


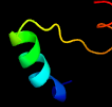
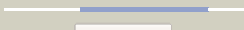


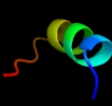
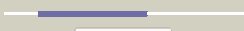



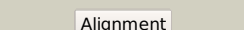

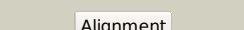


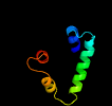
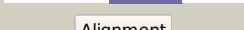




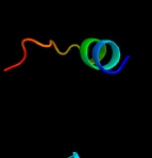


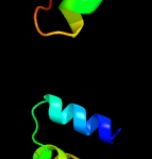



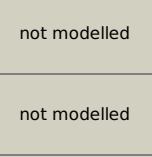


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1271c_(-)_1419967_1420308
Date	Wed Jul 31 22:05:36 BST 2019
Unique Job ID	c229fa9a2ebf105d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6c3rB_	 Alignment		37.1	14	PDB header: viral protein Chain: B: PDB Molecule: cricket paralysis virus 1a protein; PDBTitle: cricket paralysis virus rna1 suppressor protein crpv-1a
2	d2csua3	 Alignment		33.1	19	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
3	c3pvsA_	 Alignment		27.3	17	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
4	c5uqdA_	 Alignment		20.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: dummy; shorter than wild-type; PDBTitle: dpy-21 in complex with fe(ii) and alpha-ketoglutarate
5	d2j9ga2	 Alignment		19.3	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
6	c1vjqB_	 Alignment		17.8	20	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of 2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal 3 predicted stability.
7	c4rl6A_	 Alignment		17.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04i03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
8	d1mkea1	 Alignment		17.4	17	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
9	d1yqqa1	 Alignment		16.8	14	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
10	c2ekcA_	 Alignment		16.2	26	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
11	c3g2bA_	 Alignment		13.8	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: coenzyme pqq synthesis protein d; PDBTitle: crystal structure of pqqd from xanthomonas campestris

12	c5k9xA_	Alignment		12.3	24	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
13	c3ss4C_	Alignment		12.2	38	PDB header: hydrolase Chain: C; PDB Molecule: glutaminase c; PDBTitle: crystal structure of mouse glutaminase c, phosphate-bound form
14	c6g2dC_	Alignment		11.8	13	PDB header: ligase Chain: C; PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
15	c5dggB_	Alignment		11.3	27	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: central domain of uncharacterized lpg1148 protein from legionella2 pneumophila
16	c4inaA_	Alignment		11.0	14	PDB header: oxidoreductase Chain: A; PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolinella2 succinogenes. northeast structural genomics consortium target wsr35
17	c6jx3B_	Alignment		10.8	19	PDB header: peptide binding protein Chain: B; PDB Molecule: tfub1; PDBTitle: lasso peptide synthetase b1 complexed with the leader peptide
18	c2lweA_	Alignment		10.6	20	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
19	c5v1uB_	Alignment		10.4	11	PDB header: protein binding Chain: B; PDB Molecule: tbib1; PDBTitle: tbib1 in complex with the tbia(beta) leader peptide
20	c2jd3B_	Alignment		10.2	11	PDB header: dna binding protein Chain: B; PDB Molecule: stbb protein; PDBTitle: parr from plasmid pb171
21	d2ahra1	Alignment	not modelled	10.2	16	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
22	c2n2aA_	Alignment	not modelled	9.6	29	PDB header: membrane protein Chain: A; PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
23	d1ulza2	Alignment	not modelled	9.5	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
24	d1ca1a1	Alignment	not modelled	9.4	24	Fold: Phospholipase C/P1 nuclease Superfamily: Phospholipase C/P1 nuclease Family: Phospholipase C
25	c2kktA_	Alignment	not modelled	9.2	50	PDB header: transcription Chain: A; PDB Molecule: ataxin-7-like protein 3; PDBTitle: solution structure of the sca7 domain of human ataxin-7-l3 protein
26	d3ctda1	Alignment	not modelled	9.1	20	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
27	c2ifsA_	Alignment	not modelled	9.0	17	PDB header: signaling protein Chain: A; PDB Molecule: wiskott-aldrich syndrome protien interacting protein and PDBTitle: structure of the n-wasp evh1 domain in complex with an extended wip2 peptide
28	c4yajA_	Alignment	not modelled	8.7	7	PDB header: ligase Chain: A; PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-

						coenzyme a2 synthetase 1 (apo form) PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: crystal structure of human gac in complex with glutamate and bptes
29	c3uo9B_	Alignment	not modelled	7.9	38	PDB header: hydrolase Chain: B: PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: multidomain structure of human kidney-type glutaminase(kga/gls)
30	c5uqeB_	Alignment	not modelled	7.5	38	PDB header: signaling protein Chain: A: PDB Molecule: stromal interaction molecule 2; PDBTitle: nmr structure of calcium-loaded stim2 ef-sam.
31	c2l5yA_	Alignment	not modelled	7.4	15	PDB header: chaperone Chain: A: PDB Molecule: bifunctional coenzyme pqq synthesis protein c/d; PDBTitle: the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
32	c5sxyA_	Alignment	not modelled	7.3	17	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
33	d1xoda1	Alignment	not modelled	7.0	27	PDB header: toxin/antitoxin/dna Chain: C: PDB Molecule: toxin-antitoxin system antidote transcriptional repressor PDBTitle: shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
34	c4pu4C_	Alignment	not modelled	7.0	21	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
35	d1eucb1	Alignment	not modelled	6.9	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative atpase, aaa family; PDBTitle: crystal structure of a putative aaa family atpase from prochlorococcus2 marinus subsp. pastoris
36	c3ctdB_	Alignment	not modelled	6.8	22	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
37	d1w2za3	Alignment	not modelled	6.8	28	PDB header: de novo protein Chain: A: PDB Molecule: heterogeneous-backbone variant of the sp1-3 zinc finger: n- PDBTitle: heterogeneous-backbone foldamer mimic of the sp1-3 zinc finger
38	c5us3A_	Alignment	not modelled	6.3	75	Fold: Gametocyte protein Pfg27 Superfamily: Gametocyte protein Pfg27 Family: Gametocyte protein Pfg27
39	d1n81a_	Alignment	not modelled	6.2	67	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
40	c5kinC_	Alignment	not modelled	6.1	29	PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
41	c3f6wE_	Alignment	not modelled	6.0	17	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrVn C-terminal domain-like
42	d2r9ga1	Alignment	not modelled	5.9	21	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
43	d1d6za3	Alignment	not modelled	5.8	33	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
44	c5kzmA_	Alignment	not modelled	5.7	29	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Pleiotropic translational regulator Hfq
45	d1u1sa1	Alignment	not modelled	5.7	8	PDB header: ribosome Chain: S: PDB Molecule: mitoribosomal protein ul18m, mrp118; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
46	c4v19S_	Alignment	not modelled	5.6	24	Fold: Phospholipase C/P1 nuclease Superfamily: Phospholipase C/P1 nuclease Family: Phospholipase C
47	d1khoa1	Alignment	not modelled	5.6	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
48	c2ppxA_	Alignment	not modelled	5.4	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
49	d2ppxa1	Alignment	not modelled	5.4	8	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Anticodon-binding domain
50	d1bbua1	Alignment	not modelled	5.4	23	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Pleiotropic translational regulator Hfq
51	d1hk9a_	Alignment	not modelled	5.4	15	PDB header: immune system Chain: A: PDB Molecule: acan1; PDBTitle: nmr solution structure of acan1 from the ancylostoma caninum hookworm
52	c6driA_	Alignment	not modelled	5.4	50	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins
53	d1kq1a_	Alignment	not modelled	5.3	0	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins

						Family: Pleiotropic translational regulator Hfq
54	c2gacD	Alignment	not modelled	5.3	20	PDB header: hydrolase Chain: D: PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
55	c3cjA	Alignment	not modelled	5.3	26	PDB header: unknown function Chain: A: PDB Molecule: domain of unknown function; PDBTitle: crystal structure of a protein of unknown function (eca1910) from2 pectobacterium atrosepticum scri1043 at 2.20 a resolution
56	d3bgea1	Alignment	not modelled	5.2	18	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like