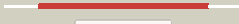



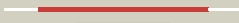












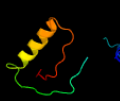

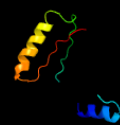


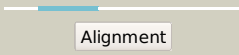

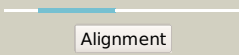

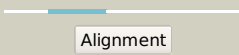
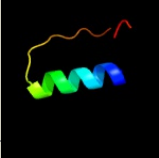
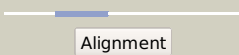
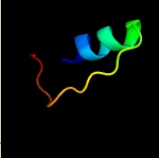
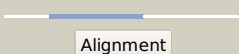

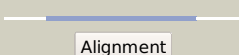
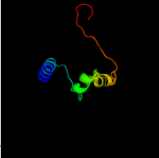

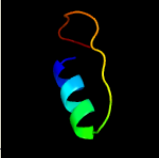
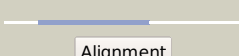

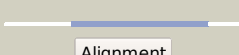


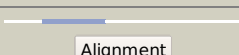

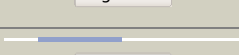
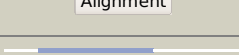
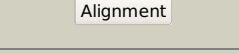
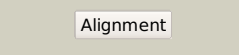
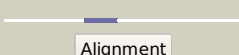



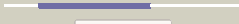

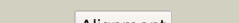
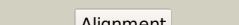
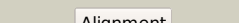
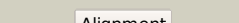
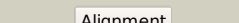
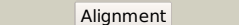
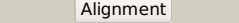
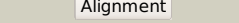
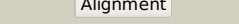
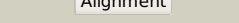
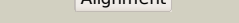
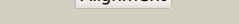
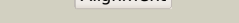
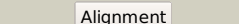




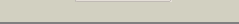


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1898 (-)_2144947_2145255
Date	Fri Aug 2 13:30:51 BST 2019
Unique Job ID	8f19a866eeaf9ee4

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lxja_	 Alignment		100.0	21	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
2	d1lxna_	 Alignment		100.0	23	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
3	c2epiA_	 Alignment		100.0	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0045 protein mj1052; PDBTitle: crystal structure pf hypothetical protein mj1052 from2 methanocaldococcus jannaschii (form 2)
4	d1yqha1	 Alignment		100.0	34	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
5	d1vk8a_	 Alignment		100.0	21	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
6	d2iboa1	 Alignment		100.0	22	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: MTH1187-like
7	d1s99a_	 Alignment		96.7	12	Fold: Ferredoxin-like Superfamily: MTH1187/YkoF-like Family: Putative thiamin/HMP-binding protein YkoF
8	c4mp4B_	 Alignment		72.3	11	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of a glutathione transferase family member from2 acinetobacter baumannii, target efi-501785, apo structure
9	d1lfpa_	 Alignment		44.1	14	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
10	d1kona_	 Alignment		34.5	15	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
11	c2kbzA_	 Alignment		33.6	35	PDB header: viral protein Chain: A: PDB Molecule: 15 protein (bacteriophage spp1 complete PDBTitle: nmr structure of protein gp15 of bacteriophage spp1

12	c4yamA	 Alignment		33.5	11	PDB header: transferase Chain: A: PDB Molecule: beta-etherase; PDBTitle: crystal structure of lige-apo form from sphingobium sp. strain syk-6
13	d1nyra1	 Alignment		33.1	11	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
14	c3nivD	 Alignment		30.3	4	PDB header: isomerase Chain: D: PDB Molecule: glutathione s-transferase; PDBTitle: the crystal structure of glutathione s-transferase from legionella2 pneumophila
15	d1k25a1	 Alignment		28.4	17	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
16	c2y9jt	 Alignment		27.3	18	PDB header: protein transport Chain: T: PDB Molecule: protein prgh; PDBTitle: three-dimensional model of salmonella's needle complex at subnanometer2 resolution
17	c5t9jB	 Alignment		26.9	14	PDB header: hydrolase Chain: B: PDB Molecule: flap endonuclease gen homolog 1; PDBTitle: crystal structure of human gen1 in complex with holliday junction dna2 in the upper interface
18	d1pyya1	 Alignment		26.7	13	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
19	c5x62A	 Alignment		24.2	13	PDB header: transferase Chain: A: PDB Molecule: carnosine n-methyltransferase; PDBTitle: crystal structure of a carnosine n-methyltransferase bound by adohcy
20	c4oxxA	 Alignment		23.1	15	PDB header: electron transport Chain: A: PDB Molecule: cindoxin; PDBTitle: crystal structure of cindoxin, surface entropy reduction mutant
21	c4f3qA	 Alignment	not modelled	22.3	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein cbu_1566; PDBTitle: structure of a yebc family protein (cbu_1566) from coxiella burnetii
22	c3bbyA	 Alignment	not modelled	21.4	18	PDB header: transferase Chain: A: PDB Molecule: uncharacterized gst-like protein yfcf; PDBTitle: crystal structure of glutathione s-transferase (np_416804.1) from2 escherichia coli k12 at 1.85 a resolution
23	d1nj1a1	 Alignment	not modelled	21.4	19	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
24	d1qf6a1	 Alignment	not modelled	21.3	16	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
25	c4exqA	 Alignment	not modelled	21.1	6	PDB header: biosynthetic protein Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
26	c5xftA	 Alignment	not modelled	20.2	8	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydroascorbate reductase; PDBTitle: crystal structure of chlamydomonas reinhardtii dehydroascorbate2 reductase
27	c2k3dA	 Alignment	not modelled	19.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0334 protein; PDBTitle: solution nmr structure of the folded 79 residue fragment of2 lin0334 from listeria innocua. northeast structural3 genomics consortium target lkr15
28	d1y81a1	 Alignment	not modelled	19.5	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain

29	c4f03A_	 Alignment	not modelled	19.4	11	PDB header: transferase Chain: A: PDB Molecule: glutathione transferase; PDBTitle: crystal structure of the glutathione transferase gte1 from2 phanerochaete chrysosporium
30	c2ejaB_	 Alignment	not modelled	18.7	10	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
31	c3ff4A_	 Alignment	not modelled	18.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
32	d1lt7a_	 Alignment	not modelled	18.2	6	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
33	c3ehgA_	 Alignment	not modelled	18.0	12	PDB header: transferase Chain: A: PDB Molecule: sensor kinase (yocf protein); PDBTitle: crystal structure of the atp-binding domain of desk in complex with2 atp
34	c2pmfA_	 Alignment	not modelled	17.9	21	PDB header: ligase Chain: A: PDB Molecule: glycyl-trna synthetase; PDBTitle: the crystal structure of a human glycyl-trna synthetase mutant
35	c5w7sA_	 Alignment	not modelled	17.9	16	PDB header: transferase Chain: A: PDB Molecule: oxac; PDBTitle: crystal structure of oxac in complex with sinefungin and meleagrins
36	c5e6mA_	 Alignment	not modelled	17.4	22	PDB header: ligase/rna Chain: A: PDB Molecule: glycine--trna ligase; PDBTitle: crystal structure of human wild type glyrs bound with trnagly
37	c4zmmB_	 Alignment	not modelled	17.3	29	PDB header: transferase Chain: B: PDB Molecule: diguanylate cyclase; PDBTitle: ggdef domain of dcsbis complexed with c-di-gmp
38	c6mspA_	 Alignment	not modelled	17.3	10	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein foldit3; PDBTitle: de novo designed protein foldit3
39	d1z9ha2	 Alignment	not modelled	17.1	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
40	d1rp5a2	 Alignment	not modelled	16.3	12	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
41	c6q8jA_	 Alignment	not modelled	16.2	14	PDB header: splicing Chain: A: PDB Molecule: wd40 repeat-containing protein smu1; PDBTitle: nterminal domain of human smu1 in complex with lsp641
42	c4heqB_	 Alignment	not modelled	16.1	16	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: the crystal structure of flavodoxin from desulfovibrio gigas
43	d1edza2	 Alignment	not modelled	15.5	6	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
44	c4zmuD_	 Alignment	not modelled	14.5	16	PDB header: lyase Chain: D: PDB Molecule: diguanylate cyclase; PDBTitle: dcsbis, a diguanylate cyclase from pseudomonas aeruginosa
45	d1k25a2	 Alignment	not modelled	14.5	8	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
46	c1tola_	 Alignment	not modelled	14.4	16	PDB header: viral protein Chain: A: PDB Molecule: protein (fusion protein consisting of minor coat protein, PDBTitle: fusion of n-terminal domain of the minor coat protein from gene iii in2 phage m13, and c-terminal domain of e. coli protein-tola
47	c6j3fB_	 Alignment	not modelled	13.9	13	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of the glutathione s-transferase, csgst63524, of2 ceriporiopsis subvermispors in complex with glutathione
48	c5yf1A_	 Alignment	not modelled	13.8	13	PDB header: transferase Chain: A: PDB Molecule: carnosine n-methyltransferase; PDBTitle: crystal structure of carnm1 bound to carnosine and sfg
49	c3zxoB_	 Alignment	not modelled	13.7	29	PDB header: transferase Chain: B: PDB Molecule: redox sensor histidine kinase response regulator devs; PDBTitle: crystal structure of the mutant atp-binding domain of2 mycobacterium tuberculosis doss
50	c5dqsA_	 Alignment	not modelled	13.6	14	PDB header: translation Chain: A: PDB Molecule: elongation factor 1-gamma; PDBTitle: complex structure of human elongation factor 1b alpha and gamma gst-2 like domains
51	c5y63E_	 Alignment	not modelled	13.6	16	PDB header: oxidoreductase Chain: E: PDB Molecule: alkyl hydroperoxide reductase, c subunit; PDBTitle: crystal structure of enterococcus faecalis ahpc
52	d1mw7a_	 Alignment	not modelled	13.5	19	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
53	c3hr4C_	 Alignment	not modelled	13.3	9	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
54	c6iwbB_	 Alignment	not modelled	13.0	13	PDB header: isomerase Chain: B: PDB Molecule: probable glutathione s-transferase;

54	c0jwkb	Alignment	not modelled	13.0	12	PDBTitle: crystal structure of maleylpyruvate isomerase from pseudomonas2 aeruginosa pao1 PDB header: ligase
55	c4kqeA	Alignment	not modelled	12.9	21	Chain: A: PDB Molecule: glycine--trna ligase; PDBTitle: the mutant structure of the human glycyl-trna synthetase e71g
56	d2fiua1	Alignment	not modelled	12.9	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
57	d1atia1	Alignment	not modelled	12.8	19	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
58	d1gwca2	Alignment	not modelled	12.7	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
59	d2b8ta1	Alignment	not modelled	12.2	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
60	d1b1ca	Alignment	not modelled	11.3	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
61	c1z9hb	Alignment	not modelled	10.7	15	PDB header: isomerase Chain: B: PDB Molecule: membrane-associated prostaglandin e synthase-2; PDBTitle: microsomal prostaglandin e synthase type-2
62	d1pyya2	Alignment	not modelled	10.6	12	Fold: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Superfamily: Penicillin-binding protein 2x (pbp-2x), c-terminal domain Family: Penicillin-binding protein 2x (pbp-2x), c-terminal domain
63	d1a4ia2	Alignment	not modelled	10.4	13	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
64	c4jbbA	Alignment	not modelled	10.4	13	PDB header: transferase Chain: A: PDB Molecule: putative glutathione s-transferase; PDBTitle: crystal structure of glutathione s-transferase a6tb7(target efi-2 507184) from klebsiella pneumoniae mgh 78578, gsh complex
65	d1g7oa2	Alignment	not modelled	10.4	9	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
66	d1d1da1	Alignment	not modelled	10.2	30	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: Retrovirus capsid protein C-terminal domain
67	c4g6uA	Alignment	not modelled	10.2	13	PDB header: toxin Chain: A: PDB Molecule: ec869 cdia-ct; PDBTitle: cdia-ct/cdii toxin and immunity complex from escherichia coli
68	d1zpdal	Alignment	not modelled	10.1	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
69	d1oyja2	Alignment	not modelled	10.0	11	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
70	c2b8tA	Alignment	not modelled	10.0	9	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in complex2 with thymidine
71	c5z5eB	Alignment	not modelled	10.0	18	PDB header: ligase Chain: B: PDB Molecule: neq417; PDBTitle: crystal structure of the glycyl-trna synthetase (glyrs) in2 nanoarchaeum equitans
72	c1oyjC	Alignment	not modelled	9.9	13	PDB header: transferase Chain: C: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure solution of rice gst1 (osgstu1) in complex with2 glutathione.
73	c3i5aA	Alignment	not modelled	9.8	10	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
74	d1pvdal	Alignment	not modelled	9.7	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
75	c5en7A	Alignment	not modelled	9.6	16	PDB header: splicing Chain: A: PDB Molecule: smu-1; PDBTitle: crystal structure of the smu1-red complex (native) of caenorhabditis2 elegans.
76	c4uw2C	Alignment	not modelled	9.5	26	PDB header: immune system Chain: C: PDB Molecule: csm1; PDBTitle: crystal structure of csm1 in t.onnurineus
77	c6j3gA	Alignment	not modelled	9.5	14	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of an apo form of the glutathione s-transferase,2 csgst83044, of ceriporiopsis subvermispora
78	c3re3B	Alignment	not modelled	9.3	8	PDB header: lyase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
79	c4zquA	Alignment	not modelled	9.2	13	PDB header: toxin Chain: A: PDB Molecule: cdia-ct toxin, conserved domain protein; PDBTitle: cdia-ct/cdii toxin and immunity complex from yersinia2 pseudotuberculosis
80	d2guka1	Alianment	not modelled	9.2	18	Fold: PG1857-like Superfamily: PG1857-like

						Family: PG1857-like
81	d2g4ca1	Alignment	not modelled	9.1	3	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
82	c3m6yA	Alignment	not modelled	8.9	21	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
83	c3l6sA	Alignment	not modelled	8.8	15	PDB header: hydrolase Chain: A: PDB Molecule: aspartyl aminopeptidase; PDBTitle: crystal structure of human aspartyl aminopeptidase (dnpep), in complex2 with aspartic acid hydroxamate
84	c3nglA	Alignment	not modelled	8.7	10	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
85	c3muxB	Alignment	not modelled	8.6	19	PDB header: lyase Chain: B: PDB Molecule: putative 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
86	d1rrma	Alignment	not modelled	8.4	13	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
87	c3csxA	Alignment	not modelled	8.4	6	PDB header: metal binding protein,unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structural characterization of a protein in the duf6832 family- crystal structure of cce_0567 from the3 cyanobacterium cyanothece 51142.
88	c4kr3A	Alignment	not modelled	8.4	22	PDB header: ligase/rna Chain: A: PDB Molecule: glycine--trna ligase; PDBTitle: glycyL-trna synthetase mutant e71g in complex with trna-gly
89	c3gqeA	Alignment	not modelled	8.4	12	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of macro domain of venezuelan equine encephalitis2 virus
90	d1ovma1	Alignment	not modelled	8.4	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
91	d2fi9a1	Alignment	not modelled	8.3	17	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
92	d1hc7a1	Alignment	not modelled	8.2	19	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
93	c2js5B	Alignment	not modelled	8.1	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein q60c73_metca. northeast structural2 genomics consortium target mcr1
94	d1y0na	Alignment	not modelled	8.1	20	Fold: YehU-like Superfamily: YehU-like Family: YehU-like
95	d1j3ma	Alignment	not modelled	8.0	30	Fold: TBP-like Superfamily: TT1751-like Family: TT1751-like
96	c3a7mA	Alignment	not modelled	8.0	11	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: flagellar protein flit; PDBTitle: structure of flit, the flagellar type iii chaperone for flid
97	c3b6nA	Alignment	not modelled	8.0	6	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase pv003920 from plasmodium vivax
98	c1jpkA	Alignment	not modelled	7.9	13	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
99	c5ucmB	Alignment	not modelled	7.9	15	PDB header: ligase Chain: B: PDB Molecule: proline--trna ligase; PDBTitle: crystal structure of prolyl-trna synthetase from pseudomonas2 aeruginosa