

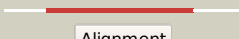

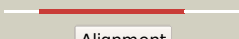



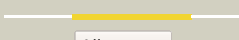


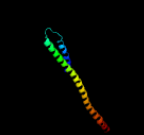

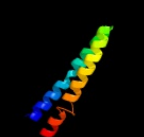
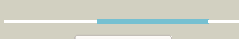
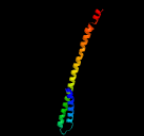
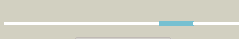
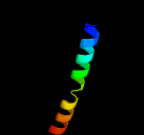






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3657c_(-)_4095718_4096293
Date	Fri Aug 9 18:20:34 BST 2019
Unique Job ID	1475d2f1c1fa2dbb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5nbgA_	 Alignment		98.9	15	PDB header: membrane protein Chain: A: PDB Molecule: general secretion pathway protein f; PDBTitle: structure of the cytoplasmic domain i of outf in the d. dadantii type2 ii secretion system
2	c3c1qA_	 Alignment		98.9	14	PDB header: transport protein Chain: A: PDB Molecule: general secretion pathway protein f; PDBTitle: the three-dimensional structure of the cytoplasmic domains of epsf2 from the type 2 secretion system of vibrio cholerae
3	c2whnA_	 Alignment		98.4	16	PDB header: protein transport Chain: A: PDB Molecule: pilus assembly protein pilc; PDBTitle: n-terminal domain from the pilc type iv pilus biogenesis protein
4	c4hhxA_	 Alignment		97.6	11	PDB header: membrane protein Chain: A: PDB Molecule: toxin coregulated pilus biosynthesis protein e; PDBTitle: structure of cytoplasmic domain of tcpe from vibrio cholerae
5	c6bs9A_	 Alignment		79.4	13	PDB header: transport protein Chain: A: PDB Molecule: stage iii sporulation protein ab; PDBTitle: stage iii sporulation protein ab (spoiiaab)
6	c5n9yB_	 Alignment		46.1	11	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
7	c4i0xA_	 Alignment		36.3	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxf (mab_3112-2 mab_3113) complex
8	c4ev6E_	 Alignment		36.3	4	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
9	c5ezeG_	 Alignment		31.0	29	PDB header: de novo protein Chain: G: PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-i22h-2 i25e
10	c6j7jA_	 Alignment		28.8	16	PDB header: transferase Chain: A: PDB Molecule: pseudomonas aeruginosa earp; PDBTitle: crystal structure of pseudomonas aeruginosa earp
11	c5f42B_	 Alignment		27.9	10	PDB header: transferase Chain: B: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: activity and crystal structure of francisella novicida udp-n-2 acetylglucosamine acyltransferase

12	c5nv8A_	Alignment		22.4	16	PDB header: transferase Chain: A; PDB Molecule: ef-p arginine 32 rhamnosyl-transferase; PDBTitle: structural basis for earp-mediated arginine glycosylation of 2 translation elongation factor ef-p
13	c5ezeE_	Alignment		21.8	27	PDB header: de novo protein Chain: E; PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
14	c5ezeC_	Alignment		21.8	27	PDB header: de novo protein Chain: C; PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
15	c5f2yE_	Alignment		21.8	27	PDB header: de novo protein Chain: E; PDB Molecule: cc-hept-hcys-h-e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-homocys-h-e
16	c5ezeA_	Alignment		21.3	27	PDB header: de novo protein Chain: A; PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
17	c5ezeF_	Alignment		21.3	27	PDB header: de novo protein Chain: F; PDB Molecule: cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-i18betamecys-l22h-2 i25e
18	c5f2yA_	Alignment		21.3	27	PDB header: de novo protein Chain: A; PDB Molecule: cc-hept-hcys-h-e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-homocys-h-e
19	c5f2yG_	Alignment		21.3	27	PDB header: de novo protein Chain: G; PDB Molecule: cc-hept-hcys-h-e; PDBTitle: a de novo designed heptameric coiled coil cc-hept-homocys-h-e
20	c2bbjB_	Alignment		20.1	12	PDB header: metal transport/membrane protein Chain: B; PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
21	d2ezla_	Alignment	not modelled	19.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
22	c6a6xC_	Alignment	not modelled	15.0	29	PDB header: toxin Chain: C; PDB Molecule: antitoxin maze7; PDBTitle: the crystal structure of the mtb maze-mazf-mt9 complex
23	d2gtad1	Alignment	not modelled	10.6	11	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: MazG-like
24	c5wxkA_	Alignment	not modelled	9.6	12	PDB header: transferase Chain: A; PDB Molecule: earp; PDBTitle: earp bound with domain i of ef-p
25	c4l6v7_	Alignment	not modelled	9.6	35	PDB header: electron transport Chain: 7; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
26	c6hqbm_	Alignment	not modelled	9.6	35	PDB header: photosynthesis Chain: M; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: monomeric cyanobacterial photosystem i
27	c4l6vM_	Alignment	not modelled	9.6	35	PDB header: electron transport Chain: M; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
28	c5oy09_	Alignment	not modelled	9.6	35	PDB header: photosynthesis Chain: 9; PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
29	c5oy0m_	Alignment	not modelled	9.6	35	PDB header: photosynthesis Chain: M; PDB Molecule: photosystem i reaction center subunit xii;

29	c5oy0M_	Alignment	not modelled	9.0	35	PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution PDB header: photosynthesis
30	c5oy0M_	Alignment	not modelled	9.6	35	Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: structure of synechocystis photosystem i trimer at 2.5a resolution
31	c5avoA_	Alignment	not modelled	8.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of the reduced form of homoserine dehydrogenase from <i>Sulfolobus tokodaii</i> .
32	c2jx4A_	Alignment	not modelled	8.5	50	PDB header: membrane protein Chain: A: PDB Molecule: vasopressin v2 receptor; PDBTitle: nmr structure of the intracellular loop (i3) of the 2 vasopressin v2 receptor (gpcr)
33	c2kv5A_	Alignment	not modelled	6.5	27	PDB header: toxin Chain: A: PDB Molecule: putative uncharacterized protein rna1; PDBTitle: solution structure of the par toxin fst in dpc micelles
34	c5dg3D_	Alignment	not modelled	6.2	12	PDB header: transferase Chain: D: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: structure of pseudomonas aeruginosa lpxa in complex with udp-3-o-(r-3-2 hydroxydecanoyl)-glcnac
35	c2ldjA_	Alignment	not modelled	6.0	64	PDB header: de novo protein Chain: A: PDB Molecule: trp-cage mini-protein; PDBTitle: 1h chemical shift assignments and structure of trp-cage mini-protein2 with d-amino acid
36	c3c8mA_	Alignment	not modelled	5.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
37	d1ef4a_	Alignment	not modelled	5.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: RNA polymerase subunit RPB10 Family: RNA polymerase subunit RPB10
38	c1f93F_	Alignment	not modelled	5.3	24	PDB header: transcription Chain: F: PDB Molecule: hepatocyte nuclear factor 1-alpha; PDBTitle: crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoH
39	d1f93f_	Alignment	not modelled	5.3	24	Fold: Dimerisation interlock Superfamily: Dimerization cofactor of HNF-1 alpha Family: Dimerization cofactor of HNF-1 alpha
40	c3io8D_	Alignment	not modelled	5.3	27	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: biml12f in complex with bcl-xl
41	c2pmzN_	Alignment	not modelled	5.2	10	PDB header: translation, transferase Chain: N: PDB Molecule: dna-directed rna polymerase subunit n; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
42	c3io8B_	Alignment	not modelled	5.1	29	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: biml12f in complex with bcl-xl