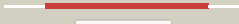

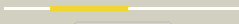


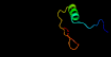

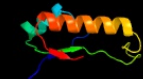

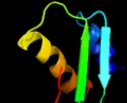





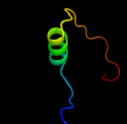

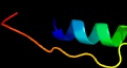




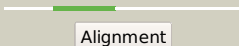
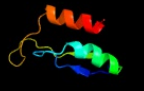
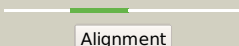


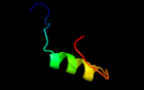
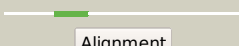

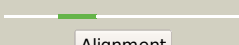
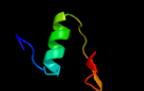
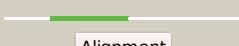

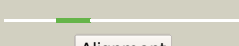


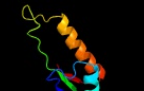

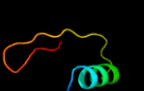
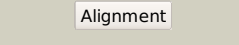

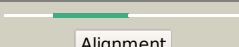

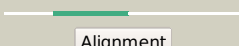


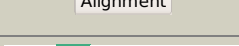
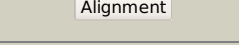


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1154c_(-)_1280848_1281489
Date	Wed Jul 31 22:05:24 BST 2019
Unique Job ID	4c741e39bbd8afcc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hiya1	 Alignment		100.0	19	Fold: SP0830-like Superfamily: SP0830-like Family: SP0830-like
2	c2oylB_	 Alignment		75.2	18	PDB header: hydrolase Chain: B: PDB Molecule: endoglycoceramidase ii; PDBTitle: endo-glycoceramidase ii from rhodococcus sp.: cellobiose-like2 imidazole complex
3	c3p9kD_	 Alignment		71.4	26	PDB header: transferase Chain: D: PDB Molecule: caffeic acid o-methyltransferase; PDBTitle: crystal structure of perennial ryegrass lpomt1 complexed with s-2 adenosyl-l-homocysteine and coniferaldehyde
4	c4xzbA_	 Alignment		69.4	14	PDB header: hydrolase Chain: A: PDB Molecule: cela; PDBTitle: endo-glucanase gscela p1
5	c3uz0A_	 Alignment		67.6	7	PDB header: transport protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: crystal structure of spoiiiiah and spoiiq complex
6	d7a3ha_	 Alignment		64.9	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
7	c3tufA_	 Alignment		64.3	7	PDB header: signaling protein Chain: A: PDB Molecule: stage iii sporulation protein ah; PDBTitle: structure of the spoiiq-spoiiiiah pore forming complex.
8	d1kyza2	 Alignment		63.4	24	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
9	d1im8a_	 Alignment		57.8	20	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Hypothetical protein HI0319 (YecO)
10	c5i2uB_	 Alignment		56.1	13	PDB header: hydrolase Chain: B: PDB Molecule: cellulase; PDBTitle: crystal structure of a novel halo-tolerant cellulase from soil2 metagenome
11	c3f55A_	 Alignment		55.7	28	PDB header: hydrolase, allergen Chain: A: PDB Molecule: beta-1,3-glucanase; PDBTitle: crystal structure of the native endo beta-1,3-glucanase (hev b 2), a2 major allergen from hevea brasiliensis (space group p41)

12	c4fk9A_	 Alignment		55.5	18	PDB header: hydrolase Chain: A: PDB Molecule: cellulose-binding family ii; PDBTitle: high resolution structure of the catalytic domain of mannanase2 sacte_2347 from streptomyces sp. sirexaa-e
13	c2rogA_	 Alignment		55.4	33	PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: solution structure of thermus thermophilus hb8 ttha17182 protein in living e. coli cells
14	d1fp1d2	 Alignment		52.8	18	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Plant O-methyltransferase, C-terminal domain
15	c4w7wA_	 Alignment		52.3	25	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: high-resolution structure of xaccl5a in complex with cellopentaose
16	c1kyzC_	 Alignment		52.1	25	PDB header: transferase Chain: C: PDB Molecule: caffeic acid 3-o-methyltransferase; PDBTitle: crystal structure analysis of caffeic acid/5-hydroxyferulic acid 3/5-o-methyltransferase ferulic acid complex
17	c5ccuA_	 Alignment		50.6	14	PDB header: hydrolase Chain: A: PDB Molecule: putative secreted endoglycosylceramidase; PDBTitle: crystal structure of endoglycosylceramidase i from rhodococ-cus equi
18	d2cyga1	 Alignment		50.5	28	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
19	c5oydA_	 Alignment		49.7	24	PDB header: hydrolase Chain: A: PDB Molecule: cellulase, putative, cel5d; PDBTitle: gh5 endo-xyloglucanase from cellvibrio japonicus
20	c4e70A_	 Alignment		49.0	26	PDB header: transferase Chain: A: PDB Molecule: coniferyl alcohol 9-o-methyltransferase; PDBTitle: crystal structure analysis of coniferyl alcohol 9-o-methyltransferase2 from linum nodiflorum in complex with coniferyl alcohol
21	c5cvvB_	 Alignment	not modelled	48.6	22	PDB header: transferase Chain: B: PDB Molecule: (iso)eugenol o-methyltransferase; PDBTitle: coniferyl alcohol bound monolignol 4-o-methyltransferase 9
22	c4htyA_	 Alignment	not modelled	48.5	13	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of a metagenome-derived cellulase cel5a
23	c2cksB_	 Alignment	not modelled	47.3	10	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase e-5; PDBTitle: x-ray crystal structure of the catalytic domain of thermobifida fusca2 endoglucanase cel5a (e5)
24	d1ttza_	 Alignment	not modelled	46.6	31	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
25	c3mmwB_	 Alignment	not modelled	46.0	17	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase cel5a from the hyperthermophilic2 thermotoga maritima
26	c5xohA_	 Alignment	not modelled	45.7	30	PDB header: transferase Chain: A: PDB Molecule: bergaptol o-methyltransferase; PDBTitle: crystal structure of bergaptol o-methyltransferase complex
27	c5uhxA_	 Alignment	not modelled	45.5	13	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate-active enzyme; PDBTitle: structure of cellulase cel5c_1
28	d1aq0a_	 Alignment	not modelled	45.3	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
		 Alignment				PDB header: structural genomics, unknown function

29	c3dtnA	Alignment	not modelled	44.9	24	Chain: A: PDB Molecule: putative methyltransferase mm_2633; PDBTitle: crystal structure of putative methyltransferase-mm_2633 from2 methanosarcina mazel.
30	d1ecea	Alignment	not modelled	43.5	7	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
31	c1xsza	Alignment	not modelled	42.5	17	PDB header: signaling protein Chain: A: PDB Molecule: guanine nucleotide exchange protein; PDBTitle: the structure of ralf
32	d1ghsa	Alignment	not modelled	42.5	28	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
33	c4d7kB	Alignment	not modelled	42.0	24	PDB header: transferase Chain: B: PDB Molecule: sam-dependent methyltransferases; PDBTitle: crystal structure of n,n-8-amino-8-demethyl-d-riboflavin2 dimethyltransferase (rosa) from streptomyces davawensis
34	c6n0tA	Alignment	not modelled	41.7	24	PDB header: ligase Chain: A: PDB Molecule: trna ligase; PDBTitle: trna ligase
35	c2jepB	Alignment	not modelled	41.5	19	PDB header: hydrolase Chain: B: PDB Molecule: xyloglucanase; PDBTitle: native family 5 xyloglucanase from paenibacillus pabuli
36	c5cm2Z	Alignment	not modelled	41.3	14	PDB header: transferase Chain: Z: PDB Molecule: trna methyltransferase; PDBTitle: insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
37	c4u5iB	Alignment	not modelled	41.0	19	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase h; PDBTitle: complex structure of mutant ctcel5e (e314a) with xylobiose
38	c2k2pA	Alignment	not modelled	40.5	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1203; PDBTitle: solution nmr structure of protein atu1203 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att10, ontario center for structural proteomics target atc1183
39	c4qvgC	Alignment	not modelled	40.2	23	PDB header: transferase Chain: C: PDB Molecule: sibl; PDBTitle: crystal structure of s-adenosylmethionine-dependent methyltransferase2 sibl in its apo form
40	c4im4F	Alignment	not modelled	40.0	18	PDB header: hydrolase Chain: F: PDB Molecule: endoglucanase e; PDBTitle: multifunctional cellulase, xylanase, mannanase
41	c4ee9A	Alignment	not modelled	39.8	18	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of the rbccl1 endo-1,4-glucanase
42	c1fpqA	Alignment	not modelled	38.2	19	PDB header: transferase Chain: A: PDB Molecule: isoliquiritigenin 2'-o-methyltransferase; PDBTitle: crystal structure analysis of selenomethionine substituted chalcone o-2 methyltransferase
43	d1ceoa	Alignment	not modelled	38.1	35	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
44	c2rrnA	Alignment	not modelled	38.1	13	PDB header: protein transport Chain: A: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: solution structure of secdf periplasmic domain p4
45	c5uzgA	Alignment	not modelled	37.1	11	PDB header: rna binding protein Chain: A: PDB Molecule: at27789p; PDBTitle: crystal structure of glorund qrrm1 domain
46	d2phna1	Alignment	not modelled	36.8	19	Fold: CofE-like Superfamily: CofE-like Family: CofE-like
47	c5hosA	Alignment	not modelled	36.8	31	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of the endo-beta-1,4-glucanase xac0029 from2 xanthomonas axonopodis pv. citri
48	d1egza	Alignment	not modelled	36.0	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
49	c4c0aA	Alignment	not modelled	34.4	23	PDB header: protein transport Chain: A: PDB Molecule: iq motif and sec7 domain-containing protein 1; PDBTitle: arf1(delta1-17)in complex with brag2 sec7-ph domain
50	c3pzvB	Alignment	not modelled	34.1	14	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase; PDBTitle: c2 crystal form of the endo-1,4-beta-glucanase from bacillus subtilis2 168
51	c5i2hB	Alignment	not modelled	33.7	20	PDB header: transferase Chain: B: PDB Molecule: o-methyltransferase family 2; PDBTitle: crystal structure of o-methyltransferase family 2 protein plim_11472 from planctomyces limnophilus dsm 3776 complex with apigenin
52	c3vupB	Alignment	not modelled	33.6	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-1,4-mannanase; PDBTitle: beta-1,4-mannanase from the common sea hare aplysia kurodai
53	c3bijC	Alignment	not modelled	33.5	21	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein gsu0716; PDBTitle: crystal structure of protein gsu0716 from geobacter sulfurreducens.2 northeast structural genomics target gsr13
54	c4iyB	Alignment	not modelled	32.5	19	PDB header: hydrolase Chain: B: PDB Molecule: caspase-6; PDBTitle: crystal structure of full-length caspase-6 zymogen

55	d2r25b1	Alignment	not modelled	32.5	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
56	d1xsza1	Alignment	not modelled	32.3	19	Fold: alpha-alpha superhelix Superfamily: Sec7 domain Family: Sec7 domain
57	d1cc8a_	Alignment	not modelled	32.2	21	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
58	c3jugA_	Alignment	not modelled	31.9	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-mannanase; PDBTitle: crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
59	c3ocjA_	Alignment	not modelled	31.3	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported protein; PDBTitle: the crystal structure of a possilbe exported protein from bordetella2 parapertussis
60	d1vbka2	Alignment	not modelled	31.2	13	Fold: THUMP domain Superfamily: THUMP domain-like Family: THUMP domain
61	c3i53A_	Alignment	not modelled	29.7	24	PDB header: transferase Chain: A: PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of an o-methyltransferase (ncsb1) from2 neocarcinostatin biosynthesis in complex with s-adenosyl-l-3 homocysteine (sah)
62	d1h1na_	Alignment	not modelled	29.6	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
63	c4kifB_	Alignment	not modelled	28.9	24	PDB header: transferase Chain: B: PDB Molecule: methyltransferase mppj; PDBTitle: crystal structure of methyltransferase from streptomyces hygroscopicus2 complexed with phenylpyruvic acid
64	d1jcb5	Alignment	not modelled	28.8	29	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
65	c5fipA_	Alignment	not modelled	27.9	16	PDB header: hydrolase Chain: A: PDB Molecule: gh5 cellulase; PDBTitle: discovery and characterization of a novel thermostable and2 highly halotolerant gh5 cellulase from an icelandic hot3 spring isolate
66	c6ccaA_	Alignment	not modelled	27.9	20	PDB header: transferase Chain: A: PDB Molecule: disa protein; PDBTitle: crystal structure of dsza carbon methyltransferase
67	d1bqca_	Alignment	not modelled	27.8	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
68	d1fe0a_	Alignment	not modelled	27.1	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
69	c3ur8A_	Alignment	not modelled	26.4	21	PDB header: hydrolase Chain: A: PDB Molecule: glucan endo-1,3-beta-d-glucosidase; PDBTitle: lower-density crystal structure of potato endo-1,3-beta-glucanase
70	c3v7qB_	Alignment	not modelled	26.3	7	PDB header: rna binding protein Chain: B: PDB Molecule: probable ribosomal protein ylxq; PDBTitle: crystal structure of b. subtilis ylxq at 1.55 a resolution
71	d1tvna1	Alignment	not modelled	26.1	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
72	c3qr3B_	Alignment	not modelled	26.0	16	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase eg-ii; PDBTitle: crystal structure of cel5a (eg2) from hypocreia jecorina (trichoderma2 reesei)
73	c2y4oA_	Alignment	not modelled	25.8	15	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
74	c4nf7A_	Alignment	not modelled	25.4	19	PDB header: hydrolase Chain: A: PDB Molecule: endo-1,4-beta-glucanase cel5c; PDBTitle: crystal structure of the gh5 family catalytic domain of endo-1,4-beta-2 glucanase cel5c from butyrivibrio proteoclasticus.
75	c5iceA_	Alignment	not modelled	25.1	24	PDB header: transferase Chain: A: PDB Molecule: (s)-norcoclaurine 6-o-methyltransferase; PDBTitle: crystal structure of (s)-norcoclaurine 6-o-methyltransferase with s-2 adenosyl-l-homocysteine and norlaudanosoline
76	d2ysca1	Alignment	not modelled	24.9	47	Fold: WW domain-like Superfamily: WW domain Family: WW domain
77	d1qupa2	Alignment	not modelled	24.9	10	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
78	c1uj6A_	Alignment	not modelled	24.8	12	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
79	c3laxA_	Alignment	not modelled	24.4	15	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
80	c5ady6_	Alignment	not modelled	24.2	13	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hflx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hflx

81	c3civA_	Alignment	not modelled	23.6	23	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-mannanase; PDBTitle: crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
82	c3i55B_	Alignment	not modelled	23.0	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: b-1,4-endoglucanase/cellulase; PDBTitle: crystal structure of a putative beta-1,4-endoglucanase / cellulase2 from prevotella bryantii
83	c3icaB_	Alignment	not modelled	22.8	29	PDB header: ligase Chain: B: PDB Molecule: phenylalanyl-trna synthetase beta chain; PDBTitle: the crystal structure of the beta subunit of a phenylalanyl-trna2 synthetase from porphyromonas gingivalis w83
84	c1zgaA_	Alignment	not modelled	22.5	21	PDB header: plant protein, transferase Chain: A: PDB Molecule: isoflavanone 4'-o-methyltransferase'; PDBTitle: crystal structure of isoflavanone 4'-o-methyltransferase complexed2 with (+)-6a-hydroxymaackiin
85	c3qovD_	Alignment	not modelled	22.4	15	PDB header: ligase Chain: D: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
86	c6bbqA_	Alignment	not modelled	22.3	20	PDB header: lipid binding protein Chain: A: PDB Molecule: cytohesin-3,adp-ribosylation factor 6; PDBTitle: model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein
87	c6gl2A_	Alignment	not modelled	22.2	18	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase, family gh5; PDBTitle: structure of zengagh5_4 wild type at 1.2 angstrom resolution
88	c2ip2B_	Alignment	not modelled	22.1	28	PDB header: transferase Chain: B: PDB Molecule: probable phenazine-specific methyltransferase; PDBTitle: structure of the pyocyanin biosynthetic protein phzm
89	c2kyzA_	Alignment	not modelled	21.8	21	PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima
90	c3gwzB_	Alignment	not modelled	21.8	28	PDB header: transferase Chain: B: PDB Molecule: mmcr; PDBTitle: structure of the mitomycin 7-o-methyltransferase mmcr
91	d2obpa1	Alignment	not modelled	21.7	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ReutB4095-like
92	c1qupA_	Alignment	not modelled	21.5	10	PDB header: chaperone Chain: A: PDB Molecule: superoxide dismutase 1 copper chaperone; PDBTitle: crystal structure of the copper chaperone for superoxide dismutase
93	c3fnpB_	Alignment	not modelled	21.1	14	PDB header: dna binding protein Chain: B: PDB Molecule: geobacillus stearothermophilus uvrB interaction domain; PDBTitle: crystal structure of uvra-uvrB interaction domains
94	c3s2uA_	Alignment	not modelled	20.9	20	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) PDBTitle: crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
95	c3qbcB_	Alignment	not modelled	20.9	19	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine PDBTitle: structure and design of a new pterin site inhibitor of s. aureus hppk
96	c4gekG_	Alignment	not modelled	20.9	22	PDB header: transferase Chain: G: PDB Molecule: trna (cmo5u34)-methyltransferase; PDBTitle: crystal structure of wild-type cmoa from e.coli
97	c4z2yA_	Alignment	not modelled	20.6	27	PDB header: transferase Chain: A: PDB Molecule: calo6; PDBTitle: crystal structure of methyltransferase calo6
98	c5a94B_	Alignment	not modelled	20.2	13	PDB header: hydrolase Chain: B: PDB Molecule: putative retaining b-glycosidase; PDBTitle: crystal structure of beta-glucanase sdgluc5_26a from saccharophagus2 degradans in complex with tetrasaccharide a, form 1
99	d1wkya2	Alignment	not modelled	19.8	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases