

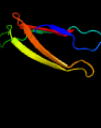

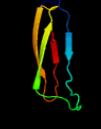



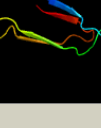


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3118_(sseC1_3484806_3485108)
 Date Thu Aug 8 16:20:30 BST 2019
 Unique Job ID 9029bec1170deb67

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1h8lA_	Alignment		97.6	20	PDB header: carboxypeptidase Chain: A: PDB Molecule: carboxypeptidase gp180 residues 503-882; PDBTitle: duck carboxypeptidase d domain ii in complex with gemsA
2	d1h8la1	Alignment		97.5	20	Fold: Prealbumin-like Superfamily: Carboxypeptidase regulatory domain-like Family: Carboxypeptidase regulatory domain
3	c3mn8A_	Alignment		97.3	23	PDB header: hydrolase Chain: A: PDB Molecule: lp15968p; PDBTitle: structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
4	c2nsmA_	Alignment		97.3	21	PDB header: hydrolase Chain: A: PDB Molecule: carboxypeptidase n catalytic chain; PDBTitle: crystal structure of the human carboxypeptidase n (kinase i)2 catalytic domain
5	c5aq0B_	Alignment		97.0	20	PDB header: hydrolase Chain: B: PDB Molecule: carboxypeptidase d; PDBTitle: the structure of the transthyretin-like domain of the first2 catalytic domain of the human carboxypeptidase d
6	c1uwvA_	Alignment		96.4	16	PDB header: hydrolase Chain: A: PDB Molecule: carboxypeptidase m; PDBTitle: crystal structure of human carboxypeptidase m
7	d3pccm_	Alignment		96.3	20	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
8	d1uwya1	Alignment		96.1	19	Fold: Prealbumin-like Superfamily: Carboxypeptidase regulatory domain-like Family: Carboxypeptidase regulatory domain
9	c4ilvB_	Alignment		95.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: intradiol ring-cleavage dioxygenase; PDBTitle: structure of the dioxygenase domain of sacte_2871, a novel dioxygenase2 carbohydrate-binding protein fusion from the cellulolytic bacterium3 streptomyces sp. sirexaa-e
10	c3n9tA_	Alignment		95.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: pnpc; PDBTitle: cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
11	d2burb1	Alignment		95.4	19	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase

12	d1nkgA1	Alignment		95.3	15	Fold: Prealbumin-like Superfamily: Starch-binding domain-like Family: Rhamnogalacturonase B, RhgB, middle domain
13	c2xsuA	Alignment		95.1	18	PDB header: oxidoreductase Chain: A; PDB Molecule: catechol 1,2 dioxygenase; PDBTitle: crystal structure of the a72g mutant of acinetobacter2 radioresistens catechol 1,2 dioxygenase
14	c2azqA	Alignment		95.1	22	PDB header: oxidoreductase Chain: A; PDB Molecule: catechol 1,2-dioxygenase; PDBTitle: crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
15	c1tmxA	Alignment		94.8	23	PDB header: oxidoreductase Chain: A; PDB Molecule: hydroxyquinol 1,2-dioxygenase; PDBTitle: crystal structure of hydroxyquinol 1,2-dioxygenase from nocardiooides2 simplex 3e
16	c3th1C	Alignment		94.7	25	PDB header: oxidoreductase Chain: C; PDB Molecule: chlorocatechol 1,2-dioxygenase; PDBTitle: crystal structure of chlorocatechol 1,2-dioxygenase from pseudomonas2 putida
17	c2boyC	Alignment		94.3	17	PDB header: oxidoreductase Chain: C; PDB Molecule: 3-chlorocatechol 1,2-dioxygenase; PDBTitle: crystal structure of 3-chlorocatechol 1,2-dioxygenase from rhodococcus2 opacus 1cp
18	d1s9aa	Alignment		94.2	23	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
19	c5td3B	Alignment		93.3	38	PDB header: oxidoreductase Chain: B; PDB Molecule: catechol 1,2-dioxygenase; PDBTitle: crystal structure of catechol 1,2-dioxygenase from burkholderia2 vietnamiensis
20	c3hj8A	Alignment		93.3	28	PDB header: oxidoreductase Chain: A; PDB Molecule: catechol 1,2-dioxygenase; PDBTitle: crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol
21	d3pcca	Alignment	not modelled	93.0	21	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
22	d1dmha	Alignment	not modelled	92.8	17	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
23	c3kptA	Alignment	not modelled	92.7	18	PDB header: cell adhesion Chain: A; PDB Molecule: collagen adhesion protein; PDBTitle: crystal structure of bcpa, the major pilin subunit of2 bacillus cereus
24	c3irpX	Alignment	not modelled	92.5	24	PDB header: cell adhesion Chain: X; PDB Molecule: uro-adherence factor a; PDBTitle: crystal structure of functional region of uafa from staphylococcus2 saprophyticus at 1.50 angstrom resolution
25	d2bura1	Alignment	not modelled	92.1	17	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
26	c2x5pA	Alignment	not modelled	91.5	26	PDB header: protein binding Chain: A; PDB Molecule: fibronectin binding protein; PDBTitle: crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
27	c4jdzA	Alignment	not modelled	91.3	12	PDB header: cell adhesion Chain: A; PDB Molecule: ser-asp rich fibrinogen/bone sialoprotein-binding protein PDBTitle: structures of sdrd from staphylococcus aureus reveal the molecular2 mechanism of how the cell surface receptors recognize their ligands
28	c2ww8A	Alignment	not modelled	89.6	23	PDB header: cell adhesion Chain: A; PDB Molecule: cell wall surface anchor family protein; PDBTitle: structure of the pilus adhesin (rrga) from streptococcus2

						pneumoniae
29	c3e8vA_	Alignment	not modelled	87.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: possible transglutaminase-family protein; PDBTitle: crystal structure of a possible transglutaminase-family protein2 proteolytic fragment from bacteroides fragilis
30	c2qz7B_	Alignment	not modelled	87.1	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein sco6318; PDBTitle: the crystal structure of a homologue of telluride resistance protein2 (terd), sco6318 from streptomyces coelicolor a3(2)
31	c5vg2B_	Alignment	not modelled	85.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: intradiol ring-cleavage dioxygenase; PDBTitle: intradiol ring-cleavage dioxygenase from tetranychus urticae
32	c2kxvA_	Alignment	not modelled	83.4	27	PDB header: unknown function Chain: A: PDB Molecule: tellurite resistance protein; PDBTitle: nmr structure and calcium-binding properties of the tellurite2 resistance protein terd from klebsiella pneumoniae
33	c3ibzA_	Alignment	not modelled	83.2	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative tellurium resistant like protein terd; PDBTitle: crystal structure of putative tellurium resistant like protein (terd)2 from streptomyces coelicolor a3(2)
34	c4acqA_	Alignment	not modelled	82.7	17	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
35	c2qngA_	Alignment	not modelled	81.4	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein sav2460; PDBTitle: crystal structure of unknown function protein sav2460
36	c4acqC_	Alignment	not modelled	77.2	17	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
37	c6fwvB_	Alignment	not modelled	75.7	15	PDB header: unknown function Chain: B: PDB Molecule: collagen adhesion protein; PDBTitle: the bacillus anthracis tie protein
38	c4u3sB_	Alignment	not modelled	75.6	24	PDB header: protein binding Chain: B: PDB Molecule: cellulosomal scaffoldin; PDBTitle: crystal structure of coh3scab-xdoc_m1scaa complex: a n-terminal2 interface mutant of type ii cohesin-x-dockerin complex from3 acetivibrio cellulolyticus
39	c4rtdA_	Alignment	not modelled	72.2	19	PDB header: lipid binding protein Chain: A: PDB Molecule: uncharacterized lipoprotein yfhm; PDBTitle: escherichia coli alpha-2-macroglobulin activated by porcine elastase
40	d1jhna4	Alignment	not modelled	71.9	29	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Calnexin/calreticulin
41	c1jhnA_	Alignment	not modelled	71.6	29	PDB header: chaperone Chain: A: PDB Molecule: calnexin; PDBTitle: crystal structure of the luminal domain of calnexin
42	c5k39B_	Alignment	not modelled	70.3	13	PDB header: structural protein Chain: B: PDB Molecule: dockerin module from a protein of unknown function; PDBTitle: the type ii cohesin dockerin complex from clostridium thermocellum
43	c1ti2F_	Alignment	not modelled	68.5	30	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici
44	c4uzgA_	Alignment	not modelled	66.6	20	PDB header: structural protein Chain: A: PDB Molecule: surface protein spb1; PDBTitle: crystal structure of group b streptococcus pilus 2b backbone protein2 sak_1440
45	c3uafA_	Alignment	not modelled	64.2	16	PDB header: protein binding Chain: A: PDB Molecule: ttr-52; PDBTitle: crystal structure of a ttr-52 mutant of c. elegans
46	c4kdwA_	Alignment	not modelled	63.4	20	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of a bacterial immunoglobulin-like domain from the2 m. primoryensis ice-binding adhesin
47	c3rg0A_	Alignment	not modelled	62.5	21	PDB header: chaperone Chain: A: PDB Molecule: calreticulin; PDBTitle: structural and functional relationships between the lectin and arm2 domains of calreticulin
48	c4u48A_	Alignment	not modelled	62.3	25	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: putative inner membrane lipoprotein; PDBTitle: crystal structure of salmonella alpha-2-macroglobulin
49	c3mxnB_	Alignment	not modelled	61.5	40	PDB header: replication Chain: B: PDB Molecule: recq-mediated genome instability protein 2; PDBTitle: crystal structure of the rmi core complex
50	c5hcfF_	Alignment	not modelled	58.4	27	PDB header: chaperone Chain: F: PDB Molecule: calreticulin, putative,calreticulin, putative; PDBTitle: t. cruzi calreticulin globular domain
51	c5hcaB_	Alignment	not modelled	57.3	18	PDB header: sugar binding protein Chain: B: PDB Molecule: calreticulin,calreticulin; PDBTitle: globular domain of the entamoeba histolytica calreticulin in complex2 with glucose
52	c3o0vA_	Alignment	not modelled	55.1	21	PDB header: chaperone Chain: A: PDB Molecule: calreticulin; PDBTitle: crystal structure of the calreticulin lectin domain
53	d1nqja_	Alignment	not modelled	53.7	16	Fold: CUB-like Superfamily: Collagen-binding domain Family: Collagen-binding domain

54	c4z8wA	Alignment	not modelled	49.9	24	PDB header: allergen Chain: A: PDB Molecule: major pollen allergen pla l 1; PDBTitle: crystal structure of the major plantain pollen allergen pla l 1
55	c2h0eA	Alignment	not modelled	47.9	14	PDB header: hydrolase Chain: A: PDB Molecule: transthyretin-like protein pucm; PDBTitle: crystal structure of pucm in the absence of substrate
56	c4q14B	Alignment	not modelled	42.5	24	PDB header: hydrolase Chain: B: PDB Molecule: 5-hydroxyisourate hydrolase; PDBTitle: crystal structure of 5-hydroxyisourate hydrolase from brucella2 melitensis
57	c3c12A	Alignment	not modelled	39.8	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
58	c2x9yA	Alignment	not modelled	39.2	27	PDB header: cell adhesion Chain: A: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structure of the pilus backbone (rrgb) from streptococcus2 pneumoniae
59	d1kgia	Alignment	not modelled	38.1	14	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
60	d1f86a	Alignment	not modelled	36.7	19	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
61	d1ttaa	Alignment	not modelled	33.6	19	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
62	d1ei5a2	Alignment	not modelled	32.4	50	Fold: Streptavidin-like Superfamily: D-aminopeptidase, middle and C-terminal domains Family: D-aminopeptidase, middle and C-terminal domains
63	c4e9lA	Alignment	not modelled	31.5	20	PDB header: cell adhesion Chain: A: PDB Molecule: attaching and effacing protein, pathogenesis factor; PDBTitle: fdec, a novel broadly conserved escherichia coli adhesin eliciting2 protection against urinary tract infections
64	c2xetB	Alignment	not modelled	31.3	19	PDB header: transport protein Chain: B: PDB Molecule: f1 capsule-anchoring protein; PDBTitle: conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
65	d1tfpa	Alignment	not modelled	30.6	12	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
66	c3qvaB	Alignment	not modelled	30.4	34	PDB header: hydrolase Chain: B: PDB Molecule: transthyretin-like protein; PDBTitle: structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
67	d1oo2a	Alignment	not modelled	29.9	19	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
68	c2gpzC	Alignment	not modelled	29.4	17	PDB header: hydrolase Chain: C: PDB Molecule: transthyretin-like protein; PDBTitle: transthyretin-like protein from salmonella dublin
69	c6b6lB	Alignment	not modelled	29.3	27	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 2, sugar binding domain protein; PDBTitle: the crystal structure of glycosyl hydrolase family 2 (gh2) member from2 bacteroides cellulosilyticus dsm 14838
70	c2pz4A	Alignment	not modelled	27.5	16	PDB header: cell adhesion Chain: A: PDB Molecule: protein gbs052; PDBTitle: crystal structure of spab (gbs52), the minor pilin in gram-positive2 pathogen streptococcus agalactiae
71	c4p0dA	Alignment	not modelled	23.8	12	PDB header: structural protein Chain: A: PDB Molecule: trypsin-resistant surface t6 protein; PDBTitle: the t6 backbone pilin of serotype m6 streptococcus pyogenes has a2 modular three-domain structure decorated with variable loops and3 extensions
72	d2qlvb1	Alignment	not modelled	23.8	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: AMPK-beta glycogen binding domain-like
73	c4a5wA	Alignment	not modelled	21.2	17	PDB header: immune system Chain: A: PDB Molecule: complement c5; PDBTitle: crystal structure of c5b6
74	c4n0rB	Alignment	not modelled	19.7	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative glycoside hydrolase; PDBTitle: crystal structure of a putative glycoside hydrolase (bvu_0362) from2 bacteroides vulgatus atcc 8482 at 1.80 a resolution
75	c6czjA	Alignment	not modelled	19.0	28	PDB header: de novo protein Chain: A: PDB Molecule: b10; PDBTitle: structure of a redesigned beta barrel, b10
76	d2f69a1	Alignment	not modelled	19.0	32	Fold: open-sided beta-meander Superfamily: Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain Family: Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain
77	c4cffB	Alignment	not modelled	18.0	24	PDB header: transferase Chain: B: PDB Molecule: 5'-amp-activated protein kinase subunit beta-1; PDBTitle: structure of full length human ampk in complex with a small molecule2 activator, a thienopyridone derivative (a-769662)
78	c5t0zB	Alignment	not modelled	16.9	24	PDB header: structural protein Chain: B: PDB Molecule: lipoprotein, putative; PDBTitle: pelc from geobacter metallireducens

79	c6mr1A	Alignment	not modelled	15.6	44	PDB header: protein binding Chain: A: PDB Molecule: carbon dioxide concentrating mechanism protein; PDBTitle: rbcs-like subdomain of ccm
80	d1ew4a	Alignment	not modelled	15.4	24	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
81	c4fe9A	Alignment	not modelled	15.3	20	PDB header: carbohydrate-binding protein Chain: A: PDB Molecule: outer membrane protein susf; PDBTitle: crystal structure of susf from bacteroides thetaiotaomicron
82	d1cwva2	Alignment	not modelled	15.1	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Invasin/intimin cell-adhesion fragments Family: Invasin/intimin cell-adhesion fragments
83	c6hbbA	Alignment	not modelled	14.6	56	PDB header: protein binding Chain: A: PDB Molecule: carbon dioxide concentrating mechanism protein ccm; PDBTitle: crystal structure of the small subunit-like domain 1 of ccm from2 synechococcus elongatus (strain pcc 7942)
84	c2kmcA	Alignment	not modelled	14.3	23	PDB header: cell adhesion Chain: A: PDB Molecule: fermitin family homolog 1; PDBTitle: solution structure of the n-terminal domain of kindlin-1
85	c1sddB	Alignment	not modelled	14.3	26	PDB header: blood clotting Chain: B: PDB Molecule: coagulation factor v; PDBTitle: crystal structure of bovine factor vai
86	c3cdzB	Alignment	not modelled	14.2	26	PDB header: blood clotting Chain: B: PDB Molecule: coagulation factor viii light chain; PDBTitle: crystal structure of human factor viii
87	c6cztA	Alignment	not modelled	14.0	38	PDB header: cell adhesion Chain: A: PDB Molecule: alginate biosynthesis protein algf; PDBTitle: cs-rosetta determined structures of the n-terminal domain of algf from2 p. aeruginosa
88	d1knva	Alignment	not modelled	13.8	15	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Cfr10I/Bse634I
89	c3n6yA	Alignment	not modelled	13.7	23	PDB header: unknown function Chain: A: PDB Molecule: immunoglobulin-like protein; PDBTitle: crystal structure of an immunoglobulin-like protein (pa1606) from2 pseudomonas aeruginosa at 1.50 a resolution
90	c6qm2A	Alignment	not modelled	12.9	44	PDB header: hydrolase Chain: A: PDB Molecule: type-2 restriction enzyme nlaiv; PDBTitle: nlaiv restriction endonuclease
91	d1rbli	Alignment	not modelled	12.7	22	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
92	d2k49a2	Alignment	not modelled	12.5	33	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
93	d2k8ea1	Alignment	not modelled	12.4	42	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
94	c2ybvN	Alignment	not modelled	12.2	22	PDB header: lyase Chain: N: PDB Molecule: ribulose biphosphate carboxylase small subunit; PDBTitle: structure of rubisco from thermosynechococcus elongatus
95	d1cwva3	Alignment	not modelled	11.8	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Invasin/intimin cell-adhesion fragments Family: Invasin/intimin cell-adhesion fragments
96	c1txkA	Alignment	not modelled	11.7	41	PDB header: biosynthetic protein Chain: A: PDB Molecule: glucans biosynthesis protein g; PDBTitle: crystal structure of escherichia coli opgg
97	d1ir1s	Alignment	not modelled	11.7	33	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
98	c3wmvA	Alignment	not modelled	11.7	41	PDB header: sugar binding protein Chain: A: PDB Molecule: lectin; PDBTitle: the structure of an anti-cancer lectin mytilec with ligand from the2 mussel mytilus galloprovincialis
99	d1svdm1	Alignment	not modelled	11.6	22	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit