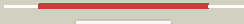

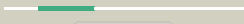
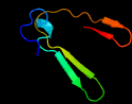







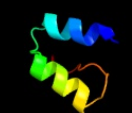



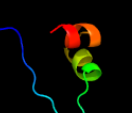

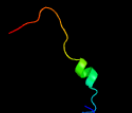

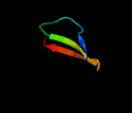










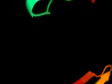


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3902c_(-)_4387543_4388073
Date	Sat Aug 10 22:05:09 BST 2019
Unique Job ID	f77c6e418681c1fc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4o6gA_	 Alignment		100.0	100	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: rv3902c from m. tuberculosis
2	c4aqzA_	 Alignment		44.0	11	PDB header: transport protein Chain: A: PDB Molecule: type iv pilus biogenesis and competence protein pilq; PDBTitle: b2 domain of neisseria meningitidis pilus assembly protein pilq
3	c3fymA_	 Alignment		43.3	8	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of yfmf, a putative dna-binding membrane2 protein from staphylococcus aureus
4	c2g7rA_	 Alignment		29.6	28	PDB header: hydrolase Chain: A: PDB Molecule: mucosa-associated lymphoid tissue lymphoma translocation PDBTitle: x-ray structure of the death domain of the human mucosa associated2 lymphoid tissue lymphoma translocation protein 1
5	d2ofya1	 Alignment		28.3	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
6	c4o6xA_	 Alignment		23.1	23	PDB header: protein binding Chain: A: PDB Molecule: ankyrin-3; PDBTitle: crystal structure of human ankyrin g death domain
7	d1r69a_	 Alignment		20.9	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
8	c5k2IA_	 Alignment		19.1	20	PDB header: hydrolase Chain: A: PDB Molecule: chitinase, lysozyme; PDBTitle: crystal structure of lysm domain from volvox carteri chitinase
9	c2rfpA_	 Alignment		17.2	16	PDB header: hydrolase Chain: A: PDB Molecule: putative ntp pyrophosphohydrolase; PDBTitle: crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
10	c3dkmA_	 Alignment		15.9	25	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase hectd1; PDBTitle: crystal structure of the hectd1 cph domain
11	c5wllD_	 Alignment		15.1	45	PDB header: de novo protein Chain: D: PDB Molecule: helical bundle 4dh1; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4dh1

12	c5wllA_	Alignment		15.1	45	PDB header: de novo protein Chain: A: PDB Molecule: helical bundle 4dh1; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4dh1
13	c5wllC_	Alignment		15.1	45	PDB header: de novo protein Chain: C: PDB Molecule: helical bundle 4dh1; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4dh1
14	c5wllB_	Alignment		15.1	45	PDB header: de novo protein Chain: B: PDB Molecule: helical bundle 4dh1; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4dh1
15	c5wljD_	Alignment		14.9	45	PDB header: de novo protein Chain: D: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1
16	c5wljA_	Alignment		14.9	45	PDB header: de novo protein Chain: A: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1
17	c5wljB_	Alignment		14.9	45	PDB header: de novo protein Chain: B: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1
18	c5wljC_	Alignment		14.9	45	PDB header: de novo protein Chain: C: PDB Molecule: de novo metal binding helical bundle; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh1
19	d1sq8a_	Alignment		14.6	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
20	c4jglA_	Alignment		14.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a streptavidin-like protein (bacegg_01519) from2 bacteroides eggerthii dsm 20697 at 1.25 a resolution
21	c6c5rF_	Alignment	not modelled	12.1	18	PDB header: cytosolic protein Chain: F: PDB Molecule: calcium uniporter; PDBTitle: crystal structure of the soluble domain of the mitochondrial calcium2 uniporter
22	c5wlmC_	Alignment	not modelled	11.3	50	PDB header: de novo protein Chain: C: PDB Molecule: helical bundle 4dh2; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4dh2
23	c5wlmD_	Alignment	not modelled	11.3	50	PDB header: de novo protein Chain: D: PDB Molecule: helical bundle 4dh2; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4dh2
24	c5wlmA_	Alignment	not modelled	11.3	50	PDB header: de novo protein Chain: A: PDB Molecule: helical bundle 4dh2; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4dh2
25	c5wlmB_	Alignment	not modelled	11.3	50	PDB header: de novo protein Chain: B: PDB Molecule: helical bundle 4dh2; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4dh2
26	c5wlkB_	Alignment	not modelled	11.2	50	PDB header: de novo protein Chain: B: PDB Molecule: helical bundle 4eh2; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh2
27	c5wlkC_	Alignment	not modelled	11.2	50	PDB header: de novo protein Chain: C: PDB Molecule: helical bundle 4eh2; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh2
28	c5wlkD_	Alignment	not modelled	11.2	50	PDB header: de novo protein Chain: D: PDB Molecule: helical bundle 4eh2; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh2

29	c5wlkA	Alignment	not modelled	11.2	50	PDB header: de novo protein Chain: A: PDB Molecule: helical bundle 4eh2; PDBTitle: de novo design of polynuclear transition metal clusters in helix2 bundles-4eh2
30	c2ewtA	Alignment	not modelled	10.8	30	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
31	d1w2ya	Alignment	not modelled	10.7	13	Fold: all-alpha NTP pyrophosphatases Superfamily: all-alpha NTP pyrophosphatases Family: Type II deoxyuridine triphosphatase
32	c3kxaD	Alignment	not modelled	10.5	26	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
33	d1de4c1	Alignment	not modelled	10.3	23	Fold: N-cbl like Superfamily: Transferrin receptor-like dimerisation domain Family: Transferrin receptor-like dimerisation domain
34	c3iraA	Alignment	not modelled	10.2	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazeri go1
35	c3k1qC	Alignment	not modelled	9.8	14	PDB header: PDB COMPND:
36	c4gqmA	Alignment	not modelled	9.8	19	PDB header: unknown function Chain: A: PDB Molecule: ct009; PDBTitle: crystal structure of a helix-turn-helix containing hypothetical2 protein (ct009) from chlamydia trachomatis in a sub-domain swap3 conformation
37	c3n2oA	Alignment	not modelled	9.6	11	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
38	c3ox4D	Alignment	not modelled	9.1	12	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
39	c3k1qB	Alignment	not modelled	9.0	14	PDB header: PDB COMPND:
40	c3bs3A	Alignment	not modelled	8.9	24	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
41	c5m41A	Alignment	not modelled	8.8	31	PDB header: toxin Chain: A: PDB Molecule: nigritoxine; PDBTitle: crystal structure of nigritoxine
42	c2oo4B	Alignment	not modelled	8.3	22	PDB header: cell cycle,signaling protein Chain: B: PDB Molecule: neurogenic locus notch homolog protein 2; PDBTitle: structure of lnr-hd (negative regulatory region) from human notch 2
43	c4aw7A	Alignment	not modelled	8.2	60	PDB header: hydrolase Chain: A: PDB Molecule: gh86a beta-porphyrinase; PDBTitle: bpggh86a: a beta-porphyrinase of glycoside hydrolase family 86 from the2 human gut bacterium bacteroides plebeius
44	c3nzqB	Alignment	not modelled	7.5	19	PDB header: lyase Chain: B: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
45	d2croa	Alignment	not modelled	7.4	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
46	c2cseW	Alignment	not modelled	7.3	14	PDB header: virus Chain: W: PDB Molecule: major core protein lambda 1; PDBTitle: features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
47	c3m62B	Alignment	not modelled	7.1	14	PDB header: ligase/protein binding Chain: B: PDB Molecule: uv excision repair protein rad23; PDBTitle: crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of rad23
48	d1qr0a1	Alignment	not modelled	7.1	25	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: 4'-Phosphopantetheinyl transferase SFP
49	c3omtA	Alignment	not modelled	6.7	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
50	c3gqrA	Alignment	not modelled	6.6	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein with a ntf2-like fold; PDBTitle: crystal structure of an uncharacterized protein with a cystatin-like fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
51	d2icta1	Alignment	not modelled	6.6	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
52	c2ctoA	Alignment	not modelled	6.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: novel protein; PDBTitle: solution structure of the hmg box like domain from human2 hypothetical protein fj14904
53	d2dk3a1	Alignment	not modelled	6.5	25	Fold: SH3-like barrel Superfamily: Mib/herc2 domain-like Family: Mib/herc2 domain
						PDB header: ligase

54	c4ex8A_	Alignment	not modelled	6.4	19	Chain: A: PDB Molecule: alna; PDBTitle: crystal structure of the prealnumycin c-glycosynthasealna
55	c5kvrA_	Alignment	not modelled	6.4	24	PDB header: translation Chain: A: PDB Molecule: pyruvate dehydrogenase complex repressor; PDBTitle: x-ray crystal structure of a fragment (1-75) of a transcriptional2 regulator pdhr from escherichia coli cft073
56	c4gijC_	Alignment	not modelled	6.2	29	PDB header: hydrolase Chain: C: PDB Molecule: pseudouridine-5'-phosphate glycosidase; PDBTitle: crystal structure of pseudouridine monophosphate glycosidase complexed2 with sulfate
57	d1vkma_	Alignment	not modelled	6.0	24	Fold: Indigoidine synthase A-like Superfamily: Indigoidine synthase A-like Family: Indigoidine synthase A-like
58	c3shgB_	Alignment	not modelled	5.9	26	PDB header: transferase/protein binding Chain: B: PDB Molecule: vbha; PDBTitle: vbht fic protein from bartonella schoenbuchensis in complex with vbha2 antitoxin
59	c3zhiA_	Alignment	not modelled	5.7	24	PDB header: transcription Chain: A: PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage tp901-1
60	d1wggA_	Alignment	not modelled	5.6	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
61	c4maiA_	Alignment	not modelled	5.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: aa11 lytic polysaccharide monoxygenase; PDBTitle: structure of aspergillus oryzae aa11 lytic polysaccharide2 monoxygenase with cu(i)
62	d2csba5	Alignment	not modelled	5.5	19	Fold: Topoisomerase V catalytic domain-like Superfamily: Topoisomerase V catalytic domain-like Family: Topoisomerase V catalytic domain-like
63	d16vpa_	Alignment	not modelled	5.4	22	Fold: Conserved core of transcriptional regulatory protein vp16 Superfamily: Conserved core of transcriptional regulatory protein vp16 Family: Conserved core of transcriptional regulatory protein vp16
64	c3t76A_	Alignment	not modelled	5.4	27	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
65	d3e11a1	Alignment	not modelled	5.3	12	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like
66	c2of5K_	Alignment	not modelled	5.3	11	PDB header: apoptosis Chain: K: PDB Molecule: leucine-rich repeat and death domain-containing protein; PDBTitle: oligomeric death domain complex
67	d3bi1a1	Alignment	not modelled	5.2	31	Fold: N-cbl like Superfamily: Transferrin receptor-like dimerisation domain Family: Transferrin receptor-like dimerisation domain