
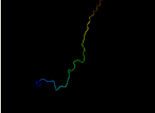
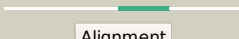

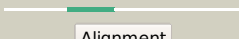
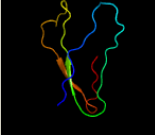

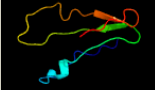



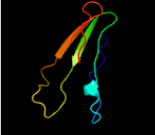







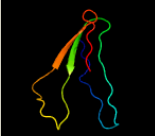


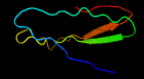
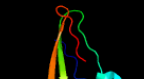
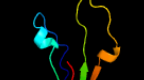
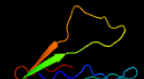
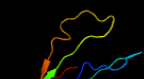
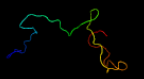
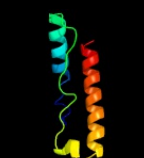
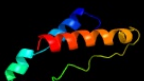
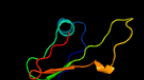


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0383c (-)_458462_459316
Date	Tue Jul 23 14:50:45 BST 2019
Unique Job ID	d57eed2c39ad804c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2miiA_	 Alignment		93.4	18	PDB header: protein binding Chain: A: PDB Molecule: penicillin-binding protein activator lpob; PDBTitle: nmr structure of e. coli lpob
2	d1muwa_	 Alignment		47.5	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
3	c5buvC_	 Alignment		46.5	14	PDB header: isomerase Chain: C: PDB Molecule: putative epimerase; PDBTitle: x-ray structure of wbca from yersinia enterocolitica
4	c6c46E_	 Alignment		45.2	21	PDB header: isomerase Chain: E: PDB Molecule: dtdp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: crystal structure of dtdp-4-dehydrorhamnose 3,5-epimerase from2 elizabethkingia anophelis nuhp1
5	d1xlma_	 Alignment		44.5	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
6	d1dzra_	 Alignment		43.9	16	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: dTDP-sugar isomerase
7	d1m0da_	 Alignment		43.9	20	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)
8	d1e7la1	 Alignment		43.2	19	Fold: LEM/SAP HeH motif Superfamily: Recombination endonuclease VII, C-terminal and dimerization domains Family: Recombination endonuclease VII, C-terminal and dimerization domains
9	d1wlta1	 Alignment		41.1	19	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: dTDP-sugar isomerase
10	c3rykB_	 Alignment		39.2	23	PDB header: isomerase Chain: B: PDB Molecule: dtdp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: 1.63 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 3,5-epimerase (rfbc) from bacillus anthracis str. ames with tdp and3 ppi bound
11	d2ixca1	 Alignment		38.3	26	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: dTDP-sugar isomerase

12	d2c0za1	Alignment		37.5	26	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
13	c1lupiA	Alignment		36.6	26	PDB header: epimerase Chain: A; PDB Molecule: dtdp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: mycobacterium tuberculosis rmlc epimerase (rv3465)
14	c4hmzD	Alignment		36.2	28	PDB header: unknown function Chain: D; PDB Molecule: putative 3-epimerase in d-allose pathway; PDBTitle: crystal structure of chmj, a 3'-monoepimerase from streptomyces2 bikiniensis in complex with dtdp-quinovose
15	c2c0zA	Alignment		36.1	26	PDB header: isomerase Chain: A; PDB Molecule: novw; PDBTitle: the 1.6 a resolution crystal structure of novw: a 4-keto-6-2 deoxy sugar epimerase from the novobiocin biosynthetic3 gene cluster of streptomyces spheroides
16	d1oi6a	Alignment		33.7	25	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
17	c4nl6C	Alignment		32.4	18	PDB header: splicing Chain: C; PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
18	c4k3zA	Alignment		31.0	6	PDB header: oxidoreductase Chain: A; PDB Molecule: d-erythrulose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrulose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
19	d1bxca	Alignment		27.5	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
20	c6ndrA	Alignment		26.9	18	PDB header: sugar binding protein Chain: A; PDB Molecule: dtdp-4-dehydrorhamnose 3,5-epimerase; PDBTitle: crystal structure of dtdp-6-deoxy-d-glucose-3,5-epimerase rmlc from2 legionella pneumophila philadelphia 1 in complex with dtdp-4-keto-l-3 rhamnose
21	c3g9hA	Alignment	not modelled	25.5	15	PDB header: endocytosis Chain: A; PDB Molecule: suppressor of yeast profilin deletion; PDBTitle: crystal structure of the c-terminal mu homology domain of2 syp1
22	d1qt1a	Alignment	not modelled	24.3	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
23	c2kngA	Alignment	not modelled	22.5	33	PDB header: dna binding protein Chain: A; PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2
24	d2qlka1	Alignment	not modelled	21.4	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
25	c4xtnj	Alignment	not modelled	21.4	12	PDB header: membrane protein Chain: J; PDB Molecule: sodium pumping rhodopsin; PDBTitle: crystal structure of the light-driven sodium pump kr2 in the2 pentameric red form, ph 4.9
26	c2yopB	Alignment	not modelled	21.0	16	PDB header: apoptosis Chain: B; PDB Molecule: protein fam3b; PDBTitle: long wavelength s-sad structure of fam3b pander
27	c3d3rA	Alignment	not modelled	19.2	13	PDB header: chaperone Chain: A; PDB Molecule: hydrogenase assembly chaperone hycp/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hycp/hupf2 family protein from shewanella oneidensis mr-1
28	d2ixha1	Alignment	not modelled	18.8	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase

29	c2jagA_	Alignment	not modelled	18.6	13	PDB header: membrane protein Chain: A; PDB Molecule: halorhodopsin; PDBTitle: I1-intermediate of halorhodopsin t203v
30	d2z1ca1	Alignment	not modelled	18.0	13	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
31	d1qzza2	Alignment	not modelled	17.9	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
32	d1e12a_	Alignment	not modelled	17.7	13	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
33	d1uaza_	Alignment	not modelled	17.4	10	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
34	d3d3ra1	Alignment	not modelled	17.4	13	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
35	d1xioa_	Alignment	not modelled	16.6	9	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
36	c1xioA_	Alignment	not modelled	16.6	9	PDB header: signaling protein Chain: A; PDB Molecule: anabaena sensory rhodopsin; PDBTitle: anabaena sensory rhodopsin
37	c5gzxD_	Alignment	not modelled	16.4	18	PDB header: hydrolase Chain: D; PDB Molecule: (r)-2-haloacid dehalogenase; PDBTitle: the complex structure of d-2-haloacid dehalogenase mutant with d-2-cpa
38	c5azdA_	Alignment	not modelled	16.1	24	PDB header: transport protein Chain: A; PDB Molecule: bacteriorhodopsin; PDBTitle: crystal structure of thermophilic rhodopsin.
39	c6eyuA_	Alignment	not modelled	15.2	15	PDB header: membrane protein Chain: A; PDB Molecule: bacteriorhodopsin; PDBTitle: crystal structure of the inward h(+) pump xenorhodopsin
40	c3re2A_	Alignment	not modelled	15.1	19	PDB header: unknown function Chain: A; PDB Molecule: predicted protein; PDBTitle: crystal structure of menin reveals the binding site for mixed lineage2 leukemia (ml) protein
41	d1h2sa_	Alignment	not modelled	14.7	18	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
42	c3a7kD_	Alignment	not modelled	14.7	15	PDB header: membrane protein Chain: D; PDB Molecule: halorhodopsin; PDBTitle: crystal structure of halorhodopsin from natronomonas2 pharaonis
43	d1xima_	Alignment	not modelled	14.7	11	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
44	c2x7IP_	Alignment	not modelled	14.6	33	PDB header: immune system Chain: P; PDB Molecule: protein rev; PDBTitle: implications of the hiv-1 rev dimer structure at 3.2a resolution for2 multimeric binding to the rev response element
45	c2kncB_	Alignment	not modelled	14.2	11	PDB header: cell adhesion Chain: B; PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
46	c3ddlB_	Alignment	not modelled	13.9	25	PDB header: transport protein Chain: B; PDB Molecule: xanthorhodopsin; PDBTitle: crystallographic structure of xanthorhodopsin, a light-driven ion pump2 with dual chromophore
47	c3u88B_	Alignment	not modelled	13.6	32	PDB header: transcription Chain: B; PDB Molecule: menin; PDBTitle: crystal structure of human menin in complex with ml1 and ledgf
48	c3mk7F_	Alignment	not modelled	13.1	23	PDB header: oxidoreductase Chain: F; PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
49	c4jr8A_	Alignment	not modelled	12.9	12	PDB header: proton transport Chain: A; PDB Molecule: cruxrhodopsin-3; PDBTitle: crystal structure of cruxrhodopsin-3 from haloarcula vallismortis at2 2.3 angstrom resolution
50	c2ghjD_	Alignment	not modelled	12.7	32	PDB header: structural protein Chain: D; PDB Molecule: 50s ribosomal protein l20; PDBTitle: crystal structure of folded and partially unfolded forms of aquifex2 aeolicus ribosomal protein l20
51	c3ug9A_	Alignment	not modelled	12.4	8	PDB header: membrane protein Chain: A; PDB Molecule: archaeal-type opsin 1, archaeal-type opsin 2; PDBTitle: crystal structure of the closed state of channelrhodopsin
52	c4fbzA_	Alignment	not modelled	12.4	9	PDB header: membrane protein Chain: A; PDB Molecule: deltarhodopsin; PDBTitle: crystal structure of deltarhodopsin from haloterrigena thermotolerans
53	d2ot2a1	Alignment	not modelled	12.0	20	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
54	d1ep0a_	Alignment	not modelled	12.0	20	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: dTDP-sugar isomerase
55	d1gz0a2	Alignment	not modelled	11.8	14	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain

56	c2n1pA_	Alignment	not modelled	11.7	30	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein
57	c4qidB_	Alignment	not modelled	11.6	12	PDB header: membrane protein Chain: B: PDB Molecule: bacteriorhodopsin-i; PDBTitle: crystal structure of haloquadratum walsbyi bacteriorhodopsin
58	d1tw3a2	Alignment	not modelled	11.4	9	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
59	c3kdpG_	Alignment	not modelled	11.2	21	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
60	c3kdpH_	Alignment	not modelled	11.2	21	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
61	c3lphD_	Alignment	not modelled	11.2	33	PDB header: viral protein Chain: D: PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer
62	d1z01a1	Alignment	not modelled	11.1	16	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
63	d1bxbA_	Alignment	not modelled	10.9	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
64	c3bjxB_	Alignment	not modelled	10.3	14	PDB header: hydrolase Chain: B: PDB Molecule: halocarboxylic acid dehalogenase dehi; PDBTitle: structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
65	c4gq6A_	Alignment	not modelled	10.2	32	PDB header: transcription/transcription inhibitor Chain: A: PDB Molecule: menin; PDBTitle: human menin in complex with mll peptide
66	c2mkvA_	Alignment	not modelled	10.1	24	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
67	d1ygya4	Alignment	not modelled	10.1	19	Fold: FwdE/GAPDH domain-like Superfamily: Serine metabolism enzymes domain Family: SerA intervening domain-like
68	c1rfoC_	Alignment	not modelled	10.0	33	PDB header: viral protein Chain: C: PDB Molecule: whisker antigen control protein; PDBTitle: trimeric foldon of the t4 phagehead fibrin
69	c6hwhB_	Alignment	not modelled	9.9	22	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
70	c5xtdo_	Alignment	not modelled	9.8	10	PDB header: oxidoreductase/electron transport Chain: O: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 2, PDBTitle: cryo-em structure of human respiratory complex i
71	c2kvoA_	Alignment	not modelled	9.7	13	PDB header: photosynthesis Chain: A: PDB Molecule: photosystem ii reaction center psb28 protein; PDBTitle: solution nmr structure of photosystem ii reaction center psb28 protein2 from synechocystis sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171
72	c2l82A_	Alignment	not modelled	9.5	13	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or32; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
73	c5ggoB_	Alignment	not modelled	9.4	18	PDB header: sugar binding protein Chain: B: PDB Molecule: protein o-linked-mannose beta-1,2-n- PDBTitle: crystal structure of n-terminal domain of human protein o-mannose2 beta-1,2-n-acetylglucosaminyltransferase in complex with galnac-3 beta1,3-glcnac-beta-pnp
74	c5zihA_	Alignment	not modelled	9.3	7	PDB header: membrane protein Chain: A: PDB Molecule: sensory opsin a,chromson; PDBTitle: crystal structure of the red light-activated channelrhodopsin2 chromson.
75	c3qxbB_	Alignment	not modelled	9.0	6	PDB header: isomerase Chain: B: PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
76	c4v19U_	Alignment	not modelled	8.7	25	PDB header: ribosome Chain: U: PDB Molecule: mitoribosomal protein bl20m, mrpl20; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
77	d2nn6c2	Alignment	not modelled	8.4	16	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
78	c5o60R_	Alignment	not modelled	8.4	39	PDB header: ribosome Chain: R: PDB Molecule: 50s ribosomal protein l20; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
79	d2zjr1	Alignment	not modelled	8.3	39	Fold: PABP domain-like Superfamily: Ribosomal protein L20 Family: Ribosomal protein L20
80	d1c4ka2	Alignment	not modelled	8.3	24	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases

						Family: Ornithine decarboxylase major domain
81	c4hyjB_	Alignment	not modelled	8.3	6	PDB header: proton transport Chain: B: PDB Molecule: rhodopsin; PDBTitle: crystal structure of exiguobacterium sibiricum rhodopsin
82	c5mlc4_	Alignment	not modelled	8.2	65	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l34, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
83	c6csmC_	Alignment	not modelled	8.0	18	PDB header: membrane protein Chain: C: PDB Molecule: gtacr1; PDBTitle: crystal structure of the natural light-gated anion channel gtacr1
84	c5mc9C_	Alignment	not modelled	7.9	19	PDB header: cell adhesion Chain: C: PDB Molecule: laminin subunit gamma-1; PDBTitle: crystal structure of the heterotrimeric integrin-binding region of2 laminin-111
85	c3j3wQ_	Alignment	not modelled	7.9	39	PDB header: ribosome Chain: Q: PDB Molecule: 50s ribosomal protein l20; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
86	c3wt9A_	Alignment	not modelled	7.7	5	PDB header: proton transport Chain: A: PDB Molecule: rhodopsin i; PDBTitle: crystal structure of the cell-free synthesized membrane protein,2 acetabularia rhodopsin i, at 1.48 angstrom
87	d2j01u1	Alignment	not modelled	7.5	32	Fold: PABP domain-like Superfamily: Ribosomal protein L20 Family: Ribosomal protein L20
88	c4hqjG_	Alignment	not modelled	7.5	25	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
89	c3am6C_	Alignment	not modelled	7.3	10	PDB header: transport protein Chain: C: PDB Molecule: rhodopsin-2; PDBTitle: crystal structure of the proton pumping rhodopsin ar2 from marine alga2 acetabularia acetabulum
90	c6q8iK_	Alignment	not modelled	7.2	27	PDB header: splicing Chain: K: PDB Molecule: protein red; PDBTitle: nterminal domain of human smu1 in complex with human redmid
91	d2gtaa1	Alignment	not modelled	6.9	9	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
92	d2iuba2	Alignment	not modelled	6.8	8	Fold: Transmembrane helix hairpin Superfamily: Magnesium transport protein CorA, transmembrane region Family: Magnesium transport protein CorA, transmembrane region
93	c2e1cA_	Alignment	not modelled	6.8	8	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
94	d1eb7a2	Alignment	not modelled	6.7	14	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
95	c4hqjE_	Alignment	not modelled	6.6	25	PDB header: hydrolase/transport protein Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
96	c4eb5B_	Alignment	not modelled	6.5	19	PDB header: transferase/metal binding protein Chain: B: PDB Molecule: probable cysteine desulfurase 2; PDBTitle: a. fulgidus iscs-iscu complex structure
97	c3a24A_	Alignment	not modelled	6.4	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of bt1871 retaining glycosidase
98	c2ostC_	Alignment	not modelled	6.3	19	PDB header: hydrolase/dna Chain: C: PDB Molecule: putative endonuclease; PDBTitle: the structure of a bacterial homing endonuclease : i-ssp6803i
99	c3d0fA_	Alignment	not modelled	6.3	20	PDB header: transferase Chain: A: PDB Molecule: penicillin-binding 1 transmembrane protein mrca; PDBTitle: structure of the big_1156.2 domain of putative penicillin-binding2 protein mrca from nitrosomonas europaea atcc 19718