






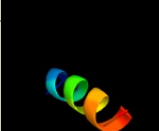
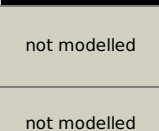


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3922c_(-)_4410230_4410592
Date	Sat Aug 10 22:05:11 BST 2019
Unique Job ID	8823adc803198367

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5lc5q_	Alignment		35.0	25	PDB header: oxidoreductase Chain: Q: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 4, PDBTitle: structure of mammalian respiratory complex i, class2
2	c4nqkD_	Alignment		30.3	12	PDB header: hydrolase/apoptosis Chain: D: PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: structure of an ubiquitin complex
3	c3zj1A_	Alignment		20.4	44	PDB header: rna binding protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: structure of nab2p tandem zinc finger 12
4	c3oruA_	Alignment		18.6	32	PDB header: metal binding protein Chain: A: PDB Molecule: duf1989 family protein; PDBTitle: crystal structure of a duf1989 family protein (tm1040_0329) from2 silicibacter sp. tm1040 at 1.11 a resolution
5	c6e8dA_	Alignment		17.8	36	PDB header: dna binding protein Chain: A: PDB Molecule: beta sliding clamp,dna mismatch repair protein mutl; PDBTitle: crystal structure of the bacillus subtilis sliding clamp-mutl complex.
6	c5i0cA_	Alignment		17.6	21	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein yjdj; PDBTitle: crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12
7	c6ekrA_	Alignment		17.4	38	PDB header: hydrolase Chain: A: PDB Molecule: type ii site-specific deoxyribonuclease; PDBTitle: crystal structure of type iip restriction endonuclease kpn2i
8	c5b37A_	Alignment		15.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan dehydrogenase; PDBTitle: crystal structure of l-tryptophan dehydrogenase from nostoc2 punctiforme
9	c1cdIH_	Alignment		14.9	50	PDB header: calcium-binding protein Chain: H: PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
10	c5jthB_	Alignment		14.8	50	PDB header: transferase Chain: B: PDB Molecule: myosin light chain kinase, smooth muscle; PDBTitle: crystal structure of e67a calmodulin - cam:rm20 complex
11	c5jqab_	Alignment		14.8	50	PDB header: calcium binding protein/protein binding Chain: B: PDB Molecule: myosin light chain kinase, smooth muscle; PDBTitle: cam:rm20 complex

12	c1cdIE_	Alignment		14.8	50	PDB header: calcium-binding protein Chain: E; PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
13	c1cdIF_	Alignment		14.8	50	PDB header: calcium-binding protein Chain: F; PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
14	c1cdIG_	Alignment		14.7	50	PDB header: calcium-binding protein Chain: G; PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
15	d3blha1	Alignment		14.7	20	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit
16	c2cseB_	Alignment		14.5	20	PDB header: virus Chain: B; PDB Molecule: major outer-capsid protein mu1; PDBTitle: features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
17	c1qtxB_	Alignment		14.5	50	PDB header: signaling protein Chain: B; PDB Molecule: protein (rs20); PDBTitle: the 1.65 angstrom structure of calmodulin rs20 peptide2 complex
18	c2o5gB_	Alignment		14.3	50	PDB header: metal binding protein Chain: B; PDB Molecule: smooth muscle myosin light chain kinase peptide; PDBTitle: calmodulin-smooth muscle light chain kinase peptide complex
19	c1qs7B_	Alignment		13.8	50	PDB header: metal binding protein/peptide Chain: B; PDB Molecule: rs20; PDBTitle: the 1.8 angstrom structure of calmodulin rs20 peptide2 complex
20	c1vrkB_	Alignment		13.7	50	PDB header: complex(calcium-binding protein/peptide) Chain: B; PDB Molecule: rs20; PDBTitle: the 1.9 angstrom structure of e84k-calmodulin rs20 peptide2 complex
21	c1qs7D_	Alignment	not modelled	12.6	50	PDB header: metal binding protein/peptide Chain: D; PDB Molecule: rs20; PDBTitle: the 1.8 angstrom structure of calmodulin rs20 peptide2 complex
22	c1jmuD_	Alignment	not modelled	12.4	23	PDB header: viral protein Chain: D; PDB Molecule: protein mu-1; PDBTitle: crystal structure of the reovirus mu1/sigma3 complex
23	c2lweA_	Alignment	not modelled	10.8	11	PDB header: signaling protein Chain: A; PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: solution structure of mutant (t170e) second card of human rig-i
24	d2j0141	Alignment	not modelled	10.5	43	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
25	c2j034_	Alignment	not modelled	10.5	43	PDB header: ribosome Chain: 4; PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
26	c2n5xA_	Alignment	not modelled	10.0	44	PDB header: chaperone Chain: A; PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: c-terminal domain of cdc37 cochaperone
27	c3bbo1_	Alignment	not modelled	9.1	29	PDB header: ribosome Chain: 1; PDB Molecule: ribosomal protein l31; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
28	c3k8zD_	Alignment	not modelled	8.2	30	PDB header: oxidoreductase Chain: D; PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudb1 a decrypted secondary glutamate2 dehydrogenase from b. subtilis

29	c5c6gA_	Alignment	not modelled	7.9	12	PDB header: cell cycle Chain: A: PDB Molecule: agr133cp; PDBTitle: structural insights into the scc2-scc4 cohesin loader
30	c3k1qP_	Alignment	not modelled	7.8	21	PDB header: PDB COMPND:
31	c6dzpg_	Alignment	not modelled	7.6	29	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: cryo-em structure of mycobacterium smegmatis c(minus) 50s ribosomal2 subunit
32	c2nx6A_	Alignment	not modelled	7.5	50	PDB header: structural protein Chain: A: PDB Molecule: nematocyst outer wall antigen; PDBTitle: structure of nowa cysteine rich domain 6
33	c2b664_	Alignment	not modelled	7.5	29	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
34	d1vs6z1	Alignment	not modelled	6.8	43	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
35	c3zj2A_	Alignment	not modelled	6.8	50	PDB header: rna binding protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: structure of nab2p tandem zinc finger 34
36	c1q68A_	Alignment	not modelled	6.8	42	PDB header: membrane protein/transferase Chain: A: PDB Molecule: t-cell surface glycoprotein cd4; PDBTitle: solution structure of t-cell surface glycoprotein cd4 and2 proto-oncogene tyrosine-protein kinase lck fragments
37	d1bgva2	Alignment	not modelled	6.8	27	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
38	c6nuwD_	Alignment	not modelled	6.7	10	PDB header: cell cycle Chain: D: PDB Molecule: inner kinetochore subunit ctf19; PDBTitle: yeast ctf19 complex
39	d1shyb2	Alignment	not modelled	6.6	42	Fold: Trefoil/Plexin domain-like Superfamily: Plexin repeat Family: Plexin repeat
40	c2hgj3_	Alignment	not modelled	6.6	43	PDB header: ribosome Chain: 3: PDB Molecule: 50s ribosomal protein l31; PDBTitle: crystal structure of the 70s thermus thermophilus ribosome showing how2 the 16s 3'-end mimicks mrna e and p codons. this entry 2hgj contains3 50s ribosomal subunit. the 30s ribosomal subunit can be found in pdb4 entry 2hgi.
41	c5o60g_	Alignment	not modelled	5.9	43	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
42	c1bvuf_	Alignment	not modelled	5.8	27	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: glutamate dehydrogenase from thermococcus litoralis
43	c2mj2A_	Alignment	not modelled	5.5	31	PDB header: viral protein Chain: A: PDB Molecule: agnoprotein; PDBTitle: structure of the dimerization domain of the human polyoma, jc virus2 agnoprotein is an amphipathic alpha-helix.
44	d1ut7a_	Alignment	not modelled	5.3	50	Fold: NAC domain Superfamily: NAC domain Family: NAC domain
45	c2tmgD_	Alignment	not modelled	5.1	33	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
46	c5n4cG_	Alignment	not modelled	5.0	40	PDB header: hydrolase Chain: G: PDB Molecule: alpha-amanitin proprotein; PDBTitle: prolyl oligopeptidase b from galerina marginata bound to 35mer2 hydrolysis and macrocyclization substrate - s577a mutant
47	c3aoeC_	Alignment	not modelled	5.0	30	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)