



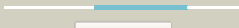

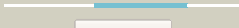
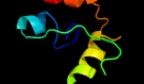


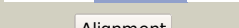
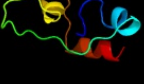
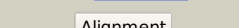

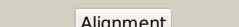

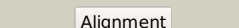
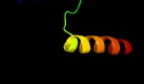
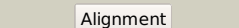


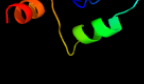
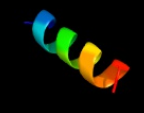










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3067_(-)_3431425_3431835
Date	Thu Aug 8 16:20:24 BST 2019
Unique Job ID	dcac68591e33ea35

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5k9xA_	 Alignment		61.3	17	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
2	c2ekcA_	 Alignment		58.9	19	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
3	c3vndD_	 Alignment		34.8	21	PDB header: lyase Chain: D; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
4	c5tchG_	 Alignment		31.6	23	PDB header: lyase Chain: G; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
5	c5kzmA_	 Alignment		30.7	23	PDB header: lyase Chain: A; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
6	c3navB_	 Alignment		26.9	21	PDB header: lyase Chain: B; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
7	c5ey5A_	 Alignment		25.9	29	PDB header: lyase Chain: A; PDB Molecule: lbcats-a; PDBTitle: lbcats
8	c6c3rB_	 Alignment		21.9	12	PDB header: viral protein Chain: B; PDB Molecule: cricket paralysis virus 1a protein; PDBTitle: cricket paralysis virus rna1 suppressor protein crpv-1a
9	d2csua3	 Alignment		20.6	11	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
10	c3thaB_	 Alignment		18.2	27	PDB header: lyase Chain: B; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
11	c5kinC_	 Alignment		16.6	32	PDB header: lyase Chain: C; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae

12	c2hzdA	Alignment		15.3	33	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional enhancer factor tef-1; PDBTitle: nmr structure of the dna-binding tea domain and insights2 into tef-1 function
13	d1mkea1	Alignment		14.9	30	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
14	c5gzba	Alignment		14.2	33	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional enhancer factor tef-3; PDBTitle: crystal structure of transcription factor tead4 in complex with m-cat2 dna
15	d1qopa	Alignment		11.9	29	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
16	c5uqda	Alignment		11.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: dummy; shorter than wild-type; PDBTitle: dpy-21 in complex with fe(ii) and alpha-ketoglutarate
17	c2mula	Alignment		11.4	45	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: solution structure of the ubm1 domain of human huwe1/arf-bp1
18	c4furD	Alignment		10.9	20	PDB header: hydrolase Chain: D: PDB Molecule: urease subunit gamma 2; PDBTitle: crystal structure of urease subunit gamma 2 from brucella melitensis2 biovar abortus 2308
19	c2fvhb	Alignment		10.1	17	PDB header: hydrolase Chain: B: PDB Molecule: urease gamma subunit; PDBTitle: crystal structure of rv1848, a urease gamma subunit urea (urea2 amidohydrolase), from mycobacterium tuberculosis
20	c2hl7A	Alignment		9.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c-type biogenesis protein ccmh; PDBTitle: crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
21	c4rl6A	Alignment	not modelled	9.0	21	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
22	c3dmyA	Alignment	not modelled	9.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein fdra; PDBTitle: crystal structure of a predicated acyl-coa synthetase from e.coli
23	d4ubpa	Alignment	not modelled	8.9	20	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
24	c4z42A	Alignment	not modelled	8.9	15	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit gamma; PDBTitle: crystal structure of urease from yersinia enterocolitica
25	d1ejxa	Alignment	not modelled	8.7	13	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
26	c2kw0A	Alignment	not modelled	8.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ccmh protein; PDBTitle: solution structure of n-terminal domain of ccmh from escherichia.coli
27	d3ctda1	Alignment	not modelled	8.5	12	Fold: post-AAA+ oligomerization domain-like Superfamily: post-AAA+ oligomerization domain-like Family: MgsA/YrvN C-terminal domain-like
28	d1geqa	Alignment	not modelled	8.4	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes

29	d1eucb1	Alignment	not modelled	7.9	19	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
30	c4krrA	Alignment	not modelled	7.7	21	PDB header: signaling protein Chain: A: PDB Molecule: wnt inhibitor of dorsal protein; PDBTitle: crystal structure of drosophila wntd n-terminal domain-linker2 (residues 31-240)
31	c3pvsA	Alignment	not modelled	7.7	16	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
32	c5cm2M	Alignment	not modelled	7.6	23	PDB header: transferase Chain: M: PDB Molecule: trna methyltransferase activator subunit; PDBTitle: insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
33	c4v19S	Alignment	not modelled	7.4	12	PDB header: ribosome Chain: S: PDB Molecule: mitoribosomal protein ul18m, mrp18; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
34	c2lweA	Alignment	not modelled	7.3	13	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
35	c1apzB	Alignment	not modelled	7.2	8	PDB header: complex (hydrolase/peptide) Chain: B: PDB Molecule: aspartylglucosaminidase; PDBTitle: human aspartylglucosaminidase complex with reaction product
36	c3ss4C	Alignment	not modelled	7.2	25	PDB header: hydrolase Chain: C: PDB Molecule: glutaminase c; PDBTitle: crystal structure of mouse glutaminase c, phosphate-bound form
37	d1xoda1	Alignment	not modelled	7.2	18	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
38	c4inaA	Alignment	not modelled	6.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolinetella2 succinogenes. northeast structural genomics consortium target wsr35
39	c2mqkA	Alignment	not modelled	6.8	7	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
40	c3v53E	Alignment	not modelled	6.8	13	PDB header: rna binding protein Chain: E: PDB Molecule: rna-binding protein 25; PDBTitle: crystal structure of human rbm25
41	c2gacD	Alignment	not modelled	6.8	20	PDB header: hydrolase Chain: D: PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
42	c6ahyD	Alignment	not modelled	6.6	24	PDB header: signaling protein Chain: D: PDB Molecule: proto-oncogene wnt-3; PDBTitle: wnt signaling complex
43	c6fnnB	Alignment	not modelled	6.6	50	PDB header: hydrolase Chain: B: PDB Molecule: 26s proteasome regulatory subunit n11-like protein; PDBTitle: caldiarchaeum subterraneum ubiquitin:rpn11-homolog complex
44	c5us3A	Alignment	not modelled	6.4	75	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
45	c4f0aB	Alignment	not modelled	6.3	18	PDB header: signaling protein Chain: B: PDB Molecule: protein wnt-8; PDBTitle: crystal structure of xwnt8 in complex with the cysteine-rich domain of2 frizzled 8
46	c1zbuB	Alignment	not modelled	6.0	18	PDB header: hydrolase Chain: B: PDB Molecule: 3'-5' exonuclease eri1; PDBTitle: crystal structure of full-length 3'-exonuclease
47	c4naeA	Alignment	not modelled	6.0	16	PDB header: transferase Chain: A: PDB Molecule: heptaprenylglyceryl phosphate synthase; PDBTitle: pcrb from geobacillus kaustophilus, with bound g1p
48	c3ctdB	Alignment	not modelled	6.0	12	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
49	d1e9ya2	Alignment	not modelled	5.9	13	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
50	d1ujpa	Alignment	not modelled	5.8	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
51	c3g2bA	Alignment	not modelled	5.7	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: coenzyme pqq synthesis protein d; PDBTitle: crystal structure of pqqd from xanthomonas campestris
52	c4nn7A	Alignment	not modelled	5.6	13	PDB header: cytokine/cytokine receptor Chain: A: PDB Molecule: thymic stromal lymphopoietin; PDBTitle: cytokine receptor complex - crystal form 2
53	c2v75A	Alignment	not modelled	5.6	17	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: n-terminal domain of nab2
						Fold: Cystatin-like

54	d1w2za3	Alignment	not modelled	5.6	17	Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
55	c3h7hA_	Alignment	not modelled	5.5	24	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt4; PDBTitle: crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
56	d1jqga2	Alignment	not modelled	5.5	16	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
57	c5j12A_	Alignment	not modelled	5.4	13	PDB header: signaling protein Chain: A: PDB Molecule: thymic stromal lymphopoietin; PDBTitle: structure of human tslp:tslpr in complex with mouse il-7ralpha
58	d1pbaa_	Alignment	not modelled	5.2	5	Fold: Ferredoxin-like Superfamily: Protease propeptides/inhibitors Family: Pancreatic carboxypeptidase, activation domain
59	c2jd3B_	Alignment	not modelled	5.1	18	PDB header: dna binding protein Chain: B: PDB Molecule: stbb protein; PDBTitle: parr from plasmid pb171