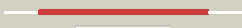








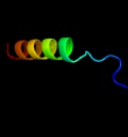



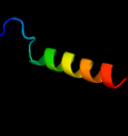

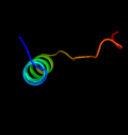

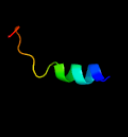



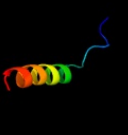


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2142c_(-)_2402201_2402518
Date	Mon Aug 5 13:25:26 BST 2019
Unique Job ID	18dbce7d5ce54f8b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5cw7H_	 Alignment		96.1	22	PDB header: toxin Chain: H; PDB Molecule: plasmid stabilization protein pare; PDBTitle: crystal structure of the paaa2-pare2 antitoxin-toxin complex
2	c5cegB_	 Alignment		94.5	23	PDB header: toxin Chain: B; PDB Molecule: plasmid stabilization system; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
3	c3kxeB_	 Alignment		93.8	19	PDB header: protein binding Chain: B; PDB Molecule: toxin protein pare-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
4	d1j7ga_	 Alignment		22.8	24	Fold: DTD-like Superfamily: DTD-like Family: DTD-like
5	c5xaqB_	 Alignment		22.5	25	PDB header: hydrolase Chain: B; PDB Molecule: probable d-tyrosyl-trna(tyr) deacylase 2; PDBTitle: crystal structure of animalia-specific trna deacylase from mus2 musculus
6	c6dftE_	 Alignment		19.5	20	PDB header: transferase Chain: E; PDB Molecule: deoxyhypusine synthase; PDBTitle: trypanosoma brucei deoxyhypusine synthase
7	c2dboA_	 Alignment		17.2	29	PDB header: hydrolase Chain: A; PDB Molecule: d-tyrosyl-trna(tyr) deacylase; PDBTitle: crystal structure of d-tyr-trna(tyr) deacylase from aquifex aeolicus
8	c5mwwA_	 Alignment		16.8	18	PDB header: transferase Chain: A; PDB Molecule: rna polymerase sigma factor sigma; PDBTitle: sigma1.1 domain of sigmaaa from bacillus subtilis
9	c5lxIA_	 Alignment		16.8	45	PDB header: viral protein Chain: A; PDB Molecule: decoration protein; PDBTitle: nmr structure of the n-terminal domain of the bacteriophage t52 decoration protein pb10
10	c5xbcB_	 Alignment		16.5	70	PDB header: hydrolase Chain: B; PDB Molecule: nsp1 protein; PDBTitle: crystal structure basis for pedv nsp1
11	d1jkea_	 Alignment		14.5	33	Fold: DTD-like Superfamily: DTD-like Family: DTD-like

12	c4y0lA_	Alignment		13.4	54	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein mmp111; PDBTitle: mycobacterial membrane protein mmp11d2
13	c2okvC_	Alignment		12.8	21	PDB header: hydrolase Chain: C: PDB Molecule: probable d-tyrosyl-trna(Tyr) deacylase 1; PDBTitle: c-myc dna unwinding element binding protein
14	c4gq6A_	Alignment		11.8	32	PDB header: transcription/transcription inhibitor Chain: A: PDB Molecule: menin; PDBTitle: human menin in complex with mll peptide
15	d8rucj_	Alignment		10.6	20	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
16	d1klxa_	Alignment		10.5	39	Fold: alpha-alpha superhelix Superfamily: HCP-like Family: HCP-like
17	c4kmhB_	Alignment		10.4	67	PDB header: protein binding Chain: B: PDB Molecule: suppressor of fused homolog; PDBTitle: crystal structure of suppressor of fused d20
18	d1luzdc1	Alignment		10.4	29	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
19	c6nx4A_	Alignment		10.3	33	PDB header: translation Chain: A: PDB Molecule: eukaryotic elongation factor 2 kinase; PDBTitle: structure of the c-terminal helical repeat domain of eukaryotic2 elongation factor 2 kinase (eef-2k)
20	d1rbli_	Alignment		10.3	47	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
21	d1ej7s_	Alignment	not modelled	10.3	17	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
22	d2v6ai1	Alignment	not modelled	10.2	30	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
23	d1gk8i_	Alignment	not modelled	10.1	30	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
24	d1wdds_	Alignment	not modelled	9.8	15	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
25	c4tpsA_	Alignment	not modelled	9.8	24	PDB header: replication Chain: A: PDB Molecule: sporulation inhibitor of replication protein sira; PDBTitle: sporulation inhibitor of dna replication, sira, in complex with domain2 i of dnaa
26	c2k6xA_	Alignment	not modelled	9.3	15	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
27	d2yzca2	Alignment	not modelled	9.3	35	Fold: T-fold Superfamily: Tetrahydrobiopterin biosynthesis enzymes-like Family: Urate oxidase (uricase)
28	c3ko7E_	Alignment	not modelled	9.0	21	PDB header: hydrolase Chain: E: PDB Molecule: d-tyrosyl-trna(Tyr) deacylase; PDBTitle: dtd from plasmodium falciparum in complex with d-lysine

29	c1gz3B_	Alignment	not modelled	8.5	39	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent malic enzyme, mitochondrial; PDBTitle: molecular mechanism for the regulation of human mitochondrial nad(p)+-2 dependent malic enzyme by atp and fumarate
30	c2ybvN_	Alignment	not modelled	8.5	40	PDB header: lyase Chain: N: PDB Molecule: ribulose bisphosphate carboxylase small subunit; PDBTitle: structure of rubisco from thermosynechococcus elongatus
31	d1pj3a2	Alignment	not modelled	7.8	39	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
32	c3oakD_	Alignment	not modelled	7.7	46	PDB header: transcription Chain: D: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of a spn1 (iws1)-spt6 complex
33	c5he9E_	Alignment	not modelled	7.7	43	PDB header: protein binding Chain: E: PDB Molecule: phage inhibitor protein; PDBTitle: bacterial initiation protein in complex with phage inhibitor protein
34	d1gq2a2	Alignment	not modelled	7.6	39	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
35	d1uzhc1	Alignment	not modelled	7.5	35	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
36	d1lr1s_	Alignment	not modelled	7.4	26	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
37	d1svdm1	Alignment	not modelled	7.0	33	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
38	c1qr6A_	Alignment	not modelled	6.8	39	PDB header: oxidoreductase Chain: A: PDB Molecule: malic enzyme 2; PDBTitle: human mitochondrial nad(p)-dependent malic enzyme
39	c1fsvA_	Alignment	not modelled	6.5	75	PDB header: beta beta alpha motif Chain: A: PDB Molecule: full sequence design 1 of beta beta alpha motif; PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, minimized average structure
40	c1fsdA_	Alignment	not modelled	6.5	75	PDB header: novel sequence Chain: A: PDB Molecule: full sequence design 1 of beta beta alpha motif; PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures
41	c2yzbA_	Alignment	not modelled	6.4	35	PDB header: oxidoreductase Chain: A: PDB Molecule: uricase; PDBTitle: crystal structure of uricase from arthrobacter globiformis2 in complex with uric acid (substrate)
42	c3mjhD_	Alignment	not modelled	6.2	50	PDB header: protein transport Chain: D: PDB Molecule: early endosome antigen 1; PDBTitle: crystal structure of early human rab5a in complex with the c2h2 zinc finger2 of eea1
43	d1dhsa_	Alignment	not modelled	5.8	38	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Deoxyhypusine synthase, DHS
44	c2aw5A_	Alignment	not modelled	5.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent malic enzyme; PDBTitle: crystal structure of a human malic enzyme
45	c4xruE_	Alignment	not modelled	5.5	19	PDB header: protein binding Chain: E: PDB Molecule: rnl; PDBTitle: structure of pnp1/rnl/hen1 complex
46	c1psvA_	Alignment	not modelled	5.3	75	PDB header: designed peptide Chain: A: PDB Molecule: pda8d; PDBTitle: computationally designed peptide with a beta-beta-alpha2 fold selection, nmr, 32 structures
47	d2pgda1	Alignment	not modelled	5.1	36	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
48	c3oakC_	Alignment	not modelled	5.1	50	PDB header: transcription Chain: C: PDB Molecule: transcription elongation factor spt6; PDBTitle: crystal structure of a spn1 (iws1)-spt6 complex