
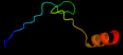

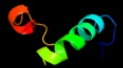

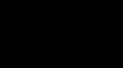



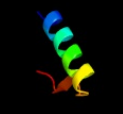

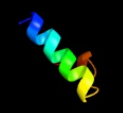


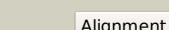

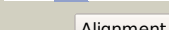
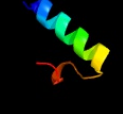
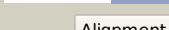
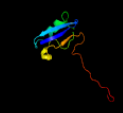
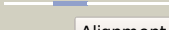
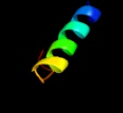




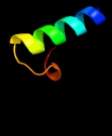






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3033_(-)_3393391_3393939
Date	Thu Aug 8 16:20:20 BST 2019
Unique Job ID	f9de84416ea68b09

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qooA_	 Alignment		56.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of hot-dog-like taci_0573 protein from2 thermanaerovibrio acidaminovorans
2	c2kwIA_	 Alignment		46.1	13	PDB header: lipid binding protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of acyl carrier protein from borrelia burgdorferi
3	d2q78a1	 Alignment		37.4	22	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
4	c3kuvB_	 Alignment		35.9	15	PDB header: hydrolase Chain: B: PDB Molecule: fluoroacetyl coenzyme a thioesterase; PDBTitle: structural basis of the activity and substrate specificity of the2 fluoroacetyl-coa thioesterase flk - t42s mutant in complex with3 acetate.
5	d1otfa_	 Alignment		33.1	25	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
6	c2op8A_	 Alignment		29.8	17	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
7	c3ry0A_	 Alignment		28.9	25	PDB header: isomerase Chain: A: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of tomn, a 4-oxalocrotonate tautomerase homologue in2 tomaymycin biosynthetic pathway
8	c4fazB_	 Alignment		28.4	33	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate isomerase protein; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
9	c4fdxB_	 Alignment		27.8	21	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonase tautomerase isozyme; PDBTitle: kinetic and structural characterization of the 4-oxalocrotonate2 tautomerase isozymes from methylbium petroleiphilum
10	c3pgeA_	 Alignment		26.5	13	PDB header: dna binding protein Chain: A: PDB Molecule: sumo-modified proliferating cell nuclear antigen; PDBTitle: structure of sumoylated pcna
11	c2ormA_	 Alignment		26.2	13	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.

12	d2imha1	Alignment		25.0	22	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: SPO2555-like
13	c3m20A_	Alignment		24.9	21	PDB header: isomerase Chain: A: PDB Molecule: 4-oxalocrotonate tautomerase, putative; PDBTitle: crystal structure of dmp1 from archaeoglobus fulgidus determined to 2.37 angstroms resolution
14	c3abfB_	Alignment		23.6	29	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
15	d1bjpa_	Alignment		23.5	17	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
16	c3mb2G_	Alignment		22.5	33	PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexameric 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the 4 tautomerase superfamily
17	c2k5dA_	Alignment		22.1	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sag0934; PDBTitle: solution nmr structure of sag0934 from streptococcus2 agalactiae. northeast structural genomics target sar32[1-3 108].
18	d1mwwa_	Alignment		21.1	13	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
19	d1wm3a_	Alignment		19.1	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
20	c4lkbA_	Alignment		18.2	22	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein alr4568/putative 4-oxalocrotonate PDBTitle: crystal structure of a putative 4-oxalocrotonate tautomerase from2 nostoc sp. pcc 7120
21	d1gyxa_	Alignment	not modelled	17.8	29	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
22	c2x4kB_	Alignment	not modelled	17.5	8	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
23	d1x9la_	Alignment	not modelled	16.9	17	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: DR1885-like metal-binding protein Family: DR1885-like metal-binding protein
24	d2cwza1	Alignment	not modelled	16.9	15	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: TTHA0967-like
25	d2io3b1	Alignment	not modelled	14.1	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
26	d2aala1	Alignment	not modelled	13.9	22	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MSAD-like
27	c2dnwA_	Alignment	not modelled	13.5	10	PDB header: transport protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of rsg1 ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
28	d2af8a_	Alignment	not modelled	12.6	6	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
						PDB header: phosphopantetheine binding protein

29	c4hkgB	Alignment	not modelled	12.3	17	Chain: B: PDB Molecule: phosphopantetheine attachment site family protein; PDBTitle: crystal structure of free-standing peptidyl carrier protein from2 uncharacterized acinetobacter baumannii secondary metabolic pathway
30	d1mfbl2	Alignment	not modelled	11.6	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
31	c5mtwD	Alignment	not modelled	11.4	17	PDB header: chaperone Chain: D: PDB Molecule: secb-like chaperone rv1957; PDBTitle: mycobacterium tuberculosis rv1957 secb-like chaperone in complex with2 a chad peptide from rv1956 higa1 antitoxin
32	d3by5a1	Alignment	not modelled	10.3	14	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
33	c3by5A	Alignment	not modelled	10.3	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: cobalamin biosynthesis protein; PDBTitle: crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
34	d1h3ua1	Alignment	not modelled	10.2	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
35	c5uifC	Alignment	not modelled	9.4	22	PDB header: hydrolase Chain: C: PDB Molecule: ps01740; PDBTitle: crystal structure of native ps01740
36	c4jvuA	Alignment	not modelled	9.3	25	PDB header: protein binding Chain: A: PDB Molecule: ig mu chain c region membrane-bound form; PDBTitle: igm c2-domain from mouse
37	c2mvaA	Alignment	not modelled	9.3	46	PDB header: toxin Chain: A: PDB Molecule: rhtx toxin; PDBTitle: solution structure of the toxin, rhtx
38	c5xqmA	Alignment	not modelled	9.2	15	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin-related modifier; PDBTitle: nmr solution structure of smo1, sumo homologue in caenorhabditis2 elegans
39	d1hc9a	Alignment	not modelled	9.2	40	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
40	c5tdqA	Alignment	not modelled	9.1	12	PDB header: transport protein Chain: A: PDB Molecule: golgi resident protein gcp60; PDBTitle: crystal structure of the gold domain of acbd3
41	d1rzf2	Alignment	not modelled	8.8	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
42	d1mr6a	Alignment	not modelled	8.8	42	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
43	c4ca3A	Alignment	not modelled	8.5	18	PDB header: ribosomal protein Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: solution structure of streptomyces virginiae vira acp5b
44	d1q46a1	Alignment	not modelled	8.1	50	Fold: SAM domain-like Superfamily: eIF2alpha middle domain-like Family: eIF2alpha middle domain-like
45	c4rudA	Alignment	not modelled	8.0	29	PDB header: toxin Chain: A: PDB Molecule: three-finger toxin 3b; PDBTitle: crystal structure of a three finger toxin
46	c4rudB	Alignment	not modelled	8.0	29	PDB header: toxin Chain: B: PDB Molecule: three-finger toxin 3b; PDBTitle: crystal structure of a three finger toxin
47	d1pg7w2	Alignment	not modelled	7.9	5	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
48	d1a5ra	Alignment	not modelled	7.8	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
49	d1l6xa1	Alignment	not modelled	7.8	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
50	c5jp1B	Alignment	not modelled	7.4	23	PDB header: hydrolase Chain: B: PDB Molecule: small ubiquitin-related modifier; PDBTitle: structure of xanthomonas campestris effector protein xopd bound to2 tomato sumo
51	c2lo1A	Alignment	not modelled	7.4	7	PDB header: lipid transport Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: nmr structure of an acyl-carrier protein from rickettsia prowazekii,2 seattle structural genomics center for infectious disease (ssgcid)
52	d3eeqa1	Alignment	not modelled	7.1	23	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
53	d1fp5a2	Alignment	not modelled	7.0	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C1 set domains (antibody constant domain-like)
54	c3nbxX	Alignment	not modelled	6.9	17	PDB header: hydrolase Chain: X: PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
55	c2fvfA	Alignment	not modelled	6.8	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: acyl carrier protein;

						PDBTitle: structure of 10:0-acp (protein with docked fatty acid)
56	c3n4dF_	Alignment	not modelled	6.7	26	PDB header: hydrolase Chain: F: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
57	c2l76A_	Alignment	not modelled	6.7	20	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
58	c4q9bA_	Alignment	not modelled	6.5	20	PDB header: immune system Chain: A: PDB Molecule: novel antigen receptor; PDBTitle: ignar antibody domain c2
59	c3d2uE_	Alignment	not modelled	6.4	12	PDB header: immune system Chain: E: PDB Molecule: ul18 protein; PDBTitle: structure of ul18, a peptide-binding viral mhc mimic, bound to a host2 inhibitory receptor
60	d1dx5i2	Alignment	not modelled	6.3	25	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
61	c6c4qA_	Alignment	not modelled	6.1	16	PDB header: transport protein Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: 1.16 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1-100) of polyketide synthase pks13 from3 mycobacterium tuberculosis
62	d2ozna1	Alignment	not modelled	6.1	19	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III
63	d2dyja1	Alignment	not modelled	6.1	23	Fold: Alpha-lytic protease prodomain-like Superfamily: Ribosome-binding factor A, RbfA Family: Ribosome-binding factor A, RbfA
64	d1kl9a1	Alignment	not modelled	6.1	43	Fold: SAM domain-like Superfamily: eIF2alpha middle domain-like Family: eIF2alpha middle domain-like
65	d2oz4a1	Alignment	not modelled	6.1	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: immunoglobulin Family: C2 set domains
66	c4ba8A_	Alignment	not modelled	5.9	12	PDB header: immune system Chain: A: PDB Molecule: sig mu chain c region secreted form; PDBTitle: high resolution nmr structure of the c mu3 domain from igm
67	c4b1yM_	Alignment	not modelled	5.9	25	PDB header: structural protein Chain: M: PDB Molecule: phosphatase and actin regulator 1; PDBTitle: structure of the phactr1 rpe1-3 bound to g-actin
68	d1o0va1	Alignment	not modelled	5.7	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: immunoglobulin Family: C1 set domains (antibody constant domain-like)
69	c3woaA_	Alignment	not modelled	5.6	13	PDB header: dna binding protein, sugar binding prote Chain: A: PDB Molecule: repressor protein ci, maltose-binding periplasmic protein; PDBTitle: crystal structure of lambda repressor (1-45) fused with maltose-2 binding protein
70	c2mk1C_	Alignment	not modelled	5.6	16	PDB header: immune system Chain: C: PDB Molecule: novel antigen receptor; PDBTitle: solution structure of the fourth constant immunoglobulin domain of2 nurse shark ignar
71	c3dj9A_	Alignment	not modelled	5.6	23	PDB header: immune system Chain: A: PDB Molecule: ig gamma-1 chain c region; PDBTitle: crystal structure of an isolated, unglycosylated antibody ch2 domain
72	c1jnhC_	Alignment	not modelled	5.5	12	PDB header: immune system Chain: C: PDB Molecule: monoclonal anti-estradiol 10g6d6 fab light chain; PDBTitle: crystal structure of fab-estradiol complexes
73	c3cgnA_	Alignment	not modelled	5.4	24	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of thermophilic slyd
74	d1fnna2	Alignment	not modelled	5.4	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
75	d2w6ka1	Alignment	not modelled	5.4	9	Fold: CobE/GbiG C-terminal domain-like Superfamily: CobE/GbiG C-terminal domain-like Family: CobE/GbiG C-terminal domain-like
76	d1kbaa_	Alignment	not modelled	5.4	25	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
77	d1deeb2	Alignment	not modelled	5.3	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: immunoglobulin Family: C1 set domains (antibody constant domain-like)
78	c4q97B_	Alignment	not modelled	5.3	15	PDB header: immune system Chain: B: PDB Molecule: novel antigen receptor; PDBTitle: ignar antibody domain c1
79	d1whqa_	Alignment	not modelled	5.2	15	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
80	d1txba_	Alignment	not modelled	5.1	40	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
81	c4nfuB_	Alignment	not modelled	5.1	21	PDB header: signaling protein Chain: B: PDB Molecule: senescence-associated carboxylesterase 101;

					PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
82	dlntna_	Alignment	not modelled	5.1	30 Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins