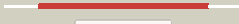



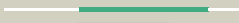






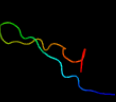





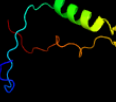

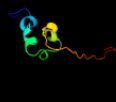



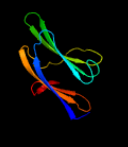
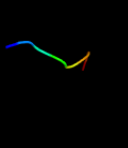
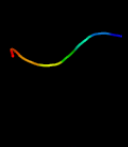


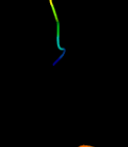
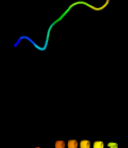
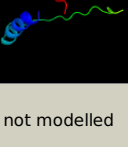


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0098 (-) _107597_108148
Date	Tue Jul 23 14:50:13 BST 2019
Unique Job ID	fc9d1d8a9d4cd4bd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pfcA_	 Alignment		100.0	100	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein rv0098/mt0107; PDBTitle: structure of mycobacterium tuberculosis rv0098
2	c5wsxA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of sav606
3	c4k00A_	 Alignment		46.2	12	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-dihydroxy-2-naphthoyl-coa hydrolase; PDBTitle: crystal structure of slr0204, a 1,4-dihydroxy-2-naphthoyl-coa2 thioesterase from synechocystis
4	d2hlja1	 Alignment		43.7	17	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
5	c4rmmA_	 Alignment		35.3	24	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the q7nvp2_chrvo protein from chromobacterium2 violaceum. northeast structural genomics consortium target cvr191
6	c6b48K_	 Alignment		29.3	28	PDB header: immune system / rna Chain: K: PDB Molecule: anti-crispr protein acrf10; PDBTitle: cryo-em structure of type i-f crispr crrna-guided csy surveillance2 complex with bound anti-crispr protein acrf10
7	c2lm0A_	 Alignment		25.4	53	PDB header: nuclear protein Chain: A: PDB Molecule: af4/fmr2 family member 1/protein af-9 chimera; PDBTitle: solution structure of the af4-af9 complex
8	c3ck1B_	 Alignment		24.5	10	PDB header: hydrolase Chain: B: PDB Molecule: putative thioesterase; PDBTitle: crystal structure of a putative thioesterase (reut_a2179) from2 ralstonia eutropha jmp134 at 1.74 a resolution
9	c5xk9F_	 Alignment		23.2	8	PDB header: transferase Chain: F: PDB Molecule: undecaprenyl diphosphate synthase; PDBTitle: crystal structure of isosesquilandulyl diphosphate synthase from2 streptomyces sp. strain cnh-189 in complex with gssp and dmapp
10	c5cajB_	 Alignment		22.5	16	PDB header: unknown function Chain: B: PDB Molecule: upf0246 protein yaaa; PDBTitle: crystal structure of e. coli yaaa, a member of the duf328/upf02462 family
11	c3kspA_	 Alignment		20.1	5	PDB header: unknown function Chain: A: PDB Molecule: calcium/calmodulin-dependent kinase ii association domain; PDBTitle: crystal structure of a putative ca/calmodulin-dependent kinase ii2 association domain (exig_1688) from exiguobacterium sibiricum 255-153 at 2.59 a resolution

12	c2egiE_	Alignment		19.4	17	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: hypothetical protein aq_1494; PDBTitle: crystal structure of a hypothetical protein(aq1494) from aquifex2 aeolicus
13	c3nv4A_	Alignment		19.2	20	PDB header: sugar binding protein Chain: A: PDB Molecule: galectin 9 short isoform variant; PDBTitle: crystal structure of human galectin-9 c-terminal crd in complex with 2 sialyllactose
14	d1ntxa_	Alignment		19.1	25	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
15	d1iq9a_	Alignment		18.2	38	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
16	d1lcla_	Alignment		17.6	15	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Galectin (animal S-lectin)
17	c2w3xE_	Alignment		16.9	18	PDB header: hydrolase Chain: E: PDB Molecule: cale7; PDBTitle: crystal structure of a bifunctional hotdog fold2 thioesterase in enediyne biosynthesis, cale7
18	d1dfxa2	Alignment		16.8	56	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Desulfiredoxin
19	d2dmda1	Alignment		16.7	55	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
20	c1w25B_	Alignment		15.9	15	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
21	d1fsoa_	Alignment	not modelled	15.8	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
22	d3ebxa_	Alignment	not modelled	15.2	38	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
23	d1ut9a2	Alignment	not modelled	14.9	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
24	c4fr9A_	Alignment	not modelled	14.9	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a blip-like protein (bf1215) from bacteroides2 fragilis nctc 9343 at 1.20 a resolution
25	c3r87A_	Alignment	not modelled	14.9	15	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf6 protein from photobacterium profundum
26	d1rhoa_	Alignment	not modelled	14.8	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
27	d1vpva_	Alignment	not modelled	14.5	38	Fold: TIM beta/alpha-barrel Superfamily: TM1631-like Family: TM1631-like
28	d1z54a1	Alignment	not modelled	14.2	11	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
29	c4g92C_	Alignment	not modelled	13.9	25	PDB header: transcription/dna Chain: C: PDB Molecule: hape;

						PDBTitle: ccaat-binding complex from aspergillus nidulans with dna
30	d1vzia2	Alignment	not modelled	13.6	44	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Desulfiredoxin
31	d1vb0a_	Alignment	not modelled	13.5	38	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
32	c2kfvA_	Alignment	not modelled	13.3	24	PDB header: isomerase Chain: A: PDB Molecule: fk506-binding protein 3; PDBTitle: structure of the amino-terminal domain of human fk506-2 binding protein 3 / northeast structural genomics3 consortium target ht99a
33	d1v43a2	Alignment	not modelled	13.1	12	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
34	d1tfsa_	Alignment	not modelled	13.0	17	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
35	d1v6pa_	Alignment	not modelled	12.9	38	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
36	c2kvfA_	Alignment	not modelled	12.8	56	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
37	d1s5ua_	Alignment	not modelled	12.7	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
38	d1vpqa_	Alignment	not modelled	12.7	50	Fold: TIM beta/alpha-barrel Superfamily: TM1631-like Family: TM1631-like
39	c2kimA_	Alignment	not modelled	12.4	28	PDB header: transferase Chain: A: PDB Molecule: o6-methylguanine-dna methyltransferase; PDBTitle: 1.7-mm microcryoprobe solution nmr structure of an o6-methylguanine2 dna methyltransferase family protein from vibrio parahaemolyticus.3 northeast structural genomics consortium target vpr247.
40	c3gx4X_	Alignment	not modelled	12.4	50	PDB header: dna binding protein/dna Chain: X: PDB Molecule: alkyltransferase-like protein 1; PDBTitle: crystal structure analysis of s. pombe atl in complex with dna
41	c2vg2C_	Alignment	not modelled	11.8	15	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
42	d1g6ma_	Alignment	not modelled	11.6	50	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
43	c3kreA_	Alignment	not modelled	11.2	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylaminoimidazole-succinocarboxamide synthase; PDBTitle: crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from ehrlichia chaffeensis at 1.8a resolution
44	d1doab_	Alignment	not modelled	10.9	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
45	c3nuaB_	Alignment	not modelled	10.8	36	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylaminoimidazole-succinocarboxamide synthase; PDBTitle: crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from clostridium perfringens
46	d1ajwa_	Alignment	not modelled	10.8	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
47	c3gekA_	Alignment	not modelled	10.8	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thioesterase yhda; PDBTitle: crystal structure of putative thioesterase yhda from lactococcus2 lactis. northeast structural genomics consortium target kr113
48	d2owna2	Alignment	not modelled	10.7	12	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Acyl-ACP thioesterase-like
49	c3btpA_	Alignment	not modelled	10.7	40	PDB header: dna binding protein, chaperone Chain: A: PDB Molecule: single-strand dna-binding protein; PDBTitle: crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
50	d1hh4e_	Alignment	not modelled	10.5	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
51	d1vh5a_	Alignment	not modelled	10.4	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
52	d1qm7a_	Alignment	not modelled	10.4	17	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Snake venom toxins
53	c2m83A_	Alignment	not modelled	10.2	33	PDB header: hydrolase Chain: A: PDB Molecule: protein phosphatase 1 regulatory subunit 3a; PDBTitle: solution structure of the carbohydrate binding module of the muscle2 glycogen-targeting subunit of protein phosphatase-1

54	d1ds6b_	Alignment	not modelled	10.2	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
55	c4mjgB_	Alignment	not modelled	10.1	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf4853 family protein (actodo_00621) from <i>Mycobacterium goodii</i> atcc 17982 at 2.65 a resolution
56	d1sc0a_	Alignment	not modelled	9.9	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like
57	d1sfea1	Alignment	not modelled	9.8	42	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
58	d1qnta1	Alignment	not modelled	9.8	67	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
59	d1libx_	Alignment	not modelled	9.8	39	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: CAD domain
60	c1ibxB_	Alignment	not modelled	9.8	39	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: chimera of igg binding protein g and dna PDBTitle: nmr structure of dff40 and dff45 n-terminal domain complex
61	d2gjva1	Alignment	not modelled	9.7	25	Fold: Phage tail protein-like Superfamily: Phage tail protein-like Family: STM4215-like
62	c3lmbA_	Alignment	not modelled	9.6	5	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein olei01261 with unknown function2 from <i>Chlorobaculum tepidum</i> t1s
63	c2pzhC_	Alignment	not modelled	9.5	16	PDB header: hydrolase Chain: C: PDB Molecule: hypothetical protein hp_0496; PDBTitle: ybgc thioesterase (hp0496) from <i>Helicobacter pylori</i>
64	d1mgta1	Alignment	not modelled	9.5	50	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
65	d1njka_	Alignment	not modelled	9.5	13	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
66	c1zx3A_	Alignment	not modelled	9.4	57	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ne0241; PDBTitle: structure of ne0241 protein of unknown function from <i>Nitrosomonas europaea</i>
67	d1zx3a1	Alignment	not modelled	9.4	57	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: NE0241-like
68	c1geaA_	Alignment	not modelled	9.4	31	PDB header: neuropeptide Chain: A: PDB Molecule: pituitary adenylate cyclase activating PDBTitle: receptor-bound conformation of pacap21
69	d1lqva_	Alignment	not modelled	9.3	18	Fold: MHC antigen-recognition domain Superfamily: MHC antigen-recognition domain Family: MHC antigen-recognition domain
70	c3ulxA_	Alignment	not modelled	9.2	31	PDB header: dna binding protein Chain: A: PDB Molecule: stress-induced transcription factor nac1; PDBTitle: crystal structural of the conserved domain of rice stress-responsive2 nac1
71	c2z02A_	Alignment	not modelled	9.1	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylaminoimidazole-succinocarboxamide PDBTitle: crystal structure of f2 phosphoribosylaminoimidazole-succinocarboxamide synthase3 wit atp from <i>Methanocaldococcus jannaschii</i>
72	c2gqsA_	Alignment	not modelled	8.9	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylaminoimidazole-succinocarboxamide synthase; PDBTitle: saicar synthetase complexed with cair-mg2+ and adp
73	c3r9rA_	Alignment	not modelled	8.7	14	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylaminoimidazole-succinocarboxamide synthase; PDBTitle: structure of a phosphoribosylaminoimidazole-succinocarboxamide2 synthase from <i>Mycobacterium abscessus</i> atcc 19977 / dsm 44196
74	c2eefA_	Alignment	not modelled	8.4	28	PDB header: sugar binding protein Chain: A: PDB Molecule: protein phosphatase 1, regulatory (inhibitor) PDBTitle: solution structure of the cbm_21 domain from human protein2 phosphatase 1, regulatory (inhibitor) subunit 3b
75	d1kmta_	Alignment	not modelled	8.3	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
76	c3e8pA_	Alignment	not modelled	8.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the protein q8e9m7 from <i>Shewanella oneidensis</i> 2 related to thioesterase superfamily. northeast structural genomics3 consortium target sor246.
77	c3dadA_	Alignment	not modelled	8.2	23	PDB header: signaling protein Chain: A: PDB Molecule: fh1/fh2 domain-containing protein 1; PDBTitle: crystal structure of the n-terminal regulatory domains of2 the formin fhod1

78	c5cfmA	Alignment	not modelled	8.1	11	PDB header: immune system Chain: A: PDB Molecule: stimulator of interferon genes; PDBTitle: crystal structure of anemone sting (nematostella vectensis) in complex2 with 3', 3' cgamp, c(g(3', 5')pa(3', 5')p]
79	d1rxjA	Alignment	not modelled	8.0	21	Fold: Streptavidin-like Superfamily: Avidin/streptavidin Family: Avidin/streptavidin
80	c2gjfV	Alignment	not modelled	7.8	24	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative cytoplasmic protein; PDBTitle: crystal structure of a protein of unknown function from salmonella2 typhimurium
81	d1x3aa1	Alignment	not modelled	7.8	0	Fold: BSD domain-like Superfamily: BSD domain-like Family: BSD domain
82	c4i4jE	Alignment	not modelled	7.8	17	PDB header: hydrolase Chain: E: PDB Molecule: acp-polyene thioesterase; PDBTitle: the structure of sgce10, the acp-polyene thioesterase involved in c-2 1027 biosynthesis
83	c3l7mC	Alignment	not modelled	7.7	42	PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a
84	c5ibxB	Alignment	not modelled	7.7	13	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: 1.65 angstrom crystal structure of triosephosphate isomerase (tim)2 from streptococcus pneumoniae
85	c2djmA	Alignment	not modelled	7.7	33	PDB header: sugar binding protein Chain: A: PDB Molecule: glucoamylase a; PDBTitle: solution structure of n-terminal starch-binding domain of2 glucoamylase from rhizopus oryzae
86	c4f5yA	Alignment	not modelled	7.6	0	PDB header: immune system Chain: A: PDB Molecule: transmembrane protein 173; PDBTitle: crystal structure of human sting ctd complex with c-di-gmp
87	d2o5ua1	Alignment	not modelled	7.4	20	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: 4HBT-like
88	d2c9aa1	Alignment	not modelled	7.2	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
89	d1ttja	Alignment	not modelled	7.1	17	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
90	c2mphA	Alignment	not modelled	7.0	26	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp3; PDBTitle: solution structure of human fk506 binding protein 25
91	c4ef4B	Alignment	not modelled	6.8	0	PDB header: immune system Chain: B: PDB Molecule: transmembrane protein 173; PDBTitle: crystal structure of sting ctd complex with c-di-gmp
92	c1jp3A	Alignment	not modelled	6.8	17	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of e.coli undecaprenyl pyrophosphate synthase
93	c2xglB	Alignment	not modelled	6.7	19	PDB header: antibiotic Chain: B: PDB Molecule: colicin-m immunity protein; PDBTitle: the x-ray structure of the escherichia coli colicin m immunity protein2 demonstrates the presence of a disulphide bridge, which is3 functionally essential
94	c2xznB	Alignment	not modelled	6.6	22	PDB header: ribosome Chain: B: PDB Molecule: rps0e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
95	d2cnqa1	Alignment	not modelled	6.3	29	Fold: SAICAR synthase-like Superfamily: SAICAR synthase-like Family: SAICAR synthase
96	c1unhD	Alignment	not modelled	6.2	14	PDB header: cell cycle Chain: D: PDB Molecule: cyclin-dependent kinase 5 activator 1; PDBTitle: structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
97	d1unld	Alignment	not modelled	6.2	14	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
98	c3ugsB	Alignment	not modelled	6.1	21	PDB header: transferase Chain: B: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
99	d1vh9a	Alignment	not modelled	6.1	18	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: Paal/Ydil-like