
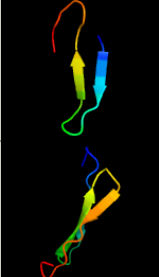
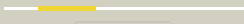
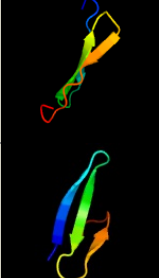





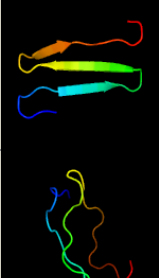

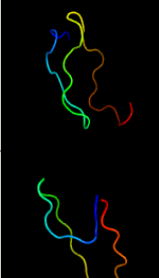

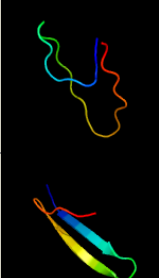

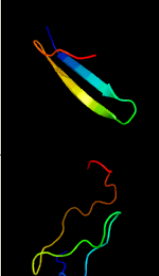

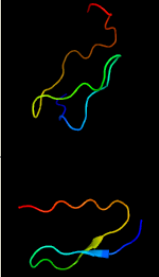

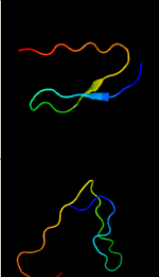




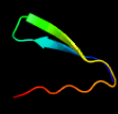

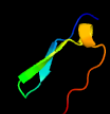
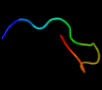
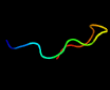
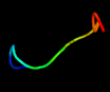



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0397 (-)_475819_476187
Date	Tue Jul 23 14:50:47 BST 2019
Unique Job ID	8b6bba937338538c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ysca1	 Alignment		78.2	38	Fold: WW domain-like Superfamily: WW domain Family: WW domain
2	c4by2C_	 Alignment		72.2	19	PDB header: structural protein Chain: C: PDB Molecule: anastral spindle 2, sas 4; PDBTitle: sas-4 (dcpap) tcp domain in complex with a proline rich motif of ana22 (dstil) of drosophila melanogaster
3	d2ho2a1	 Alignment		71.9	37	Fold: WW domain-like Superfamily: WW domain Family: WW domain
4	c4bxB_	 Alignment		71.6	20	PDB header: cell cycle Chain: B: PDB Molecule: cpap; PDBTitle: structure of the wild-type tcp10 domain of danio rerio cpap in complex2 with a peptide of danio rerio stil
5	c4ld3A_	 Alignment		71.0	16	PDB header: structural protein, protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structural analysis of the microcephaly protein cpap g-box domain2 suggests a role in centriole elongation.
6	d2bcoa1	 Alignment		51.2	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like
7	d1o5ua_	 Alignment		40.2	31	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Hypothetical protein TM1112
8	c3bcwB_	 Alignment		40.1	19	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
9	d2g9da1	 Alignment		39.0	19	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like
10	c3es4B_	 Alignment		38.4	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein duf861 with a rmlc-like cupin fold; PDBTitle: crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
11	d1yw6a1	 Alignment		36.3	22	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like

12	d2e45a1	Alignment		35.9	38	Fold: WW domain-like Superfamily: WW domain Family: WW domain
13	d2gprra	Alignment		35.6	13	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
14	c3myxA	Alignment		31.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pspto_0244; PDBTitle: crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
15	d1glaf	Alignment		31.0	20	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
16	d2pyta1	Alignment		30.9	16	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: EutQ-like
17	d2f3ga	Alignment		30.1	20	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
18	d1gprra	Alignment		29.6	13	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
19	d2sn3a	Alignment		29.2	42	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
20	c2k8iA	Alignment		29.0	21	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure of e.coli slyd
21	d2b3ca	Alignment	not modelled	28.2	47	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
22	d1iuqa	Alignment	not modelled	24.3	22	Fold: Glycerol-3-phosphate (1)-acyltransferase Superfamily: Glycerol-3-phosphate (1)-acyltransferase Family: Glycerol-3-phosphate (1)-acyltransferase
23	c2vldA	Alignment	not modelled	22.2	23	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease nucs; PDBTitle: crystal structure of a repair endonuclease from pyrococcus abyssi
24	c2kfwA	Alignment	not modelled	21.5	21	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase PDBTitle: solution structure of full-length slyd from e.coli
25	c2jrtA	Alignment	not modelled	21.5	47	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
26	c3lwcA	Alignment	not modelled	21.4	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of structural genomics, unknown function2 (yp_766765.1) from rhizobium leguminosarum bv. viciae 3841 at 1.40 a3 resolution
27	c5gkeB	Alignment	not modelled	21.2	23	PDB header: hydrolase/dna Chain: B: PDB Molecule: endonuclease endoms; PDBTitle: structure of endoms-dsdna1 complex
28	d2oa4a1	Alignment	not modelled	20.7	37	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: SPO1678-like

29	c5j67C_	Alignment	not modelled	20.7	31	PDB header: membrane protein Chain: C: PDB Molecule: astrotactin-2; PDBTitle: structure of astrotactin-2, a conserved vertebrate-specific and2 perforin-like membrane protein involved in neuronal development
30	c2mx4A_	Alignment	not modelled	18.8	42	PDB header: translation,protein binding Chain: A: PDB Molecule: eukaryotic translation initiation factor 4e-binding protein PDBTitle: nmr structure of phosphorylated 4e-bp2
31	c5ljyA_	Alignment	not modelled	16.3	37	PDB header: viral protein Chain: A: PDB Molecule: envelopment polyprotein; PDBTitle: structure of hantavirus envelope glycoprotein gc in complex with scfv2 a5
32	d1jnua_	Alignment	not modelled	15.7	29	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
33	d1mswd_	Alignment	not modelled	15.5	33	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: T7 RNA polymerase
34	c3ue6C_	Alignment	not modelled	11.9	20	PDB header: signaling protein Chain: C: PDB Molecule: aureochrome1; PDBTitle: the dark structure of the blue-light photoreceptor aureochrome1 lov
35	c2qsdB_	Alignment	not modelled	11.9	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of a protein il1583 from idiomarina loihiensis
36	d1bywa_	Alignment	not modelled	11.7	14	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
37	c3t50B_	Alignment	not modelled	11.4	27	PDB header: transferase Chain: B: PDB Molecule: blue-light-activated histidine kinase; PDBTitle: x-ray structure of the lov domain from the lov-hk sensory protein from2 brucella abortus (dark state).
38	c2ljmA_	Alignment	not modelled	11.3	33	PDB header: toxin Chain: A: PDB Molecule: beta-mammal toxin css2; PDBTitle: solution structure of cssii
39	d2r4qa1	Alignment	not modelled	10.9	33	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
40	c4axoA_	Alignment	not modelled	10.5	20	PDB header: structural protein Chain: A: PDB Molecule: ethanolamine utilization protein; PDBTitle: structure of the clostridium difficile eutq protein
41	c4mxeA_	Alignment	not modelled	10.1	36	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase esco1; PDBTitle: human esco1 (eco1/ctf7 ortholog), acetyltransferase domain in complex2 with acetyl-coa
42	c4m0hB_	Alignment	not modelled	9.9	44	PDB header: signaling protein Chain: B: PDB Molecule: conserved hypothetical protein, putative anti-sigma factor; PDBTitle: crystal structure of a putative anti-sigma factor (bdi_1681) from2 parabacteroides distasonis atcc 8503 at 2.50 a resolution
43	c3o10C_	Alignment	not modelled	8.7	32	PDB header: de novo protein Chain: C: PDB Molecule: de novo designed monomer trefoil-fold sub-domain which PDBTitle: crystal structure of monofoil-4p homo-trimer: de novo designed monomer2 trefoil-fold sub-domain which forms homo-trimer assembly
44	c3i38E_	Alignment	not modelled	8.5	20	PDB header: chaperone Chain: E: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
45	c3i38C_	Alignment	not modelled	8.5	20	PDB header: chaperone Chain: C: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
46	c2mz8A_	Alignment	not modelled	8.4	100	PDB header: transcription regulator Chain: A: PDB Molecule: sigma factor-binding protein crl; PDBTitle: solution nmr structure of salmonella typhimurium transcriptional2 regulator protein crl
47	d1n9la_	Alignment	not modelled	8.3	20	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
48	c2je2A_	Alignment	not modelled	8.3	57	PDB header: metal binding protein Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cytochrome p460 from nitrosomonas europaea - probable2 nonphysiological oxidized form
49	c6amgA_	Alignment	not modelled	8.3	71	PDB header: metal binding protein Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cyt p460 of nitrosomonas sp. al212
50	c4afhE_	Alignment	not modelled	8.0	45	PDB header: acetylcholine-binding protein Chain: E: PDB Molecule: achbp; PDBTitle: capitella teleta achbp in complex with lobeline
51	d1jzaa_	Alignment	not modelled	7.9	42	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
52	c6hihB_	Alignment	not modelled	7.8	57	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: cytochrome c prime beta from methylococcus capsulatus (bath)
53	c3jqoC_	Alignment	not modelled	7.7	29	PDB header: transport protein Chain: C: PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system PDB header: transport protein

54	c3jqoF_	Alignment	not modelled	7.7	29	Chain: F; PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
55	c3jqoj_	Alignment	not modelled	7.7	29	PDB header: transport protein Chain: J; PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
56	c3jqog_	Alignment	not modelled	7.7	29	PDB header: transport protein Chain: G; PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
57	c3jqol_	Alignment	not modelled	7.7	29	PDB header: transport protein Chain: I; PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
58	c3jqom_	Alignment	not modelled	7.7	29	PDB header: transport protein Chain: M; PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
59	c3jqoX_	Alignment	not modelled	7.6	29	PDB header: transport protein Chain: X; PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
60	c3jqoO_	Alignment	not modelled	7.6	29	PDB header: transport protein Chain: O; PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
61	c3jqoa_	Alignment	not modelled	7.6	29	PDB header: transport protein Chain: A; PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
62	c3jqod_	Alignment	not modelled	7.6	29	PDB header: transport protein Chain: D; PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
63	c5u75A_	Alignment	not modelled	7.6	14	PDB header: toxin Chain: A; PDB Molecule: enterotoxin-like toxin x; PDBTitle: the structure of staphylococcal enterotoxin-like x (selx), a unique2 superantigen
64	c3spaA_	Alignment	not modelled	7.5	38	PDB header: transferase Chain: A; PDB Molecule: dna-directed rna polymerase, mitochondrial; PDBTitle: crystal structure of human mitochondrial rna polymerase
65	c3jqoR_	Alignment	not modelled	7.5	29	PDB header: transport protein Chain: R; PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
66	c3jqop_	Alignment	not modelled	7.5	29	PDB header: transport protein Chain: P; PDB Molecule: traf protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
67	c3jqoU_	Alignment	not modelled	7.4	29	PDB header: transport protein Chain: U; PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
68	c3zbia_	Alignment	not modelled	7.4	29	PDB header: cell adhesion Chain: A; PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
69	c3zbiU_	Alignment	not modelled	7.4	29	PDB header: cell adhesion Chain: U; PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
70	c3zbiP_	Alignment	not modelled	7.4	29	PDB header: cell adhesion Chain: P; PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
71	c3zbid_	Alignment	not modelled	7.4	29	PDB header: cell adhesion Chain: D; PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
72	c3zbiO_	Alignment	not modelled	7.4	29	PDB header: cell adhesion Chain: O; PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
73	c3zbig_	Alignment	not modelled	7.4	29	PDB header: cell adhesion Chain: G; PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
74	c3zbiC_	Alignment	not modelled	7.4	29	PDB header: cell adhesion Chain: C; PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
75	c3jqoL_	Alignment	not modelled	7.4	29	PDB header: transport protein Chain: L; PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
76	c3zbiX_	Alignment	not modelled	7.4	29	PDB header: cell adhesion Chain: X; PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
77	c3zbiM_	Alignment	not modelled	7.4	29	PDB header: cell adhesion Chain: M; PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex

							digested with3 elastase
78	c3zbiF_	Alignment	not modelled	7.4	29		PDB header: cell adhesion Chain: F: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
79	c3zbiR_	Alignment	not modelled	7.4	29		PDB header: cell adhesion Chain: R: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
80	c3zbiL_	Alignment	not modelled	7.4	29		PDB header: cell adhesion Chain: I: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
81	c3zbiU_	Alignment	not modelled	7.4	29		PDB header: cell adhesion Chain: L: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
82	c3zbij_	Alignment	not modelled	7.4	29		PDB header: cell adhesion Chain: J: PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
83	c3cnrA_	Alignment	not modelled	7.3	60		PDB header: unknown function Chain: A: PDB Molecule: type iv fimbriae assembly protein; PDBTitle: crystal structure of pilz (xac1133) from xanthomonas axonopodis pv2 citri
84	c3p45F_	Alignment	not modelled	6.9	27		PDB header: hydrolase Chain: F: PDB Molecule: caspase-6; PDBTitle: crystal structure of apo-caspase-6 at physiological ph
85	c3rpiA_	Alignment	not modelled	6.9	100		PDB header: transcription regulator Chain: A: PDB Molecule: curlin genes transcriptional regulator; PDBTitle: structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.
86	c4c24A_	Alignment	not modelled	6.8	9		PDB header: lyase Chain: A: PDB Molecule: l-fucose phosphate aldolase; PDBTitle: l-fucose 1-phosphate aldolase
87	c4hoiB_	Alignment	not modelled	6.5	14		PDB header: transport protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily h member 1; PDBTitle: crystal structure of pas domain from the mouse eag1 potassium channel
88	c6hiuA_	Alignment	not modelled	6.4	43		PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p460; PDBTitle: cytochrome p460 from methylococcus capsulatus (bath)
89	c2bj0D_	Alignment	not modelled	6.3	36		PDB header: glycoprotein Chain: D: PDB Molecule: acetylcholine-binding protein; PDBTitle: crystal structure of achbp from bulinus truncatus reveals2 the conserved structural scaffold and sites of variation3 in nicotinic acetylcholine receptors
90	c2vn4A_	Alignment	not modelled	6.1	35		PDB header: hydrolase Chain: A: PDB Molecule: glucoamylase; PDBTitle: glycoside hydrolase family 15 glucoamylase from hypocrea jecorina
91	c2i45C_	Alignment	not modelled	6.0	12		PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein nmb1881 from neisseria meningitidis
92	c2ofqB_	Alignment	not modelled	5.9	33		PDB header: protein transport/protein transport Chain: B: PDB Molecule: tran; PDBTitle: nmr solution structure of a complex between the virb9/virb72 interaction domains of the pkm101 type iv secretion system
93	c2ixsB_	Alignment	not modelled	5.9	31		PDB header: hydrolase Chain: B: PDB Molecule: sdaI restriction endonuclease; PDBTitle: structure of sdaI restriction endonuclease
94	c6ergA_	Alignment	not modelled	5.9	38		PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase, mitochondrial; PDBTitle: structure of the human mitochondrial transcription initiation complex2 at the hsp promoter
95	c2byqC_	Alignment	not modelled	5.9	17		PDB header: receptor Chain: C: PDB Molecule: soluble acetylcholine receptor; PDBTitle: crystal structure of aplysia californica achbp in complex with2 epibatidine
96	c5cd6C_	Alignment	not modelled	5.8	13		PDB header: unknown function Chain: C: PDB Molecule: tpr-domain containing protein; PDBTitle: crystal structure of a tpr-domain containing protein (bdi_1685) from2 parabacteroides distasonis atcc 8503 at 2.26 a resolution
97	d2d40a1	Alignment	not modelled	5.8	18		Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Gentisate 1,2-dioxygenase-like
98	c4dt4A_	Alignment	not modelled	5.7	28		PDB header: isomerase Chain: A: PDB Molecule: fkbp-type 16 kda peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of the ppiase-chaperone slpa with the chaperone2 binding site occupied by the linker of the purification tag
99	d2afaa1	Alignment	not modelled	5.7	23		Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: N-acylglucosamine (NAG) epimerase