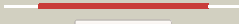



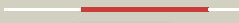


















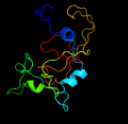


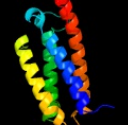






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3703c_(-)_4145792_4147069
Date	Fri Aug 9 18:20:39 BST 2019
Unique Job ID	65fefbe684c4581bf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4x8bA_	 Alignment		100.0	81	PDB header: oxidoreductase Chain: A; PDB Molecule: sulfoxide synthase egtb; PDBTitle: ergothioneine-biosynthetic sulfoxide synthase egtb, apo form
2	c6qkjA_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: egtb from chloracidobacterium thermophilum, a type ii sulfoxide2 synthase in complex with n,n,n-trimethyl-histidine
3	c5hhaB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B; PDB Molecule: pvdo; PDBTitle: structure of pvdo from pseudomonas aeruginosa
4	d1z70x1	 Alignment		100.0	28	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Sulfatase-modifying factor-like
5	c2q17C_	 Alignment		100.0	31	PDB header: unknown function Chain: C; PDB Molecule: formylglycine generating enzyme; PDBTitle: formylglycine generating enzyme from streptomyces coelicolor
6	c1y1fx_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: X; PDB Molecule: c-alpha-formylglycine-generating enzyme; PDBTitle: human formylglycine generating enzyme with cysteine sulfenic acid
7	c5nyyA_	 Alignment		100.0	29	PDB header: transferase Chain: A; PDB Molecule: non-specific serine/threonine protein kinase; PDBTitle: formylglycine generating enzyme from t. curvata in complex with cd(ii)
8	d1y4ja1	 Alignment		100.0	32	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Sulfatase-modifying factor-like
9	c2y3cA_	 Alignment		100.0	23	PDB header: unknown function Chain: A; PDB Molecule: treponema denticola variable protein 1; PDBTitle: treponema denticola variable protein 1
10	c5aohA_	 Alignment		100.0	24	PDB header: unknown function Chain: A; PDB Molecule: carf; PDBTitle: crystal structure of carf
11	d1yu0a2	 Alignment		100.0	16	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Mtd variable domain

12	d1yu3a2	Alignment		100.0	18	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Mtd variable domain
13	c2iouC	Alignment		100.0	18	PDB header: viral protein/membrane protein Chain: C: PDB Molecule: major tropism determinant p1; PDBTitle: major tropism determinant p1 (mtd-p1) variant complexed with2 bordetella brochiseptica virulence factor pertactin extracellular3 domain (prn-e).
14	c5vf4A	Alignment		100.0	23	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: thermus aquaticus variable protein (taqvp) from diversity-generating2 retroelements (dgr)
15	c5wk0A	Alignment		99.6	11	PDB header: unknown function Chain: A: PDB Molecule: damage-inducible protein dinb; PDBTitle: crystal structure of the bacillithiol transferase bsta from2 staphylococcus aureus.
16	c6iz2A	Alignment		99.2	17	PDB header: unknown function Chain: A: PDB Molecule: dinb/yfit family protein; PDBTitle: crystal structure of dinb/yfit protein dr0053 from d. radiodurans r1
17	d2ou6a1	Alignment		99.2	18	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
18	c3cexB	Alignment		99.1	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the conserved protein of locus ef_3021 from2 enterococcus faecalis
19	c3di5A	Alignment		98.8	18	PDB header: metal binding protein Chain: A: PDB Molecule: dinb-like protein; PDBTitle: crystal structure of a dinb-like protein (bce_4655) from bacillus2 cereus atcc 10987 at 2.01 a resolution
20	c3dkaA	Alignment		98.7	13	PDB header: unknown function Chain: A: PDB Molecule: dinb-like protein; PDBTitle: crystal structure of a dinb-like protein (yjoa, bsu12410) from2 bacillus subtilis at 2.30 a resolution
21	c3e4xB	Alignment	not modelled	98.6	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: apc36150; PDBTitle: crystal structure of putative metal-dependent hydrolases2 apc36150
22	c2qe9B	Alignment	not modelled	98.3	16	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein yiza; PDBTitle: crystal structure of a putative metal-dependent hydrolase (yiza,2 bsu10800) from bacillus subtilis at 1.90 a resolution
23	d2p1aa1	Alignment	not modelled	98.0	15	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
24	d1rxqa	Alignment	not modelled	97.7	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: YfiT-like putative metal-dependent hydrolases
25	d2hkva1	Alignment	not modelled	97.5	13	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
26	c2rd9C	Alignment	not modelled	97.4	10	PDB header: hydrolase Chain: C: PDB Molecule: bh0186 protein; PDBTitle: crystal structure of a putative yfit-like metal-dependent hydrolase2 (bh0186) from bacillus halodurans c-125 at 2.30 a resolution
27	c2qn1A	Alignment	not modelled	95.1	16	PDB header: signaling protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dna damage-inducible protein2 (chu_0679) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
28	c5cogB	Alignment	not modelled	82.0	13	PDB header: unknown function Chain: B: PDB Molecule: irc4; PDBTitle: crystal structure of yeast irc4

29	c1e5uL	Alignment	not modelled	80.3	32	PDB header: intimin Chain: I: PDB Molecule: intimin; PDBTitle: nmr representative structure of intimin-190 (int190) from 2 enteropathogenic e. coli
30	c5civA	Alignment	not modelled	72.5	22	PDB header: unknown function Chain: A: PDB Molecule: sibling bacteriocin; PDBTitle: sibling lethal factor precursor - dfsb
31	d2pf5a1	Alignment	not modelled	61.4	30	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Link domain
32	d1byfa	Alignment	not modelled	59.0	26	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
33	c1eslA	Alignment	not modelled	55.5	32	PDB header: cell adhesion protein Chain: A: PDB Molecule: human e-selectin; PDBTitle: insight into e-selectin(/slash)ligand interaction from the crystal2 structure and mutagenesis of the lec(/slash)egf domains
34	c3k7bA	Alignment	not modelled	55.0	19	PDB header: viral protein Chain: A: PDB Molecule: protein a33; PDBTitle: the structure of the poxvirus a33 protein reveals a dimer of unique c-2 type lectin-like domains.
35	c1fm5A	Alignment	not modelled	54.8	26	PDB header: immune system Chain: A: PDB Molecule: early activation antigen cd69; PDBTitle: crystal structure of human cd69
36	c5cofA	Alignment	not modelled	54.4	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterised protein q1r1x2 from escherichia2 coli uti89
37	d1uuha	Alignment	not modelled	54.1	30	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Link domain
38	d2msba	Alignment	not modelled	53.7	5	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
39	d1rjha	Alignment	not modelled	52.6	26	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
40	d2f22a1	Alignment	not modelled	52.2	16	Fold: DinB/YfiT-like putative metalloenzymes Superfamily: DinB/YfiT-like putative metalloenzymes Family: DinB-like
41	d1fifa1	Alignment	not modelled	51.3	5	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
42	d1g1ta1	Alignment	not modelled	51.3	32	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
43	d1rdl1	Alignment	not modelled	50.4	16	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
44	d1wk1a	Alignment	not modelled	49.5	35	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
45	d1g1sa1	Alignment	not modelled	49.4	16	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
46	c5xtwH	Alignment	not modelled	49.2	16	PDB header: sugar binding protein Chain: H: PDB Molecule: macrophage mannose receptor 1; PDBTitle: crystal structure of the cysr-ctld2 fragment of human mr at acidic ph
47	d1ja3a	Alignment	not modelled	47.4	5	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
48	d1hupa1	Alignment	not modelled	45.7	16	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
49	c2vuvA	Alignment	not modelled	45.6	21	PDB header: sugar-binding protein Chain: A: PDB Molecule: codakine; PDBTitle: crystal structure of codakine at 1.3a resolution
50	c2yqyB	Alignment	not modelled	45.4	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ttha0303; PDBTitle: crystal structure of tt2238, a four-helix bundle protein
51	c4qkhB	Alignment	not modelled	45.4	11	PDB header: immune system Chain: B: PDB Molecule: c-type lectin domain family 2 member d; PDBTitle: dimeric form of human llt1, a ligand for nkr-p1
52	c5ao6A	Alignment	not modelled	45.1	37	PDB header: endocytosis Chain: A: PDB Molecule: c-type mannose receptor 2; PDBTitle: endo180 d1-4, trigonal form
53	c1g1qD	Alignment	not modelled	44.4	16	PDB header: immune system, membrane protein Chain: D: PDB Molecule: p-selectin; PDBTitle: crystal structure of p-selectin lectin/egf domains
54	d3c8ja1	Alignment	not modelled	43.5	11	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
55	c6jliA	Alignment	not modelled	43.1	16	PDB header: immune system Chain: A: PDB Molecule: secretory phospholipase a2 receptor; PDBTitle: crystal structure of ctld7 domain of human pla2r
						PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein:

56	c4n6cB_	Alignment	not modelled	42.8	15	PDBTitle: crystal structure of the b1rzq2 protein from streptococcus pneumoniae.2 northeast structural genomics consortium (nesg) target spr36.
57	c1kwwC_	Alignment	not modelled	41.2	5	PDB header: immune system, sugar binding protein Chain: C: PDB Molecule: mannose-binding protein a; PDBTitle: rat mannose protein a complexed with a-me-fuc.
58	d1f00i3	Alignment	not modelled	40.8	32	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Invasin/intimin cell-adhesion fragment, C-terminal domain
59	c3rs1A_	Alignment	not modelled	40.5	21	PDB header: immune system Chain: A: PDB Molecule: c-type lectin domain family 2 member i; PDBTitle: mouse c-type lectin-related protein clrg
60	d1e87a_	Alignment	not modelled	39.8	26	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
61	c4c16B_	Alignment	not modelled	39.0	32	PDB header: cell adhesion Chain: B: PDB Molecule: e-selectin; PDBTitle: e-selectin lectin, egf-like and two scr domains complexed2 with glycomimetic antagonist
62	c3dbzB_	Alignment	not modelled	38.7	26	PDB header: sugar binding protein Chain: B: PDB Molecule: pulmonary surfactant-associated protein d; PDBTitle: human surfactant protein d
63	c5b1rA_	Alignment	not modelled	38.2	21	PDB header: immune system Chain: A: PDB Molecule: b-cell differentiation antigen cd72; PDBTitle: crystal structure of mouse cd72a ctd
64	c3bdwD_	Alignment	not modelled	37.8	11	PDB header: immune system receptor Chain: D: PDB Molecule: nkg2-a/nkg2-b type ii integral membrane protein; PDBTitle: human cd94/nkg2a
65	c2b6bD_	Alignment	not modelled	37.6	16	PDB header: virus/receptor Chain: D: PDB Molecule: cd209 antigen; PDBTitle: cryo em structure of dengue complexed with crd of dc-sign
66	c1hupA_	Alignment	not modelled	36.8	16	PDB header: c-type lectin Chain: A: PDB Molecule: mannose-binding protein; PDBTitle: human mannose binding protein carbohydrate recognition domain2 trimerizes through a triple alpha-helical coiled-coil
67	d1ufia_	Alignment	not modelled	36.8	25	Fold: ROP-like Superfamily: Dimerisation domain of CENP-B Family: Dimerisation domain of CENP-B
68	c1ufiD_	Alignment	not modelled	36.1	25	PDB header: dna binding protein Chain: D: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of the dimerization domain of human cenp-b
69	c5mgsF_	Alignment	not modelled	35.7	11	PDB header: immune system Chain: F: PDB Molecule: killer cell lectin-like receptor subfamily b member 1; PDBTitle: human receptor nkr-p1 in deglycosylated form, extracellular domain
70	d1egga_	Alignment	not modelled	35.6	21	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
71	c3ff7C_	Alignment	not modelled	35.4	5	PDB header: cell adhesion/immune system Chain: C: PDB Molecule: killer cell lectin-like receptor subfamily g member 1; PDBTitle: structure of nk cell receptor klrp1 bound to e-cadherin
72	c3cfwA_	Alignment	not modelled	35.3	11	PDB header: cell adhesion Chain: A: PDB Molecule: l-selectin; PDBTitle: l-selectin lectin and egf domains
73	d1r13a1	Alignment	not modelled	34.9	16	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
74	c5e4lB_	Alignment	not modelled	33.8	37	PDB header: sugar binding protein Chain: B: PDB Molecule: c-type mannose receptor 2; PDBTitle: structure of ligand binding region of uparap at ph 5.3
75	c3fd4B_	Alignment	not modelled	33.4	15	PDB header: viral protein Chain: B: PDB Molecule: glycoprotein gp42; PDBTitle: crystal structure of epstein-barr virus gp42 protein
76	c4iopA_	Alignment	not modelled	33.2	11	PDB header: immune system Chain: A: PDB Molecule: c-type lectin domain family 2 member a; PDBTitle: crystal structure of nkp65 bound to its ligand kacl
77	c6anrA_	Alignment	not modelled	32.4	11	PDB header: hydrolase Chain: A: PDB Molecule: colibactin self-protection protein clbs; PDBTitle: crystal structure of a self resistance protein clbs from colibactin2 biosynthetic gene cluster
78	d1hq8a_	Alignment	not modelled	32.3	11	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
79	d1mpua_	Alignment	not modelled	32.3	21	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
80	d1t8da1	Alignment	not modelled	31.9	11	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
81	c3m9zA_	Alignment	not modelled	31.7	21	PDB header: signaling protein Chain: A: PDB Molecule: killer cell lectin-like receptor subfamily b member 1a; PDBTitle: crystal structure of extracellular domain of mouse nkr-p1a PDB header: cell adhesion/immune system

82	c3ff8D_	Alignment	not modelled	31.5	21	Chain: D: PDB Molecule: killer cell lectin-like receptor subfamily g member 1; PDBTitle: structure of nk cell receptor klrp1 bound to e-cadherin
83	c1r13A_	Alignment	not modelled	31.4	16	PDB header: sugar binding protein Chain: A: PDB Molecule: pulmonary surfactant-associated protein a; PDBTitle: carbohydrate recognition and neck domains of surfactant protein a (sp-2 a)
84	d1kg0c_	Alignment	not modelled	31.1	16	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
85	d1qo3c_	Alignment	not modelled	31.1	5	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
86	c3c8jB_	Alignment	not modelled	31.0	11	PDB header: immune system Chain: B: PDB Molecule: natural killer cell receptor ly49c; PDBTitle: the crystal structure of natural killer cell receptor ly49c
87	c6a7tA_	Alignment	not modelled	29.4	16	PDB header: sugar binding protein Chain: A: PDB Molecule: n-acetylglucosamine-specific lectin; PDBTitle: ca2+-independent c-type lectin spl-1 from saxidomus purpuratus
88	d1ypqa1	Alignment	not modelled	29.0	11	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
89	c2nanA_	Alignment	not modelled	28.9	16	PDB header: immune system Chain: A: PDB Molecule: cd302 antigen; PDBTitle: nmr structure of human dcl-1 (cd302) extracellular domain
90	c3j82A_	Alignment	not modelled	28.0	16	PDB header: membrane protein/adp-binding protein Chain: A: PDB Molecule: c-type lectin domain family 9 member a; PDBTitle: electron cryo-microscopy of dngn-1 in complex with f-actin
91	d1jwia_	Alignment	not modelled	27.7	13	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
92	c3wbrC_	Alignment	not modelled	27.0	15	PDB header: carbohydrate binding protein Chain: C: PDB Molecule: c-type lectin domain family 4 member c; PDBTitle: crystal structure of carbohydrate recognition domain of blood2 dendritic cell antigen-2 (bdca2) lectin (crystal form-3)
93	c5j2sA_	Alignment	not modelled	26.7	21	PDB header: immune system Chain: A: PDB Molecule: killer cell lectin-like receptor subfamily b member 1b PDBTitle: nkr-p1b from rattus norvegicus
94	d3e9va1	Alignment	not modelled	26.6	15	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
95	c1f00I_	Alignment	not modelled	26.5	32	PDB header: cell adhesion Chain: I: PDB Molecule: intimin; PDBTitle: crystal structure of c-terminal 282-residue fragment of2 enteropathogenic e. coli intimin
96	d2z15a1	Alignment	not modelled	25.6	15	Fold: BTG domain-like Superfamily: BTG domain-like Family: BTG domain-like
97	c1cwwA_	Alignment	not modelled	23.9	22	PDB header: structural protein Chain: A: PDB Molecule: invasin; PDBTitle: crystal structure of invasin: a bacterial integrin-binding protein
98	d1dv8a_	Alignment	not modelled	23.5	21	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
99	d1tn3a_	Alignment	not modelled	22.7	24	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
100	c3g8ID_	Alignment	not modelled	22.7	5	PDB header: immune system Chain: D: PDB Molecule: lectin-related nk cell receptor ly49i1; PDBTitle: crystal structure of murine natural killer cell receptor,2 ly49i4
101	c4w7bG_	Alignment	not modelled	22.3	17	PDB header: lyase Chain: G: PDB Molecule: hydratase chsh1; PDBTitle: crystal structure of the chsh1:chsh2: complex from mycobacterium2 tuberculosis
102	c1htnA_	Alignment	not modelled	21.8	26	PDB header: lectin Chain: A: PDB Molecule: tetranectin; PDBTitle: human tetranectin, a trimeric plasminogen binding protein2 with an alpha-helical coiled coil
103	d1qo3d_	Alignment	not modelled	21.8	8	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
104	d3bdwa1	Alignment	not modelled	21.4	17	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
105	c4iopB_	Alignment	not modelled	21.2	16	PDB header: immune system Chain: B: PDB Molecule: killer cell lectin-like receptor subfamily f member 2; PDBTitle: crystal structure of nkp65 bound to its ligand kacl
106	c4kzvB_	Alignment	not modelled	20.9	21	PDB header: carbohydrate-binding protein Chain: B: PDB Molecule: c-type lectin mincle; PDBTitle: structure of the carbohydrate-recognition domain of the c-type lectin2 mincle bound to trehalose