


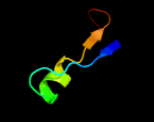
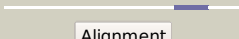
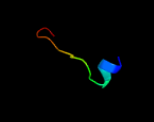
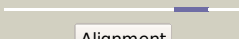
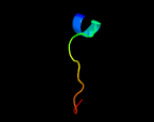
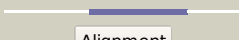

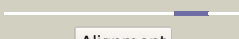
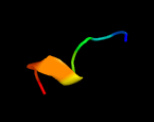

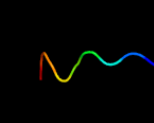

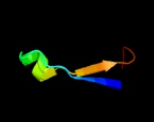

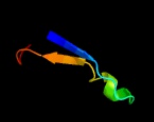




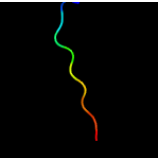
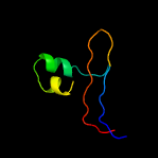


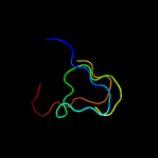
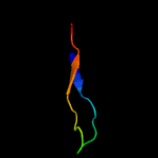

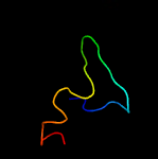
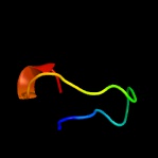


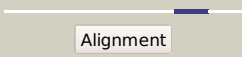
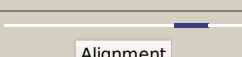
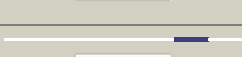
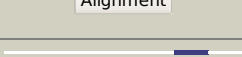
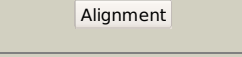

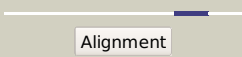
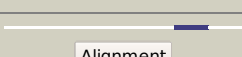
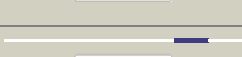
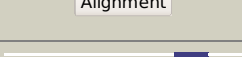
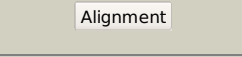

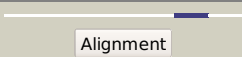
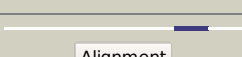
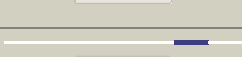
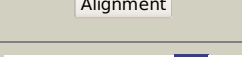
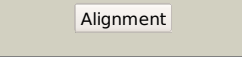

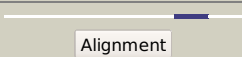
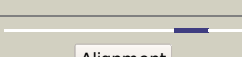
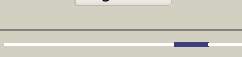
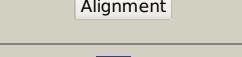
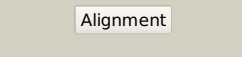

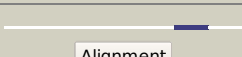

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1228_(lpqX)_1370926_1371483
Date	Wed Jul 31 22:05:31 BST 2019
Unique Job ID	b18742260bd5a44d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1d0rA_	 Alignment		20.1	78	PDB header: hormone/growth factor Chain: A: PDB Molecule: glucagon-like peptide-1-(7-36)-amide; PDBTitle: solution structure of glucagon-like peptide-1-(7-36)-amide in 2 trifluoroethanol/water
2	d2a1ba1	 Alignment		17.1	30	Fold: Ferredoxin-like Superfamily: CcmK-like Family: CcmK-like
3	d1p65a_	 Alignment		16.8	53	Fold: Nucleocapsid protein dimerization domain Superfamily: Nucleocapsid protein dimerization domain Family: Arterivirus nucleocapsid protein
4	c1p65A_	 Alignment		16.8	53	PDB header: viral protein Chain: A: PDB Molecule: nucleocapsid protein; PDBTitle: crystal structure of the nucleocapsid protein of porcine reproductive 2 and respiratory syndrome virus (prrsv)
5	c6qe7A_	 Alignment		15.8	19	PDB header: sugar binding protein Chain: A: PDB Molecule: anti-sigma factor domain-containing protein; PDBTitle: anti-sigma factor domain-containing protein
6	c2l64A_	 Alignment		15.4	44	PDB header: hormone Chain: A: PDB Molecule: glucagon-like peptide 2; PDBTitle: nmr solution structure of glp-2 in dhpc micelles
7	c1lrjA_	 Alignment		14.7	67	PDB header: hormone/growth factor Chain: A: PDB Molecule: exendin-4; PDBTitle: solution structure of exendin-4 in 30-vol% trifluoroethanol
8	c4qivA_	 Alignment		14.5	39	PDB header: structural protein Chain: A: PDB Molecule: bacterial microcompartments family protein; PDBTitle: crystal structure of hexameric microcompart ment shell protein from 2 aeromonas hydrophila
9	c3ngkA_	 Alignment		13.8	30	PDB header: unknown function Chain: A: PDB Molecule: propanediol utilization protein pdua; PDBTitle: pdua from salmonella enterica typhimurium
10	c5waiC_	 Alignment		13.8	26	PDB header: transcription Chain: C: PDB Molecule: zinc finger protein aebp2; PDBTitle: crystal structure of a suz12-rbbp4-jarid2-aebp2 heterotetrameric 2 complex
11	d1e8ob_	 Alignment		13.3	50	Fold: Signal recognition particle alu RNA binding heterodimer, SRP9/14 Superfamily: Signal recognition particle alu RNA binding heterodimer, SRP9/14 Family: Signal recognition particle alu RNA binding heterodimer, SRP9/14

12	c6qk7C_	Alignment		12.7	50	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
13	c4gr5B_	Alignment		12.3	30	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
14	d1kzyc2	Alignment		12.3	25	Fold: BRCT domain Superfamily: BRCT domain Family: 53BP1
15	c5djbD_	Alignment		11.6	35	PDB header: structural protein Chain: D: PDB Molecule: microcompartments protein; PDBTitle: structure of the haliangium ochraceum bmc-h shell protein
16	c6n2cA_	Alignment		11.3	39	PDB header: cell adhesion Chain: A: PDB Molecule: tapirin; PDBTitle: the crystal structure of caldicellulosiruptor hydrothermalis tapirin2 c-terminal domain
17	d3deoa1	Alignment		11.1	38	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
18	c6cfzA_	Alignment		11.0	36	PDB header: nuclear protein Chain: A: PDB Molecule: ask1; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
19	c2qx0A_	Alignment		10.8	28	PDB header: transferase Chain: A: PDB Molecule: 7,8-dihydro-6-hydroxymethylpterin- PDBTitle: crystal structure of yersinia pestis hppk (ternary complex)
20	c5o9zN_	Alignment		10.6	24	PDB header: splicing Chain: N: PDB Molecule: zinc finger matrin-type protein 2; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
21	c3j38h_	Alignment	not modelled	10.2	47	PDB header: ribosome Chain: H: PDB Molecule: 40s ribosomal protein s7; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
22	c3t5cA_	Alignment	not modelled	9.4	40	PDB header: ligase Chain: A: PDB Molecule: probable chain-fatty-acid-coa ligase fadd13; PDBTitle: crystal structure of n-terminal domain of fac13 from mycobacterium2 tuberculosis in different space group c2
23	c3i6pF_	Alignment	not modelled	9.3	22	PDB header: structural protein Chain: F: PDB Molecule: ethanolamine utilization protein eutm; PDBTitle: ethanolamine utilization microcompartment shell subunit, eutm
24	d1t6aa_	Alignment	not modelled	9.0	44	Fold: TBP-like Superfamily: Rbstp2229 protein Family: Rbstp2229 protein
25	c5hpnA_	Alignment	not modelled	8.8	30	PDB header: de novo protein Chain: A: PDB Molecule: permuted pdua; PDBTitle: a circularly permuted pdua forming an icosahedral cage
26	c1t5qA_	Alignment	not modelled	8.8	88	PDB header: hormone/growth factor Chain: A: PDB Molecule: gastric inhibitory polypeptide; PDBTitle: solution structure of gip(1-30)amide in tfe/water
27	c6n3cM_	Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: M: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
28	c6n3cO_	Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: Q: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a

29	c6n3cO	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: O: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
30	c6n3cG	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: G: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
31	c6n3cA	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: A: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
32	c6n3cS	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: S: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
33	c6n3cK	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: K: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
34	c6n3cC	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: C: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
35	c6n3cE	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: E: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
36	c6n3cI	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: I: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
37	c6n3cH	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: H: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
38	c6n3cP	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: P: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
39	c6n3cB	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: B: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
40	c6n3cR	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: R: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
41	c6n3cN	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: N: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
42	c6n3cJ	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: J: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
43	c6n3cL	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: L: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
44	c6n3cD	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: D: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
45	c6n3cT	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: T: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
46	c6n3cF	 Alignment	not modelled	8.7	38	PDB header: dna binding protein, protein fibril Chain: F: PDB Molecule: tar dna-binding protein 43; PDBTitle: segb, conformation of tdp-43 low complexity domain segment a
47	c3rrrM	 Alignment	not modelled	8.4	53	PDB header: viral protein Chain: M: PDB Molecule: fusion glycoprotein f0; PDBTitle: structure of the rsv f protein in the post-fusion conformation
48	c3qs3I	 Alignment	not modelled	8.3	31	PDB header: cell adhesion Chain: I: PDB Molecule: fimbrillin matb homolog, ecpd; PDBTitle: crystal structure of the biofilm forming subunit of the e. coli common2 pilus: donor strand complemented (dsc) ecpa
49	c2nawA	 Alignment	not modelled	8.2	54	PDB header: toxin Chain: A: PDB Molecule: exendin-4, alpha/kappa-conotoxin pl14a chimera; PDBTitle: nmr solution structure of exendin-4/conotoxin chimera (ex-4[1-2 27]/pl14a)
50	c3I52A	 Alignment	not modelled	8.2	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of putative orotidine 5'-phosphate decarboxylase2 from streptomyces avermitilis ma-4680
51	c6nerS	 Alignment	not modelled	8.0	36	PDB header: structural protein Chain: S: PDB Molecule: bmc-h tandem fusion protein; PDBTitle: synthetic haliangium ochraceum bmc shell
52	c2ekjA	 Alignment	not modelled	7.9	26	PDB header: signaling protein Chain: A: PDB Molecule: collagen alpha-1(xx) chain; PDBTitle: solution structures of the fn3 domain of human collagen2 alpha-1(xx) chain
53	d1xcra1	 Alignment	not modelled	7.7	33	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: PTD012-like
54	c5vcpB	 Alignment	not modelled	7.7	38	PDB header: transferase Chain: B: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n

54	c3vcsb_	Alignment	not modelled	7.7	30	PDBTitle: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound acceptor Fold: Ferredoxin-like Superfamily: 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
55	d1cbka_	Alignment	not modelled	7.6	24	PDB header: photosynthesis Chain: D: PDB Molecule: photosystem i p700 chlorophyll a apoprotein a2; PDBTitle: crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
56	c6fosD_	Alignment	not modelled	7.4	33	PDB header: transferase Chain: A: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
57	c3rxya_	Alignment	not modelled	7.3	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nif3 protein; PDBTitle: crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
58	c5vcmA_	Alignment	not modelled	7.1	33	PDB header: transferase Chain: A: PDB Molecule: alpha-1,6-mannosyl-glycoprotein 2-beta-n-acetylglucosaminyltransferase2 with bound udp and manganese
59	d1h7za_	Alignment	not modelled	7.0	40	Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Adenovirus fiber protein "knob" domain
60	c2obuA_	Alignment	not modelled	7.0	88	PDB header: hormone/growth factor Chain: A: PDB Molecule: gastric inhibitory polypeptide; PDBTitle: solution structure of gip in tfe/water
61	c5dihE_	Alignment	not modelled	7.0	27	PDB header: structural protein Chain: E: PDB Molecule: microcompartments protein; PDBTitle: structure of haliangium ochraceum bmc-t ho-5812
62	d2cuia1	Alignment	not modelled	7.0	30	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
63	c2cg8B_	Alignment	not modelled	6.8	21	PDB header: lyase/transferase Chain: B: PDB Molecule: dihydroneopterin aldolase 6-hydroxymethyl-7,8- PDBTitle: the bifunctional dihydroneopterin aldolase 6-hydroxymethyl-2 7,8-dihydropterin synthase from streptococcus pneumoniae
64	c2navA_	Alignment	not modelled	6.8	86	PDB header: toxin Chain: A: PDB Molecule: exendin-4, alpha/kappa-conotoxin pl14a chimera; PDBTitle: nmr solution structure of ex-4[1-16]/pl14a
65	d2a10a1	Alignment	not modelled	6.7	17	Fold: Ferredoxin-like Superfamily: CcmK-like Family: CcmK-like
66	c2dleA_	Alignment	not modelled	6.6	22	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase eta; PDBTitle: solution structure of the fourth fn3 domain of human2 receptor-type tyrosine-protein phosphatase eta
67	d1wxqa2	Alignment	not modelled	6.4	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
68	d2ewha1	Alignment	not modelled	6.4	22	Fold: Ferredoxin-like Superfamily: CcmK-like Family: CcmK-like
69	c1bh0A_	Alignment	not modelled	6.3	71	PDB header: synthetic hormone Chain: A: PDB Molecule: glucagon; PDBTitle: structure of a glucagon analog
70	c3b83B_	Alignment	not modelled	6.3	26	PDB header: unknown function Chain: B: PDB Molecule: ten-d3; PDBTitle: computer-based redesign of a beta sandwich protein suggests that2 extensive negative design is not required for de novo beta sheet3 design.
71	d2pu9b1	Alignment	not modelled	6.2	29	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
72	c5i38A_	Alignment	not modelled	6.2	30	PDB header: structural protein Chain: A: PDB Molecule: msm0272 - rmm microcompartment shell protein; PDBTitle: the structure of the hexagonal shell protein msm0272 from the rmm2 microcompartment
73	d1f9ya_	Alignment	not modelled	6.1	28	Fold: Ferredoxin-like Superfamily: 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK Family: 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK
74	d1fnha3	Alignment	not modelled	6.1	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
75	c5vitC_	Alignment	not modelled	5.9	26	PDB header: transferase Chain: C: PDB Molecule: mdcc; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with malonate
76	c4qo6A_	Alignment	not modelled	5.9	31	PDB header: structural protein Chain: A: PDB Molecule: adenylate cyclase-like protein; PDBTitle: structural studies of cdsd, a structural protein of the type iii2 secretion system (tss) of chlamydia trachomatis
77	d1inla_	Alignment	not modelled	5.8	35	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Spermidine synthase
78	d1fnfa3	Alignment	not modelled	5.8	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
						Fold: Immunoglobulin-like beta-sandwich

79	d1qr4a2	Alignment	not modelled	5.7	13	Superfamily: Fibronectin type III Family: Fibronectin type III
80	d2b3ta1	Alignment	not modelled	5.7	56	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N5-glutamine methyltransferase, HemK
81	d1x5ja1	Alignment	not modelled	5.6	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
82	c3hlzA_	Alignment	not modelled	5.2	55	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bt_1490; PDBTitle: crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution