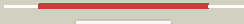










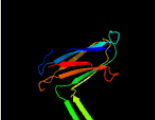















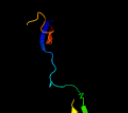


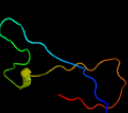


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0669c_(-)_767687_769600
Date	Fri Jul 26 01:50:23 BST 2019
Unique Job ID	dd8a7b0c86c70c96

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4wgb	 Alignment		100.0	35	PDB header: hydrolase Chain: B: PDB Molecule: neutral ceramidase; PDBTitle: crystal structure of human neutral ceramidase with zn-bound phosphate
2	c2zxcA	 Alignment		100.0	42	PDB header: hydrolase Chain: A: PDB Molecule: neutral ceramidase; PDBTitle: ceramidase complexed with c2
3	c2p9rA	 Alignment		96.9	25	PDB header: signaling protein Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: human alpha2-macroglobulin is composed of multiple domains,2 as predicted by homology with complement component c3
4	c4a5wA	 Alignment		94.6	17	PDB header: immune system Chain: A: PDB Molecule: complement c5; PDBTitle: crystal structure of c5b6
5	c2pn5A	 Alignment		94.5	11	PDB header: immune system Chain: A: PDB Molecule: thioester-containing protein i; PDBTitle: crystal structure of tep1r
6	c4fxgA	 Alignment		94.4	18	PDB header: immune system Chain: A: PDB Molecule: complement c4 beta chain; PDBTitle: complement c4 in complex with masp-2
7	c3cu7A	 Alignment		93.0	16	PDB header: immune system Chain: A: PDB Molecule: complement c5; PDBTitle: human complement component 5
8	c2b39B	 Alignment		91.9	17	PDB header: immune system Chain: B: PDB Molecule: c3; PDBTitle: structure of mammalian c3 with an intact thioester at 3a resolution
9	c3pvmB	 Alignment		88.9	16	PDB header: immune system Chain: B: PDB Molecule: cobra venom factor; PDBTitle: structure of complement c5 in complex with cvf
10	c4acqA	 Alignment		88.8	22	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
11	c6i2xB	 Alignment		88.2	16	PDB header: immune system Chain: B: PDB Molecule: cobra venom factor; PDBTitle: structure of complement c5 in complex with small molecule inhibitor2 and cvf

12	c2qkiA	Alignment		88.0	15	PDB header: immune system/hydrolase inhibitor Chain: A: PDB Molecule: complement c3; PDBTitle: human c3c in complex with the inhibitor compstatin
13	c4eisA	Alignment		87.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: polysaccharide monooxygenase-3; PDBTitle: structural basis for substrate targeting and catalysis by fungal2 polysaccharide monooxygenases (pmo-3)
14	d1vja1	Alignment		85.9	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
15	c4acqC	Alignment		85.4	22	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
16	c3hrzA	Alignment		85.3	16	PDB header: immune system Chain: A: PDB Molecule: cobra venom factor; PDBTitle: cobra venom factor (cvf) in complex with human factor b
17	c3lkwA	Alignment		83.0	26	PDB header: viral protein,hydrolase Chain: A: PDB Molecule: fusion protein of nonstructural protein 2b and PDBTitle: crystal structure of dengue virus 1 ns2b/ns3 protease active site2 mutant
18	c5o2xA	Alignment		78.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: glycoside hydrolase family 61; PDBTitle: extended catalytic domain of h. jecorina lpmo9a a.k.a eg4
19	c4eirB	Alignment		76.9	23	PDB header: oxidoreductase Chain: B: PDB Molecule: polysaccharide monooxygenase-2; PDBTitle: structural basis for substrate targeting and catalysis by fungal2 polysaccharide monooxygenases (pmo-2)
20	c3ejaB	Alignment		70.0	25	PDB header: unknown function Chain: B: PDB Molecule: protein gh61e; PDBTitle: magnesium-bound glycoside hydrolase 61 isoform e from thielavia2 terrestris
21	c2vy9A	Alignment	not modelled	66.9	4	PDB header: gene regulation Chain: A: PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub
22	c4maiA	Alignment	not modelled	66.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aa11 lytic polysaccharide monooxygenase; PDBTitle: structure of aspergillus oryzae aa11 lytic polysaccharide2 monooxygenase with cu(i)
23	c5fohA	Alignment	not modelled	65.3	23	PDB header: oxidoreductase Chain: A: PDB Molecule: polysaccharide monooxygenase; PDBTitle: crystal structure of the catalytic domain of nclpmo9a
24	c5nltD	Alignment	not modelled	65.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: cvaa9a; PDBTitle: cvaa9a
25	d1ndsA2	Alignment	not modelled	62.0	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
26	c4rtdA	Alignment	not modelled	60.7	14	PDB header: lipid binding protein Chain: A: PDB Molecule: uncharacterized lipoprotein yfhm; PDBTitle: escherichia coli alpha-2-macroglobulin activated by porcine elastase
27	c1l9mB	Alignment	not modelled	60.7	14	PDB header: transferase Chain: B: PDB Molecule: protein-glutamine glutamyltransferase e3; PDBTitle: three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
28	c4d7uB	Alignment	not modelled	60.5	28	PDB header: oxidoreductase Chain: B: PDB Molecule: endoglucanase ii; PDBTitle: the structure of the catalytic domain of nclpmo9c from

						the filamentous2 fungus neurospora crassa
29	d1ex0a1	Alignment	not modelled	58.7	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
30	c2yetB	Alignment	not modelled	57.8	22	PDB header: hydrolase Chain: B: PDB Molecule: gh61 isozyme a; PDBTitle: thermoascus gh61 isozyme a
31	c5ufvE	Alignment	not modelled	57.5	29	PDB header: hydrolase/oxidoreductase Chain: E: PDB Molecule: glycoside hydrolase family 61 protein; PDBTitle: crystal structure of a cellulose-active polysaccharide monooxygenase2 from m. thermophila (mtpmo3*)
32	d1owwa	Alignment	not modelled	55.5	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
33	c5i0pB	Alignment	not modelled	52.9	14	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of a beta-lactamase domain protein from burkholderia2 ambifaria
34	d2q3za1	Alignment	not modelled	52.7	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Transglutaminase N-terminal domain
35	c2vtcB	Alignment	not modelled	51.2	25	PDB header: hydrolase Chain: B: PDB Molecule: cel61b; PDBTitle: the structure of a glycoside hydrolase family 61 member,2 cel61b from the hypocrea jecorina.
36	c3isyA	Alignment	not modelled	49.9	18	PDB header: protein binding Chain: A: PDB Molecule: intracellular proteinase inhibitor; PDBTitle: crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
37	c2zz8B	Alignment	not modelled	49.9	26	PDB header: unknown function Chain: B: PDB Molecule: lipl32 protein; PDBTitle: crystal structure of lipl32, the most abundant surface protein of 2 pathogenic leptospira spp
38	d1fnfa3	Alignment	not modelled	49.3	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
39	c5axhA	Alignment	not modelled	49.1	19	PDB header: hydrolase Chain: A: PDB Molecule: dextranase; PDBTitle: crystal structure of thermophilic dextranase from thermoanaerobacter2 pseudethanolicus, d312g mutant in complex with isomaltohexaase
40	d1v5ja	Alignment	not modelled	48.3	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
41	c3tesD	Alignment	not modelled	46.2	10	PDB header: de novo protein Chain: D: PDB Molecule: tencon; PDBTitle: crystal structure of tencon
42	d1azca	Alignment	not modelled	45.1	25	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
43	c5m0aA	Alignment	not modelled	43.4	22	PDB header: cell adhesion Chain: A: PDB Molecule: fibronectin; PDBTitle: solution structure of isolated 15th fibronectin iii domain from human2 fibronectin
44	c2z1dA	Alignment	not modelled	41.3	12	PDB header: metal binding protein Chain: A: PDB Molecule: hydrogenase expression/formation protein hypd; PDBTitle: crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
45	c2h45A	Alignment	not modelled	40.5	13	PDB header: cell adhesion, structural protein Chain: A: PDB Molecule: fibronectin; PDBTitle: solution structure of the second type iii domain of human2 fibronectin: ensemble of 25 structures
46	c4ax3A	Alignment	not modelled	40.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: copper-containing nitrite reductase; PDBTitle: structure of three-domain heme-cu nitrite reductase from ralstonia2 pickettii at 1.6 a resolution
47	c5a0zA	Alignment	not modelled	40.1	27	PDB header: sugar binding protein Chain: A: PDB Molecule: putative cellulosomal scaffoldin protein; PDBTitle: high resolution semet structure of the third cohesin from2 ruminococcus flavefaciens scaffoldin protein, scab
48	c3qhtD	Alignment	not modelled	39.2	18	PDB header: de novo protein Chain: D: PDB Molecule: monobody ysmb-1; PDBTitle: crystal structure of the monobody ysmb-1 bound to yeast sumo
49	c4m8rA	Alignment	not modelled	38.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf4784 family protein (baccac_01631) from2 bacteroides caccae atcc 43185 at 2.50 a resolution
50	c4u48A	Alignment	not modelled	37.7	11	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: putative inner membrane lipoprotein; PDBTitle: crystal structure of salmonella alpha-2-macroglobulin
51	c4dibF	Alignment	not modelled	37.0	19	PDB header: oxidoreductase Chain: F: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: the crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 bacillus anthracis str. Sterne
52	d1rkra	Alignment	not modelled	36.6	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
53	d2mfna2	Alignment	not modelled	36.4	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
						PDB header: signaling protein

54	c2ekjA_	Alignment	not modelled	36.3	9	Chain: A: PDB Molecule: collagen alpha-1(xx) chain; PDBTitle: solution structures of the fn3 domain of human collagen2 alpha-1(xx) chain
55	c4lsdF_	Alignment	not modelled	35.8	16	PDB header: hormone Chain: F: PDB Molecule: fibronectin type iii domain-containing protein 5; PDBTitle: myokine structure
56	d1ddwa_	Alignment	not modelled	35.7	31	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
57	c5nnsB_	Alignment	not modelled	35.5	25	PDB header: oxidoreductase Chain: B: PDB Molecule: glycosyl hydrolase family 61, 2 protein; PDBTitle: crystal structure of hilpmo9b
58	d1fnha3	Alignment	not modelled	34.8	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
59	c4hylB_	Alignment	not modelled	34.3	13	PDB header: transcription regulator Chain: B: PDB Molecule: stage ii sporulation protein; PDBTitle: the crystal structure of an anti-sigma-factor antagonist from2 haliangium ochraceum dsm 14365
60	d1j8ka_	Alignment	not modelled	34.2	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
61	c2dkmA_	Alignment	not modelled	33.9	9	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
62	d1h4xa_	Alignment	not modelled	33.8	14	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
63	c4zchA_	Alignment	not modelled	33.0	18	PDB header: cytokine Chain: A: PDB Molecule: tumor necrosis factor ligand superfamily member 13,tumor PDBTitle: single-chain human april-baff-baff heterotrimer
64	d1tdqa1	Alignment	not modelled	32.9	7	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
65	d1oe1a2	Alignment	not modelled	32.8	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
66	d1fnfa2	Alignment	not modelled	31.9	6	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
67	c5n5pA_	Alignment	not modelled	31.2	23	PDB header: protein binding Chain: A: PDB Molecule: putative cellulosomal scaffoldin protein; PDBTitle: crystal structure of ruminococcus flavefaciens' type iii complex2 containing the fifth cohesin from scaffoldin b and the dockerin from3 scaffoldin a
68	d3d48r2	Alignment	not modelled	31.0	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
69	d1v10a2	Alignment	not modelled	30.8	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
70	c3lb6D_	Alignment	not modelled	30.6	11	PDB header: signaling protein/signaling protein Chain: D: PDB Molecule: interleukin-13 receptor subunit alpha-2; PDBTitle: the structure of il-13 in complex with il-13ralpha2
71	c2qeaB_	Alignment	not modelled	30.5	25	PDB header: oxidoreductase Chain: B: PDB Molecule: putative general stress protein 26; PDBTitle: crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
72	c2ck2B_	Alignment	not modelled	30.3	18	PDB header: signaling protein Chain: B: PDB Molecule: human fibronectin; PDBTitle: structure of core-swapped mutant of fibronectin
73	d1vj1a1	Alignment	not modelled	30.3	23	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
74	d1f86a_	Alignment	not modelled	29.5	18	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
75	c2yolA_	Alignment	not modelled	28.8	24	PDB header: hydrolase Chain: A: PDB Molecule: serine protease subunit ns2b, serine protease ns3; PDBTitle: west nile virus ns2b-ns3 protease in complex with 3,4-2 dichlorophenylacetyl-lys-lys-gcma
76	d1vc1a_	Alignment	not modelled	28.6	6	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
77	c2h1xB_	Alignment	not modelled	27.8	18	PDB header: hydrolase Chain: B: PDB Molecule: 5-hydroxyisourate hydrolase (formerly known as PDBTitle: crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
78	d1ttaa_	Alignment	not modelled	27.6	20	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
79	c2zouB_	Alignment	not modelled	27.3	15	PDB header: cell adhesion Chain: B: PDB Molecule: spondin-1; PDBTitle: crystal structure of human f-spondin reeler domain (fragment 2)
						Fold: Immunoglobulin-like beta-sandwich

80	d1bpva_	Alignment	not modelled	27.1	22	Superfamily: Fibronectin type III Family: Fibronectin type III
81	d1w8oa1	Alignment	not modelled	26.2	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
82	c2myvA_	Alignment	not modelled	26.2	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of m. oryzae protein avr1-co39
83	c3uyoD_	Alignment	not modelled	25.6	20	PDB header: signaling protein/protein binding Chain: D: PDB Molecule: monobody sh13; PDBTitle: crystal structure of monobody sh13/abl1 sh2 domain complex
84	d1h54a2	Alignment	not modelled	25.4	27	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Glycosyltransferase family 36 N-terminal domain
85	c4b5qA_	Alignment	not modelled	24.9	15	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 61 protein d; PDBTitle: the lytic polysaccharide monooxygenase gh61d structure from the2 basidiomycota fungus phanerochaete chrysosporium
86	c3tcmB_	Alignment	not modelled	24.8	10	PDB header: transferase Chain: B: PDB Molecule: alanine aminotransferase 2; PDBTitle: crystal structure of alanine aminotransferase from hordeum vulgare
87	c2ocfD_	Alignment	not modelled	24.7	22	PDB header: hormone/growth factor Chain: D: PDB Molecule: fibronectin; PDBTitle: human estrogen receptor alpha ligand-binding domain in complex with2 estradiol and the e2#23 fn3 monobody
88	d2vkwA2	Alignment	not modelled	24.5	8	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
89	c3m9qA_	Alignment	not modelled	24.4	15	PDB header: dna binding protein Chain: A: PDB Molecule: protein male-specific lethal-3; PDBTitle: drosophila msl3 chromodomain
90	c3t5sA_	Alignment	not modelled	24.2	4	PDB header: immune system Chain: A: PDB Molecule: macrophage migration inhibitory factor; PDBTitle: structure of macrophage migration inhibitory factor from giardia2 lamblia
91	c1ttfA_	Alignment	not modelled	23.8	23	PDB header: glycoprotein Chain: A: PDB Molecule: fibronectin; PDBTitle: the three-dimensional structure of the tenth type iii module of2 fibronectin: an insight into rgd-mediated interactions
92	c1ttgA_	Alignment	not modelled	23.8	23	PDB header: glycoprotein Chain: A: PDB Molecule: fibronectin; PDBTitle: the three-dimensional structure of the tenth type iii module of2 fibronectin: an insight into rgd-mediated interactions
93	c2fp3A_	Alignment	not modelled	23.4	16	PDB header: hydrolysis/apoptosis Chain: A: PDB Molecule: caspase nc; PDBTitle: crystal structure of the drosophila initiator caspase dronc
94	c2e7hA_	Alignment	not modelled	23.1	16	PDB header: transferase, signaling protein Chain: A: PDB Molecule: ephrin type-b receptor 4; PDBTitle: solution structure of the second fn3 domain from human2 ephrin type-b receptor 4
95	d2fnba_	Alignment	not modelled	22.1	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
96	c3rzwA_	Alignment	not modelled	21.8	18	PDB header: protein binding Chain: A: PDB Molecule: monobody ysmb-9; PDBTitle: crystal structure of the monobody ysmb-9 bound to human sumo1
97	c2gysB_	Alignment	not modelled	21.1	11	PDB header: signaling protein, cytokine Chain: B: PDB Molecule: cytokine receptor common beta chain; PDBTitle: 2.7 a structure of the extracellular domains of the human beta common2 receptor involved in il-3, il-5, and gm-csf signalling
98	c2gfcC_	Alignment	not modelled	20.9	13	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: upf0204 protein ph0006; PDBTitle: structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
99	c1f13A_	Alignment	not modelled	20.9	11	PDB header: coagulation factor Chain: A: PDB Molecule: cellular coagulation factor xiii zymogen; PDBTitle: recombinant human cellular coagulation factor xiii
100	c3k2mD_	Alignment	not modelled	20.0	19	PDB header: signaling protein/protein binding Chain: D: PDB Molecule: monobody ha4; PDBTitle: crystal structure of monobody ha4/abl1 sh2 domain complex