
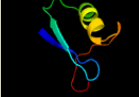
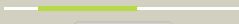


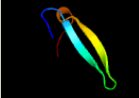

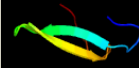
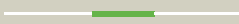


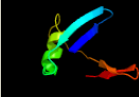







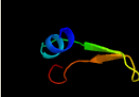






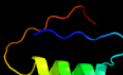

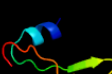




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3208A_(TB9.4)_3585673_3585945
 Date Thu Aug 8 16:20:40 BST 2019
 Unique Job ID 0c6a30ddee34d3e5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ip9a_	 Alignment		68.0	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
2	c4tkzA_	 Alignment		62.5	21	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein gbs1890; PDBTitle: crystal structure of phosphotransferase system component eiia from2 streptococcus agalactiae
3	c3hfoC_	 Alignment		61.5	35	PDB header: rna binding protein Chain: C: PDB Molecule: ssr3341 protein; PDBTitle: crystal structure of an hfq protein from synechocystis sp.
4	d2k57a1	 Alignment		52.4	17	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
5	d2jn0a1	 Alignment		50.4	28	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
6	d1wmha_	 Alignment		42.1	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
7	d1tksa_	 Alignment		40.8	19	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
8	d2rb6a1	 Alignment		38.9	27	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
9	d2rd1a1	 Alignment		38.8	24	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
10	c3mioA_	 Alignment		38.7	10	PDB header: lyase Chain: A: PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
11	d1pdoa_	 Alignment		36.2	24	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like

12	d3bdua1	Alignment		35.6	24	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
13	c4p6dA_	Alignment		34.7	30	PDB header: lyase Chain: A: PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: structure of ribb complexed with po4 ion
14	d2ra2a1	Alignment		34.0	20	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: YgdI/YgdR-like
15	c3ffhF_	Alignment		31.2	14	PDB header: transferase Chain: F: PDB Molecule: phosphotransferase system, mannose/fructose-specific PDBTitle: crystal structure of manxa from thermoanaerobacter tengcongensis
16	c5t3uA_	Alignment		30.5	28	PDB header: transport protein Chain: A: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the pts iia protein associated with the fucose2 utilization operon from streptococcus pneumoniae
17	d2hiya1	Alignment		29.1	14	Fold: SP0830-like Superfamily: SP0830-like Family: SP0830-like
18	d1k4ia_	Alignment		25.9	17	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
19	c3iprC_	Alignment		25.2	17	PDB header: transferase Chain: C: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
20	c4ffjA_	Alignment		24.3	13	PDB header: lyase Chain: A: PDB Molecule: riboflavin biosynthesis protein ribba; PDBTitle: the crystal structure of spdhbps from s.pneumoniae
21	d2a90a2	Alignment	not modelled	23.4	15	Fold: WWE domain Superfamily: WWE domain Family: WWE domain
22	c6fmgC_	Alignment	not modelled	22.6	21	PDB header: transferase Chain: C: PDB Molecule: pts system mannose-specific transporter subunit iiab; PDBTitle: structure of the mannose transporter iia domain from streptococcus2 pneumoniae
23	d1g57a_	Alignment	not modelled	20.2	23	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
24	c4bzbP_	Alignment	not modelled	19.8	18	PDB header: transferase Chain: B: PDB Molecule: bifunctional enzyme cysn/cysc; PDBTitle: structure of the mycobacterium tuberculosis aps kinase cysc2 in complex with adp
25	c2kmaA_	Alignment	not modelled	19.0	20	PDB header: structural protein Chain: A: PDB Molecule: taln1; PDBTitle: nmr structure of the f0f1 double domain (residues 1-202) of2 the talin ferm domain
26	c3gx1A_	Alignment	not modelled	18.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1832 protein; PDBTitle: crystal structure of a domain of lin1832 from listeria innocua
27	d1cr5a2	Alignment	not modelled	17.7	11	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
28	c4i14B_	Alignment	not modelled	17.4	10	PDB header: hydrolase, lyase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribba; PDBTitle: crystal structure of mtb-riba2 (rv1415)

29	c1xs3A_	Alignment	not modelled	17.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein xc975; PDBTitle: solution structure analysis of the xc975 protein
30	d1snaa_	Alignment	not modelled	16.9	23	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
31	d1v86a_	Alignment	not modelled	15.4	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
32	c6gf8B_	Alignment	not modelled	14.9	22	PDB header: cell adhesion Chain: B: PDB Molecule: zona pellucida sperm-binding protein 1,zona pellucida PDBTitle: molecular basis of egg coat filament cross-linking: structure of the2 glycosylated zp1 zp-n1 domain homodimer
33	c3hfnA_	Alignment	not modelled	14.5	30	PDB header: rna binding protein Chain: A: PDB Molecule: asl2047 protein; PDBTitle: crystal structure of an hfq protein from anabaena sp.
34	d1wi9a_	Alignment	not modelled	14.5	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PCI domain (PINT motif)
35	c6mnzB_	Alignment	not modelled	14.4	19	PDB header: lyase Chain: B: PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: crystal structure of ribbx, a two domain 3,4-dihydroxy-2-butanone 4-2 phosphate synthase from a. baumannii.
36	c6g09A_	Alignment	not modelled	14.0	19	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 8 domain protein; PDBTitle: crystal structure of a gh8 xylobiose complex from teredinibacter2 turnerae
37	c6nbpA_	Alignment	not modelled	13.4	30	PDB header: transferase Chain: A: PDB Molecule: n-formyltransferase; PDBTitle: crystal structure of a sugar n-formyltransferase from the plant2 pathogen pantoea ananatis
38	d1d3bl_	Alignment	not modelled	12.7	9	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Sm motif of small nuclear ribonucleoproteins, SNRNP
39	c2pmzL_	Alignment	not modelled	11.9	21	PDB header: translation, transferase Chain: L: PDB Molecule: dna-directed rna polymerase subunit I; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
40	c4nv1D_	Alignment	not modelled	11.4	14	PDB header: transferase Chain: D: PDB Molecule: formyltransferase; PDBTitle: crystal structure of a 4-n formyltransferase from francisella2 tularensis
41	c2v9vA_	Alignment	not modelled	11.1	13	PDB header: transcription Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of moorella thermoacetica selb(377-511)
42	d2fq1a1	Alignment	not modelled	11.0	22	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
43	c3cbnA_	Alignment	not modelled	11.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mth639; PDBTitle: crystal structure of a conserved protein (mth639) from2 methanobacterium thermoautotrophicum
44	c3ip5A_	Alignment	not modelled	10.8	29	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (amino acid); PDBTitle: structure of atu2422-gaba receptor in complex with alanine
45	c3g1zB_	Alignment	not modelled	10.5	36	PDB header: ligase Chain: B: PDB Molecule: putative lysyl-trna synthetase; PDBTitle: structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
46	d1nvmb1	Alignment	not modelled	10.2	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
47	d2znvb1	Alignment	not modelled	10.2	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
48	c5d4pA_	Alignment	not modelled	10.2	12	PDB header: signaling protein Chain: A: PDB Molecule: putative nitrogen regulatory protein p-ii glnb; PDBTitle: structure of cp11 bound to adp and bicarbonate, from thiomonas2 intermedia k12
49	c3tr3A_	Alignment	not modelled	10.1	13	PDB header: unknown function Chain: A: PDB Molecule: bola; PDBTitle: structure of a bola protein homologue from coxiella burnetii
50	d1bbua2	Alignment	not modelled	9.3	25	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
51	c4qiwU_	Alignment	not modelled	9.0	13	PDB header: transcription Chain: U: PDB Molecule: dna-directed rna polymerase subunit I; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
52	d2ga5a1	Alignment	not modelled	8.7	21	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
53	d1e1oa2	Alignment	not modelled	8.6	36	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
						Fold: Class II aaRS and biotin synthetases

54	d1b8aa2	Alignment	not modelled	8.6	25	Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
55	d3beda1	Alignment	not modelled	8.6	17	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
56	d1ir1s_	Alignment	not modelled	8.4	17	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
57	d2a90a1	Alignment	not modelled	8.4	13	Fold: WWE domain Superfamily: WWE domain Family: WWE domain
58	c2kd0A_	Alignment	not modelled	8.4	9	PDB header: signaling protein Chain: A; PDB Molecule: lrr repeats and ubiquitin-like domain-containing PDBTitle: nmr solution structure of o64736 protein from arabidopsis2 thaliana. northeast structural genomics consortium mega3 target ar3445a
59	d1tdha3	Alignment	not modelled	8.1	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
60	c2rrnA_	Alignment	not modelled	8.1	11	PDB header: protein transport Chain: A; PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: solution structure of secdf periplasmic domain p4
61	c5kdvA_	Alignment	not modelled	8.0	16	PDB header: hydrolase Chain: A; PDB Molecule: metallopeptidase; PDBTitle: impa metallopeptidase from pseudomonas aeruginosa
62	d2vzsa2	Alignment	not modelled	8.0	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
63	c4yfvA_	Alignment	not modelled	7.9	14	PDB header: transferase Chain: A; PDB Molecule: viof; PDBTitle: x-ray structure of the 4-n-formyltransferase viof from providencia2 alcalifaciens o30
64	d1h4vb2	Alignment	not modelled	7.9	38	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
65	d1eova2	Alignment	not modelled	7.8	19	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
66	d1ekga_	Alignment	not modelled	7.7	31	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
67	c2x4IA_	Alignment	not modelled	7.6	19	PDB header: transport Chain: A; PDB Molecule: ferric-siderophore receptor protein; PDBTitle: crystal structure of dese, a ferric-siderophore receptor protein from2 streptomyces coelicolor
68	d1ndda_	Alignment	not modelled	7.6	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
69	d1fxkc_	Alignment	not modelled	7.6	16	Fold: Long alpha-hairpin Superfamily: Prefoldin Family: Prefoldin
70	c3v9pA_	Alignment	not modelled	7.5	9	PDB header: transferase Chain: A; PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of thymidylate kinase from burkholderia2 thailandensis
71	c2mqjA_	Alignment	not modelled	7.5	17	PDB header: ligase Chain: A; PDB Molecule: ubiquitin-like protein; PDBTitle: solution structure of ubiquitin-like protein from caldiarchaeum2 subterraneum
72	c3ts3D_	Alignment	not modelled	7.4	29	PDB header: viral protein Chain: D; PDB Molecule: capsid polyprotein; PDBTitle: crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
73	d1kmma2	Alignment	not modelled	7.3	31	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
74	c4hs5B_	Alignment	not modelled	7.3	19	PDB header: metal binding protein Chain: B; PDB Molecule: protein cyay; PDBTitle: frataxin from psychromonas ingrahamii as a model to study stability2 modulation within cyay protein family PDB header: structural genomics, unknown function
75	c2klcA_	Alignment	not modelled	7.1	14	Chain: A; PDB Molecule: ubiquilin-1; PDBTitle: nmr solution structure of human ubiquitin-like domain of ubiquilin 1,2 northeast structural genomics consortium (nesg) target ht5a
76	c4mo9A_	Alignment	not modelled	7.0	25	PDB header: solute-binding protein Chain: A; PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of troa-like periplasmic binding protein fepb from2 veillonella parvula
77	d1ew4a_	Alignment	not modelled	7.0	41	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
78	d1nnha_	Alignment	not modelled	7.0	36	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
79	d2fnjb1	Alignment	not modelled	7.0	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related

80	c6b0nG_	 Alignment	not modelled	6.9	30	PDB header: viral protein/immune system Chain: G: PDB Molecule: envelope glycoprotein gp140; PDBTitle: crystal structure of the cleavage-independent prefusion hiv env2 glycoprotein trimer of the clade a bg505 isolate (nfl construct) in3 complex with fabs pgt122 and pgv19 at 3.39 a
81	c3d6wA_	 Alignment	not modelled	6.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: methyl-accepting/dna response regulator; PDBTitle: lyttr dna-binding domain of putative methyl-accepting/dna response2 regulator from bacillus cereus.
82	c5ur0B_	 Alignment	not modelled	6.8	25	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystallographic structure of glyceraldehyde-3-phosphate dehydrogenase2 from naegleria gruberi
83	c3t61A_	 Alignment	not modelled	6.7	21	PDB header: transferase Chain: A: PDB Molecule: gluconokinase; PDBTitle: crystal structure of a gluconokinase from sinorhizobium meliloti 1021
84	c4k95G_	 Alignment	not modelled	6.7	14	PDB header: ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase parkin; PDBTitle: crystal structure of parkin
85	c5nfmA_	 Alignment	not modelled	6.5	16	PDB header: ligase Chain: A: PDB Molecule: yrba; PDBTitle: crystal structure of yrba from sinorhizobium meliloti in complex with2 copper.
86	d1knqa_	 Alignment	not modelled	6.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Gluconate kinase
87	d1qe0a2	 Alignment	not modelled	6.5	15	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
88	d1wx7a1	 Alignment	not modelled	6.5	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
89	c1yx5B_	 Alignment	not modelled	6.4	12	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin; PDBTitle: solution structure of s5a uim-1/ubiquitin complex
90	c3be5D_	 Alignment	not modelled	6.4	21	PDB header: metal transport Chain: D: PDB Molecule: putative iron compound-binding protein of abc transporter PDBTitle: crystal structure of fite (crystal form 1), a group iii periplasmic2 siderophore binding protein
91	d1p9ya_	 Alignment	not modelled	6.4	15	Fold: Ribosome binding domain-like Superfamily: Trigger factor ribosome-binding domain Family: Trigger factor ribosome-binding domain
92	d1e6yb2	 Alignment	not modelled	6.4	17	Fold: Ferredoxin-like Superfamily: Methyl-coenzyme M reductase subunits Family: Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
93	c4l0jA_	 Alignment	not modelled	6.3	20	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase i; PDBTitle: structure of a translocation signal domain mediating conjugative2 transfer by type iv secretion systems
94	d1v2ya_	 Alignment	not modelled	6.2	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
95	c4jpdA_	 Alignment	not modelled	6.1	38	PDB header: metal binding protein Chain: A: PDB Molecule: protein cyay; PDBTitle: the structure of cyay from burkholderia cenocepacia
96	d1v5oa_	 Alignment	not modelled	6.0	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
97	c2kanA_	 Alignment	not modelled	6.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ar3433a; PDBTitle: solution nmr structure of ubiquitin-like domain of2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
98	d2phla2	 Alignment	not modelled	5.9	18	Fold: Double-stranded beta-helix Superfamily: RmC-like cupins Family: Germin/Seed storage 7S protein
99	c3w66A_	 Alignment	not modelled	5.8	17	PDB header: metal transport Chain: A: PDB Molecule: magnetosome protein mamm; PDBTitle: mamm-ctd d249a and h285a