


















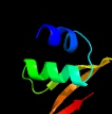




Phyre2

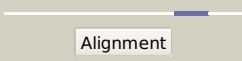
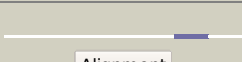
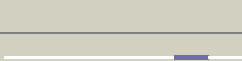
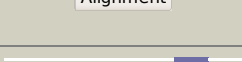
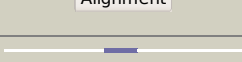
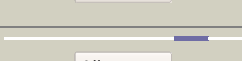
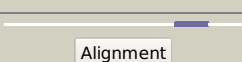
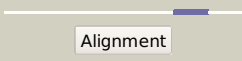
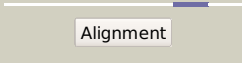
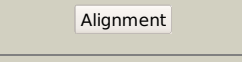
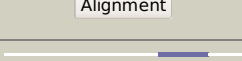
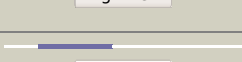
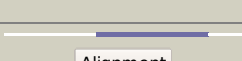
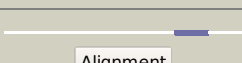
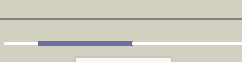
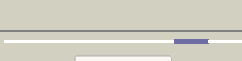
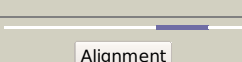
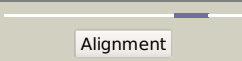
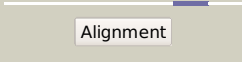
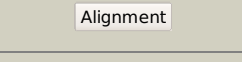
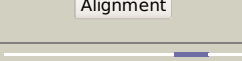
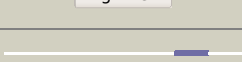
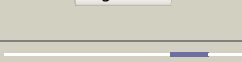
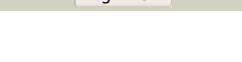

Email	mdejesus@rockefeller.edu
Description	RVBD3241c_(-)_3620607_3621251
Date	Thu Aug 8 16:20:44 BST 2019
Unique Job ID	0f8a7b0c3af8daf3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mmjy_	 Alignment		99.9	25	PDB header: ribosome Chain: Y; PDB Molecule: PDBTitle: structure of the small subunit of the chloroplast ribosome
2	c6dzkY_	 Alignment		99.9	84	PDB header: ribosome Chain: Y; PDB Molecule: ribosome hibernation promoting factor; PDBTitle: cryo-em structure of mycobacterium smegmatis c(minus) 30s ribosomal2 subunit with mpy
3	c3ka5A_	 Alignment		99.9	43	PDB header: chaperone Chain: A; PDB Molecule: ribosome-associated protein y (psrp-1); PDBTitle: crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
4	d1l4sa_	 Alignment		99.9	17	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)
5	c2rqlA_	 Alignment		99.9	29	PDB header: translation Chain: A; PDB Molecule: probable sigma-54 modulation protein; PDBTitle: solution structure of the e. coli ribosome hibernation2 promoting factor hpf
6	c6qbzA_	 Alignment		99.9	24	PDB header: ribosomal protein Chain: A; PDB Molecule: ribosome hibernation promoting factor; PDBTitle: solution structure of the n-terminal domain of the staphylococcus2 aureus hibernation promoting factor
7	c3tqmD_	 Alignment		99.9	22	PDB header: protein binding Chain: D; PDB Molecule: ribosome-associated factor y; PDBTitle: structure of an ribosomal subunit interface protein from coxiella2 burnetii
8	d1imua_	 Alignment		99.9	18	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)
9	c4fylB_	 Alignment		99.9	34	PDB header: translation Chain: B; PDB Molecule: ribosome hibernation protein yhbh; PDBTitle: high-resolution x-ray structure of hpf from vibrio cholerae
10	c3k2tA_	 Alignment		99.9	46	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: lmo2511 protein; PDBTitle: crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
11	d2ywqa1	 Alignment		99.9	38	Fold: Ribosome binding protein Y (YfiA homologue) Superfamily: Ribosome binding protein Y (YfiA homologue) Family: Ribosome binding protein Y (YfiA homologue)

12	c3lyvF_	Alignment		99.8	48	PDB header: chaperone Chain: F; PDB Molecule: ribosome-associated factor y; PDBTitle: crystal structure of a domain of ribosome-associated factor y from2 streptococcus pyogenes serotype m6. northeast structural genomics3 consortium target id dr64a
13	c4jw1A_	Alignment		47.3	36	PDB header: hydrolase activator Chain: A; PDB Molecule: effector protein b; PDBTitle: crystal structure of n-terminal 618-residue fragment of lepb from2 legionella pneumophila
14	c3zf7R_	Alignment		45.2	12	PDB header: ribosome Chain: R; PDB Molecule: 60s ribosomal protein l17, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
15	d1ohea1	Alignment		40.1	12	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
16	c2j43A_	Alignment		40.0	8	PDB header: carbohydrate-binding module Chain: A; PDB Molecule: spydX; PDBTitle: alpha-glucan recognition by family 41 carbohydrate-binding2 modules from streptococcal virulence factors
17	c1oheA_	Alignment		39.2	12	PDB header: hydrolase Chain: A; PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
18	d1m0wa1	Alignment		35.8	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Eukaryotic glutathione synthetase, substrate-binding domain
19	c3vcaA_	Alignment		34.9	5	PDB header: oxidoreductase Chain: A; PDB Molecule: ring-hydroxylating dioxygenase; PDBTitle: quaternary ammonium oxidative demethylation: x-ray crystallographic,2 resonance raman and uv-visible spectroscopic analysis of a rieske-3 type demethylase
20	c4v19W_	Alignment		33.6	39	PDB header: ribosome Chain: W; PDB Molecule: mitoribosomal protein ul22m, mrpl22; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
21	c2j44A_	Alignment	not modelled	33.2	19	PDB header: carbohydrate-binding module Chain: A; PDB Molecule: alkaline amylopullulanase; PDBTitle: alpha-glucan binding by a streptococcal virulence factor
22	c5nwmA_	Alignment	not modelled	31.4	0	PDB header: signaling protein Chain: A; PDB Molecule: nuclear receptor coactivator 1; PDBTitle: insight into the molecular recognition mechanism of the coactivator2 ncoa1 by stat6
23	c3n0qA_	Alignment	not modelled	30.1	5	PDB header: oxidoreductase Chain: A; PDB Molecule: putative aromatic-ring hydroxylating dioxygenase; PDBTitle: crystal structure of a putative aromatic-ring hydroxylating2 dioxygenase (tm1040_3219) from silicibacter sp. tm1040 at 1.80 a3 resolution
24	c4ce4W_	Alignment	not modelled	29.5	37	PDB header: ribosome Chain: W; PDB Molecule: mrpl22; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
25	c3j39P_	Alignment	not modelled	27.8	21	PDB header: ribosome Chain: P; PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
26	c5o60T_	Alignment	not modelled	27.8	21	PDB header: ribosome Chain: T; PDB Molecule: 50s ribosomal protein l22; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
27	d2zjrp1	Alignment	not modelled	27.5	22	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
28	c2jvfA_	Alignment	not modelled	27.3	19	PDB header: de novo protein Chain: A; PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein PDB header: ribosome

29	c3jywN_	Alignment	not modelled	26.6	18	Chain: N: PDB Molecule: 60s ribosomal protein l17(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
30	c1vw4O_	Alignment	not modelled	25.9	16	PDB header: ribosome Chain: O: PDB Molecule: 54s ribosomal protein l22, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
31	c2xp1A_	Alignment	not modelled	24.7	11	PDB header: transcription Chain: A: PDB Molecule: spt6; PDBTitle: structure of the tandem sh2 domains from antonospora locustae2 transcription elongation factor spt6
32	c3j21S_	Alignment	not modelled	24.3	24	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l22p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
33	d1i4ja_	Alignment	not modelled	23.9	11	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
34	c5boiA_	Alignment	not modelled	23.7	21	PDB header: unknown function Chain: A: PDB Molecule: germination protein ypeb; PDBTitle: bacillus megaterium ypeb c-terminal domain
35	d1nxxa_	Alignment	not modelled	22.8	24	Fold: OB-fold Superfamily: Hypothetical protein YgiW Family: Hypothetical protein YgiW
36	c3j3wS_	Alignment	not modelled	22.6	17	PDB header: ribosome Chain: S: PDB Molecule: 50s ribosomal protein l22; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
37	c1by0A_	Alignment	not modelled	21.8	38	PDB header: rna binding protein Chain: A: PDB Molecule: protein (hepatitis delta antigen); PDBTitle: n-terminal leucine-repeat region of hepatitis delta antigen
38	c2zylA_	Alignment	not modelled	21.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: possible oxidoreductase; PDBTitle: crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
39	c2de7B_	Alignment	not modelled	21.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: terminal oxygenase component of carbazole; PDBTitle: the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
40	c3nqrD_	Alignment	not modelled	20.5	14	PDB header: transport protein Chain: D: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: a putative cbs domain-containing protein from salmonella typhimurium2 lt2
41	d2v8qe2	Alignment	not modelled	20.3	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
42	c4a17Q_	Alignment	not modelled	19.5	18	PDB header: ribosome Chain: Q: PDB Molecule: rpl17; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
43	d1egxa_	Alignment	not modelled	19.4	15	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
44	c2ftcM_	Alignment	not modelled	19.2	39	PDB header: ribosome Chain: M: PDB Molecule: mitochondrial ribosomal protein l22 isoform a; PDBTitle: structural model for the large subunit of the mammalian mitochondrial2 ribosome
45	c3u5eP_	Alignment	not modelled	18.4	15	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
46	d2k0bx1	Alignment	not modelled	18.3	29	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
47	d1vqor1	Alignment	not modelled	18.2	24	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
48	c3fwrB_	Alignment	not modelled	17.8	29	PDB header: transcription Chain: B: PDB Molecule: yqzb protein; PDBTitle: crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
49	c2zkrr_	Alignment	not modelled	17.7	24	PDB header: ribosomal protein/rna Chain: R: PDB Molecule: rna expansion segment es39 part i; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
50	d2hkja2	Alignment	not modelled	17.5	6	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
51	c1v06A_	Alignment	not modelled	17.2	22	PDB header: dna-binding protein Chain: A: PDB Molecule: hmg box-containing protein 1; PDBTitle: axh domain of the transcription factor hbp1 from m.musculus
52	c4gi3C_	Alignment	not modelled	17.1	42	PDB header: hydrolase/hydrolase inhibitor Chain: C: PDB Molecule: greglin; PDBTitle: crystal structure of greglin in complex with subtilisin
53	d2awia1	Alignment	not modelled	17.0	35	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: PrgX N-terminal domain-like

54	c5mlcU		Alignment	not modelled	16.9	21	PDB header: ribosome Chain: U: PDB Molecule: 50s ribosomal protein l22, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
55	c4wujB		Alignment	not modelled	16.9	6	PDB header: circadian clock protein Chain: B: PDB Molecule: glycoside hydrolase family 15, cellulose signaling PDBTitle: structural biochemistry of a fungal lov domain photoreceptor reveals2 an evolutionarily conserved pathway integrating blue-light and3 oxidative stress
56	c3gcfC		Alignment	not modelled	16.3	9	PDB header: oxidoreductase Chain: C: PDB Molecule: terminal oxygenase component of carbazole 1,9a- PDBTitle: terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardioides aromaticivorans ic177
57	c5xw4A		Alignment	not modelled	16.2	19	PDB header: cell cycle Chain: A: PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
58	c1gmjD		Alignment	not modelled	16.2	25	PDB header: atpase inhibitor Chain: D: PDB Molecule: atpase inhibitor; PDBTitle: the structure of bovine if1, the regulatory subunit of mitochondrial2 f-atpase
59	d2gycq1		Alignment	not modelled	16.2	16	Fold: Ribosomal protein L22 Superfamily: Ribosomal protein L22 Family: Ribosomal protein L22
60	c2vlgD		Alignment	not modelled	16.0	7	PDB header: transferase Chain: D: PDB Molecule: sporulation kinase a; PDBTitle: kina pas-a domain, homodimer
61	c1yavB		Alignment	not modelled	16.0	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein yukl2 from bacillus subtilis
62	c6h1wA		Alignment	not modelled	15.9	18	PDB header: unknown function Chain: A: PDB Molecule: mj1004; PDBTitle: crystal structure of protein mj1004 from mathanocaldococcus jannaschii
63	d2b1xa1		Alignment	not modelled	15.7	10	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
64	c3zqbB		Alignment	not modelled	15.7	16	PDB header: cell invasion Chain: B: PDB Molecule: protein prgi, cell invasion protein sipd; PDBTitle: prgi-sipd from salmonella typhimurium
65	c2m5jA		Alignment	not modelled	15.1	6	PDB header: signaling protein Chain: A: PDB Molecule: hasr protein; PDBTitle: solution structure of the periplasmic signaling domain of hasr, a2 tonb-dependent outer membrane heme transporter
66	c5ts4A		Alignment	not modelled	15.1	21	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
67	d1kx5b		Alignment	not modelled	14.8	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
68	c2outA		Alignment	not modelled	14.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mu-like prophage flumu protein gp35, protein PDBTitle: solution structure of hi1506, a novel two domain protein2 from haemophilus influenzae
69	c4ky3A		Alignment	not modelled	14.5	32	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or327; PDBTitle: three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327
70	d2bm0a4		Alignment	not modelled	14.3	14	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
71	d1rq8a		Alignment	not modelled	14.0	6	Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like
72	c3i8nB		Alignment	not modelled	13.7	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp2912; PDBTitle: a domain of a conserved functionally known protein from2 vibrio parahaemolyticus rimd 2210633.
73	d2yzia1		Alignment	not modelled	13.4	12	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
74	d1vr9a3		Alignment	not modelled	13.4	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
75	c1vr9B		Alignment	not modelled	13.4	14	PDB header: unknown function Chain: B: PDB Molecule: cbs domain protein/act domain protein; PDBTitle: crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution
76	d1nyta2		Alignment	not modelled	13.3	7	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
77	c4irtA		Alignment	not modelled	13.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative neuraminidase (bacova_03493) from2 bacteroides ovatus atcc 8483 at 1.74 a resolution
78	c3jtfB		Alignment	not modelled	13.2	14	PDB header: transport protein Chain: B: PDB Molecule: magnesium and cobalt efflux protein; PDBTitle: the cbs domain pair structure of a magnesium and cobalt

						efflux protein2 from bordetella parapertussis in complex with amp
79	d1qqfa_	Alignment	not modelled	13.1	10	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components
80	d1jo0a_	Alignment	not modelled	13.0	11	Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like
81	c2jy8A_	Alignment	not modelled	13.0	29	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin-binding protein p62; PDBTitle: nmr structure of the ubiquitin associated (uba) domain of2 p62 (sqstm1) in complex with ubiquitin. rdc refined
82	d3bb6a1	Alignment	not modelled	13.0	14	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TehB-like
83	c3lhhA_	Alignment	not modelled	12.9	11	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
84	d1lr0a_	Alignment	not modelled	12.3	14	Fold: ToIA/TonB C-terminal domain Superfamily: ToIA/TonB C-terminal domain Family: ToIA
85	d1wqla1	Alignment	not modelled	12.3	14	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
86	d2bmoa1	Alignment	not modelled	12.2	5	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
87	d1rrpb_	Alignment	not modelled	11.9	12	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Ran-binding domain
88	c3l2iB_	Alignment	not modelled	11.9	13	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinone dehydratase; PDBTitle: 1.85 angstrom crystal structure of the 3-dehydroquinone dehydratase2 (arod) from salmonella typhimurium lt2.
89	d1sr9a3	Alignment	not modelled	11.8	10	Fold: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Superfamily: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Family: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
90	d3dl3a1	Alignment	not modelled	11.7	11	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: TehB-like
91	c1p74B_	Alignment	not modelled	11.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from haemophilus2 influenzae
92	c3kxeD_	Alignment	not modelled	11.5	29	PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
93	d1pvma4	Alignment	not modelled	11.5	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
94	c1m0tB_	Alignment	not modelled	11.4	20	PDB header: ligase Chain: B: PDB Molecule: glutathione synthetase; PDBTitle: yeast glutathione synthase
95	d1ln4a_	Alignment	not modelled	11.3	9	Fold: IF3-like Superfamily: YhbY-like Family: YhbY-like
96	d2e9xd1	Alignment	not modelled	11.0	27	Fold: GINS helical bundle-like Superfamily: GINS helical bundle-like Family: SLD5 N-terminal domain-like
97	d2dy1a4	Alignment	not modelled	10.9	14	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
98	d2ooxe1	Alignment	not modelled	10.8	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
99	c5cegC_	Alignment	not modelled	10.8	6	PDB header: toxin Chain: C: PDB Molecule: addiction module antidote protein, copg/arc/metj family; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum