

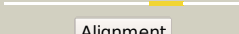
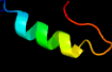
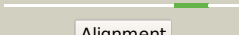
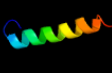



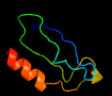

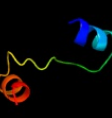










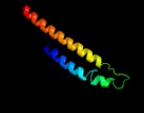


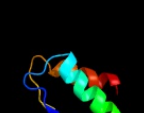



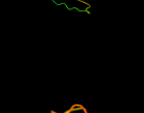



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0686 (-) _786152_786949
Date	Fri Jul 26 01:50:25 BST 2019
Unique Job ID	21fc0674f97ab5ef

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ddrC_	 Alignment		74.2	39	PDB header: membrane protein/heme binding protein Chain: C: PDB Molecule: hemophore hasa; PDBTitle: structure of the serratia marcescens hemophore receptor hasr-ile671gly2 mutant in complex with its hemophore hasa and heme
2	d1dk0a_	 Alignment		70.8	39	Fold: Heme-binding protein A (HasA) Superfamily: Heme-binding protein A (HasA) Family: Heme-binding protein A (HasA)
3	c4ynhA_	 Alignment		53.9	38	PDB header: structural protein Chain: A: PDB Molecule: spindle assembly abnormal protein 5; PDBTitle: structure of the c. elegans sas-5 implicio dimerization domain
4	c1u6tA_	 Alignment		47.5	26	PDB header: protein binding, signaling protein Chain: A: PDB Molecule: sh3 domain-binding glutamic acid-rich-like PDBTitle: crystal structure of the human sh3 binding glutamic-rich2 protein like
5	c4k2bA_	 Alignment		37.6	17	PDB header: transferase Chain: A: PDB Molecule: ntd biosynthesis operon protein ntda; PDBTitle: crystal structure of ntda from bacillus subtilis in complex with the2 internal aldimine
6	c2ct6A_	 Alignment		37.2	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sh3 domain-binding glutamic acid-rich-like PDBTitle: solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
7	c6eeqA_	 Alignment		35.5	19	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxyphenylacetaldehyde synthase; PDBTitle: crystal structure of rhodiola rosea 4-hydroxyphenylacetaldehyde2 synthase
8	d1s3ia1	 Alignment		30.4	34	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: Post formyltransferase domain
9	c3wknG_	 Alignment		29.9	36	PDB header: immune system Chain: G: PDB Molecule: affinger p17; PDBTitle: crystal structure of the artificial protein affinger p17 (af.p17)2 complexed with fc fragment of human igg
10	d1hjqa_	 Alignment		29.3	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
11	c4uz0B_	 Alignment		28.6	41	PDB header: apoptosis Chain: B: PDB Molecule: nucleolar protein 3; PDBTitle: crystal structure of apoptosis repressor with card (arc)

12	d1r3jc_	Alignment		26.8	11	Fold: Voltage-gated potassium channels Superfamily: Voltage-gated potassium channels Family: Voltage-gated potassium channels
13	d2bw0a1	Alignment		25.7	34	Fold: FMT C-terminal domain-like Superfamily: FMT C-terminal domain-like Family: Post formyltransferase domain
14	d1m5wa_	Alignment		25.3	19	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
15	d1dcja_	Alignment		24.2	16	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
16	d3bc8a1	Alignment		22.9	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: SepSecS-like
17	c2hzpA_	Alignment		21.6	13	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase
18	d2cspa1	Alignment		19.5	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
19	c4jesA_	Alignment		19.3	25	PDB header: heme binding protein, transport protein Chain: A: PDB Molecule: hemophore hasa; PDBTitle: 1.6a resolution apo structure of the hemophore hasa from yersinia2 pestis (hexagonal form)
20	c6fucA_	Alignment		18.8	26	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside phosphotransferase; PDBTitle: structure of aminoglycoside phosphotransferase aph(3'')-id from2 streptomyces rimosus atcc10970
21	d2qmwa2	Alignment	not modelled	18.7	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
22	c5dlcC_	Alignment	not modelled	18.3	23	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
23	c5mqcA_	Alignment	not modelled	18.1	40	PDB header: virus Chain: A: PDB Molecule: vp1; PDBTitle: structure of black queen cell virus
24	d1t1va_	Alignment	not modelled	17.7	28	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: SH3BGR (SH3-binding, glutamic acid-rich protein-like)
25	c6hwhB_	Alignment	not modelled	17.1	17	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
26	c3bcxA_	Alignment	not modelled	16.1	14	PDB header: transferase Chain: A: PDB Molecule: cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3-dehydrase; PDBTitle: e1 dehydrase
27	d1jdqa_	Alignment	not modelled	15.4	16	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
28	d1h3fa2	Alignment	not modelled	15.1	13	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain PDB header: metal binding protein

29	c6nxA	Alignment	not modelled	15.0	32	Chain: A: PDB Molecule: cytochrome b5; PDBTitle: hadesarchaea ynp_n21 cytochrome b5 domain protein (kuo41884.1)
30	c6eewC	Alignment	not modelled	14.5	13	PDB header: lyase Chain: C: PDB Molecule: aromatic-l-amino-acid decarboxylase; PDBTitle: crystal structure of catharanthus roseus tryptophan decarboxylase in2 complex with l-tryptophan
31	c3e9kA	Alignment	not modelled	14.2	13	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
32	c3madA	Alignment	not modelled	14.0	12	PDB header: lyase Chain: A: PDB Molecule: sphingosine-1-phosphate lyase; PDBTitle: crystal structure of stspl (symmetric form)
33	c3uh8A	Alignment	not modelled	13.9	14	PDB header: viral protein Chain: A: PDB Molecule: orf48; PDBTitle: n-terminal domain of phage tp901-1 orf48
34	c3hzaA	Alignment	not modelled	13.6	23	PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
35	d1sd4a	Alignment	not modelled	13.6	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
36	c3e2sA	Alignment	not modelled	13.5	30	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase; PDBTitle: crystal structure reduced puta86-630 mutant y540s complexed with l-2 proline
37	d1hjsa	Alignment	not modelled	13.4	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
38	c2c5sA	Alignment	not modelled	13.2	31	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
39	d2g9wa1	Alignment	not modelled	13.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
40	d1dfoa	Alignment	not modelled	12.4	7	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
41	c2dajA	Alignment	not modelled	12.4	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: kiaa0977 protein; PDBTitle: solution structure of the novel identified ubiquitin-like2 domain in the human cobl-like 1 protein
42	c2mdaB	Alignment	not modelled	11.9	5	PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosine 3-monoxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
43	c1vbka	Alignment	not modelled	11.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1313; PDBTitle: crystal structure of ph1313 from pyrococcus horikoshii ot3
44	c3cjtP	Alignment	not modelled	11.8	21	PDB header: transferase/ribosomal protein Chain: P: PDB Molecule: 50s ribosomal protein l11; PDBTitle: ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11
45	d2byla1	Alignment	not modelled	11.5	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
46	d1je3a	Alignment	not modelled	11.4	10	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
47	c4mcjC	Alignment	not modelled	11.3	17	PDB header: transferase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative nucleoside deoxyribosyltransferase2 (bdi_0649) from parabacteroides distasonis atcc 8503 at 2.40 a3 resolution
48	c3vmtA	Alignment	not modelled	11.0	23	PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: crystal structure of staphylococcus aureus membrane-bound2 transglycosylase in complex with a lipid ii analog
49	d1nm3a2	Alignment	not modelled	11.0	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
50	d2f06a1	Alignment	not modelled	10.8	30	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
51	d1i7aa	Alignment	not modelled	10.8	15	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
52	c2jo8B	Alignment	not modelled	10.8	36	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
53	d1pava	Alignment	not modelled	10.4	12	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
54	c4nz3A	Alignment	not modelled	10.3	23	PDB header: hydrolase Chain: A: PDB Molecule: deacetylase da1; PDBTitle: structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21

55	d1q25a2	Alignment	not modelled	10.2	32	Fold: Mannose 6-phosphate receptor domain Superfamily: Mannose 6-phosphate receptor domain Family: Mannose 6-phosphate receptor domain
56	c6cjbA	Alignment	not modelled	10.2	13	PDB header: lyase Chain: A: PDB Molecule: cystathionine beta-lyase; PDBTitle: crystal structure of cystathionine beta-lyase from legionella2 pneumophila philadelphia 1 covalently bound to pyridoxal phosphate
57	d2nn4a1	Alignment	not modelled	10.2	19	Fold: YqqQ-like Superfamily: YqqQ-like Family: YqqQ-like
58	c3hl2D	Alignment	not modelled	10.2	19	PDB header: transferase Chain: D: PDB Molecule: o-phosphoseryl-trna(sec) selenium transferase; PDBTitle: the crystal structure of the human sepsecs-trnasec complex
59	d1phza1	Alignment	not modelled	10.2	25	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
60	d2odgc1	Alignment	not modelled	10.1	28	Fold: LEM/SAP HeH motif Superfamily: LEM domain Family: LEM domain
61	c4l0nG	Alignment	not modelled	10.1	32	PDB header: transferase Chain: G: PDB Molecule: serine/threonine-protein kinase 3; PDBTitle: crystal structure of stk3 (mst2) sarah domain
62	d1nsja	Alignment	not modelled	9.3	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
63	c5w70B	Alignment	not modelled	9.2	8	PDB header: transferase Chain: B: PDB Molecule: l-glutamine:2-deoxy-scylo-inosose aminotransferase; PDBTitle: x-ray structure of rbmb from streptomyces ribosidificus
64	d1okra	Alignment	not modelled	9.0	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
65	c4wxfc	Alignment	not modelled	9.0	18	PDB header: transferase Chain: C: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of l-serine hydroxymethyltransferase in complex with2 glycine
66	c6bn1A	Alignment	not modelled	8.5	33	PDB header: signaling protein Chain: A: PDB Molecule: serine/threonine-protein kinase hippo; PDBTitle: salvador hippo sarah domain complex
67	d1vefa1	Alignment	not modelled	8.5	11	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
68	c5vc2A	Alignment	not modelled	8.5	13	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of a serine hydroxymethyltransferase from2 helicobacter pylori
69	c6nmiF	Alignment	not modelled	8.4	17	PDB header: transcription Chain: F: PDB Molecule: general transcription factor iih subunit 3, p34; PDBTitle: cryo-em structure of the human tfiih core complex
70	d1a6ca1	Alignment	not modelled	8.3	7	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
71	c3k1qE	Alignment	not modelled	8.2	29	PDB header: PDB COMPND:
72	d3cjsb1	Alignment	not modelled	8.1	21	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
73	c6b4eD	Alignment	not modelled	7.9	44	PDB header: transport protein Chain: D: PDB Molecule: nucleoporin nup42; PDBTitle: crystal structure of saccharomyces cerevisiae gle1 ctd-nup42 gbm2 complex
74	c3lv2A	Alignment	not modelled	7.9	14	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
75	d1p6ra	Alignment	not modelled	7.9	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
76	c3gk0H	Alignment	not modelled	7.8	16	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
77	d1xbpg2	Alignment	not modelled	7.7	16	Fold: Ribosomal L11/L12e N-terminal domain Superfamily: Ribosomal L11/L12e N-terminal domain Family: Ribosomal L11/L12e N-terminal domain
78	c4qgrA	Alignment	not modelled	7.6	15	PDB header: transferase Chain: A: PDB Molecule: degt/dnrj/eryc1/strs aminotransferase; PDBTitle: crystal structure of a degt dnrj eryc1 strs aminotransferase from2 brucella abortus
79	d1f4nb	Alignment	not modelled	7.5	46	Fold: ROP-like Superfamily: ROP protein Family: ROP protein
80	d2dih2	Alignment	not modelled	7.5	22	Fold: Epsilon subunit of F1F0-ATP synthase N-terminal domain Superfamily: Epsilon subunit of F1F0-ATP synthase N-terminal domain Family: Epsilon subunit of F1F0-ATP synthase N-terminal domain

81	c2m46A_	Alignment	not modelled	7.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase, putative; PDBTitle: solution nmr structure of sac010876 from staphylococcus aureus col,2 nesg target zr353 and csgid target idp00841
82	c2qmwa_	Alignment	not modelled	7.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
83	c2gaaA_	Alignment	not modelled	7.4	31	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 39.9 kda protein; PDBTitle: crystal structure of yfh7 from saccharomyces cerevisiae: a2 putative p-loop containing kinase with a circular3 permutation.
84	d1exta2	Alignment	not modelled	7.3	38	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
85	c3ovcA_	Alignment	not modelled	7.2	29	PDB header: transferase/antibiotic Chain: A: PDB Molecule: hygromycin-b 4-o-kinase; PDBTitle: crystal structure of aminoglycoside phosphotransferase aph(4)-ia
86	c5a6eB_	Alignment	not modelled	7.2	20	PDB header: transport Chain: B: PDB Molecule: pore domain of potassium channel subfamily t member 1; PDBTitle: cryo-em structure of the slo2.2 na-activated k channel
87	c4bhel_	Alignment	not modelled	7.2	8	PDB header: transferase Chain: I: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: methanococcus jannaschii serine hydroxymethyl-transferase2 in complex with plp
88	c3rfuC_	Alignment	not modelled	6.9	17	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
89	d1f4na_	Alignment	not modelled	6.9	46	Fold: ROP-like Superfamily: ROP protein Family: ROP protein
90	c4lubA_	Alignment	not modelled	6.8	19	PDB header: lyase Chain: A: PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
91	c6b4eC_	Alignment	not modelled	6.6	44	PDB header: transport protein Chain: C: PDB Molecule: nucleoporin nup42; PDBTitle: crystal structure of saccharomyces cerevisiae gle1 ctd-nup42 gbm2 complex
92	c2cazB_	Alignment	not modelled	6.5	16	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein vps28; PDBTitle: escrt-i core
93	d2cazb1	Alignment	not modelled	6.5	16	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
94	d1t4aa_	Alignment	not modelled	6.5	29	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
95	c6enzA_	Alignment	not modelled	6.4	25	PDB header: lyase Chain: A: PDB Molecule: acidic amino acid decarboxylase gad11; PDBTitle: crystal structure of mouse gad11
96	c2k4bA_	Alignment	not modelled	6.4	0	PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: copr repressor structure
97	d2f6mb1	Alignment	not modelled	6.3	16	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
98	c5uidC_	Alignment	not modelled	6.3	18	PDB header: transferase Chain: C: PDB Molecule: aminotransferase tlmj; PDBTitle: the crystal structure of an aminotransferase tlmj from2 streptoalloteichus hindustanus
99	d1rhzb_	Alignment	not modelled	6.2	20	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit