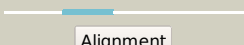

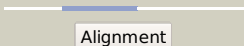
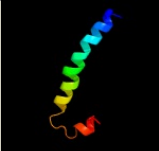
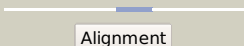



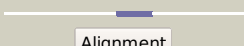
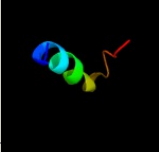
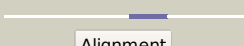
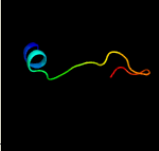
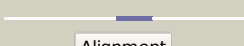
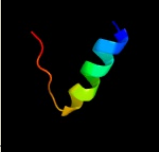

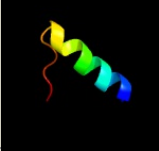





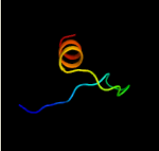




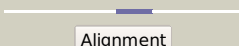
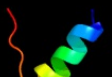
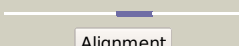
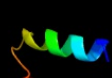
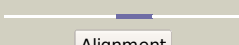
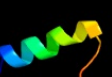
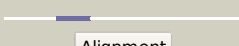


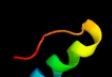

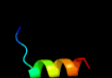




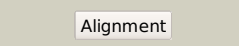
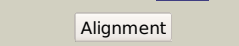
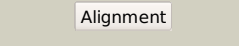
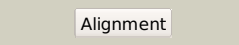




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3845_(-)_4319459_4319818
Date	Sat Aug 10 22:05:02 BST 2019
Unique Job ID	77e457625c6a9633

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5ux1D_	 Alignment		31.1	27	PDB header: lyase Chain: D: PDB Molecule: trna-(ms(2)io(6)a)-hydroxylase-like; PDBTitle: protein 43 with aldehyde deformylating oxygenase activity from2 synechococcus
2	d2itba1	 Alignment		29.2	24	Fold: Ferritin-like Superfamily: Ferritin-like Family: MiaE-like
3	c2wghA_	 Alignment		23.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large PDBTitle: human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
4	c4txoB_	 Alignment		18.3	50	PDB header: oxidoreductase/copper binding protein Chain: B: PDB Molecule: blr1131 protein; PDBTitle: crystal structure of the mixed disulfide complex of thioredoxin-like2 tlpas(c110s) and copper chaperone scois(c74s)
5	c1xjeA_	 Alignment		17.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleotide reductase, b12-dependent; PDBTitle: structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dttp-gdp complex
6	d1r5la2	 Alignment		17.1	29	Fold: Spollaa-like Superfamily: CRAL/TRIO domain Family: CRAL/TRIO domain
7	d1peqa2	 Alignment		16.0	25	Fold: PFL-like glycol radical enzymes Superfamily: PFL-like glycol radical enzymes Family: R1 subunit of ribonucleotide reductase, C-terminal domain
8	c6cgmA_	 Alignment		15.9	35	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; PDBTitle: x-ray crystal structure of bacillus subtilis ribonucleotide reductase2 nrde alpha subunit (nucleotide free)
9	d2cuqa1	 Alignment		15.4	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
10	c2cvuA_	 Alignment		15.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large chain PDBTitle: structures of yeast ribonucleotide reductase i
11	c3wl7A_	 Alignment		14.4	28	PDB header: hydrolase Chain: A: PDB Molecule: oxidized polyvinyl alcohol hydrolase; PDBTitle: the complex structure of poph s172c with ligand, aca

12	c2jphA_		Alignment		12.8	22	PDB header: signaling protein, protein binding Chain: A: PDB Molecule: plexin-b1; PDBTitle: nmr solution structure of the rho gtpase binding domain of2 human plexin-b1
13	c6n5uC_		Alignment		11.6	33	PDB header: metal binding protein Chain: C: PDB Molecule: protein sco1 homolog 1, mitochondrial; PDBTitle: crystal structure of arabidopsis thaliana sco1 with copper bound
14	c1pemA_		Alignment		11.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase 2 alpha PDBTitle: ribonucleotide reductase protein r1e from salmonella2 typhimurium
15	c6dqwD_		Alignment		10.8	20	PDB header: oxidoreductase Chain: D: PDB Molecule: ribonucleoside-diphosphate reductase, alpha chain; PDBTitle: flavobacterium johnsoniae class id ribonucleotide reductase alpha2 subunit
16	c6dqxA_		Alignment		10.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase, alpha chain; PDBTitle: actinobacillus ureae class id ribonucleotide reductase alpha subunit
17	d1xoub_		Alignment		10.1	38	Fold: EspA/CesA-like Superfamily: EspA/CesA-like Family: EspA chaperone CesA
18	c3hnfA_		Alignment		9.6	35	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large subunit; PDBTitle: crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
19	c6fh4D_		Alignment		9.3	6	PDB header: signaling protein Chain: D: PDB Molecule: transcriptional regulator ctsr; PDBTitle: ctsr c-terminal domain with bound phospho-arginine
20	d1cwva3		Alignment		8.7	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: Invasin/intimin cell-adhesion fragments Family: Invasin/intimin cell-adhesion fragments
21	c3rsrA_		Alignment	not modelled	8.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large chain 1; PDBTitle: crystal structure of 5-nitp inhibition of yeast ribonucleotide2 reductase
22	c6rlxB_		Alignment	not modelled	8.6	27	PDB header: hormone(muscle relaxant) Chain: B: PDB Molecule: relaxin, b-chain; PDBTitle: x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
23	c2k17A_		Alignment	not modelled	8.3	27	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 3; PDBTitle: solution structure of the taf3 phd domain in complex with a2 h3k4me3 peptide
24	c5b42A_		Alignment	not modelled	8.0	25	PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
25	d3bgea1		Alignment	not modelled	7.9	38	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
26	c2yh5A_		Alignment	not modelled	7.8	24	PDB header: lipid binding protein Chain: A: PDB Molecule: dapx protein; PDBTitle: structure of the c-terminal domain of bamc
27	c3r1rB_		Alignment	not modelled	7.7	30	PDB header: complex (oxidoreductase/peptide) Chain: B: PDB Molecule: ribonucleotide reductase r1 protein; PDBTitle: ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
28	c2n58C_		Alignment	not modelled	7.6	36	PDB header: transport protein/chaperone Chain: C: PDB Molecule: putative type iii secretion protein yscg;

28	c3p30C_	Alignment	not modelled	7.0	30	PDBTitle: structure of the yersinia pestis type iii secretion system needle2 protein yscf in complex with its chaperones ysce/yscg
29	c3ph0C_	Alignment	not modelled	7.5	43	PDB header: chaperone Chain: C: PDB Molecule: ascg; PDBTitle: crystal structure of the heteromolecular chaperone, asce-ascg, from2 the type iii secretion system in aeromonas hydrophila
30	d1g8fa1	Alignment	not modelled	7.5	17	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
31	d1cwva2	Alignment	not modelled	7.2	50	Fold: Immunoglobulin-like beta-sandwich Superfamily: Invasin/intimin cell-adhesion fragments Family: Invasin/intimin cell-adhesion fragments
32	c2xzmW_	Alignment	not modelled	7.2	17	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s4; 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 1
33	c2uwjG_	Alignment	not modelled	7.1	50	PDB header: chaperone Chain: G: PDB Molecule: type iii export protein pscg; PDBTitle: structure of the heterotrimeric complex which regulates type iii2 secretion needle formation
34	d2j6ba1	Alignment	not modelled	7.0	28	Fold: STIV B116-like Superfamily: STIV B116-like Family: STIV B116-like
35	c5ag8A_	Alignment	not modelled	7.0	31	PDB header: hydrolase Chain: A: PDB Molecule: gingipain r2; PDBTitle: crystal structure of a mutant (665i6h) of the c-terminal2 domain of rgpb
36	d1rlra2	Alignment	not modelled	6.6	30	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: R1 subunit of ribonucleotide reductase, C-terminal domain
37	c3n00B_	Alignment	not modelled	6.6	35	PDB header: transcription regulator Chain: B: PDB Molecule: nuclear receptor corepressor 1; PDBTitle: crystal structure of a deletion mutant of human reverba ligand binding2 domain bound with an ncor id1 peptide determined to 2.60a
38	c4an7B_	Alignment	not modelled	6.6	55	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: trypsin inhibitor; PDBTitle: kunitz type trypsin inhibitor complex with porcine trypsin
39	d1tdha3	Alignment	not modelled	6.3	31	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
40	c4tq1B_	Alignment	not modelled	6.2	33	PDB header: protein binding Chain: B: PDB Molecule: tectonin beta-propeller repeat-containing protein 1; PDBTitle: crystal structure of human atg5-tecair
41	c2kr7A_	Alignment	not modelled	6.2	63	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase slyd; PDBTitle: solution structure of helicobacter pylori slyd
42	c4yhwa_	Alignment	not modelled	5.9	38	PDB header: splicing Chain: A: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: yeast prp3 (296-469) in complex with fragment of u4/u6 di-snrna
43	d1zaka2	Alignment	not modelled	5.9	54	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
44	c2rliA_	Alignment	not modelled	5.7	19	PDB header: metal transport Chain: A: PDB Molecule: sco2 protein homolog, mitochondrial; PDBTitle: solution structure of cu(i) human sco2
45	c3jcrK_	Alignment	not modelled	5.6	38	PDB header: splicing Chain: K: PDB Molecule: hprp3; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
46	c2lv4A_	Alignment	not modelled	5.5	40	PDB header: protein binding Chain: A: PDB Molecule: putative outer membrane or exported protein; PDBTitle: zirs c-terminal domain