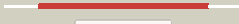



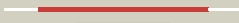




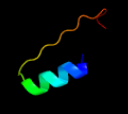

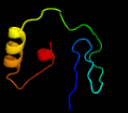

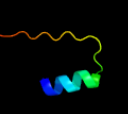



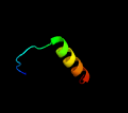

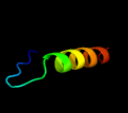

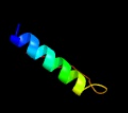
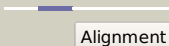
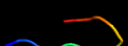
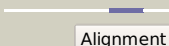

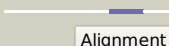

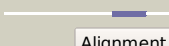

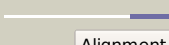

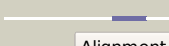
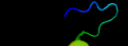
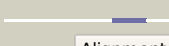

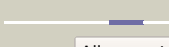



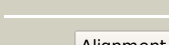
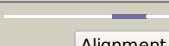
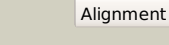
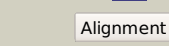
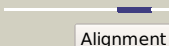




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3455c_truA_3876231_3877001
Date	Fri Aug 9 18:20:13 BST 2019
Unique Job ID	0986eb7ec385badc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dj0a_	 Alignment		100.0	35	Fold: Pseudouridine synthase Superfamily: Pseudouridine synthase Family: Pseudouridine synthase I TruA
2	c1vs3B_	 Alignment		100.0	35	PDB header: isomerase Chain: B: PDB Molecule: trna pseudouridine synthase a; PDBTitle: crystal structure of the trna pseudouridine synthase truA from thermus2 thermophilus hb8
3	c4j37A_	 Alignment		100.0	24	PDB header: rna binding protein Chain: A: PDB Molecule: trna pseudouridine synthase a, mitochondrial; PDBTitle: crystal structure of the catalytic domain of human pus1
4	c2v9kA_	 Alignment		91.7	14	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein flj32312; PDBTitle: crystal structure of human pus10, a novel pseudouridine2 synthase.
5	c1qysA_	 Alignment		50.6	22	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
6	d2hh8a1	 Alignment		49.9	23	Fold: YdfO-like Superfamily: YdfO-like Family: YdfO-like
7	c2jvfA_	 Alignment		45.4	19	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein
8	c6aefB_	 Alignment		28.2	23	PDB header: transferase Chain: B: PDB Molecule: polyketide synthase associated protein papa2; PDBTitle: papa2 acyl transferase
9	d1q9ja1	 Alignment		26.3	23	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
10	d1l5aa1	 Alignment		21.5	15	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: NRPS condensation domain (amide synthase)
11	c6gnyA_	 Alignment		18.4	11	PDB header: structural protein Chain: A: PDB Molecule: membrane-anchored junction protein; PDBTitle: crystal structure of the majin-terb2 heterotetrameric complex

12	d1e88a3	 Alignment		17.8	40	Fold: Fnl-like domain Superfamily: Fnl-like domain Family: Fibronectin type I module
13	c2xhgA_	 Alignment		17.3	12	PDB header: isomerase Chain: A; PDB Molecule: tyrocidine synthetase a; PDBTitle: crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
14	c6ad3A_	 Alignment		16.9	12	PDB header: biosynthetic protein Chain: A; PDB Molecule: lovastatin nonaketide synthase moka; PDBTitle: structural characterization of the condensation domain from monacolin2 k polyketide synthase moka
15	c1l5aA_	 Alignment		16.3	15	PDB header: biosynthetic protein Chain: A; PDB Molecule: amide synthase; PDBTitle: crystal structure of vibh, an nrps condensation enzyme
16	c6d0tA_	 Alignment		14.6	20	PDB header: de novo protein Chain: A; PDB Molecule: bb1; PDBTitle: de novo design of a fluorescence-activating beta barrel - bb1
17	c4tx3B_	 Alignment		11.6	31	PDB header: oxidoreductase Chain: B; PDB Molecule: peptide synthetase, module 7; PDBTitle: complex of the x-domain and oxyb from teicoplanin biosynthesis
18	c5t3eA_	 Alignment		11.5	15	PDB header: ligase Chain: A; PDB Molecule: bacillamide synthetase heterocyclization domain; PDBTitle: crystal structure of a nonribosomal peptide synthetase2 heterocyclization domain.
19	c5m6pB_	 Alignment		11.3	12	PDB header: isomerase Chain: B; PDB Molecule: tyrocidine synthase 2; PDBTitle: crystal structure of the epimerization domain from module 3 of2 tyrocidine synthetase b, tycb3(e)
20	c3pstA_	 Alignment		11.1	12	PDB header: nuclear protein Chain: A; PDB Molecule: protein doa1; PDBTitle: crystal structure of pul and pfu(mutate) domain
21	c2kruA_	 Alignment	not modelled	11.0	18	PDB header: oxidoreductase Chain: A; PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: solution nmr structure of the pcp_red domain of light-independent2 protochlorophyllide reductase subunit b from chlorobium tepidum.3 northeast structural genomics consortium target ctr69a
22	c4znmB_	 Alignment	not modelled	10.6	15	PDB header: ligase Chain: B; PDB Molecule: c-domain type ii peptide synthetase; PDBTitle: crystal structure of sgcc5 protein from streptomyces globisporus (apo2 form)
23	c6m7lB_	 Alignment	not modelled	9.7	31	PDB header: biosynthetic protein Chain: B; PDB Molecule: putative non-ribosomal peptide synthetase; PDBTitle: complex of oxa with the x-domain from gpa biosynthesis
24	c4jn3B_	 Alignment	not modelled	9.6	15	PDB header: biosynthetic protein Chain: B; PDB Molecule: cda peptide synthetase i; PDBTitle: crystal structures of the first condensation domain of the cda2 synthetase
25	c4u5hC_	 Alignment	not modelled	9.5	30	PDB header: toxin Chain: C; PDB Molecule: con-ikot-ikot; PDBTitle: crystal structure of con-ikot-ikot toxin
26	c1unyA_	 Alignment	not modelled	9.0	13	PDB header: four helix bundle Chain: A; PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
27	c4ky3A_	 Alignment	not modelled	8.4	19	PDB header: de novo protein Chain: A; PDB Molecule: designed protein or327; PDBTitle: three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327 Fold: FwdE/GAPDH domain-like

28	d1gr0a2	Alignment	not modelled	8.1	18	Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of e(22)(23)
29	c1u9hB_	Alignment	not modelled	7.7	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: epob; PDBTitle: rhombohedral crystal form of the epob nrps cyclization-docking2 bidomain from sorangium cellulosum
30	c5t81A_	Alignment	not modelled	7.5	27	PDB header: ligase Chain: A: PDB Molecule: enterobactin synthase component f; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 non-native mbth-like protein pa2412
31	c5ja2A_	Alignment	not modelled	7.1	12	PDB header: ligase Chain: A: PDB Molecule: polyketide synthase associated protein 5; PDBTitle: structure of polyketide synthase associated protein 5 from2 mycobacterium tuberculosis
32	c1q9jA_	Alignment	not modelled	7.0	23	PDB header: isomerase Chain: A: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlu
33	c2om1A_	Alignment	not modelled	6.9	18	PDB header: four helix bundle Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
34	c1unzA_	Alignment	not modelled	6.9	13	PDB header: four helix bundle Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure based engineering of internal molecular surfaces2 of four helix bundles
35	c1unzB_	Alignment	not modelled	6.9	13	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin-6; PDBTitle: crystal structure of human alpha-defensin 6 (h27w mutant)
36	c3qteA_	Alignment	not modelled	6.7	31	PDB header: biosynthetic protein Chain: A: PDB Molecule: txo1; PDBTitle: the structure of condensation and adenylation domains of teixobactin-2 producing nonribosomal peptide synthetase txo1 serine module in3 complex with amp
37	c6ozvA_	Alignment	not modelled	6.5	31	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a tgase
38	c4xz7A_	Alignment	not modelled	6.4	25	PDB header: cell adhesion Chain: A: PDB Molecule: fibronectin; PDBTitle: solution structure of 6f11f22f2, a compact three-module fragment of2 the gelatin-binding domain of human fibronectin
39	c1e88A_	Alignment	not modelled	6.4	40	PDB header: oxidoreductase Chain: A: PDB Molecule: asr4154 protein; PDBTitle: solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
40	c2109A_	Alignment	not modelled	6.2	6	PDB header: antimicrobial protein Chain: B: PDB Molecule: defensin 6; PDBTitle: crystal structure of human alpha-defensin-6
41	c1zmqB_	Alignment	not modelled	6.0	31	PDB header: protein binding Chain: X: PDB Molecule: protein doa1; PDBTitle: crystal structure of a pfu-pul domain pair of saccharomyces cerevisiae2 doa1/ufd3
42	c3l3fX_	Alignment	not modelled	6.0	12	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
43	c2mpnA_	Alignment	not modelled	5.9	25	PDB header: membrane protein Chain: B: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
44	c2mpnB_	Alignment	not modelled	5.9	25	PDB header: isomerase Chain: B: PDB Molecule: ribosomal large subunit pseudouridine synthase e; PDBTitle: crystal structure of e. coli pseudouridine synthase rlu
45	c2olwB_	Alignment	not modelled	5.8	18	PDB header: biosynthetic protein Chain: C: PDB Molecule: tlmii; PDBTitle: crystal structure of tallsomycin biosynthesis protein tlmii
46	c4hvmC_	Alignment	not modelled	5.6	16	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase component of branched- PDBTitle: solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
47	c2cooA_	Alignment	not modelled	5.3	14	PDB header: ribosome Chain: J: PDB Molecule: 60s ribosomal protein l19; PDBTitle: cryo-em structure of idle yeast ssh1 complex bound to the yeast 80s2 ribosome
48	c2wwaj_	Alignment	not modelled	5.2	19	PDB header: ligase Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: structure of the tycc5-6 pcp-c bidomain of the tyrocidine synthetase2 tycc
49	c2jgpA_	Alignment	not modelled	5.2	15	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
50	d2csha2	Alignment	not modelled	5.1	22	