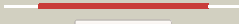



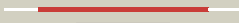
















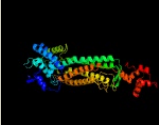
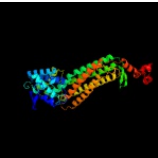

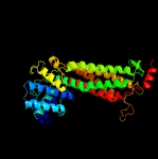
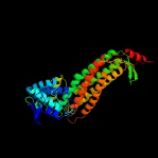


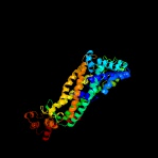




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1098c_(fumC)_1226146_1227570
 Date Wed Jul 31 22:05:17 BST 2019
 Unique Job ID 4a8fb7ac563902e2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6n1mA_	 Alignment		100.0	47	PDB header: lyase Chain: A: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of fumarate hydratase class ii from legionella2 pneumophila philadelphia 1
2	c3gtdA_	 Alignment		100.0	49	PDB header: lyase Chain: A: PDB Molecule: fumarate hydratase class ii; PDBTitle: 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
3	c3no9C_	 Alignment		100.0	99	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis
4	c1yfmA_	 Alignment		100.0	50	PDB header: lyase Chain: A: PDB Molecule: fumarase; PDBTitle: recombinant yeast fumarase
5	d1yfma_	 Alignment		100.0	50	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
6	c3e04A_	 Alignment		100.0	51	PDB header: lyase Chain: A: PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of human fumarate hydratase
7	d1vdka_	 Alignment		100.0	51	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
8	d1j3ua_	 Alignment		100.0	44	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
9	c4hgvD_	 Alignment		100.0	47	PDB header: lyase Chain: D: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of a fumarate hydratase
10	d1jswa_	 Alignment		100.0	42	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
11	d1fuoa_	 Alignment		100.0	50	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase

12	c3ocfB_	Alignment		100.0	46	PDB header: lyase Chain: B; PDB Molecule: fumarate lyase:delta crystallin; PDBTitle: crystal structure of fumarate lyase:delta crystallin from brucella2 melitensis in native form
13	c3e04C_	Alignment		100.0	53	PDB header: lyase Chain: C; PDB Molecule: fumarate hydratase; PDBTitle: crystal structure of human fumarate hydratase
14	c3gtdB_	Alignment		100.0	50	PDB header: lyase Chain: B; PDB Molecule: fumarate hydratase class ii; PDBTitle: 2.4 angstrom crystal structure of fumarate hydratase from rickettsia2 prowazekii
15	c4hgvC_	Alignment		100.0	48	PDB header: lyase Chain: C; PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of a fumarate hydratase
16	d1jswc_	Alignment		100.0	43	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
17	c3r6yG_	Alignment		100.0	46	PDB header: lyase Chain: G; PDB Molecule: aspartase; PDBTitle: crystal structure of chymotrypsin-treated aspartase from bacillus sp.2 ym55-1
18	c5xnzA_	Alignment		100.0	23	PDB header: lyase Chain: A; PDB Molecule: cred; PDBTitle: crystal structure of cred complex with fumarate
19	d1re5a_	Alignment		100.0	24	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
20	c2pfmA_	Alignment		100.0	21	PDB header: lyase Chain: A; PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase (purb) from bacillus2 anthracis
21	d1q5na_	Alignment	not modelled	100.0	23	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
22	d1c3ca_	Alignment	not modelled	100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
23	d1tj7a_	Alignment	not modelled	100.0	18	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
24	c2e9fC_	Alignment	not modelled	100.0	22	PDB header: lyase Chain: C; PDB Molecule: argininosuccinate lyase; PDBTitle: crystal structure of t.th.hb8 argininosuccinate lyase complexed with2 l-arginine
25	c6g3eA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A; PDB Molecule: argininosuccinate lyase; PDBTitle: crystal structure of edds lyase in complex with formate
26	c6igaB_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: B; PDB Molecule: argininosuccinate lyase; PDBTitle: crystal structure of argininosuccinate lyase from mycobacterium2 tuberculosis
27	d1hy0a_	Alignment	not modelled	100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
28	d1tjva_	Alignment	not modelled	100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
29	d1k62a_	Alignment	not modelled	100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like

						Family: L-aspartase/fumarase
30	d1i0aa_	Alignment	not modelled	100.0	19	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
31	c5vkwB_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase ade13 from candida2 albicans
32	c4eeiA_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from francisella2 tularensis complexed with amp and succinate
33	c3c8tA_	Alignment	not modelled	100.0	20	PDB header: lyase Chain: A: PDB Molecule: fumarate lyase; PDBTitle: crystal structure of fumarate lyase from mesorhizobium sp. bnc1
34	c4nleB_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of apo adenylosuccinate lyase from mycobacterium2 smegmatis
35	c4efcA_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from trypanosoma brucei,2 tb427tmp.160.5560
36	c3bhgA_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from legionella2 pneumophila
37	d1dofa_	Alignment	not modelled	100.0	20	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
38	c2vd6B_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: adenylosuccinate lyase; PDBTitle: human adenylosuccinate lyase in complex with its substrate2 n6-(1,2-dicarboxyethyl)-amp, and its products amp and3 fumarate.
39	c2ptsA_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of wild type escherichia coli adenylosuccinate lyase
40	c1yisA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: adenylosuccinate lyase; PDBTitle: structural genomics of caenorhabditis elegans: adenylosuccinate lyase
41	c2qgaC_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: C: PDB Molecule: adenylosuccinate lyase; PDBTitle: plasmodium vivax adenylosuccinate lyase pv003765 with amp bound
42	c5eyvB_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: B: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from schistosoma mansoni2 in apo form.
43	c4mx2C_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: C: PDB Molecule: adenylosuccinate lyase; PDBTitle: crystal structure of adenylosuccinate lyase from leishmania donovani
44	c2fenA_	Alignment	not modelled	100.0	22	PDB header: isomerase Chain: A: PDB Molecule: 3-carboxy-cis,cis-muconate lactonizing enzyme; PDBTitle: 3-carboxy-cis,cis-muconate lactonizing enzyme from agrobacterium2 radiobacter s2
45	d1f1oa_	Alignment	not modelled	100.0	20	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
46	c2xgvA_	Alignment	not modelled	48.4	18	PDB header: viral protein Chain: A: PDB Molecule: psiv capsid n-terminal domain; PDBTitle: structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
47	c5tv7A_	Alignment	not modelled	35.6	28	PDB header: hydrolase Chain: A: PDB Molecule: putative peptidoglycan-binding/hydrolysing protein; PDBTitle: 2.05 angstrom resolution crystal structure of peptidoglycan-binding2 protein from clostridioides difficile in complex with glutamine3 hydroxamate.
48	c5bmqa_	Alignment	not modelled	28.8	17	PDB header: hydrolase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of l,d-transpeptidase (yku) from stackebrandtia2 nassauensis
49	d1gkma_	Alignment	not modelled	25.3	24	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: HAL/PAL-like
50	d1lbua1	Alignment	not modelled	25.1	21	Fold: PGBD-like Superfamily: PGBD-like Family: Peptidoglycan binding domain, PGBD
51	c3bkha_	Alignment	not modelled	22.1	17	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
52	c6nyyA_	Alignment	not modelled	20.1	13	PDB header: translocase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
53	c4bolA_	Alignment	not modelled	19.2	21	PDB header: hydrolase Chain: A: PDB Molecule: ampdh2; PDBTitle: crystal structure of ampdh2 from pseudomonas aeruginosa in2 complex with pentapeptide
54	c4xytA_	Alignment	not modelled	19.1	27	PDB header: hydrolase Chain: A: PDB Molecule: fusion of predicted zn-dependent amidase/peptidase (cell

54	c4xvA	Alignment	not modelled	19.1	27	PDBTitle: crystal structure of fused zn-dependent2 amidase/peptidase/peptidoglycan-binding domain-containing protein3 from clostridium acetobutylicum atcc 824
55	d2p1ra1	Alignment	not modelled	18.6	12	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
56	c4btpl	Alignment	not modelled	16.9	29	PDB header: viral protein Chain: I: PDB Molecule: p1; PDBTitle: structure of the capsid protein p1 of the bacteriophage phi8
57	c1byvA	Alignment	not modelled	15.0	20	PDB header: hormone/growth factor Chain: A: PDB Molecule: protein (calcitonin); PDBTitle: glycosylated eel calcitonin
58	c5cx2C	Alignment	not modelled	14.1	15	PDB header: structural protein Chain: C: PDB Molecule: coronin; PDBTitle: structure of coiled coil domain of leishmania donovani coronin
59	c2ctoA	Alignment	not modelled	14.0	42	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: novel protein; PDBTitle: solution structure of the hmg box like domain from human2 hypothetical protein flj14904
60	c4g54A	Alignment	not modelled	14.0	17	PDB header: peptidoglycan-binding protein Chain: A: PDB Molecule: general secretion pathway protein; PDBTitle: crystal structure of a periplasmic domain of the epsab fusion protein2 of the vibrio vulnificus type ii secretion system
61	c4lpqA	Alignment	not modelled	13.9	30	PDB header: transferase Chain: A: PDB Molecule: erfk/ybis/ycfs/ynhg family protein; PDBTitle: crystal structure of the l,d-transpeptidase (residues 123-326) from2 xylanimonas cellulositytica dsm 15894
62	d2ce7a1	Alignment	not modelled	13.7	21	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
63	c3bbnC	Alignment	not modelled	13.7	50	PDB header: ribosome Chain: C: PDB Molecule: ribosomal protein s3; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
64	c3lq9B	Alignment	not modelled	13.4	11	PDB header: signaling protein Chain: B: PDB Molecule: dna-damage-inducible transcript 4 protein; PDBTitle: crystal structure of human redd1, a hypoxia-induced regulator of mtor
65	c2di4B	Alignment	not modelled	13.3	14	PDB header: hydrolase Chain: B: PDB Molecule: cell division protein ftsH homolog; PDBTitle: crystal structure of the ftsH protease domain
66	d2bona1	Alignment	not modelled	12.9	14	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
67	c5zdnA	Alignment	not modelled	12.4	31	PDB header: hydrolase Chain: A: PDB Molecule: fomd; PDBTitle: the complex structure of fomd with cdp
68	d1nvta2	Alignment	not modelled	11.5	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
69	d2joka1	Alignment	not modelled	11.2	24	Fold: SopE-like GEF domain Superfamily: SopE-like GEF domain Family: SopE-like GEF domain
70	d1e0ea	Alignment	not modelled	10.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
71	d1k6ya1	Alignment	not modelled	10.7	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
72	d1w27a	Alignment	not modelled	10.6	22	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: HAL/PAL-like
73	d1wjfa	Alignment	not modelled	10.5	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: N-terminal Zn binding domain of HIV integrase Family: N-terminal Zn binding domain of HIV integrase
74	d2di4a1	Alignment	not modelled	10.5	18	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
75	c2ev9B	Alignment	not modelled	9.5	29	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
76	c3j3bT	Alignment	not modelled	9.4	26	PDB header: ribosome Chain: T: PDB Molecule: 60s ribosomal protein l21; PDBTitle: structure of the human 60s ribosomal proteins
77	c1lbuA	Alignment	not modelled	9.0	18	PDB header: hydrolase Chain: A: PDB Molecule: muramoyl-pentapeptide carboxypeptidase; PDBTitle: hydrolase metallo (zn) dd-peptidase
78	c3fbtB	Alignment	not modelled	8.9	20	PDB header: oxidoreductase, lyase Chain: B: PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase fusion PDBTitle: crystal structure of a chorismate mutase/shikimate 5-dehydrogenase2 fusion protein from clostridium acetobutylicum
79	c3iz5U	Alignment	not modelled	8.9	15	PDB header: ribosome Chain: U: PDB Molecule: 60s ribosomal protein l21 (l21e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
80	c2dinA	Alignment	not modelled	8.9	56	PDB header: dna binding protein Chain: A: PDB Molecule: lamin-b receptor;

80	c2u9gA	Alignment	not modelled	8.9	30	PDBTitle: solution structure of the todor domain of human lamin-b2 receptor PDB header: hydrolase
81	c3exmA	Alignment	not modelled	8.8	16	Chain: A; PDB Molecule: phosphatase sc4828; PDBTitle: crystal structure of the phosphatase sc4828 with the non-hydrolyzable2 nucleotide gpcp
82	c5dzsA	Alignment	not modelled	8.7	29	PDB header: oxidoreductase Chain: A; PDB Molecule: shikimate dehydrogenase (nadp(+)); PDBTitle: 1.5 angstrom crystal structure of shikimate dehydrogenase 1 from2 peptoclostridium difficile.
83	c5nm7A	Alignment	not modelled	8.7	16	PDB header: hydrolase Chain: A; PDB Molecule: peptidoglycan-binding domain 1; PDBTitle: crystal structure of burkholderia ap3 phage endolysin
84	d1npya2	Alignment	not modelled	8.7	50	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
85	d2pxrc1	Alignment	not modelled	8.5	25	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
86	c6fxyA	Alignment	not modelled	8.3	39	PDB header: transferase Chain: A; PDB Molecule: procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; PDBTitle: crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with fe2+, mn2+, udp-gal - structure from long-wavelength3 s-sad
87	c5cx2B	Alignment	not modelled	7.7	16	PDB header: structural protein Chain: B; PDB Molecule: coronin; PDBTitle: structure of coiled coil domain of leishmania donovani coronin
88	d2b0ja1	Alignment	not modelled	7.6	28	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: HMD dimerization domain-like
89	d1vi2a2	Alignment	not modelled	7.4	14	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
90	c3zf7U	Alignment	not modelled	7.2	15	PDB header: ribosome Chain: U; PDB Molecule: 60s ribosomal protein l21e, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
91	c6nyyC	Alignment	not modelled	7.2	12	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
92	c3izcU	Alignment	not modelled	7.1	22	PDB header: ribosome Chain: U; PDB Molecule: 60s ribosomal protein rpl21 (l21e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
93	d1p77a2	Alignment	not modelled	7.1	33	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
94	c2k2tA	Alignment	not modelled	7.0	22	PDB header: cell adhesion Chain: A; PDB Molecule: micronemal protein 6; PDBTitle: epidermal growth factor-like domain 2 from toxoplasma2 gondii microneme protein 6
95	c2v1nA	Alignment	not modelled	7.0	25	PDB header: nuclear protein Chain: A; PDB Molecule: protein kin homolog; PDBTitle: solution structure of the region 51-160 of human kin172 reveals a winged helix fold
96	c2pmzL	Alignment	not modelled	7.0	14	PDB header: translation, transferase Chain: L; PDB Molecule: dna-directed rna polymerase subunit I; PDBTitle: archaeal rna polymerase from sulfolobus solfataricus
97	c3j38V	Alignment	not modelled	7.0	17	PDB header: ribosome Chain: V; PDB Molecule: 40s ribosomal protein s21; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
98	d1u5ta1	Alignment	not modelled	6.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
99	c1wjvA	Alignment	not modelled	6.7	44	PDB header: dna binding protein Chain: A; PDB Molecule: cell growth regulating nucleolar protein lyar; PDBTitle: solution structure of the n-terminal zinc finger domain of2 mouse cell growth regulating nucleolar protein lyar