














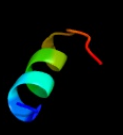

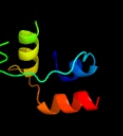

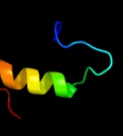

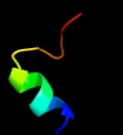
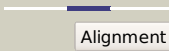

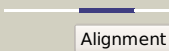

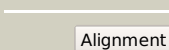
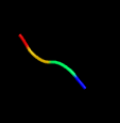
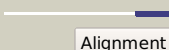
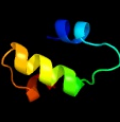




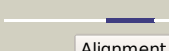
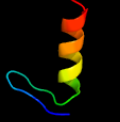
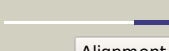

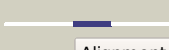


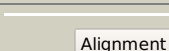
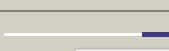
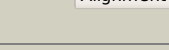
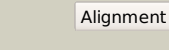

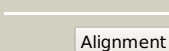



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1291c_(-)_1445505_1445840
Date	Wed Jul 31 22:05:38 BST 2019
Unique Job ID	99b5687ce01ad142

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6c3rB_</a>	 Alignment		60.0	19	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> cricket paralysis virus 1a protein; <b>PDBTitle:</b> cricket paralysis virus rna1 suppressor protein crpv-1a
2	<a href="#">d2csua3</a>	 Alignment		25.7	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
3	<a href="#">c2ekcA_</a>	 Alignment		16.8	23	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5
4	<a href="#">d1mkea1</a>	 Alignment		15.8	26	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
5	<a href="#">c5k9xA_</a>	 Alignment		15.8	24	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
6	<a href="#">c4rl6A_</a>	 Alignment		14.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> crystal structure of the q04i03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
7	<a href="#">c4inaA_</a>	 Alignment		14.8	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> crystal structure of the q7mss8_wolsu protein from wolinnella2 succinogenes. northeast structural genomics consortium target wsr35
8	<a href="#">c5uqdA_</a>	 Alignment		14.1	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dumpy: shorter than wild-type; <b>PDBTitle:</b> dpy-21 in complex with fe(ii) and alpha-ketoglutarate
9	<a href="#">c5tchG_</a>	 Alignment		13.8	25	<b>PDB header:</b> lyase <b>Chain:</b> G; <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
10	<a href="#">c2jd3B_</a>	 Alignment		12.8	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> stbb protein; <b>PDBTitle:</b> parr from plasmid pb171
11	<a href="#">c3ss4C_</a>	 Alignment		9.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> glutaminase c; <b>PDBTitle:</b> crystal structure of mouse glutaminase c, phosphate-bound form

12	<a href="#">c5dggB_</a>	 Alignment		9.5	27	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> central domain of uncharacterized lpg1148 protein from legionella2 pneumophila
13	<a href="#">d2j9ga2</a>	 Alignment		8.5	22	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
14	<a href="#">c5us3A_</a>	 Alignment		8.4	75	<b>PDB header:</b> de novo protein <b>Chain:</b> A; <b>PDB Molecule:</b> heterogeneous-backbone variant of the sp1-3 zinc finger: n- <b>PDBTitle:</b> heterogeneous-backbone foldamer mimic of the sp1-3 zinc finger
15	<a href="#">c3g2ba_</a>	 Alignment		8.3	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A; <b>PDB Molecule:</b> coenzyme pqq synthesis protein d; <b>PDBTitle:</b> crystal structure of pqqd from xanthomonas campestris
16	<a href="#">d1ulza2</a>	 Alignment		7.8	19	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
17	<a href="#">c2lweA_</a>	 Alignment		7.8	7	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> probable atp-dependent rna helicase ddx58; <b>PDBTitle:</b> solution structure of mutant (t170e) second card of human rig-i
18	<a href="#">d1qcrd2</a>	 Alignment		7.6	21	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Cytochrome bc1 domain
19	<a href="#">c1apzB_</a>	 Alignment		7.6	8	<b>PDB header:</b> complex (hydrolase/peptide) <b>Chain:</b> B; <b>PDB Molecule:</b> aspartylglucosaminidase; <b>PDBTitle:</b> human aspartylglucosaminidase complex with reaction product
20	<a href="#">c1vjqb_</a>	 Alignment		7.5	42	<b>PDB header:</b> structural genomics, de novo protein <b>Chain:</b> B; <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> designed protein based on backbone conformation of 2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal predicted stability.
21	<a href="#">c4y7iB_</a>	 Alignment	not modelled	7.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> myotubularin-related protein 8; <b>PDBTitle:</b> crystal structure of mtmr8
22	<a href="#">d2drpa1</a>	 Alignment	not modelled	7.5	55	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
23	<a href="#">d1khda1</a>	 Alignment	not modelled	7.2	3	<b>Fold:</b> Methionine synthase domain-like <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
24	<a href="#">c6fddC_</a>	 Alignment	not modelled	7.2	23	<b>PDB header:</b> structural protein <b>Chain:</b> C; <b>PDB Molecule:</b> whirlin; <b>PDBTitle:</b> crystal structure of the hhd2 domain of whirlin
25	<a href="#">c6jx3B_</a>	 Alignment	not modelled	7.0	19	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> tfub1; <b>PDBTitle:</b> lasso peptide synthetase b1 complexed with the leader peptide
26	<a href="#">c6dria_</a>	 Alignment	not modelled	6.8	50	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> acan1; <b>PDBTitle:</b> nmr solution structure of acan1 from the ancylostoma caninum hookworm
27	<a href="#">c3uo9B_</a>	 Alignment	not modelled	6.6	19	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> B; <b>PDB Molecule:</b> glutaminase kidney isoform, mitochondrial; <b>PDBTitle:</b> crystal structure of human gac in complex with glutamate and bptes
28	<a href="#">d1zsqz2</a>	 Alignment	not modelled	6.5	13	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Myotubularin-like phosphatases

29	<a href="#">c2gacD</a>	Alignment	not modelled	6.5	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> glycosylasparaginase; <b>PDBTitle:</b> t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
30	<a href="#">c5uqeB</a>	Alignment	not modelled	6.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutaminase kidney isoform, mitochondrial; <b>PDBTitle:</b> multidomain structure of human kidney-type glutaminase(kga/gls)
31	<a href="#">d1xoda1</a>	Alignment	not modelled	6.3	27	<b>Fold:</b> PH domain-like barrel <b>Superfamily:</b> PH domain-like <b>Family:</b> Enabled/VASP homology 1 domain (EVH1 domain)
32	<a href="#">c5kzmA</a>	Alignment	not modelled	6.3	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
33	<a href="#">c5e8jC</a>	Alignment	not modelled	6.2	67	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> rnmmt-activating mini protein; <b>PDBTitle:</b> crystal structure of mrna cap guanine-n7 methyltransferase in complex2 with ram
34	<a href="#">d1bbua1</a>	Alignment	not modelled	6.2	46	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Anticodon-binding domain
35	<a href="#">c1bonB</a>	Alignment	not modelled	6.1	23	<b>PDB header:</b> hormone <b>Chain:</b> B: <b>PDB Molecule:</b> bombyxin-ii,bombyxin a-6; <b>PDBTitle:</b> three-dimensional structure of bombyxin-ii, an insulin-2 related brain-secretory peptide of the silkworm bombyx3 mori: comparison with insulin and relaxin
36	<a href="#">c4yajA</a>	Alignment	not modelled	6.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha subunit of acetyl-coenzyme a synthetase <b>PDBTitle:</b> ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
37	<a href="#">c5i78A</a>	Alignment	not modelled	5.9	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-aminoadipic semialdehyde synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
38	<a href="#">c2md0A</a>	Alignment	not modelled	5.8	50	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> ack1; <b>PDBTitle:</b> solution structure of shk-like immunomodulatory peptide from2 ancylostoma caninum (hookworm)
39	<a href="#">c4v19S</a>	Alignment	not modelled	5.8	6	<b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> mitoribosomal protein ul18m, mrpl18; <b>PDBTitle:</b> structure of the large subunit of the mammalian mitoribosome, part 12 of 2
40	<a href="#">d1e1oa1</a>	Alignment	not modelled	5.5	38	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Anticodon-binding domain
41	<a href="#">c2i5yA</a>	Alignment	not modelled	5.4	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> stromal interaction molecule 2; <b>PDBTitle:</b> nmr structure of calcium-loaded stim2 ef-sam.
42	<a href="#">c1bomB</a>	Alignment	not modelled	5.4	23	<b>PDB header:</b> insulin-like brain-secretory peptide <b>Chain:</b> B: <b>PDB Molecule:</b> bombyxin-ii,bombyxin a-6; <b>PDBTitle:</b> three-dimensional structure of bombyxin-ii, an insulin-2 related brain-secretory peptide of the silkworm bombyx3 mori: comparison with insulin and relaxin
43	<a href="#">d1p9sa</a>	Alignment	not modelled	5.4	57	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
44	<a href="#">d2duca1</a>	Alignment	not modelled	5.3	57	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Viral cysteine protease of trypsin fold
45	<a href="#">c3vndD</a>	Alignment	not modelled	5.3	18	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
46	<a href="#">c5kinC</a>	Alignment	not modelled	5.2	24	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
47	<a href="#">c5v1uB</a>	Alignment	not modelled	5.1	11	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> tbib1; <b>PDBTitle:</b> tbib1 in complex with the tbia(beta) leader peptide
48	<a href="#">d1z1va1</a>	Alignment	not modelled	5.1	13	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> SAM/Pointed domain <b>Family:</b> SAM (sterile alpha motif) domain