
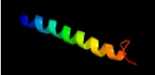



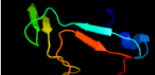





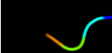

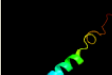

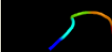



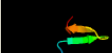





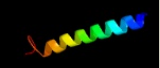


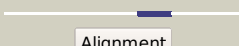
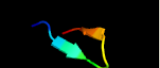
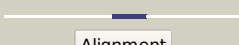

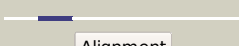

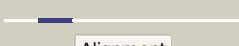
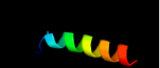
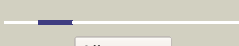


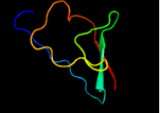

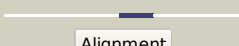
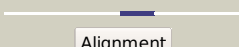


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2980_(-)_3335970_3336515
Date	Thu Aug 8 16:20:14 BST 2019
Unique Job ID	52f617a9b6789cd3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a0hj_	 Alignment		22.6	16	PDB header: electron transport Chain: J; PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
2	d2axtj1	 Alignment		22.6	16	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
3	d1f2qa1	 Alignment		15.8	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: ! set domains
4	d1su3a1	 Alignment		14.0	60	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
5	d1slma1	 Alignment		13.6	60	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
6	d1eaka1	 Alignment		12.7	60	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
7	c6f0kA_	 Alignment		11.9	11	PDB header: membrane protein Chain: A; PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
8	d1l6ja1	 Alignment		11.6	60	Fold: PGBD-like Superfamily: PGBD-like Family: MMP N-terminal domain
9	c4xtrG_	 Alignment		9.2	15	PDB header: hydrolase/transport protein Chain: G; PDB Molecule: pep12p; PDBTitle: structure of get3 bound to the transmembrane domain of pep12
10	c5eurC_	 Alignment		8.6	11	PDB header: unknown function Chain: C; PDB Molecule: uncharacterized protein; PDBTitle: hypothetical protein sf216 from shigella flexneri 5a m90t
11	c2l2ta_	 Alignment		8.3	36	PDB header: membrane protein Chain: A; PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain

12	c2lcxB_		Alignment		8.3	36	PDB header: transferase Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbB-4; PDBTitle: spatial structure of the erbB4 dimeric tm domain
13	c3jcuJ_		Alignment		8.1	10	PDB header: membrane protein Chain: J: PDB Molecule: photosystem ii reaction center protein j; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
14	c3kpaB_		Alignment		7.6	28	PDB header: ligase Chain: B: PDB Molecule: probable ubiquitin fold modifier conjugating enzyme; PDBTitle: ubiquitin fold modifier conjugating enzyme from leishmania major2 (probable)
15	c6eyvB_		Alignment		7.3	36	PDB header: oxidoreductase Chain: B: PDB Molecule: pvdP; PDBTitle: crystal structure of the pyoverdine maturation protein pvdP in complex2 with the mock substrates l-tyrosine and zinc.
16	c1ic9A_		Alignment		7.2	50	PDB header: de novo protein Chain: A: PDB Molecule: th10aoX; PDBTitle: nmr solution structure of the designed beta-sheet mini-2 protein th10aoX
17	c2kncB_		Alignment		6.9	9	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
18	c2m20B_		Alignment		6.4	14	PDB header: signaling protein Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
19	c2l8sA_		Alignment		5.8	14	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
20	d1ugna1		Alignment		5.7	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
21	d1fcga2		Alignment	not modelled	5.7	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
22	c4gvsA_		Alignment	not modelled	5.5	24	PDB header: hydrolase Chain: A: PDB Molecule: methenyltetrahydromethanopterin cyclohydrolase; PDBTitle: x-ray structure of the archaeoglobus fulgidus methenyl-2 tetrahydromethanopterin cyclohydrolase in complex with n5-formyl-3 tetrahydromethanopterin
23	c5th6D_		Alignment	not modelled	5.5	36	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: matrix metalloproteinase-9,matrix metalloproteinase-9; PDBTitle: structure determination of a potent, selective antibody inhibitor of2 human mmp9 (apo mmp9)