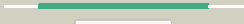

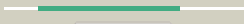






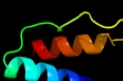











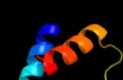


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1693_(-)_1917763_1917939
Date	Fri Aug 2 13:30:29 BST 2019
Unique Job ID	e5139e6f83a251bb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r3na1	 Alignment		47.2	11	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Bacterial dinuclear zinc exopeptidases
2	c2v8gD	 Alignment		44.5	17	PDB header: hydrolase Chain: D: PDB Molecule: beta-alanine synthase; PDBTitle: crystal structure of beta-alanine synthase from2 saccharomyces kluuyveri in complex with the product beta-3 alanine
3	c1zvzB	 Alignment		37.0	35	PDB header: protein binding Chain: B: PDB Molecule: talin 1; PDBTitle: vinculin head (0-258) in complex with the talin rod residue2 820-844
4	c3oqvA	 Alignment		35.4	30	PDB header: protein binding Chain: A: PDB Molecule: albc; PDBTitle: albc, a cyclodipeptide synthase from streptomyces noursei
5	c4exqA	 Alignment		31.1	28	PDB header: biosynthetic protein Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
6	c2ejaB	 Alignment		31.1	16	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
7	c3t38B	 Alignment		29.8	25	PDB header: oxidoreductase Chain: B: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum thioredoxin-dependent arsenate reductase2 cg_arsc1'
8	d1r3sa	 Alignment		29.4	9	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
9	d1qvra1	 Alignment		29.1	27	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
10	c4rc1B	 Alignment		26.7	39	PDB header: chaperone Chain: B: PDB Molecule: espg3; PDBTitle: structure of espg3 chaperone from the type vii (esx-3) secretion2 system, space group p43212
11	c1jpkA	 Alignment		25.8	9	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase

12	c4kxrC_	Alignment		25.6	22	PDB header: protein transport Chain: C: PDB Molecule: espg5; PDBTitle: structure of the mycobacterium tuberculosis type vii secretion system2 chaperone espg5 in complex with pe25-ppe41 dimer
13	c5yh1A_	Alignment		24.6	15	PDB header: ribosomal protein Chain: A: PDB Molecule: member of s1p family of ribosomal proteins; PDBTitle: member of s1p family of ribosomal proteins pf0399 dhh domain
14	c4pxeB_	Alignment		20.6	23	PDB header: hydrolase Chain: B: PDB Molecule: ureidoglycolate hydrolase; PDBTitle: the crystal structure of atuah in complex with glyoxylate
15	c5l8xA_	Alignment		20.5	24	PDB header: transferase Chain: A: PDB Molecule: tetrahydromethanopterin s-methyltransferase subunit a; PDBTitle: x-ray structure of apo methanocaldococcus jannaschii methyltransferase2 subunit a at 1.85 angstrom
16	d1fpoa1	Alignment		19.9	10	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
17	c5vsoA_	Alignment		19.5	17	PDB header: chaperone Chain: A: PDB Molecule: yeast dnaj protein 1; PDBTitle: nmr structure of ydj1 j-domain, a cytosolic hsp40 from saccharomyces2 cerevisiae
18	c4w4iA_	Alignment		19.4	44	PDB header: protein transport Chain: A: PDB Molecule: esx-3 secretion-associated protein espg3; PDBTitle: crystal structure of espg3 from the esx-3 type vii secretion system of2 m. tuberculosis
19	c5laaB_	Alignment		18.2	22	PDB header: transferase Chain: B: PDB Molecule: tetrahydromethanopterin s-methyltransferase subunit a; PDBTitle: x-ray structure of the methyltransferase subunit a from methanothermus2 fervidus in complex with cobalamin
20	c3oqhB_	Alignment		18.0	25	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein yvmc; PDBTitle: crystal structure of b. licheniformis cdps yvmc-blic
21	d1khya_	Alignment	not modelled	17.8	28	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
22	c2infB_	Alignment	not modelled	17.0	14	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
23	c2zshB_	Alignment	not modelled	16.8	17	PDB header: hormone receptor Chain: B: PDB Molecule: della protein gai; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
24	c2mniA_	Alignment	not modelled	15.7	23	PDB header: unknown function Chain: A: PDB Molecule: hsp_q4d059; PDBTitle: chemical shift assignments and structure of q4d059, a hypothetical2 protein from trypanosoma cruzi
25	c3ol4B_	Alignment	not modelled	15.5	29	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
26	d1j93a_	Alignment	not modelled	15.5	12	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
27	c3cyvA_	Alignment	not modelled	15.2	16	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
28	c5n6yC_	Alignment	not modelled	14.6	19	PDB header: oxidoreductase Chain: C: PDB Molecule: nitrogenase vanadium-iron protein delta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
29	c1l4wB_	Alignment	not modelled	14.5	29	PDB header: protein transport Chain: B: PDB Molecule: espg3;

29	c4hwB_	Alignment	not modelled	14.5	33	PDBTitle: structure of espg3 chaperone from the type vii (esx-3) secretion2 system PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein;
30	c2m0nA_	Alignment	not modelled	14.5	23	PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
31	d1hdja_	Alignment	not modelled	13.8	14	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
32	c5u2lA_	Alignment	not modelled	13.2	9	PDB header: protein binding Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: crystal structure of the hsp104 n-terminal domain from candida2 albicans
33	d1ul7a_	Alignment	not modelled	12.3	26	Fold: TBP-like Superfamily: KA1-like Family: Kinase associated domain 1, KA1
34	d1szaa_	Alignment	not modelled	11.8	22	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: RPR domain (SMART 00582)
35	c5vbaA_	Alignment	not modelled	11.6	33	PDB header: chaperone, hydrolase Chain: A: PDB Molecule: lysozyme, esx-1 secretion-associated protein espg1 chimera; PDBTitle: structure of espg1 chaperone from the type vii (esx-1) secretion2 system determined with the assistance of n-terminal t4 lysozyme3 fusion
36	c6jx3B_	Alignment	not modelled	11.1	28	PDB header: peptide binding protein Chain: B: PDB Molecule: tfub1; PDBTitle: lasso peptide synthetase b1 complexed with the leader peptide
37	c4xbiA_	Alignment	not modelled	10.7	20	PDB header: chaperone Chain: A: PDB Molecule: clpb protein, putative,green fluorescent protein; PDBTitle: structure of a malarial protein involved in proteostasis
38	c2qsiB_	Alignment	not modelled	10.5	37	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative hydrogenase expression/formation protein hupg; PDBTitle: crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
39	d2a26a1	Alignment	not modelled	10.5	22	Fold: Long alpha-hairpin Superfamily: Calcyclin-binding protein-like Family: Siah interacting protein N terminal domain-like
40	c3d22A_	Alignment	not modelled	10.4	33	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin h-type; PDBTitle: crystal structure of a poplar thioredoxin h mutant, pptrxh4c61s
41	c4l6wA_	Alignment	not modelled	10.3	37	PDB header: ligase Chain: A: PDB Molecule: probable propionyl-coa carboxylase beta chain 6; PDBTitle: carboxyltransferase subunit (accd6) of mycobacterium tuberculosis2 acetyl-coa carboxylase
42	c2lkyA_	Alignment	not modelled	10.2	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of msMeg_1053, the second duf3349 annotated protein2 in the genome of mycobacterium smegmatis, seattle structural genomics3 center for infectious disease target mysma.17112.b
43	c5v1uB_	Alignment	not modelled	10.0	18	PDB header: protein binding Chain: B: PDB Molecule: tbib1; PDBTitle: tbib1 in complex with the tbia(beta) leader peptide
44	c6n1fD_	Alignment	not modelled	9.9	33	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, 2og-fe(ii) oxygenase family; PDBTitle: crystal structure of oxidoreductase, 2og-fe(ii) oxygenase family, from2 burkholderia pseudomallei
45	c4y0bA_	Alignment	not modelled	9.2	14	PDB header: protein binding Chain: A: PDB Molecule: double clp-n motif protein; PDBTitle: the structure of arabidopsis clpt1
46	c2cugA_	Alignment	not modelled	8.9	19	PDB header: chaperone Chain: A: PDB Molecule: mkiaa0962 protein; PDBTitle: solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962
47	c2lndA_	Alignment	not modelled	8.5	14	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein, pfk fold; PDBTitle: solution nmr structure of de novo designed protein, pfk fold,2 northeast structural genomics consortium target or134
48	d2inwa1	Alignment	not modelled	8.2	30	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
49	d2h28a1	Alignment	not modelled	8.1	30	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
50	c4zr8B_	Alignment	not modelled	7.9	14	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
51	c5ovmA_	Alignment	not modelled	7.6	30	PDB header: chaperone Chain: A: PDB Molecule: lipase chaperone; PDBTitle: solution structure of lipase binding domain lid1 of foldase from2 pseudomonas aeruginosa
52	c3ghfA_	Alignment	not modelled	6.9	25	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium
53	c4irfA_	Alignment	not modelled	6.6	16	PDB header: chaperone Chain: A: PDB Molecule: malarial clpb2 atpase/hsp101 protein;

53	c4n1A_	Alignment	not modelled	6.6	10	PDBTitle: preliminary structural investigations of a malarial protein secretion2 system
54	d2ea9a1	Alignment	not modelled	6.5	15	Fold: Profilin-like Superfamily: YeeU-like Family: YagB/YeeU/YfjZ-like
55	c3c4rC_	Alignment	not modelled	6.5	25	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein encoded by2 cryptic prophage
56	c4cvdA_	Alignment	not modelled	6.4	20	PDB header: hydrolase Chain: A: PDB Molecule: lysozyme; PDBTitle: crystal structure of the central repeat of cell wall binding module of2 cpl7
57	d2byea1	Alignment	not modelled	6.2	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
58	c2kqxA_	Alignment	not modelled	6.0	23	PDB header: chaperone binding protein Chain: A: PDB Molecule: curved dna-binding protein; PDBTitle: nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa
59	c3zriA_	Alignment	not modelled	5.8	12	PDB header: chaperone Chain: A: PDB Molecule: clpb protein; PDBTitle: n-domain of clpv from vibrio cholerae
60	c2x5eA_	Alignment	not modelled	5.7	18	PDB header: unknown function Chain: A: PDB Molecule: upf0271 protein pa4511; PDBTitle: crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
61	c6gzuA_	Alignment	not modelled	5.6	19	PDB header: transferase Chain: A: PDB Molecule: conserved membrane protein; PDBTitle: structure of chlamydia abortus effector protein chladub
62	c1p9iA_	Alignment	not modelled	5.5	36	PDB header: unknown function Chain: A: PDB Molecule: cortexillin i/gcn4 hybrid peptide; PDBTitle: coiled-coil x-ray structure at 1.17 a resolution
63	c3eytA_	Alignment	not modelled	5.2	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein spoa0173; PDBTitle: crystal structure of thioredoxin-like superfamily protein spoa0173
64	c2lgwA_	Alignment	not modelled	5.1	20	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily b member 2; PDBTitle: solution structure of the j domain of hsj1a