
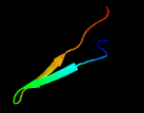

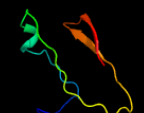



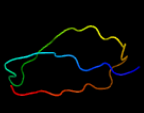

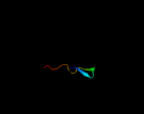

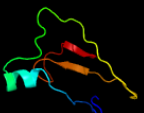

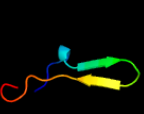

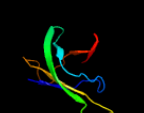

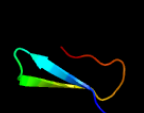

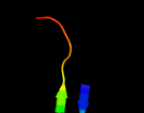





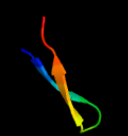



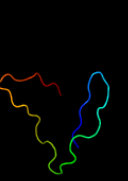
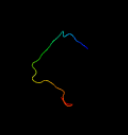


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1252c_(lprE)_1399302_1399910
 Date Wed Jul 31 22:05:34 BST 2019
 Unique Job ID 7fc00f9362bedb91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gjhA_	 Alignment		70.8	30	PDB header: de novo protein Chain: A: PDB Molecule: designed protein; PDBTitle: nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
2	c5x7hA_	 Alignment		61.9	16	PDB header: transferase Chain: A: PDB Molecule: cycloisomaltooligosaccharide glucanotransferase; PDBTitle: crystal structure of paenibacillus sp. 598k2 cycloisomaltooligosaccharide glucanotransferase complexed with3 cycloisomaltoheptaose
3	c3pdgA_	 Alignment		44.6	12	PDB header: unknown function Chain: A: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
4	d1gpla1	 Alignment		38.2	16	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Colipase-binding domain
5	c6chgB_	 Alignment		31.5	14	PDB header: transferase Chain: B: PDB Molecule: klla0c10945p; PDBTitle: crystal structure of the yeast compass catalytic module
6	d1luxxx_	 Alignment		28.4	18	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 6 carbohydrate binding module, CBM6
7	c2mbIA_	 Alignment		27.3	26	PDB header: de novo protein Chain: A: PDB Molecule: top7 fold protein top7m13; PDBTitle: solution nmr structure of de novo designed top7 fold protein top7m13,2 northeast structural genomics consortium (nesg) target or33
8	d1pj5a1	 Alignment		26.7	14	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
9	c3pe9D_	 Alignment		24.8	17	PDB header: unknown function Chain: D: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
10	c3gzbC_	 Alignment		20.6	33	PDB header: lyase Chain: C: PDB Molecule: putative snoal-like polyketide cyclase; PDBTitle: crystal structure of putative snoal-like polyketide cyclase2 (yp_001182657.1) from shewanella putrefaciens cn-32 at 1.44 a3 resolution
11	c2rnmC_	 Alignment		18.9	50	PDB header: protein fibril Chain: C: PDB Molecule: small s protein; PDBTitle: structure of the het-s(218-289) prion in its amyloid form obtained by2 solid-state nmr

12	d1etha1	Alignment		17.9	18	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Colipase-binding domain
13	c6bx3K_	Alignment		16.2	18	PDB header: gene regulation/transferase Chain: K: PDB Molecule: compass component bre2; PDBTitle: structure of histone h3k4 methyltransferase
14	d2p3pa1	Alignment		15.3	33	Fold: PG1388-like Superfamily: PG1388-like Family: PG1388-like
15	c5ggfC_	Alignment		15.3	7	PDB header: transferase, sugar binding protein Chain: C: PDB Molecule: protein o-linked-mannose beta-1,2-n- PDBTitle: crystal structure of human protein o-mannose beta-1,2-n-2 acetylglucosaminyltransferase form ii
16	d2as0a1	Alignment		14.5	13	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical RNA methyltransferase domain (HRMD)
17	c5e24D_	Alignment		14.2	45	PDB header: transport/dna binding/dna Chain: D: PDB Molecule: protein hairless; PDBTitle: structure of the su(h)-hairless-dna repressor complex
18	d1dmla1	Alignment		14.2	18	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
19	d2fnja1	Alignment		14.0	13	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: SPRY domain
20	c3cb0B_	Alignment		13.9	8	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxyphenylacetate 3- monoxygenase; PDBTitle: cobr
21	c2yfrA_	Alignment	not modelled	13.9	12	PDB header: transferase Chain: A: PDB Molecule: levansucrase; PDBTitle: crystal structure of inulosucrase from lactobacillus2 johnsonii ncc533
22	d2hfa1	Alignment	not modelled	13.7	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: HyaE-like
23	c5xebC_	Alignment	not modelled	13.3	26	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein; PDBTitle: structure of the envelope glycoprotein of dhori virus
24	c2w1wB_	Alignment	not modelled	12.7	15	PDB header: hydrolase Chain: B: PDB Molecule: lipolytic enzyme, g-d-s-l; PDBTitle: native structure of a family 35 carbohydrate binding module2 from clostridium thermocellum
25	c2rdyB_	Alignment	not modelled	12.2	17	PDB header: hydrolase Chain: B: PDB Molecule: bh0842 protein; PDBTitle: crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
26	d2g60h1	Alignment	not modelled	11.8	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
27	c1qysA_	Alignment	not modelled	11.2	20	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
28	c2k2dA_	Alignment	not modelled	10.4	12	PDB header: metal binding protein Chain: A: PDB Molecule: ring finger and chy zinc finger domain- PDBTitle: solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c PDB header: oxidoreductase

29	c4hx6D	Alignment	not modelled	10.2	16	Chain: D: PDB Molecule: oxidoreductase; PDBTitle: streptomyces globisporus c-1027 nadh:fad oxidoreductase sgce6
30	d1pz5b1	Alignment	not modelled	10.2	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
31	c2qsiB	Alignment	not modelled	10.2	0	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative hydrogenase expression/formation protein hupg; PDBTitle: crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodospseudomonas palustris cga009
32	c5y4uA	Alignment	not modelled	10.2	10	PDB header: oxidoreductase Chain: A: PDB Molecule: monothiol glutaredoxin-3; PDBTitle: crystal structure of grx domain of grx3 from saccharomyces cerevisiae
33	c4p9lA	Alignment	not modelled	9.7	12	PDB header: transport protein Chain: A: PDB Molecule: ryanodine receptor 2; PDBTitle: crystal structure of mouse ryanodine receptor 2 spry2 domain (1080-2 1253) disease mutant a1107m
34	c6f8sD	Alignment	not modelled	9.1	23	PDB header: toxin Chain: D: PDB Molecule: putative killer protein; PDBTitle: toxin-antitoxin complex grata
35	c5hx2E	Alignment	not modelled	9.0	18	PDB header: viral protein Chain: E: PDB Molecule: baseplate wedge protein gp6; PDBTitle: in vitro assembled star-shaped hubless t4 baseplate
36	c2r0xA	Alignment	not modelled	8.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: possible flavin reductase; PDBTitle: crystal structure of a putative flavin reductase (ycdh, hs_1225) from haemophilus somnus 129pt at 1.06 a resolution
37	d2afja1	Alignment	not modelled	8.9	14	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: SPRY domain
38	c1dmlG	Alignment	not modelled	8.7	18	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 of 2 hsv pol
39	d1fo5a	Alignment	not modelled	8.7	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
40	c3pe9B	Alignment	not modelled	8.6	10	PDB header: unknown function Chain: B: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
41	c3igzB	Alignment	not modelled	8.6	33	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
42	c3adyA	Alignment	not modelled	8.5	25	PDB header: proton transport Chain: A: PDB Molecule: dotd; PDBTitle: crystal structure of dotd from legionella
43	d2jelh2	Alignment	not modelled	8.4	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
44	c3pftA	Alignment	not modelled	8.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase; PDBTitle: crystal structure of untagged c54a mutant flavin reductase (dszd) in2 complex with fmn from mycobacterium goodii
45	c2yyoA	Alignment	not modelled	8.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: spry domain-containing protein 3; PDBTitle: crystal structure of human spry domain
46	d2fnjb1	Alignment	not modelled	8.2	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
47	c3m4xA	Alignment	not modelled	8.2	10	PDB header: transferase Chain: A: PDB Molecule: no11/nop2/sun family protein; PDBTitle: structure of a ribosomal methyltransferase
48	d2rdea2	Alignment	not modelled	8.1	14	Fold: Split barrel-like Superfamily: PilZ domain-like Family: PilZ domain-associated domain
49	d1eaqa	Alignment	not modelled	7.9	18	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
50	d1wosa1	Alignment	not modelled	7.7	11	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
51	d1bcoa1	Alignment	not modelled	7.7	14	Fold: mu transposase, C-terminal domain Superfamily: mu transposase, C-terminal domain Family: mu transposase, C-terminal domain
52	c3c12A	Alignment	not modelled	7.6	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
53	c2ecrA	Alignment	not modelled	7.6	10	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase component (hpac) of 4-hydroxyphenylacetate PDBTitle: crystal structure of the ligand-free form of the flavin reductase2 component (hpac) of 4-hydroxyphenylacetate 3-monooxygenase
54	c5zc2B	Alignment	not modelled	7.5	25	PDB header: flavoprotein Chain: B: PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component;

						PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
55	d1l6za2	Alignment	not modelled	7.4	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
56	d1v5va1	Alignment	not modelled	7.4	13	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
57	c4f07A_	Alignment	not modelled	7.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: styrene monooxygenase component 2; PDBTitle: structure of the styrene monooxygenase flavin reductase (smob) from2 pseudomonas putida s12
58	d1cb8a2	Alignment	not modelled	7.3	11	Fold: Hyaluronate lyase-like, C-terminal domain Superfamily: Hyaluronate lyase-like, C-terminal domain Family: Hyaluronate lyase-like, C-terminal domain
59	d1igtb1	Alignment	not modelled	7.2	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
60	c2pcjB_	Alignment	not modelled	7.2	19	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein lold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
61	c3osvC_	Alignment	not modelled	7.1	14	PDB header: structural protein Chain: C: PDB Molecule: flagellar basal-body rod modification protein flgd; PDBTitle: the crytsal structure of flgd from p. aeruginosa
62	c4madA_	Alignment	not modelled	7.1	8	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of beta-galactosidase c (bgac) from bacillus2 circulans atcc 31382
63	c3pe9C_	Alignment	not modelled	7.1	14	PDB header: unknown function Chain: C: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
64	c3pe9A_	Alignment	not modelled	7.1	14	PDB header: unknown function Chain: A: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
65	c2jacA_	Alignment	not modelled	7.0	30	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin-1; PDBTitle: glutaredoxin grx1p c30s mutant from yeast
66	d1inva_	Alignment	not modelled	7.0	19	Fold: 6-bladed beta-propeller Superfamily: Sialidases Family: Sialidases (neuraminidases)
67	d1w7ab4	Alignment	not modelled	6.9	7	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
68	d2c9wb1	Alignment	not modelled	6.9	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
69	c2mrpA_	Alignment	not modelled	6.8	14	PDB header: ubiquitin-binding protein Chain: A: PDB Molecule: dna damage-inducible protein 1; PDBTitle: nmr solution structure of the ubiquitin like domain (ubl) of dna-2 damage-inducible 1 protein (ddi1)
70	d1r0wa_	Alignment	not modelled	6.8	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
71	c6ff43_	Alignment	not modelled	6.7	50	PDB header: splicing Chain: 3: PDB Molecule: bud13 homolog; PDBTitle: human bact spliceosome core structure
72	d1ljma_	Alignment	not modelled	6.5	18	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
73	c5oltA_	Alignment	not modelled	6.4	27	PDB header: transferase Chain: A: PDB Molecule: cellulose biosynthesis protein bcsg; PDBTitle: crystal structure of the extramembrane domain of the cellulose2 biosynthetic protein bcsg from salmonella typhimurium
74	c4qn3B_	Alignment	not modelled	6.4	21	PDB header: hydrolase Chain: B: PDB Molecule: neuraminidase; PDBTitle: crystal structure of neuraminidase n7
75	c3m6wA_	Alignment	not modelled	6.3	19	PDB header: transferase Chain: A: PDB Molecule: rrna methylase; PDBTitle: multi-site-specific 16s rna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
76	c1z47B_	Alignment	not modelled	6.2	28	PDB header: ligand binding protein Chain: B: PDB Molecule: putative abc-transporter atp-binding protein; PDBTitle: structure of the atpase subunit cysa of the putative sulfate atp-2 binding cassette (abc) transporter from alicyclobacillus3 acidocaldarius
77	c2l76A_	Alignment	not modelled	6.1	21	PDB header: transcription Chain: A: PDB Molecule: nfatc2-interacting protein; PDBTitle: solution nmr structure of human nfatc2ip ubiquitin-like domain,2 nfatc2ip_244_338, nesg target ht65a/ocsp target hs00387_244_338/sgc-3 toronto
78	d2f09a1	Alignment	not modelled	6.1	17	Fold: Streptavidin-like Superfamily: YdhA-like Family: YdhA-like
79	d1y71a1	Alignment	not modelled	6.0	31	Fold: SH3-like barrel Superfamily: Kinase-associated protein B-like Family: Kinase-associated protein B-like

80	c4l0zA_	Alignment	not modelled	5.9	18	PDB header: transcription/dna Chain: A: PDB Molecule: runt-related transcription factor 1; PDBTitle: crystal structure of runx1 and ets1 bound to tcr alpha promoter2 (crystal form 2)
81	d1wika_	Alignment	not modelled	5.9	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
82	c3k87B_	Alignment	not modelled	5.8	7	PDB header: oxidoreductase Chain: B: PDB Molecule: chlorophenol-4-monooxygenase component 1; PDBTitle: crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex
83	c4r03A_	Alignment	not modelled	5.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf3836 family protein (bdi_3222) from2 parabacteroides distasonis atcc 8503 at 1.50 a resolution
84	d1nldh2	Alignment	not modelled	5.7	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
85	c3c1sA_	Alignment	not modelled	5.7	30	PDB header: oxidoreductase Chain: A: PDB Molecule: glutaredoxin-1; PDBTitle: crystal structure of grx1 in glutathionylated form
86	d1vlya2	Alignment	not modelled	5.7	44	Fold: Folate-binding domain Superfamily: Folate-binding domain Family: Aminomethyltransferase folate-binding domain
87	c2qcckA_	Alignment	not modelled	5.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein; PDBTitle: crystal structure of flavin reductase domain protein (yp_831077.1)2 from arthrobacter sp. fb24 at 1.90 a resolution
88	d1wiaa_	Alignment	not modelled	5.7	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
89	d1qgva_	Alignment	not modelled	5.6	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: spliceosomal protein U5-15Kd
90	d1i8lc_	Alignment	not modelled	5.6	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
91	d1c5cl2	Alignment	not modelled	5.6	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: immunoglobulin Family: C1 set domains (antibody constant domain-like)
92	c3ahpA_	Alignment	not modelled	5.5	20	PDB header: electron transport Chain: A: PDB Molecule: cuta1; PDBTitle: crystal structure of stable protein, cuta1, from a psychrotrophic2 bacterium shewanella sp. sib1
93	c1xbsA_	Alignment	not modelled	5.5	18	PDB header: transcription, cell cycle Chain: A: PDB Molecule: dim1-like protein; PDBTitle: crystal structure of human dim2: a dim1-like protein
94	c4c87A_	Alignment	not modelled	5.3	13	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: esterase lpest1 from lactobacillus plantarum wcf51
95	c3qmxA_	Alignment	not modelled	5.3	20	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin a; PDBTitle: x-ray crystal structure of synechocystis sp. pcc 6803 glutaredoxin a
96	c4l82D_	Alignment	not modelled	5.1	8	PDB header: oxidoreductase Chain: D: PDB Molecule: rifea.00250.a; PDBTitle: structure of a putative oxidoreductase from rickettsia felis
97	c2mixA_	Alignment	not modelled	5.1	30	PDB header: toxin Chain: A: PDB Molecule: venom peptide toxin; PDBTitle: structure of a novel venom peptide toxin from sample limited terebrid2 marine snail
98	d1uy4a_	Alignment	not modelled	5.1	15	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 6 carbohydrate binding module, CBM6
99	c5d3mA_	Alignment	not modelled	5.1	16	PDB header: transport protein Chain: A: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state