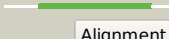
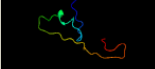





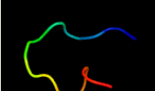
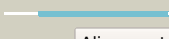





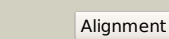

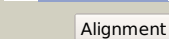

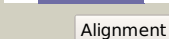
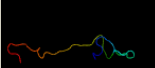




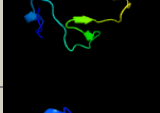

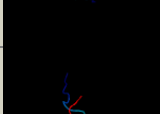
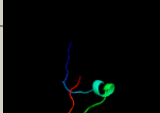
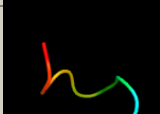

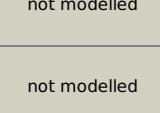


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0863 (-) _962602_962883
Date	Fri Jul 26 01:50:45 BST 2019
Unique Job ID	ca6075fde2399208

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5c0wJ_	 Alignment		59.8	21	PDB header: hydrolase/rna Chain: J; PDB Molecule: exosome complex exonuclease dis3; PDBTitle: structure of a 12-subunit nuclear exosome complex bound to single-2 stranded rna substrates
2	c2wp8J_	 Alignment		57.0	21	PDB header: hydrolase Chain: J; PDB Molecule: exosome complex exonuclease dis3; PDBTitle: yeast rrp44 nuclease
3	c6d6rK_	 Alignment		39.6	44	PDB header: hydrolase Chain: K; PDB Molecule: exosome complex exonuclease rrp44; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
4	c6md3F_	 Alignment		36.5	50	PDB header: hydrolase/rna Chain: F; PDB Molecule: rrp44p homologue; PDBTitle: structure of t. brucei rrp44 pin domain
5	d2a1ha1	 Alignment		32.5	18	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
6	c5oqj4_	 Alignment		27.9	25	PDB header: transcription Chain: 4; PDB Molecule: rna polymerase ii transcription factor b subunit 4; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
7	c5n60Q_	 Alignment		27.0	50	PDB header: transferase Chain: Q; PDB Molecule: rna polymerase i-specific transcription initiation factor PDBTitle: cryo-em structure of rna polymerase i in complex with rrn3 and core2 factor (orientation i)
8	c2r9qD_	 Alignment		24.9	23	PDB header: hydrolase Chain: D; PDB Molecule: 2'-deoxycytidine 5'-triphosphate deaminase; PDBTitle: crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
9	c2abjG_	 Alignment		22.0	18	PDB header: transferase Chain: G; PDB Molecule: branched-chain-amino-acid aminotransferase, cytosolic; PDBTitle: crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
10	c6grvA_	 Alignment		19.2	22	PDB header: metal binding protein Chain: A; PDB Molecule: metallothionein; PDBTitle: cadmium(ii) form of full-length metallothionein from pseudomonas2 fluorescens q2-87 (pflq2 mt)
11	c5jcaS_	 Alignment		14.7	40	PDB header: oxidoreductase Chain: S; PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (nfni) PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus

12	c4yifA_	Alignment		14.2	40	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase b (nad(+)), electron transfer PDBTitle: insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
13	d1rfma_	Alignment		13.5	30	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
14	c5op0B_	Alignment		13.0	13	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ligd, polymerase domain; PDBTitle: structure of prim-polc from mycobacterium smegmatis
15	c2iruA_	Alignment		12.2	10	PDB header: transferase Chain: A: PDB Molecule: putative dna ligase-like protein rv0938/mt0965; PDBTitle: crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
16	d1nxua_	Alignment		11.7	14	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
17	d1xrha_	Alignment		11.6	19	Fold: L-sulfolactate dehydrogenase-like Superfamily: L-sulfolactate dehydrogenase-like Family: L-sulfolactate dehydrogenase-like
18	c3uoeB_	Alignment		11.1	35	PDB header: oxidoreductase Chain: B: PDB Molecule: dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from sinorhizobium mellioti
19	c1ep3B_	Alignment		10.7	50	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase b (pyrk subunit); PDBTitle: crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
20	c3lq9B_	Alignment		10.6	44	PDB header: signaling protein Chain: B: PDB Molecule: dna-damage-inducible transcript 4 protein; PDBTitle: crystal structure of human redd1, a hypoxia-induced regulator of mtor
21	c6bymA_	Alignment	not modelled	10.2	22	PDB header: lipid transport Chain: A: PDB Molecule: sterol-binding protein; PDBTitle: crystal structure of the sterol-bound second start domain of yeast2 lam4
22	c5vj7B_	Alignment	not modelled	8.7	40	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp(+) reductase subunit alpha; PDBTitle: ferredoxin nadp oxidoreductase (xfn)
23	c5dmuA_	Alignment	not modelled	8.3	16	PDB header: transferase Chain: A: PDB Molecule: nhej polymerase; PDBTitle: structure of the nhej polymerase from methanocella paludicola
24	c2piaA_	Alignment	not modelled	7.4	33	PDB header: reductase Chain: A: PDB Molecule: phthalate dioxygenase reductase; PDBTitle: phthalate dioxygenase reductase: a modular structure for electron2 transfer from pyridine nucleotides to [2fe-2s]
25	c1d4cB_	Alignment	not modelled	7.2	24	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the flavocytochrome c2 fumarate reductase of shewanella putrefaciens strain mr-1
26	c2kfqA_	Alignment	not modelled	7.1	30	PDB header: de novo protein Chain: A: PDB Molecule: fp1; PDBTitle: nmr structure of fp1
27	c2n9oA_	Alignment	not modelled	6.9	33	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase rnf126; PDBTitle: solution structure of rnf126 n-terminal zinc finger domain
28	d1ep3b2	Alignment	not modelled	6.7	56	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Dihydroorotate dehydrogenase B, PyrK subunit PDB header: hydrolase/transferase

29	c2faoB_	Alignment	not modelled	6.7	19	Chain: B: PDB Molecule: probable atp-dependent dna ligase; PDBTitle: crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
30	c2m2jA_	Alignment	not modelled	6.4	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative periplasmic protein; PDBTitle: solution nmr structure of the n-terminal domain of stm1478 from2 salmonella typhimurium lt2: target str147a of the northeast3 structural genomics consortium (nesg), and apc101565 of the midwest4 center for structural genomics (mcsng).
31	d1awda_	Alignment	not modelled	6.4	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
32	c1j5mA_	Alignment	not modelled	6.3	75	PDB header: metal binding protein Chain: A: PDB Molecule: metallothionein-1; PDBTitle: solution nmr structure of the synthetic 113cd_3 beta_n domain2 of lobster metallothionein-1
33	d1frra_	Alignment	not modelled	6.2	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
34	c2g8yB_	Alignment	not modelled	6.1	23	PDB header: oxidoreductase Chain: B: PDB Molecule: malate/l-lactate dehydrogenases; PDBTitle: the structure of a putative malate/lactate dehydrogenase from e. coli.
35	c3uzbA_	Alignment	not modelled	5.8	17	PDB header: transferase Chain: A: PDB Molecule: branched-chain-amino-acid aminotransferase; PDBTitle: crystal structures of branched-chain aminotransferase from deinococcus2 radiodurans complexes with alpha-ketoisocaproate and l-glutamate3 suggest its radio-resistance for catalysis
36	d1fxia_	Alignment	not modelled	5.8	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
37	c1wtjB_	Alignment	not modelled	5.6	36	PDB header: oxidoreductase Chain: B: PDB Molecule: ureidoglycolate dehydrogenase; PDBTitle: crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
38	d2axth1	Alignment	not modelled	5.5	27	Fold: Single transmembrane helix Superfamily: Photosystem II 10 kDa phosphoprotein PsbH Family: PsbH-like
39	c2axtH_	Alignment	not modelled	5.5	27	PDB header: electron transport Chain: H: PDB Molecule: photosystem ii reaction center h protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus