

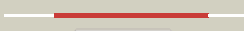
















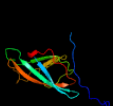



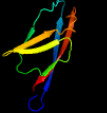






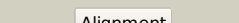
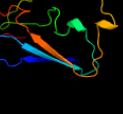
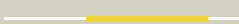

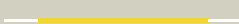






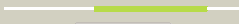
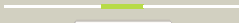
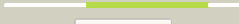
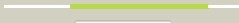
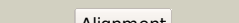




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1987 (-)_2231034_2231462
Date	Mon Aug 5 13:25:09 BST 2019
Unique Job ID	a820c2cdd01525d1

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ndyG_	 Alignment		100.0	29	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
2	d1exha_	 Alignment		100.0	39	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family II
3	c2rttA_	 Alignment		100.0	43	PDB header: hydrolase Chain: A; PDB Molecule: chic; PDBTitle: solution structure of the chitin-binding domain of chi18ac from2 streptomyces coelicolor
4	c6f7eA_	 Alignment		100.0	27	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
5	c3icgD_	 Alignment		99.9	26	PDB header: hydrolase Chain: D; PDB Molecule: endoglucanase d; PDBTitle: crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
6	c2cwrA_	 Alignment		99.9	22	PDB header: hydrolase Chain: A; PDB Molecule: chitinase; PDBTitle: crystal structure of chitin biding domain of chitinase from2 pyrococcus furiosus
7	c5dhdA_	 Alignment		99.9	28	PDB header: hydrolase Chain: A; PDB Molecule: chitinase; PDBTitle: crystal structure of chbd2 from thermococcus kodakarensis kod1
8	d1e5ba_	 Alignment		99.8	22	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family II
9	d1hehc_	 Alignment		99.8	22	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family II
10	c6bt9B_	 Alignment		99.5	33	PDB header: hydrolase Chain: B; PDB Molecule: chitinase; PDBTitle: chitinase chia74 from bacillus thuringiensis
11	d1qbaa2	 Alignment		97.9	19	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Bacterial chitobiase, n-terminal domain

12	c1qbaA	 Alignment		97.7	20	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitobiase; PDBTitle: bacterial chitobiase, glycosyl hydrolase family 20
13	c6ezrA	 Alignment		97.2	20	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylglucosaminidase nag2; PDBTitle: crystal structure of gh20 exo beta-n-acetylglucosaminidase from vibrio2 harveyi
14	c1wkyA	 Alignment		93.6	10	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-mannanase; PDBTitle: crystal structure of alkaline mannanase from bacillus sp. strain jamb-2 602: catalytic domain and its carbohydrate binding module
15	d1w8oa1	 Alignment		92.9	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
16	c2x3bB	 Alignment		89.9	16	PDB header: hydrolase Chain: B: PDB Molecule: toxic extracellular endopeptidase; PDBTitle: asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
17	c2l0dA	 Alignment		77.4	14	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
18	c4txqA	 Alignment		77.4	20	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of a family gh18 chitinase from chromobacterium2 violaceum
19	d1lfra	 Alignment		75.5	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
20	c2kl6A	 Alignment		69.8	12	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
21	c3jt0B	 Alignment	not modelled	64.9	12	PDB header: structural protein Chain: B: PDB Molecule: lamin-b1; PDBTitle: crystal structure of the c-terminal fragment (426-558) lamin-b1 from2 homo sapiens, northeast structural genomics consortium target hr5546a
22	c3qbtH	 Alignment	not modelled	64.3	16	PDB header: protein transport/hydrolase Chain: H: PDB Molecule: inositol polyphosphate 5-phosphatase ocr1-1; PDBTitle: crystal structure of ocr1 540-678 in complex with rab8a:gppnhp
23	d1ivta	 Alignment	not modelled	63.9	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
24	c5d6hA	 Alignment	not modelled	61.7	11	PDB header: chaperone/protein transport Chain: A: PDB Molecule: csuc; PDBTitle: crystal structure of csuc-csua/b chaperone-major subunit pre-assembly2 complex from csu biofilm-mediating pili of acinetobacter baumannii
25	c5xswA	 Alignment	not modelled	61.5	12	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of an archaeal chitinase in the substrate-complex2 form (p63)
26	d1lufga	 Alignment	not modelled	57.7	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: Lamin A/C globular tail domain Family: Lamin A/C globular tail domain
27	d2vzsa2	 Alignment	not modelled	50.9	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
						PDB header: structural protein Chain: A: PDB Molecule: lamin-b2;

28	c2IIIa_	Alignment	not modelled	48.2	30	PDBTitle: solution nmr structure of c-terminal globular domain of human lamin-2 b2, northeast structural genomics consortium target hr8546a
29	c1yewl_	Alignment	not modelled	44.1	16	PDB header: oxidoreductase, membrane protein Chain: I; PDB Molecule: particulate methane monooxygenase, b subunit; PDBTitle: crystal structure of particulate methane monooxygenase
30	c3rgbA_	Alignment	not modelled	42.5	15	PDB header: oxidoreductase Chain: A; PDB Molecule: methane monooxygenase subunit b2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
31	c5dfkA_	Alignment	not modelled	41.7	14	PDB header: structural protein Chain: A; PDB Molecule: probable fimbrial chaperone ecpb; PDBTitle: crystal structure of the escherichia coli common pilus chaperone, ecpb
32	c4hcgA_	Alignment	not modelled	39.4	12	PDB header: oxidoreductase Chain: A; PDB Molecule: cupredoxin 1; PDBTitle: uncharacterized cupredoxin-like domain protein cupredoxin_1 with zinc2 bound from bacillus anthracis
33	c6q7jB_	Alignment	not modelled	37.2	17	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
34	c3zmrA_	Alignment	not modelled	36.2	13	PDB header: hydrolase Chain: A; PDB Molecule: cellulase (glycosyl hydrolase family 5); PDBTitle: bacteroides ovatus gh5 xyloglucanase in complex with a xxxg2 heptasaccharide
35	c2f1eA_	Alignment	not modelled	36.2	23	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein apag; PDBTitle: solution structure of apag protein
36	c2e6jA_	Alignment	not modelled	34.8	17	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
37	c4f2eA_	Alignment	not modelled	33.5	8	PDB header: metal transport Chain: A; PDB Molecule: cupa; PDBTitle: crystal structure of the streptococcus pneumoniae d39 copper chaperone2 cupa with cu(i)
38	c3isyA_	Alignment	not modelled	33.1	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
39	d1xvsa_	Alignment	not modelled	32.8	28	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
40	c4f2fA_	Alignment	not modelled	32.2	12	PDB header: metal binding protein Chain: A; PDB Molecule: cation-transporting atpase, e1-e2 family protein; PDBTitle: crystal structure of the metal binding domain (mbd) of the2 streptococcus pneumoniae d39 cu(i) exporting p-type atpase copa with3 cu(i)
41	c5e09A_	Alignment	not modelled	28.9	10	PDB header: hydrolase Chain: A; PDB Molecule: cellulase; PDBTitle: structural insight of a trimodular halophilic cellulase with a family2 46 carbohydrate-binding module
42	d1wzla2	Alignment	not modelled	28.7	16	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
43	c3qisA_	Alignment	not modelled	27.3	16	PDB header: hydrolase/protein binding Chain: A; PDB Molecule: inositol polyphosphate 5-phosphatase ocr1; PDBTitle: recognition of the f&h motif by the lowe syndrome protein ocr1
44	d1tzaa_	Alignment	not modelled	26.9	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
45	c2kutA_	Alignment	not modelled	24.6	15	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
46	c2ahnA_	Alignment	not modelled	23.8	15	PDB header: allergen Chain: A; PDB Molecule: thaumatin-like protein; PDBTitle: high resolution structure of a cherry allergen pru av 2
47	c2nc8A_	Alignment	not modelled	23.5	23	PDB header: protein binding Chain: A; PDB Molecule: lipoprotein lppm; PDBTitle: nmr structure of the mycobacterium tuberculosis lppm (rv2171) protein2 folded domain
48	c5aj3c_	Alignment	not modelled	22.5	50	PDB header: ribosome Chain: C; PDB Molecule: mitoribosomal protein us3m, mrps24; PDBTitle: structure of the small subunit of the mammalian mitoribosome
49	d1e42a1	Alignment	not modelled	21.8	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Alpha-adaptin ear subdomain-like
50	c4ncdA_	Alignment	not modelled	21.1	12	PDB header: chaperone Chain: A; PDB Molecule: gram-negative pili assembly chaperone, n-terminal domain PDBTitle: crystal structure of class 5 fimbriae chaperone cfaa
51	c6b7lA_	Alignment	not modelled	19.4	20	PDB header: unknown function Chain: A; PDB Molecule: immune modulator a; PDBTitle: aeromonas veronii immune modulator a
52	d1xq4a_	Alignment	not modelled	19.1	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: ApaG-like Family: ApaG-like
53	c2x41A_	Alignment	not modelled	18.4	16	PDB header: hydrolase Chain: A; PDB Molecule: beta-glucosidase;

53	c6at1A	Alignment	not modelled	16.4	10	PDBTitle: structure of beta-glucosidase 3b from thermotoga neapolitana in2 complex with glucose
54	d1ehxa	Alignment	not modelled	16.5	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cellulosomal scaffoldin protein CipC, module x2.1
55	c3u07A	Alignment	not modelled	15.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vpa0106; PDBTitle: crystal structure of the vpa0106 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr106.
56	c3fn2A	Alignment	not modelled	14.7	40	PDB header: transferase Chain: A: PDB Molecule: putative sensor histidine kinase domain; PDBTitle: crystal structure of a putative sensor histidine kinase domain from2 clostridium symbiosum atcc 14940
57	c3pe9A	Alignment	not modelled	14.7	10	PDB header: unknown function Chain: A: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
58	c3pe9C	Alignment	not modelled	14.7	10	PDB header: unknown function Chain: C: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
59	d1ji1a2	Alignment	not modelled	14.2	10	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
60	c2criA	Alignment	not modelled	14.2	25	PDB header: transport protein Chain: A: PDB Molecule: vesicle-associated membrane protein-associated PDBTitle: solution structure of the msp domain of mouse vamp-2 associated proteina
61	c1e42A	Alignment	not modelled	13.7	21	PDB header: endocytosis Chain: A: PDB Molecule: ap-2 complex subunit beta; PDBTitle: beta2-adaptin appendage domain, from clathrin adaptor ap2
62	c5cn1A	Alignment	not modelled	13.5	21	PDB header: protein transport Chain: A: PDB Molecule: adp-ribosylation factor-binding protein gga1; PDBTitle: crystal structure of yeast gga1_gae domain-p21
63	c5z87B	Alignment	not modelled	13.0	13	PDB header: hydrolase Chain: B: PDB Molecule: emgh1; PDBTitle: structural of a novel b-glucosidase emgh1 at 2.3 angstrom from2 erythrobacter marinus
64	d1kyfa1	Alignment	not modelled	12.9	6	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Alpha-adaptin ear subdomain-like
65	d1jv2a3	Alignment	not modelled	12.6	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Integrin domains Family: Integrin domains
66	c1z9oB	Alignment	not modelled	12.5	18	PDB header: protein binding/lipid binding protein Chain: B: PDB Molecule: vesicle-associated membrane protein-associated protein a; PDBTitle: 1.9 angstrom crystal structure of the rat vap-a msp homology domain in2 complex with the rat orp1 ffat motif
67	d2vj0a1	Alignment	not modelled	12.4	6	Fold: Immunoglobulin-like beta-sandwich Superfamily: Clathrin adaptor appendage domain Family: Alpha-adaptin ear subdomain-like
68	c4oleD	Alignment	not modelled	12.2	21	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
69	c4rt6A	Alignment	not modelled	11.1	22	PDB header: protein binding Chain: A: PDB Molecule: heme/hemopexin-binding protein; PDBTitle: structure of a complex between hemopexin and hemopexin binding protein
70	c1ky6A	Alignment	not modelled	11.1	6	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: alpha-adaptin c; PDBTitle: ap-2 clathrin adaptor alpha-appendage in complex with epsin2 dpw peptide
71	c2ys4A	Alignment	not modelled	10.2	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 of2 hydin protein from human
72	c2aanA	Alignment	not modelled	9.8	6	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	c3ac0B	Alignment	not modelled	9.5	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluveromyces marxianus in2 complex with glucose
74	d1lmia	Alignment	not modelled	9.4	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Antigen MPT63/MPB63 (immunoprotective extracellular protein) Family: Antigen MPT63/MPB63 (immunoprotective extracellular protein)
75	d1wica	Alignment	not modelled	8.7	23	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like
76	c5wabD	Alignment	not modelled	8.7	14	PDB header: hydrolase Chain: D: PDB Molecule: putative beta-glucosidase; PDBTitle: crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase
77	c5jp0A	Alignment	not modelled	8.7	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase bogh3b; PDBTitle: bacteroides ovatus xyloglucan pul gh3b with bound glucose
78	c3mnmC	Alignment	not modelled	8.6	16	PDB header: protein transport Chain: C: PDB Molecule: adp-ribosylation factor-binding protein gga2;

						PDBTitle: crystal structure of gae domain of gga2p from saccharomyces cerevisiae
79	d1ejxb_	Alignment	not modelled	8.4	23	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
80	d1du5a_	Alignment	not modelled	8.2	18	Fold: Osmotin, thaumatin-like protein Superfamily: Osmotin, thaumatin-like protein Family: Osmotin, thaumatin-like protein
81	c3g7mA_	Alignment	not modelled	8.2	20	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: xylanase inhibitor tl-xi; PDBTitle: structure of the thaumatin-like xylanase inhibitor tlxi
82	c3u48A_	Alignment	not modelled	7.9	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
83	c2d4nA_	Alignment	not modelled	7.9	7	PDB header: hydrolase Chain: A: PDB Molecule: du; PDBTitle: crystal structure of m-pmv dutpase complexed with dupnpp, substrate2 analogue
84	c2w2sA_	Alignment	not modelled	7.8	36	PDB header: viral protein Chain: A: PDB Molecule: matrix protein; PDBTitle: structure of the lagos bat virus matrix protein
85	c2l8aA_	Alignment	not modelled	7.7	16	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: structure of a novel cbm3 lacking the calcium-binding site
86	c3m86B_	Alignment	not modelled	7.6	13	PDB header: protein binding Chain: B: PDB Molecule: amoebiasin-2; PDBTitle: crystal structure of the cysteine protease inhibitor, ehicp2, from2 entamoeba histolytica
87	d1duna_	Alignment	not modelled	7.6	20	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
88	c6rimB_	Alignment	not modelled	7.5	23	PDB header: toxin Chain: B: PDB Molecule: putative botulinum-like toxin wo; PDBTitle: crystal structure of the catalytic domain of the weissela oryzae2 botulinum like toxin
89	c2qsvA_	Alignment	not modelled	7.4	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
90	c5tf0B_	Alignment	not modelled	7.4	20	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
91	d1z45a1	Alignment	not modelled	7.2	12	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Aldose 1-epimerase (mutarotase)
92	d1pcva_	Alignment	not modelled	7.2	18	Fold: Osmotin, thaumatin-like protein Superfamily: Osmotin, thaumatin-like protein Family: Osmotin, thaumatin-like protein
93	c1mqsb_	Alignment	not modelled	7.1	67	PDB header: endocytosis/exocytosis Chain: B: PDB Molecule: integral membrane protein sed5; PDBTitle: crystal structure of sly1p in complex with an n-terminal peptide of2 sed5p
94	d4ubpb_	Alignment	not modelled	7.1	15	Fold: beta-clip Superfamily: Urease, beta-subunit Family: Urease, beta-subunit
95	c3pdgA_	Alignment	not modelled	6.9	3	PDB header: unknown function Chain: A: PDB Molecule: fibronectin(iii)-like module; PDBTitle: structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
96	c3dcdA_	Alignment	not modelled	6.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: galactose mutarotase related enzyme; PDBTitle: x-ray structure of the galactose mutarotase related enzyme q5fkd7 from2 lactobacillus acidophilus at the resolution 1.9a. northeast3 structural genomics consortium target lar33.
97	c1l9mB_	Alignment	not modelled	6.6	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
98	c3a5vA_	Alignment	not modelled	6.6	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of alpha-galactosidase i from mortierella vinacea
99	d1mspa_	Alignment	not modelled	6.6	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: PapD-like Family: MSP-like