


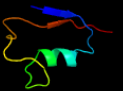

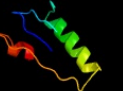

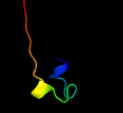

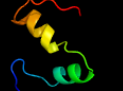

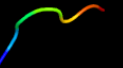





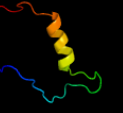

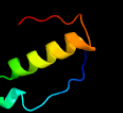


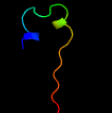

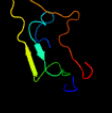




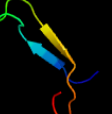
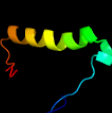


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0313 (-)_382490_382876
Date	Tue Jul 23 14:50:38 BST 2019
Unique Job ID	87f44a22373371cd

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1f7uA_	 Alignment		45.4	12	PDB header: ligase/rna Chain: A: PDB Molecule: arginyl-trna synthetase; PDBTitle: crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
2	c4r3zB_	 Alignment		30.5	20	PDB header: protein binding/ligase Chain: B: PDB Molecule: arginine--trna ligase, cytoplasmic; PDBTitle: crystal structure of human argrs-glnrs-aimp1 complex
3	c2jwlB_	 Alignment		23.8	18	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxs data
4	d1dmla1	 Alignment		21.8	38	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
5	c5xmjl_	 Alignment		19.6	30	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
6	c6eacC_	 Alignment		19.0	71	PDB header: transferase Chain: C: PDB Molecule: selo; PDBTitle: pseudomonas syringae selo
7	d2ffga1	 Alignment		17.8	15	Fold: Ykuj-like Superfamily: Ykuj-like Family: Ykuj-like
8	c2lufA_	 Alignment		16.0	41	PDB header: de novo protein Chain: A: PDB Molecule: retro trp-cage peptide; PDBTitle: retro trp-cage peptide
9	c2ys5A_	 Alignment		15.5	26	PDB header: signaling protein Chain: A: PDB Molecule: fibroblast growth factor receptor substrate 3; PDBTitle: solution structure of the complex of the ptb domain of snt-2 and 19-2 residue peptide (aa 1571-1589) of halk
10	d1kf6b2	 Alignment		14.5	39	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
11	d3etja2	 Alignment		14.5	33	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like

12	c1dmIG_	Alignment		14.4	33	PDB header: dna binding protein/transferase Chain: G: PDB Molecule: dna polymerase processivity factor; PDBTitle: crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
13	c5x3IA_	Alignment		14.0	43	PDB header: antimicrobial protein Chain: A: PDB Molecule: pilosulin-1; PDBTitle: solution structure of a novel antimicrobial peptide, p1, from jumper2 ant myrmecia pilosula
14	c4ipuA_	Alignment		13.2	17	PDB header: cell adhesion Chain: A: PDB Molecule: fimu protein; PDBTitle: crystal structure of pseudomonas aeruginosa (strain: pao1) type iv2 minor pilin fimu in space group p21
15	c4d77A_	Alignment		12.3	35	PDB header: signaling protein Chain: A: PDB Molecule: gliomedin; PDBTitle: high-resolution structure of the extracellular olfactomedin2 domain from gliomedin
16	d1jl7a_	Alignment		11.5	14	Fold: Globin-like Superfamily: Globin-like Family: Globins
17	d1jl6a_	Alignment		11.5	14	Fold: Globin-like Superfamily: Globin-like Family: Globins
18	c2iopD_	Alignment		11.5	30	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein htpg; PDBTitle: crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
19	c4wxuA_	Alignment		11.4	35	PDB header: protein binding Chain: A: PDB Molecule: myocilin; PDBTitle: crystal structure of the selenomthionine incorporated myocilin2 olfactomedin domain e396d variant.
20	d1xr0b_	Alignment		11.1	22	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)
21	c2yt2A_	Alignment	not modelled	10.9	24	PDB header: signaling protein Chain: A: PDB Molecule: fibroblast growth factor receptor substrate 3 and alk PDBTitle: solution structure of the chimera of the ptb domain of snt-2 and 19-2 residue peptide (aa 1571-1589) of halk
22	c5amoA_	Alignment	not modelled	10.9	23	PDB header: signaling protein Chain: A: PDB Molecule: noelin; PDBTitle: structure of a mouse olfactomedin-1 disulfide-linked dimer of the2 olfactomedin domain and part of the coiled coil
23	d1a6ma_	Alignment	not modelled	10.7	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
24	c3cm8A_	Alignment	not modelled	10.3	25	PDB header: rna binding protein/transferase Chain: A: PDB Molecule: polymerase acidic protein; PDBTitle: a rna polymerase subunit structure from virus
25	c4rdqA_	Alignment	not modelled	10.1	60	PDB header: transport protein Chain: A: PDB Molecule: bestrophin-1; PDBTitle: calcium-activated chloride channel bestrophin-1, from chicken, in2 complex with fab antibody fragments, chloride and calcium
26	c2bs2E_	Alignment	not modelled	9.5	11	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
27	d1a9we_	Alignment	not modelled	9.4	15	Fold: Globin-like Superfamily: Globin-like Family: Globins
28	c6en3A_	Alignment	not modelled	9.1	41	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-n-acetylglucosaminidase f2,multifunctional-

						PDBTitle: crystal structure of full length endos from streptococcus pyogenes in2 complex with g2 oligosaccharide.
29	c5by4A_	Alignment	not modelled	9.1	26	PDB header: protein transport Chain: A: PDB Molecule: protein tolr; PDBTitle: structure and function of the escherichia coli tol-pal stator protein2 tolr
30	d1hbga_	Alignment	not modelled	9.1	14	Fold: Globin-like Superfamily: Globin-like Family: Globins
31	c5d9aD_	Alignment	not modelled	9.0	29	PDB header: viral protein Chain: D: PDB Molecule: polymerase acidic protein; PDBTitle: influenza c virus rna-dependent rna polymerase - space group p212121
32	c6eslB_	Alignment	not modelled	8.3	27	PDB header: hydrolase Chain: B: PDB Molecule: bacterial leucyl aminopeptidase; PDBTitle: crystal structure of the legionella pneumoppila lapa
33	c3iaxB_	Alignment	not modelled	8.3	75	PDB header: protein transport Chain: B: PDB Molecule: colicin-a; PDBTitle: the crystal structure of the tolB box of colicin a in complex with2 tolB reveals important differences in the recruitment of the common3 tolB translocation portal used by group a colicins
34	d1hbrb_	Alignment	not modelled	8.3	15	Fold: Globin-like Superfamily: Globin-like Family: Globins
35	d3bj1b1	Alignment	not modelled	8.2	12	Fold: Globin-like Superfamily: Globin-like Family: Globins
36	d1a4fb_	Alignment	not modelled	8.2	15	Fold: Globin-like Superfamily: Globin-like Family: Globins
37	d1gcvb_	Alignment	not modelled	8.2	20	Fold: Globin-like Superfamily: Globin-like Family: Globins
38	d1fsla_	Alignment	not modelled	8.1	12	Fold: Globin-like Superfamily: Globin-like Family: Globins
39	c4dnhA_	Alignment	not modelled	7.8	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hypothetical protein smc04132 from sinorhizobium2 meliloti 1021
40	d1qpwb_	Alignment	not modelled	7.7	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
41	c3mkbD_	Alignment	not modelled	7.7	15	PDB header: oxygen storage, oxygen transport Chain: D: PDB Molecule: hemoglobin subunit beta; PDBTitle: crystal structure determination of shortfin mako (isurus oxyrinchus)2 hemoglobin at 1.9 angstrom resolution
42	d2dn3b1	Alignment	not modelled	7.6	13	Fold: Globin-like Superfamily: Globin-like Family: Globins
43	c3d5cX_	Alignment	not modelled	7.5	36	PDB header: ribosome Chain: X: PDB Molecule: peptide chain release factor 1; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
44	c2bu8A_	Alignment	not modelled	7.5	31	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 2 containing2 physiological and synthetic ligands
45	d2aa1b1	Alignment	not modelled	7.4	12	Fold: Globin-like Superfamily: Globin-like Family: Globins
46	d1v4wb_	Alignment	not modelled	7.4	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
47	d1jebb_	Alignment	not modelled	7.4	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
48	d1v0ea2	Alignment	not modelled	7.0	38	Fold: Triple-stranded beta-helix Superfamily: Phage fibre proteins Family: Endo-alpha-sialidase
49	c1s2nB_	Alignment	not modelled	7.0	24	PDB header: hydrolase Chain: B: PDB Molecule: extracellular subtilisin-like serine proteinase; PDBTitle: crystal structure of a cold adapted subtilisin-like serine proteinase
50	c2bk9A_	Alignment	not modelled	7.0	21	PDB header: oxygen transport Chain: A: PDB Molecule: cg9734-pa; PDBTitle: drosophila melanogaster globin
51	d1rq0a_	Alignment	not modelled	6.9	28	Fold: Release factor Superfamily: Release factor Family: Release factor
52	d1a4fa_	Alignment	not modelled	6.9	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
53	c5iauD_	Alignment	not modelled	6.9	20	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidase; PDBTitle: a c69-family cysteine dipeptidase from lactobacillus farcininis

54	d1cg5b_	Alignment	not modelled	6.8	13	Fold: Globin-like Superfamily: Globin-like Family: Globins
55	c4uzzB_	Alignment	not modelled	6.8	25	PDB header: motor protein Chain: B: PDB Molecule: intraflagellar transporter-like protein; PDBTitle: crystal structure of the ttift52-46 complex
56	c4wrtA_	Alignment	not modelled	6.8	29	PDB header: transferase/rna Chain: A: PDB Molecule: pa; PDBTitle: crystal structure of influenza b polymerase with bound vrna promoter2 (form flub2)
57	d3d1kb1	Alignment	not modelled	6.7	15	Fold: Globin-like Superfamily: Globin-like Family: Globins
58	d1qpwa_	Alignment	not modelled	6.6	13	Fold: Globin-like Superfamily: Globin-like Family: Globins
59	d2h8fb1	Alignment	not modelled	6.5	15	Fold: Globin-like Superfamily: Globin-like Family: Globins
60	c3dwl_	Alignment	not modelled	6.4	17	PDB header: structural protein Chain: I: PDB Molecule: actin-related protein 2/3 complex subunit 2; PDBTitle: crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
61	c2lpbB_	Alignment	not modelled	6.4	12	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: structure of the complex of the central activation domain of gcn42 bound to the mediator co-activator domain 1 of gal11/med15
62	c3bjxB_	Alignment	not modelled	6.4	22	PDB header: hydrolase Chain: B: PDB Molecule: halocarboxylic acid dehalogenase dehi; PDBTitle: structure of a group i haloacid dehalogenase from2 pseudomonas putida strain pp3
63	c2wa0A_	Alignment	not modelled	6.3	29	PDB header: immune system Chain: A: PDB Molecule: melanoma-associated antigen 4; PDBTitle: crystal structure of the human magea4
64	d1scta_	Alignment	not modelled	6.2	23	Fold: Globin-like Superfamily: Globin-like Family: Globins
65	c3k90C_	Alignment	not modelled	6.2	29	PDB header: hormone receptor, hydrolase regulator Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: the abscisic acid receptor pyr1 in complex with abscisic acid
66	c4biuB_	Alignment	not modelled	6.1	35	PDB header: transferase Chain: B: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (orthorhombic form 1)
67	c6gcsR_	Alignment	not modelled	6.1	14	PDB header: oxidoreductase Chain: R: PDB Molecule: ni2m subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
68	d1ch4a_	Alignment	not modelled	6.1	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
69	c3crB_	Alignment	not modelled	6.0	24	PDB header: transferase Chain: B: PDB Molecule: pyruvate dehydrogenase [lipoamide] kinase isozyme 2, PDBTitle: crystal structure of the pdhk2-l2 complex.
70	d1hdsb_	Alignment	not modelled	6.0	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
71	c6oawA_	Alignment	not modelled	6.0	24	PDB header: immune system Chain: A: PDB Molecule: wyl1; PDBTitle: crystal structure of a crispr cas-related protein
72	d2d5xa1	Alignment	not modelled	6.0	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
73	c3a0rA_	Alignment	not modelled	6.0	18	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
74	d3e11a1	Alignment	not modelled	5.9	41	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: TTHA0227-like
75	c2ihr1_	Alignment	not modelled	5.9	32	PDB header: translation Chain: 1: PDB Molecule: peptide chain release factor 2; PDBTitle: rf2 of thermus thermophilus
76	d1i3da_	Alignment	not modelled	5.7	14	Fold: Globin-like Superfamily: Globin-like Family: Globins
77	c5afbA_	Alignment	not modelled	5.7	35	PDB header: signaling protein Chain: A: PDB Molecule: latrophilin-3; PDBTitle: crystal structure of the latrophilin3 lectin and2 olfactomedin domains
78	d1shrb_	Alignment	not modelled	5.6	13	Fold: Globin-like Superfamily: Globin-like Family: Globins
79	d1f3ta2	Alignment	not modelled	5.6	10	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
						PDB header: translation Chain: A: PDB Molecule: probable peptide chain release factor

80	c2rsmA_	Alignment	not modelled	5.4	20	c12orf65 homolog, PDBTitle: solution structure and sirna-mediated knockdown analysis of the 2 mitochondrial disease-related protein c12orf65 (ict2)
81	c4l67B_	Alignment	not modelled	5.4	36	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: crystal structure of catalytic domain of pak4
82	d1lnza1	Alignment	not modelled	5.4	16	Fold: Obg-fold Superfamily: Obg GTP-binding protein N-terminal domain Family: Obg GTP-binding protein N-terminal domain
83	d1ecda_	Alignment	not modelled	5.3	18	Fold: Globin-like Superfamily: Globin-like Family: Globins
84	c4n2xF_	Alignment	not modelled	5.3	22	PDB header: hydrolase Chain: F: PDB Molecule: dl-2-haloacid dehalogenase; PDBTitle: crystal structure of dl-2-haloacid dehalogenase
85	c4v0pA_	Alignment	not modelled	5.3	24	PDB header: immune system Chain: A: PDB Molecule: melanoma-associated antigen 3; PDBTitle: crystal structure of the mage homology domain of human mage-a3
86	d1cqxa1	Alignment	not modelled	5.2	10	Fold: Globin-like Superfamily: Globin-like Family: Globins
87	c4biyD_	Alignment	not modelled	5.2	35	PDB header: transferase Chain: D: PDB Molecule: sensor protein cpxa; PDBTitle: crystal structure of cpxahdc (monoclinic form 2)
88	d1spga_	Alignment	not modelled	5.1	13	Fold: Globin-like Superfamily: Globin-like Family: Globins
89	c3s1jC_	Alignment	not modelled	5.1	8	PDB header: oxygen transport, oxygen storage Chain: C: PDB Molecule: hemoglobin-like flavoprotein; PDBTitle: crystal structure of acetate-bound hell's gate globin i
90	d1jdqa_	Alignment	not modelled	5.0	45	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
91	c3nw0B_	Alignment	not modelled	5.0	24	PDB header: metal binding protein Chain: B: PDB Molecule: melanoma-associated antigen g1; PDBTitle: crystal structure of mageg1 and nse1 complex
92	d1u84a_	Alignment	not modelled	5.0	50	Fold: YugE-like Superfamily: YugE-like Family: YugE-like