










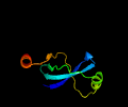







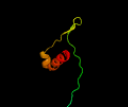




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1073_(-)_1197236_1198087
Date	Wed Jul 31 22:05:15 BST 2019
Unique Job ID	cbc4c035299e376d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r3pB_	 Alignment		99.6	18	PDB header: hydrolase Chain: B: PDB Molecule: mobile intron protein; PDBTitle: homing endonuclease i-bth0305i catalytic domain
2	c3hrIA_	 Alignment		99.3	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: endonuclease-like protein; PDBTitle: crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
3	d1cw0a_	 Alignment		99.3	14	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
4	d1vsra_	 Alignment		98.0	15	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Very short patch repair (VSR) endonuclease
5	c4oq2A_	 Alignment		97.3	21	PDB header: hydrolase Chain: A: PDB Molecule: restriction endonuclease pvurts1 i; PDBTitle: 5hmc specific restriction endonuclease pvurts1i
6	c4parC_	 Alignment		96.9	24	PDB header: dna binding protein/dna Chain: C: PDB Molecule: uncharacterized protein abasi; PDBTitle: the 5-hydroxymethylcytosine-specific restriction enzyme abasi in a2 complex with product-like dna
7	c6rdu2_	 Alignment		94.8	11	PDB header: proton transport Chain: 2: PDB Molecule: asa-2: polytomella f-atp synthase associated subunit 2; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 monomer-masked refinement
8	c1zela_	 Alignment		91.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2827c; PDBTitle: crystal structure of rv2827c protein from mycobacterium tuberculosis
9	d1zela2	 Alignment		82.0	23	Fold: Rv2827c C-terminal domain-like Superfamily: Rv2827c C-terminal domain-like Family: Rv2827c C-terminal domain-like
10	d1m0da_	 Alignment		80.7	22	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Endonuclease I (Holliday junction resolvase)
11	c4p6iB_	 Alignment		27.9	18	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of the cas1-cas2 complex from escherichia coli

12	c4gqzB_	Alignment		21.3	22	PDB header: metal binding protein Chain: B: PDB Molecule: putative periplasmic or exported protein; PDBTitle: crystal structure of s.cuep
13	d2fcla1	Alignment		16.8	19	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: TM1012-like
14	c3dupB_	Alignment		13.8	7	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
15	c2uwjG_	Alignment		11.5	14	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
16	c4makA_	Alignment		11.1	12	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of a putative ssrna endonuclease cas2, crispr2 adaptation protein from e.coli
17	d2fuka1	Alignment		10.1	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Atu1826-like
18	c3wbzD_	Alignment		9.9	16	PDB header: transferase Chain: D: PDB Molecule: likely histidyl trna-specific guanylyltransferase; PDBTitle: crystal structure of c. albicans trna(his) guanylyltransferase (thg1)2 with atp
19	c5xoxD_	Alignment		9.8	21	PDB header: transferase Chain: D: PDB Molecule: trna(his) guanylyltransferase; PDBTitle: crystal structure of trna(his) guanylyltransferase from saccharomyces2 cerevisiae
20	c3otbB_	Alignment		9.5	21	PDB header: transferase Chain: B: PDB Molecule: trna(his) guanylyltransferase; PDBTitle: crystal structure of human trnahis guanylyltransferase (thg1) - dtgp2 complex
21	d1tfea_	Alignment	not modelled	7.8	16	Fold: EF-Ts domain-like Superfamily: Elongation factor Ts (EF-Ts), dimerisation domain Family: Elongation factor Ts (EF-Ts), dimerisation domain
22	d1jg5a_	Alignment	not modelled	6.9	7	Fold: GTP cyclohydrolase I feedback regulatory protein, GFRP Superfamily: GTP cyclohydrolase I feedback regulatory protein, GFRP Family: GTP cyclohydrolase I feedback regulatory protein, GFRP
23	c4kgkB_	Alignment	not modelled	6.4	24	PDB header: transferase Chain: B: PDB Molecule: thg1-like uncharacterized protein; PDBTitle: bacterial trna(his) guanylyltransferase (thg1)-like protein in complex2 with gtp
24	c2pjpA_	Alignment	not modelled	6.2	14	PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
25	d1ccwa_	Alignment	not modelled	6.2	7	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
26	c5vrvA_	Alignment	not modelled	6.1	22	PDB header: hydrolase,oxidoreductase Chain: A: PDB Molecule: protein regulated by acid ph; PDBTitle: 2.05 angstrom resolution crystal structure of c-terminal domain2 (duf2156) of putative lysylphosphatidylglycerol synthetase from3 agrobacterium fabrum.
27	d1ynha1	Alignment	not modelled	6.0	35	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Succinylarginine dihydrolase-like
28	d1hh1a_	Alignment	not modelled	5.6	18	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Hjc-like

29	c2wj0B_	Alignment	not modelled	5.5	25	PDB header: hydrolase/dna Chain: B: PDB Molecule: archaeal hjc; PDBTitle: crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
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