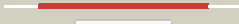



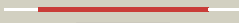









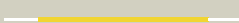




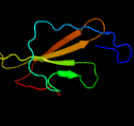

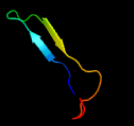
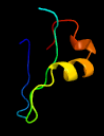

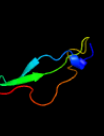
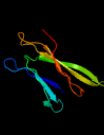
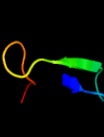
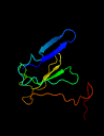
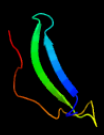

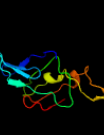


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0913c_(-)_1017221_1018729
Date	Fri Jul 26 01:50:50 BST 2019
Unique Job ID	eae2b1cd7168ceff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5j54A_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A; PDB Molecule: carotenoid oxygenase; PDBTitle: the structure and mechanism of nov1, a resveratrol-cleaving2 dioxygenase
2	c5v2dA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A; PDB Molecule: dioxygenase; PDBTitle: crystal structure of pseudomonas brassicacearum lignostilbene2 dioxygenase
3	c5u90A_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A; PDB Molecule: carotenoid oxygenase 1; PDBTitle: crystal structure of co-cao1 in complex with resveratrol
4	c3npeA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A; PDB Molecule: 9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; PDBTitle: structure of vp14 in complex with oxygen
5	c2biwC_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: C; PDB Molecule: apocarotenoid-cleaving oxygenase; PDBTitle: crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme
6	c3fsnA_	 Alignment		100.0	18	PDB header: isomerase Chain: A; PDB Molecule: retinal pigment epithelium-specific 65 kda protein; PDBTitle: crystal structure of rpe65 at 2.14 angstrom resolution
7	c6rteB_	 Alignment		83.4	16	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
8	c4cvcA_	 Alignment		77.4	10	PDB header: oxidoreductase Chain: A; PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of quinone-dependent alcohol dehydrogenase from2 pseudogluconobacter saccharoketogenes with zinc in the active site
9	c1nnoA_	 Alignment		57.4	14	PDB header: oxidoreductase Chain: A; PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa
10	d1mdah_	 Alignment		39.4	11	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
11	c5dilA_	 Alignment		31.2	32	PDB header: rna-binding protein, viral protein Chain: A; PDB Molecule: non-structural protein 1; PDBTitle: crystal structure of the effector domain of the ns1 protein from2 influenza virus b

12	d2hu7a1	Alignment		26.9	15	Fold: 7-bladed beta-propeller Superfamily: Peptidase/esterase 'gauge' domain Family: Acylamino-acid-releasing enzyme, N-terminal donain
13	c3qc2A_	Alignment		26.4	28	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase; PDBTitle: crystal structure of a glycosyl hydrolase (bacova_03624) from2 bacteroides ovatus at 2.30 a resolution
14	c5aycA_	Alignment		25.2	21	PDB header: transferase Chain: A: PDB Molecule: 4-o-beta-d-mannosyl-d-glucose phosphorylase; PDBTitle: crystal structure of ruminococcus albus 4-o-beta-d-mannosyl-d-glucose2 phosphorylase (ramp1) in complexes with sulfate and 4-o-beta-d-3 mannosyl-d-glucose
15	c5f30B_	Alignment		21.4	18	PDB header: oxidoreductase Chain: B: PDB Molecule: thiocyanate dehydrogenase; PDBTitle: thiocyanate dehydrogenase from thioalkalivibrio paradoxus
16	d1zaka2	Alignment		21.4	32	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
17	c5c2wD_	Alignment		21.2	13	PDB header: oxidoreductase Chain: D: PDB Molecule: hydrazine synthase alpha subunit; PDBTitle: kuenenia stuttgartiensis hydrazine synthase pressurized with 20 bar2 xenon
18	c3watA_	Alignment		17.2	17	PDB header: transferase Chain: A: PDB Molecule: 4-o-beta-d-mannosyl-d-glucose phosphorylase; PDBTitle: crystal structure of 4-o-beta-d-mannosyl-d-glucose phosphorylase mgp2 complexed with man+glc
19	c3metB_	Alignment		15.8	18	PDB header: transcription Chain: B: PDB Molecule: saga-associated factor 29 homolog; PDBTitle: crystal structure of sgf29 in complex with h3k4me2
20	c3elqA_	Alignment		14.5	11	PDB header: transferase Chain: A: PDB Molecule: arylsulfate sulfotransferase; PDBTitle: crystal structure of a bacterial arylsulfate2 sulfotransferase
21	d1jmx_b_	Alignment	not modelled	14.4	18	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
22	c4ozuA_	Alignment	not modelled	12.8	14	PDB header: structural protein Chain: A: PDB Molecule: coronin; PDBTitle: crystal structure of wd40 domain from toxoplasma gondii coronin
23	c6cmkB_	Alignment	not modelled	12.8	17	PDB header: metal binding protein Chain: B: PDB Molecule: aztd protein; PDBTitle: crystal structure of citrobacter koseri aztd
24	d1m7ja2	Alignment	not modelled	12.6	35	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: D-aminoacylase
25	c2vb6A_	Alignment	not modelled	12.0	20	PDB header: motor protein Chain: A: PDB Molecule: myosin vi; PDBTitle: myosin vi (md-insert2-cam, delta insert1) post-rigor state (2 crystal form 2)
26	d1mspa_	Alignment	not modelled	11.5	36	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
27	c1gq1B_	Alignment	not modelled	11.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome cd1 nitrite reductase; PDBTitle: cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
28	c3knuD_	Alignment	not modelled	11.3	25	PDB header: transferase Chain: D: PDB Molecule: trna (guanine-n(1)-)-methyltransferase; PDBTitle: crystal structure of trna (guanine-n1)-methyltransferase from2 anaplasma phagocytophilum
						PDB header: oxidoreductase

29	c5i5iA_	Alignment	not modelled	11.2	8	Chain: A: PDB Molecule: nitrous-oxide reductase; PDBTitle: shewanella denitrificans nitrous oxide reductase, app form
30	d1jofa_	Alignment	not modelled	11.2	8	Fold: 7-bladed beta-propeller Superfamily: 3-carboxy-cis,cis-muocoante lactonizing enzyme Family: 3-carboxy-cis,cis-muocoante lactonizing enzyme
31	c1kv9A_	Alignment	not modelled	10.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: type ii quinohemoprotein alcohol dehydrogenase; PDBTitle: structure at 1.9 a resolution of a quinohemoprotein alcohol2 dehydrogenase from pseudomonas putida hk5
32	d1k91a_	Alignment	not modelled	10.5	13	Fold: P-domain of calnexin/calreticulin Superfamily: P-domain of calnexin/calreticulin Family: P-domain of calnexin/calreticulin
33	c5c2mA_	Alignment	not modelled	10.2	35	PDB header: structural protein Chain: A: PDB Molecule: predicted protein; PDBTitle: the de novo evolutionary emergence of a symmetrical protein is shaped2 by folding constraints
34	d2oz4a1	Alignment	not modelled	9.7	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C2 set domains
35	c5uqdA_	Alignment	not modelled	9.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dummy: shorter than wild-type; PDBTitle: dpy-21 in complex with fe(ii) and alpha-ketoglutarate
36	d2cu6a1	Alignment	not modelled	8.6	24	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
37	d2noha2	Alignment	not modelled	7.8	8	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: DNA repair glycosylase, N-terminal domain
38	c2bkiA_	Alignment	not modelled	7.7	20	PDB header: motor protein/metal-binding protein Chain: A: PDB Molecule: unconventional myosin; PDBTitle: myosin vi nucleotide-free (mdinsert2-iq) crystal structure
39	c6cslA_	Alignment	not modelled	7.6	25	PDB header: metal binding protein Chain: A: PDB Molecule: histidine triad protein d; PDBTitle: pneumococcal phtd protein 269-339 fragment with bound zn(ii)
40	c1bb9A_	Alignment	not modelled	7.6	18	PDB header: transferase Chain: A: PDB Molecule: amphiphysin 2; PDBTitle: crystal structure of the sh3 domain from rat amphiphysin 2
41	d1bb9a_	Alignment	not modelled	7.6	18	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
42	c3e7hA_	Alignment	not modelled	7.4	53	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: the crystal structure of the beta subunit of the dna-directed rna2 polymerase from vibrio cholerae o1 biovar eltor
43	c1mv3A_	Alignment	not modelled	7.2	16	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: myc box dependent interacting protein 1; PDBTitle: nmr structure of the tumor suppressor bin1: alternative2 splicing in melanoma and interaction with c-myc
44	d2fe0a1	Alignment	not modelled	7.2	12	Fold: Smp-1-like Superfamily: Smp-1-like Family: Smp-1-like
45	d1xpna_	Alignment	not modelled	7.1	12	Fold: Prealbumin-like Superfamily: Hypothetical protein PA1324 Family: Hypothetical protein PA1324
46	d1njha_	Alignment	not modelled	7.1	26	Fold: Hypothetical protein YojF Superfamily: Hypothetical protein YojF Family: Hypothetical protein YojF
47	c6cfwl_	Alignment	not modelled	7.0	15	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
48	c2fu4B_	Alignment	not modelled	6.9	27	PDB header: dna binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
49	c5oxzB_	Alignment	not modelled	6.8	22	PDB header: splicing Chain: B: PDB Molecule: neq528; PDBTitle: crystal structure of neqn/neqc complex from nanoarchaeum equitans at2 1.2a
50	c4c95C_	Alignment	not modelled	6.8	11	PDB header: dna replication Chain: C: PDB Molecule: dna polymerase alpha-binding protein; PDBTitle: crystal structure of the carboxy-terminal domain of yeast2 ctf4 bound to sld5
51	c2bkhA_	Alignment	not modelled	6.7	20	PDB header: motor protein/metal-binding protein Chain: A: PDB Molecule: unconventional myosin; PDBTitle: myosin vi nucleotide-free (mdinsert2) crystal structure
52	c6g72A_	Alignment	not modelled	6.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-ubiquinone oxidoreductase chain 3; PDBTitle: mouse mitochondrial complex i in the deactive state
53	d2cs7a1	Alignment	not modelled	6.5	25	Fold: IL8-like Superfamily: PhtA domain-like Family: PhtA domain-like
54	c2ghsA_	Alignment	not modelled	6.4	13	PDB header: calcium-binding protein Chain: A: PDB Molecule: agr_c_1268p; PDBTitle: crystal structure of a calcium-binding protein, regucalcin2 (agr_c_1268) from agrobacterium tumefaciens str. c58 at 1.55 a3 resolution
55	d2ghsa1	Alignment	not modelled	6.4	13	Fold: 6-bladed beta-propeller Superfamily: Calcium-dependent phosphotriesterase

						Family: SGL-like
56	c5tbyA_	Alignment	not modelled	6.3	3	PDB header: contractile protein Chain: A: PDB Molecule: myosin-7; PDBTitle: human beta cardiac heavy meromyosin interacting-heads motif obtained2 by homology modeling (using swiss-model) of human sequence from3 aphonopelma homology model (pdb-3jbh), rigidly fitted to human beta-4 cardiac negatively stained thick filament 3d-reconstruction (emd-5 2240)
57	d1bf2a1	Alignment	not modelled	6.2	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
58	c4fc9B_	Alignment	not modelled	6.0	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: structure of the c-terminal domain of the type iii effector xcv32202 (xopl)
59	c3q54A_	Alignment	not modelled	6.0	16	PDB header: lipid binding protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfgl; PDBTitle: crystal structure of escherichia coli bamb
60	d1xv2a_	Alignment	not modelled	5.9	19	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: Alpha-acetolactate decarboxylase-like
61	c4wndB_	Alignment	not modelled	5.9	13	PDB header: signaling protein/protein binding Chain: B: PDB Molecule: ferm and pdz domain-containing protein 4; PDBTitle: crystal structure of the tpr domain of lgn in complex with2 frmpd4/preso1 at 1.5 angstrom resolution
62	c5v1dA_	Alignment	not modelled	5.9	14	PDB header: transferase/substrate Chain: A: PDB Molecule: eif2ak3 protein; PDBTitle: complex structure of the bovine perk luminal domain and its substrate2 peptide
63	c1yr2A_	Alignment	not modelled	5.8	11	PDB header: hydrolase Chain: A: PDB Molecule: prolyl oligopeptidase; PDBTitle: structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
64	c4c8hC_	Alignment	not modelled	5.8	12	PDB header: dna replication Chain: C: PDB Molecule: ctf4; PDBTitle: crystal structure of the c-terminal region of yeast ctf4,2 selenomethionine protein.
65	c5yhoA_	Alignment	not modelled	5.7	28	PDB header: metal binding protein Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterobacter2 cloacae
66	c4wneB_	Alignment	not modelled	5.7	13	PDB header: signaling protein/protein binding Chain: B: PDB Molecule: peptide from ferm and pdz domain-containing protein 4; PDBTitle: crystal structure of the tpr domain of lgn in complex with2 frmpd4/preso1 at 2.0 angstrom resolution
67	c3mbrX_	Alignment	not modelled	5.6	13	PDB header: transferase Chain: X: PDB Molecule: glutamine cyclotransferase; PDBTitle: crystal structure of the glutamyl cyclase from xanthomonas2 campestris
68	d1lmia_	Alignment	not modelled	5.4	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Antigen MPT63/MPB63 (immunoprotective extracellular protein) Family: Antigen MPT63/MPB63 (immunoprotective extracellular protein)
69	c3grdA_	Alignment	not modelled	5.4	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized ntf2-superfamily protein; PDBTitle: crystal structure of ntf2-superfamily protein with unknown function2 (np_977240.1) from bacillus cereus atcc 10987 at 1.25 a resolution
70	c4mveB_	Alignment	not modelled	5.3	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of tcur_1030 protein from thermomonospora curvata
71	c5gvbA_	Alignment	not modelled	5.2	10	PDB header: replication, peptide binding protein Chain: A: PDB Molecule: wd repeat and hmg-box dna-binding protein 1; PDBTitle: sepb domain of human and-1
72	c3mjjD_	Alignment	not modelled	5.2	16	PDB header: hydrolase Chain: D: PDB Molecule: predicted acetamidase/formamidase; PDBTitle: crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
73	d1kv9a2	Alignment	not modelled	5.2	9	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
74	c2kyyA_	Alignment	not modelled	5.1	20	PDB header: hydrolase Chain: A: PDB Molecule: possible atp-dependent dna helicase recg-related protein; PDBTitle: solution nmr structure of the n-terminal domain of putative atp-2 dependent dna helicase recg-related protein from nitrosomonas3 europaea, northeast structural genomics consortium target ner70a
75	c6dk4A_	Alignment	not modelled	5.1	15	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni peroxide stress regulator
76	d1dq3a4	Alignment	not modelled	5.0	18	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
77	c5nsaA_	Alignment	not modelled	5.0	30	PDB header: transport protein Chain: A: PDB Molecule: transcobalamin-2; PDBTitle: beta domain of human transcobalamin bound to co-beta-[2-(2,4-2 difluorophenyl)ethyl]nicobalamin