



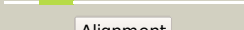

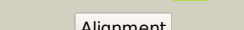







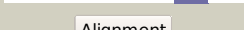

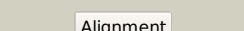
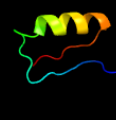



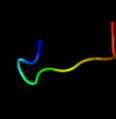








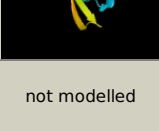


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1226c_(-)_1368838_1370301
Date	Wed Jul 31 22:05:31 BST 2019
Unique Job ID	14a554a0b75ae8a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gcla1	 Alignment		83.0	15	Fold: PH domain-like barrel Superfamily: PH domain-like Family: SSRP1-like
2	d3dcxa1	 Alignment		71.0	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: BPHL domain
3	c3fssa_	 Alignment		66.5	11	PDB header: chaperone Chain: A: PDB Molecule: histone chaperone rtt106; PDBTitle: structure of the tandem ph domains of rtt106
4	c4tyzB_	 Alignment		66.1	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the c-terminal domain of an unknown protein from2 leishmania infantum
5	c3gypA_	 Alignment		37.2	11	PDB header: chaperone Chain: A: PDB Molecule: histone chaperone rtt106; PDBTitle: rtt106p
6	c4khhF_	 Alignment		17.3	13	PDB header: transcription/replication Chain: F: PDB Molecule: uncharacterized protein pob3n; PDBTitle: structure of the spt16d pob3n heterodimer
7	d1ujpa_	 Alignment		13.5	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
8	c5tchG_	 Alignment		12.8	24	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
9	c5k9xA_	 Alignment		9.7	30	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
10	c1lqvD_	 Alignment		8.8	60	PDB header: blood clotting Chain: D: PDB Molecule: vitamin-k dependent protein c; PDBTitle: crystal structure of the endothelial protein c receptor with2 phospholipid in the groove in complex with gla domain of protein c.
11	c3jtcD_	 Alignment		8.8	60	PDB header: blood clotting Chain: D: PDB Molecule: vitamin k-dependent protein c; PDBTitle: importance of mg2+ in the ca2+-dependent folding of the gamma-2 carboxyglutamic acid domains of vitamin k-dependent clotting and3 anticlotting proteins

12	c3jtcC	Alignment		8.8	60	PDB header: blood clotting Chain: C: PDB Molecule: vitamin k-dependent protein c; PDBTitle: importance of mg2+ in the ca2+-dependent folding of the gamma-2 carboxyglutamic acid domains of vitamin k-dependent clotting and3 anticlotting proteins
13	c1lqvC	Alignment		8.8	60	PDB header: blood clotting Chain: C: PDB Molecule: vitamin-k dependent protein c; PDBTitle: crystal structure of the endothelial protein c receptor with2 phospholipid in the groove in complex with gla domain of protein c.
14	c5umrA	Alignment		8.1	10	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit ssrp1; PDBTitle: crystal structure of n-terminal domain of human fact complex subunit2 ssrp1
15	c5yqrA	Alignment		7.8	12	PDB header: transport protein Chain: A: PDB Molecule: endolysin/membrane-anchored lipid-binding protein lam6 PDBTitle: crystal structure of the ph-like domain of lam6
16	c5x3xq	Alignment		7.8	21	PDB header: transport protein Chain: Q: PDB Molecule: uncharacterized protein cbiq; PDBTitle: 2.8a resolution structure of a cobalt energy-coupling factor2 transporter-cbimqo
17	d1zj8a1	Alignment		7.5	22	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
18	c5uz9K	Alignment		7.3	38	PDB header: immune system/rna Chain: K: PDB Molecule: anti-crispr protein 30; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
19	d3b77a1	Alignment		6.6	4	Fold: PH domain-like barrel Superfamily: PH domain-like Family: BPHL domain
20	c3f5rA	Alignment		6.5	17	PDB header: transcription regulator Chain: A: PDB Molecule: fact complex subunit pob3; PDBTitle: the crystal structure of a subunit of the heterodimeric fact complex2 (spt16p-pob3p).
21	d2fbla1	Alignment	not modelled	6.3	7	Fold: CYTH-like phosphatases Superfamily: CYTH-like phosphatases Family: CYTH domain
22	d2q09a1	Alignment	not modelled	6.2	20	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
23	c3aaoD	Alignment	not modelled	6.2	20	PDB header: membrane protein Chain: D: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: structure and function of a membrane component secdf that enhances2 protein export
24	d2hthb1	Alignment	not modelled	6.1	10	Fold: PH domain-like barrel Superfamily: PH domain-like Family: VPS36 N-terminal domain-like
25	c5nocA	Alignment	not modelled	5.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: stage 0 sporulation protein j; PDBTitle: solution nmr structure of the c-terminal domain of parb (spo0j)
26	c4z3uC	Alignment	not modelled	5.7	7	PDB header: viral protein Chain: C: PDB Molecule: ul34 protein; PDBTitle: prv nuclear egress complex
27	c4e1pA	Alignment	not modelled	5.5	23	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 1 21 1 space group
28	c4e1rA	Alignment	not modelled	5.5	23	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: crystal structure of the dimerization domain of lsr2 from2 mycobacterium tuberculosis in the p 31 2 1 space group
						Fold: YqqU-like

