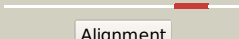
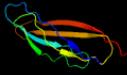
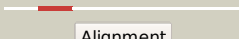

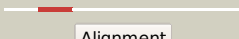


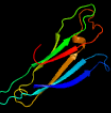









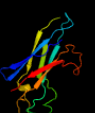



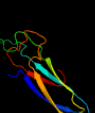
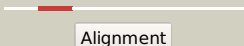
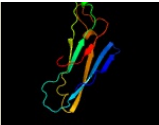
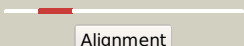
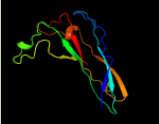

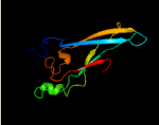
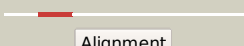
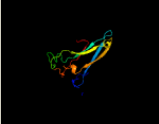
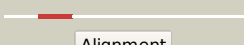

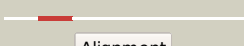
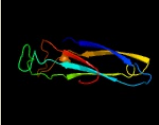






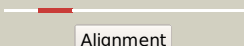
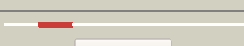
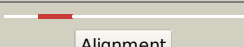

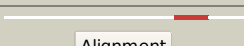
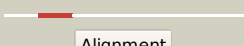
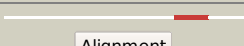
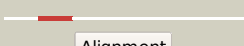


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3909_(-)_4394370_4396778
Date	Sat Aug 10 22:05:09 BST 2019
Unique Job ID	e2554d66aea504b7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fxkB_	 Alignment		97.1	20	PDB header: immune system Chain: B: PDB Molecule: complement c4-a alpha chain; PDBTitle: human complement c4
2	d1w8oa1	 Alignment		96.9	28	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
3	c3u48A_	 Alignment		96.8	19	PDB header: hydrolase Chain: A: PDB Molecule: jmb19063; PDBTitle: from soil to structure: a novel dimeric family 3-beta-glucosidase2 isolated from compost using metagenomic analysis
4	c5wvpA_	 Alignment		96.8	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: expression, characterization and crystal structure of a novel beta-2 glucosidase from paenibacillus barengoltzii
5	c2l0dA_	 Alignment		96.6	20	PDB header: cell adhesion Chain: A: PDB Molecule: cell surface protein; PDBTitle: solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
6	c3hs0B_	 Alignment		96.5	17	PDB header: immune system Chain: B: PDB Molecule: cobra venom factor; PDBTitle: cobra venom factor (cvf) in complex with human factor b
7	c2x41A_	 Alignment		96.4	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structure of beta-glucosidase 3b from thermotoga neapolitana in2 complex with glucose
8	c5nbsA_	 Alignment		96.3	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structural studies of a glycoside hydrolase family 3 beta-glucosidase2 from the model fungus neurospora crassa
9	c4i3gB_	 Alignment		96.3	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of desr, a beta-glucosidase from streptomyces2 venezuelae in complex with d-glucose.
10	c3zz1A_	 Alignment		96.3	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-d-glucoside glucohydrolase; PDBTitle: crystal structure of a glycoside hydrolase family 3 beta-glucosidase,2 bgl1 from hypocrea jecorina at 2.1a resolution.
11	c5k6lA_	 Alignment		96.2	25	PDB header: hydrolase Chain: A: PDB Molecule: b-glucosidase; PDBTitle: structure of a gh3 b-glucosidase from cow rumen metagenome

12	c5tf0B_	 Alignment		96.1	25	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3 n-terminal domain protein; PDBTitle: crystal structure of glycosyl hydrolase family 3 n-terminal domain2 protein from bacteroides intestinalis
13	c5jp0A_	 Alignment		96.1	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase bogh3b; PDBTitle: bacteroides ovatus xyloglucan pul gh3b with bound glucose
14	c4d0jD_	 Alignment		96.1	21	PDB header: hydrolase Chain: D: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of glycoside hydrolase family 3 beta-2 glucosidase cel3a from the moderately thermophilic fungus rasamsonia emersonii
15	c5z87B_	 Alignment		96.0	20	PDB header: hydrolase Chain: B: PDB Molecule: emgh1; PDBTitle: structural of a novel b-glucosidase emgh1 at 2.3 angstrom from erythrobacter marinus
16	c3ac0B_	 Alignment		96.0	22	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
17	c4zo9B_	 Alignment		95.9	23	PDB header: hydrolase Chain: B: PDB Molecule: lin1840 protein; PDBTitle: crystal structure of mutant (d270a) beta-glucosidase from listeria2 innocua in complex with laminaribiose
18	c6q7jB_	 Alignment		95.8	19	PDB header: hydrolase Chain: B: PDB Molecule: exo-1,4-beta-xylosidase xlnD; PDBTitle: gh3 exo-beta-xylosidase (xlnD) in complex with xylobiose aziridine2 activity based probe
19	c4iidB_	 Alignment		95.7	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase 1; PDBTitle: crystal structure of beta-glucosidase 1 from aspergillus aculeatus in2 complex with 1-deoxynojirimycin
20	c5yotB_	 Alignment		95.7	24	PDB header: hydrolase Chain: B: PDB Molecule: isoprimeverose-producing enzyme; PDBTitle: isoprimeverose-producing enzyme from aspergillus oryzae in complex2 with isoprimeverose
21	c5z9sB_	 Alignment	not modelled	95.7	19	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3 protein; PDBTitle: functional and structural characterization of a beta-glucosidase2 involved in saponin metabolism from intestinal bacteria
22	c5a7mA_	 Alignment	not modelled	95.6	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylosidase; PDBTitle: the structure of hypocrea jecorina beta-xylosidase xyl3a (bx11)
23	c5wabD_	 Alignment	not modelled	95.5	22	PDB header: hydrolase Chain: D: PDB Molecule: putative beta-glucosidase; PDBTitle: crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
24	c5wabC_	 Alignment	not modelled	95.4	24	PDB header: hydrolase Chain: C: PDB Molecule: putative beta-glucosidase; PDBTitle: crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
25	c4a5wA_	 Alignment	not modelled	95.1	14	PDB header: immune system Chain: A: PDB Molecule: complement c5; PDBTitle: crystal structure of c5b6
26	c2kutA_	 Alignment	not modelled	95.1	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
27	c6i2xB_	 Alignment	not modelled	95.0	20	PDB header: immune system Chain: B: PDB Molecule: cobra venom factor; PDBTitle: structure of complement c5 in complex with small molecule inhibitor2 and cvf
28	c2kl6A_	 Alignment	not modelled	94.1	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a

29	c2x3bB	Alignment	not modelled	93.8	26	PDB header: hydrolase Chain: B: PDB Molecule: toxic extracellular endopeptidase; PDBTitle: asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
30	c4acqA	Alignment	not modelled	93.7	20	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
31	c3g6jB	Alignment	not modelled	93.5	22	PDB header: immune system Chain: B: PDB Molecule: complement c3 alpha chain; PDBTitle: c3b in complex with a c3b specific fab
32	c1l9mB	Alignment	not modelled	93.3	23	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
33	c2a73B	Alignment	not modelled	93.1	20	PDB header: immune system Chain: B: PDB Molecule: complement c3; PDBTitle: human complement component c3
34	c2a74B	Alignment	not modelled	92.6	22	PDB header: immune system Chain: B: PDB Molecule: complement component c3c; PDBTitle: human complement component c3c
35	c3cu7A	Alignment	not modelled	92.5	15	PDB header: immune system Chain: A: PDB Molecule: complement c5; PDBTitle: human complement component 5
36	c4acqC	Alignment	not modelled	91.7	20	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
37	c3e9tD	Alignment	not modelled	91.7	19	PDB header: membrane protein Chain: D: PDB Molecule: na/ca exchange protein; PDBTitle: crystal structure of apo-form calx cbd1 domain
38	c1yewI	Alignment	not modelled	89.9	20	PDB header: oxidoreductase, membrane protein Chain: I: PDB Molecule: particulate methane monooxygenase, b subunit; PDBTitle: crystal structure of particulate methane monooxygenase
39	c3rgbA	Alignment	not modelled	89.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: methane monooxygenase subunit b2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
40	c2h47C	Alignment	not modelled	88.3	14	PDB header: oxidoreductase/electron transport Chain: C: PDB Molecule: azurin; PDBTitle: crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from alcaligenes3 faecalis (form 1)
41	c3isyA	Alignment	not modelled	87.4	16	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
42	c3rfrI	Alignment	not modelled	87.2	15	PDB header: oxidoreductase Chain: I: PDB Molecule: pmob; PDBTitle: crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
43	d1cc3a	Alignment	not modelled	84.6	16	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
44	d1exha	Alignment	not modelled	84.1	23	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family II
45	c3pvmB	Alignment	not modelled	83.5	17	PDB header: immune system Chain: B: PDB Molecule: cobra venom factor; PDBTitle: structure of complement c5 in complex with cvf
46	c5icuA	Alignment	not modelled	82.5	13	PDB header: chaperone Chain: A: PDB Molecule: copc; PDBTitle: the crystal structure of copc from methylosinus trichosporium ob3b
47	d2vzsa2	Alignment	not modelled	82.3	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
48	c2b39B	Alignment	not modelled	80.6	19	PDB header: immune system Chain: B: PDB Molecule: c3; PDBTitle: structure of mammalian c3 with an intact thioester at 3a resolution
49	c3h6aB	Alignment	not modelled	78.5	17	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-4; PDBTitle: structure of the calx-beta domain of integrin beta42 crystallized in the presence of calcium
50	c2r39A	Alignment	not modelled	77.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fixg-related protein; PDBTitle: crystal structure of fixg-related protein from vibrio parahaemolyticus
51	c3ndyG	Alignment	not modelled	76.1	16	PDB header: hydrolase Chain: G: PDB Molecule: endoglucanase d; PDBTitle: the structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
52	c4u48A	Alignment	not modelled	75.7	15	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: putative inner membrane lipoprotein; PDBTitle: crystal structure of salmonella alpha-2-macroglobulin
53	c4rtDA	Alignment	not modelled	75.4	12	PDB header: lipid binding protein Chain: A: PDB Molecule: uncharacterized lipoprotein yfhm; PDBTitle: escherichia coli alpha-2-macroglobulin activated by porcine elastase
54	c2rttA	Alignment	not modelled	73.8	20	PDB header: hydrolase Chain: A: PDB Molecule: chic; PDBTitle: solution structure of the chitin-binding domain of chi18ac from2 streptomyces coelicolor

55	d2ccwa1	Alignment	not modelled	73.7	11	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
56	d1ex0a3	Alignment	not modelled	69.7	11	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
57	d1jzga_	Alignment	not modelled	69.6	17	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
58	d1nwpa_	Alignment	not modelled	69.3	15	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
59	c6nfgC_	Alignment	not modelled	69.3	6	PDB header: metal binding protein Chain: C: PDB Molecule: copc; PDBTitle: copc from pseudomonas fluorescens
60	c3ginB_	Alignment	not modelled	69.0	13	PDB header: metal binding protein Chain: B: PDB Molecule: sodium/calcium exchanger 1; PDBTitle: crystal structure of e454k-cbd1
61	c2pn5A_	Alignment	not modelled	67.8	18	PDB header: immune system Chain: A: PDB Molecule: thioester-containing protein i; PDBTitle: crystal structure of tep1r
62	d1cuoa_	Alignment	not modelled	65.0	11	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
63	d3es6b1	Alignment	not modelled	63.1	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: SVA-like
64	c4oleD_	Alignment	not modelled	62.9	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: next to brca1 gene 1 protein; PDBTitle: crystal structure of a neighbor of brca1 gene 1 (nbr1) from homo2 sapiens at 2.52 a resolution
65	c6f7eA_	Alignment	not modelled	62.8	17	PDB header: carbohydrate Chain: A: PDB Molecule: putative secreted cellulose binding protein; PDBTitle: nmr solution structure of the cellulose-binding family 2 carbohydrate2 binding domain (cbm2) from sclpmo9c
66	c2xzza_	Alignment	not modelled	59.3	11	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase k; PDBTitle: crystal structure of the human transglutaminase 1 beta-barrel domain
67	d1joia_	Alignment	not modelled	59.3	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
68	c2qvka_	Alignment	not modelled	59.2	13	PDB header: metal binding protein Chain: A: PDB Molecule: sodium/calcium exchanger 1; PDBTitle: the second ca2+-binding domain of the na+-ca2+ exchanger is2 essential for regulation: crystal structures and3 mutational analysis
69	d1rkra_	Alignment	not modelled	55.2	14	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
70	d1g0da3	Alignment	not modelled	54.7	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
71	c3ay2A_	Alignment	not modelled	53.5	17	PDB header: antitumor protein, antiviral protein Chain: A: PDB Molecule: lipid modified azurin protein; PDBTitle: crystal structure of neisserial azurin
72	c2aanA_	Alignment	not modelled	53.4	17	PDB header: electron transport Chain: A: PDB Molecule: auracyanin a; PDBTitle: auracyanin a: a "blue" copper protein from the green thermophilic2 photosynthetic bacterium, chloroflexus aurantiacus
73	d1qhqa_	Alignment	not modelled	52.2	17	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
74	c5z6pB_	Alignment	not modelled	50.4	7	PDB header: hydrolase Chain: B: PDB Molecule: b-agarase; PDBTitle: the crystal structure of an agarase, agwh50c
75	d1ix2a_	Alignment	not modelled	47.2	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
76	c6c14A_	Alignment	not modelled	46.0	10	PDB header: membrane protein, metal transport Chain: A: PDB Molecule: protocadherin-15; PDBTitle: cryoem structure of mouse pcdh15-1ec-lhfp15 complex
77	c2kncA_	Alignment	not modelled	45.4	17	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfaib-beta3 transmembrane-cytoplasmic2 heterocomplex
78	c2e6jA_	Alignment	not modelled	44.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hydin protein; PDBTitle: solution structure of the c-terminal papd-like domain from2 human hydin protein
79	c5sydA_	Alignment	not modelled	41.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: azurin, chimeric construct; PDBTitle: circularly permuted azurin (cpaz) based on p. aeruginosa azurin2 sequence
80	c5e6wA_	Alignment	not modelled	38.2	21	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: re-refinement of the crystal structure of the plexin-semaphorin-2 integrin domain/hybrid domain/i-egf1 segment from the human integrin3 b2 subunit

81	d1azca_	Alignment	not modelled	36.5	10	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
82	d3pccm_	Alignment	not modelled	33.9	27	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
83	c4b97A_	Alignment	not modelled	32.8	19	PDB header: sugar binding protein Chain: A: PDB Molecule: cellulose binding domain-containing protein; PDBTitle: biomass sensing modules from putative rsgi-like proteins2 of clostridium thermocellum resemble family 3 carbohydrate-3 binding module of cellulosome
84	c2ys4A_	Alignment	not modelled	32.8	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hydrocephalus-inducing protein homolog; PDBTitle: solution structure of the n-terminal papd-like domain of f2 hydin protein from human
85	c4ilvB_	Alignment	not modelled	32.5	26	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
86	c3rkoK_	Alignment	not modelled	27.2	28	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit k; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
87	d2bura1	Alignment	not modelled	27.2	23	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
88	d1k1xa3	Alignment	not modelled	26.3	21	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: 4-alpha-glucanotransferase, N-terminal domain
89	c4bq3A_	Alignment	not modelled	24.8	9	PDB header: hydrolase Chain: A: PDB Molecule: b-agarase; PDBTitle: structural analysis of an exo-beta-agarase
90	d2burb1	Alignment	not modelled	23.3	33	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
91	c5v2sA_	Alignment	not modelled	22.8	19	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
92	d3pcca_	Alignment	not modelled	22.8	26	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
93	c6cpdB_	Alignment	not modelled	22.8	15	PDB header: metal binding protein Chain: B: PDB Molecule: pmod; PDBTitle: crystal structure of pmod soluble domain from methylocystis sp. atcc2 49242 (rockwell)
94	d2dpka1	Alignment	not modelled	22.7	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: CaIX-like Family: CaIX-beta domain
95	c3us9A_	Alignment	not modelled	22.4	11	PDB header: metal binding protein Chain: A: PDB Molecule: sodium/calcium exchanger 1; PDBTitle: crystal structure of the ncx1 intracellular tandem calcium binding2 domains(cbd12)
96	d1vjja3	Alignment	not modelled	21.5	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Transglutaminase, two C-terminal domains Family: Transglutaminase, two C-terminal domains
97	c1f13A_	Alignment	not modelled	21.2	11	PDB header: coagulation factor Chain: A: PDB Molecule: cellular coagulation factor xiii zymogen; PDBTitle: recombinant human cellular coagulation factor xiii
98	c6e8wC_	Alignment	not modelled	20.2	24	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein gp160; PDBTitle: mper-tm domain of hiv-1 envelope glycoprotein (env)
99	c3rb7E_	Alignment	not modelled	19.5	14	PDB header: metal binding protein Chain: E: PDB Molecule: na/ca exchange protein; PDBTitle: crystal structure of cbd12 from calx1.2