1	Alignment	not modelled	7.3	27	Fold: Type III secretion system domain Superfamily: Type III secretion system domain Family: YopR Core
72	d5gata_	Alignment	not modelled	7.3	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
73	c4e0hA_	Alignment	not modelled	7.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: mitochondrial fad-linked sulfhydryl oxidase erv1; PDBTitle: crystal structure of fad binding domain of erv1 from saccharomyces2 cerevisiae
74	d2ahob1	Alignment	not modelled	7.2	14	Fold: SAM domain-like Superfamily: eIF2alpha middle domain-like Family: eIF2alpha middle domain-like
75	c4dl0I_	Alignment	not modelled	7.2	23	PDB header: hydrolase Chain: I: PDB Molecule: v-type proton atpase subunit c; PDBTitle: crystal structure of the heterotrimeric egthead peripheral stalk2 complex of the yeast vacuolar atpase
76	c6a73B_	Alignment	not modelled	7.1	19	PDB header: signaling protein Chain: B: PDB Molecule: cop9 signalosome complex subunit 2, endolysin; PDBTitle: complex structure of csn2 with ip6
77	c3uaiC_	Alignment	not modelled	7.1	29	PDB header: isomerase/chaperone Chain: C: PDB Molecule: h/aca ribonucleoprotein complex subunit 1; PDBTitle: structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
78	c3zey8_	Alignment	not modelled	7.1	78	PDB header: ribosome Chain: 8: PDB Molecule: ribosomal protein s29, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

79	c5ch6B_	Alignment	not modelled	7.0	15	PDB header: transcription Chain: B: PDB Molecule: frigida; PDBTitle: crystal structure of frigida flowering-time regulator
80	c6nhwD_	Alignment	not modelled	7.0	64	PDB header: immune system Chain: D: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
81	c6nhwF_	Alignment	not modelled	7.0	64	PDB header: immune system Chain: F: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
82	c6nhwE_	Alignment	not modelled	7.0	64	PDB header: immune system Chain: E: PDB Molecule: tumor necrosis factor receptor superfamily member 10b; PDBTitle: structure of the transmembrane domain of the death receptor 5 - dimer2 of trimer
83	d1w07a2	Alignment	not modelled	7.0	11	Fold: Bromodomain-like Superfamily: Acyl-CoA dehydrogenase C-terminal domain-like Family: acyl-CoA oxidase C-terminal domains
84	c3h6sE_	Alignment	not modelled	6.9	28	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: clitocypin analog; PDBTitle: structure of clitocypin - cathepsin v complex
85	d1y0ja1	Alignment	not modelled	6.8	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
86	d1j2za_	Alignment	not modelled	6.7	18	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
87	c2kaeA_	Alignment	not modelled	6.6	10	PDB header: transcription/dna Chain: A: PDB Molecule: gata-type transcription factor; PDBTitle: data-driven model of med1:dna complex
88	d2bmob1	Alignment	not modelled	6.6	27	Fold: Cystatin-like Superfamily: NTF2-like Family: Ring hydroxylating beta subunit
89	c5vbaA_	Alignment	not modelled	6.5	35	PDB header: chaperone, hydrolase Chain: A: PDB Molecule: lysozyme, esx-1 secretion-associated protein espg1 chimera; PDBTitle: structure of espg1 chaperone from the type vii (esx-1) secretion2 system determined with the assistance of n-terminal t4 lysozyme3 fusion
90	c5od9B_	Alignment	not modelled	6.3	18	PDB header: de novo protein hydrolase Chain: B: PDB Molecule: mid1sc9; PDBTitle: structure of the engineered metalloesterase mid1sc9
91	d2vuti1	Alignment	not modelled	6.3	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
92	c6b5bA_	Alignment	not modelled	6.2	31	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: cryo-em structure of the naip5-nlr4-flagellin inflammasome
93	c4k30B_	Alignment	not modelled	6.2	31	PDB header: transferase Chain: B: PDB Molecule: n-acetylglutamate synthase, mitochondrial; PDBTitle: structure of the n-acetyltransferase domain of human n-acetylglutamate2 synthase
94	c3jyvN_	Alignment	not modelled	6.1	67	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s29(a); PDBTitle: structure of the 40s rna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
95	c2xz nN_	Alignment	not modelled	6.1	67	PDB header: ribosome Chain: N: PDB Molecule: rps29e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
96	c5i2rA_	Alignment	not modelled	6.0	20	PDB header: lyase Chain: A: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of fumarate hydratase from leishmania major
97	c3j20P_	Alignment	not modelled	5.8	56	PDB header: ribosome Chain: P: PDB Molecule: 30s ribosomal protein s14p type z; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
98	c5xxud_	Alignment	not modelled	5.8	67	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein us3; PDBTitle: small subunit of toxoplasma gondii ribosome
99	c4inmV_	Alignment	not modelled	5.8	80	PDB header: structural protein/dna Chain: V: PDB Molecule: cenp-c; PDBTitle: crystal structure of cenp-c in complex with the nucleosome core2 particle