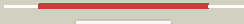



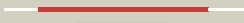






















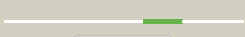








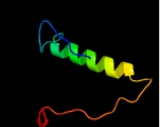
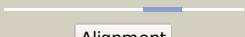


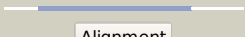


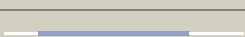
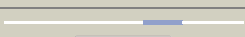
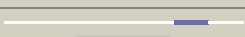
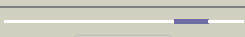


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0727c_(fucA)_819846_820502
 Date Fri Jul 26 01:50:30 BST 2019
 Unique Job ID 19025d106cfd5fb1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ojra_	 Alignment		100.0	21	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
2	c4c24A_	 Alignment		100.0	35	PDB header: lyase Chain: A: PDB Molecule: l-fucose phosphate aldolase; PDBTitle: l-fucose 1-phosphate aldolase
3	d1e4cp_	 Alignment		100.0	29	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
4	c6btdA_	 Alignment		100.0	35	PDB header: lyase Chain: A: PDB Molecule: fucose phosphate aldolase; PDBTitle: crystal structure of deoxyribose-phosphate aldolase from bacillus2 thuringiensis involved in dispatching the ubiquitous radical sam3 enzyme byproduct 5-deoxyribose
5	c3ocrA_	 Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: class ii aldolase/adducin domain protein; PDBTitle: crystal structure of aldolase ii superfamily protein from pseudomonas2 syringae
6	c4xxfA_	 Alignment		100.0	22	PDB header: lyase Chain: A: PDB Molecule: fucose-1-phosphate aldolase; PDBTitle: l-fucose 1-phosphate aldolase from glaciozyma antarctica pi12
7	c2z7bA_	 Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: mlr6791 protein; PDBTitle: crystal structure of mesorhizobium loti 3-hydroxy-2-methylpyridine-4,2 5-dicarboxylate decarboxylase
8	c2opiB_	 Alignment		100.0	21	PDB header: lyase Chain: B: PDB Molecule: l-fucose-1-phosphate aldolase; PDBTitle: crystal structure of l-fucose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
9	d1k0wa_	 Alignment		100.0	30	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase
10	c2fk5B_	 Alignment		100.0	27	PDB header: lyase Chain: B: PDB Molecule: fucose-1-phosphate aldolase; PDBTitle: crystal structure of l-fucose-1-phosphate aldolase from thermus2 thermophilus hb8
11	d1pvta_	 Alignment		100.0	27	Fold: AraD/HMP-PK domain-like Superfamily: AraD/HMP-PK domain-like Family: AraD-like aldolase/epimerase

12	c4m6rA_	 Alignment		100.0	20	PDB header: lyase Chain: A: PDB Molecule: methylthioribulose-1-phosphate dehydratase; PDBTitle: structural and biochemical basis for the inhibition of cell death by2 apip, a methionine salvage enzyme
13	c2irpA_	 Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: putative aldolase class 2 protein aq_1979; PDBTitle: crystal structure of the l-fuculose-1-phosphate aldolase (aq_1979)2 from aquifex aeolicus vf5
14	c3m4rA_	 Alignment		100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the n-terminal class ii aldolase domain of a conserved2 protein from thermoplasma acidophilum
15	c4xaeB_	 Alignment		59.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: feruloyl coa ortho-hydroxylase 1; PDBTitle: structure of feruloyl-coa 6-hydroxylase (f6h) from arabidopsis2 thaliana
16	d1w9ya1	 Alignment		27.7	14	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Penicillin synthase-like
17	d1odma_	 Alignment		27.6	17	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Penicillin synthase-like
18	c5gj9A_	 Alignment		26.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate oxidase 2; PDBTitle: crystal structure of arabidopsis thaliana aco2 in complex with poa
19	c6g1cV_	 Alignment		26.1	14	PDB header: antitoxin Chain: V: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the n-terminal domain of burkholderia2 pseudomallei antitoxin hicb
20	d1gp6a_	 Alignment		26.0	16	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Penicillin synthase-like
21	c2kouA_	 Alignment	not modelled	24.8	16	PDB header: hydrolase Chain: A: PDB Molecule: dicer-like protein 4; PDBTitle: dicer like protein
22	c4q0mA_	 Alignment	not modelled	23.0	16	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of pyrococcus furiosus l-asparaginase
23	c2yztA_	 Alignment	not modelled	21.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha1756; PDBTitle: crystal structure of uncharacterized conserved protein from thermus2 thermophilus hb8
24	c2yz3B_	 Alignment	not modelled	21.2	12	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
25	c2d6fA_	 Alignment	not modelled	20.9	17	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
26	c3on7C_	 Alignment	not modelled	20.3	15	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, iron/ascorbate family; PDBTitle: crystal structure of a putative oxygenase (so_2589) from shewanella2 oneidensis at 2.20 a resolution
27	c2k06A_	 Alignment	not modelled	17.8	16	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of the aminoterminal domain of e. coli nusg
28	d1nz8a_	 Alignment	not modelled	17.6	36	Fold: Ferredoxin-like Superfamily: N-utilization substance G protein NusG, N-terminal domain

						Family: N-utilization substance G protein NusG, N-terminal domain PDB header: metal binding protein Chain: A: PDB Molecule: probable iron/ascorbate oxidoreductase; PDBTitle: structure of an isopenicillin n synthase from pseudomonas aeruginosa2 pao1
29	c6jyvA	Alignment	not modelled	17.4	23	
30	d1dcsa	Alignment	not modelled	16.3	17	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: Penicillin synthase-like
31	c5ot0A	Alignment	not modelled	15.8	18	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: the thermostable l-asparaginase from thermococcus kodakarensis
32	c4ad8A	Alignment	not modelled	15.6	13	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of a deletion mutant of deinococcus radiodurans2 recn
33	d2bfdb2	Alignment	not modelled	14.1	19	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
34	c3ju3A	Alignment	not modelled	13.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; PDBTitle: crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
35	c1ecjB	Alignment	not modelled	13.7	15	PDB header: transferase Chain: B: PDB Molecule: glutamine phosphoribosylpyrophosphate PDBTitle: escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
36	c3pvjB	Alignment	not modelled	13.6	10	PDB header: oxidoreductase Chain: B: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
37	c1wnfA	Alignment	not modelled	12.5	16	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of ph0066 from pyrococcus horikoshii
38	c4awyB	Alignment	not modelled	11.3	10	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase aim-1; PDBTitle: crystal structure of the mobile metallo-beta-lactamase aim-1 from2 pseudomonas aeruginosa: insights into antibiotic binding and the role3 of gln157
39	c5apqA	Alignment	not modelled	11.2	20	PDB header: transferase Chain: A: PDB Molecule: tsr3; PDBTitle: structure of the sam-dependent rrna:acp-transferase tsr32 from vulcanisaeta distributa
40	c5iqkB	Alignment	not modelled	11.0	11	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase rm3; PDBTitle: rm3 metallo-beta-lactamase
41	c2yheD	Alignment	not modelled	10.7	19	PDB header: hydrolase Chain: D: PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
42	d1j5ua	Alignment	not modelled	10.5	11	Fold: MTH1598-like Superfamily: MTH1598-like Family: MTH1598-like
43	d1w85b2	Alignment	not modelled	10.3	16	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
44	c4n2pC	Alignment	not modelled	10.1	16	PDB header: chaperone Chain: C: PDB Molecule: protein archease; PDBTitle: structure of archease from pyrococcus horikoshii
45	c3zieC	Alignment	not modelled	10.0	20	PDB header: cell cycle Chain: C: PDB Molecule: sepf-like protein; PDBTitle: sepf-like protein from archaeoglobus fulgidus
46	c5yzlA	Alignment	not modelled	9.9	21	PDB header: chaperone Chain: A: PDB Molecule: protein archease; PDBTitle: crystal structure of human archease d178a
47	c5lqmA	Alignment	not modelled	9.9	38	PDB header: transcription Chain: A: PDB Molecule: fusion protein 5.5/5.7; PDBTitle: gp5.7 mutant l42a
48	c5ld9B	Alignment	not modelled	9.8	19	PDB header: hydrolase Chain: B: PDB Molecule: jamm1; PDBTitle: structure of debiquitinating enzyme homolog, pyrococcus furiosus2 jamm1.
49	c2ra9A	Alignment	not modelled	9.8	25	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein duf1285; PDBTitle: crystal structure of a duf1285 family protein (sba1_2486) from2 shewanella baltica os155 at 1.40 a resolution
50	c5yrzC	Alignment	not modelled	9.8	19	PDB header: antitoxin/hydrolase Chain: C: PDB Molecule: hicb; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
51	c1zq1B	Alignment	not modelled	9.7	15	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
52	d1jw3a	Alignment	not modelled	9.4	32	Fold: MTH1598-like Superfamily: MTH1598-like Family: MTH1598-like
53	c6d1oD	Alignment	not modelled	9.3	19	PDB header: oxidoreductase Chain: D: PDB Molecule: (r)-phenoxypropionate/alpha-ketoglutarate-dioxygenase; PDBTitle: ft_5 dioxygenase apoenzyme Fold: SH2-like

54	d2c9wa2	Alignment	not modelled	9.1	18	Superfamily: SH2 domain Family: SH2 domain
55	d1m1ha2	Alignment	not modelled	9.0	30	Fold: Ferredoxin-like Superfamily: N-utilization substance G protein NusG, N-terminal domain Family: N-utilization substance G protein NusG, N-terminal domain
56	c4ux3A_	Alignment	not modelled	9.0	3	PDB header: protein binding Chain: A: PDB Molecule: structural maintenance of chromosomes protein 3; PDBTitle: cohesin smc3-hd:scc1-n complex from yeast
57	c4p7dA_	Alignment	not modelled	9.0	22	PDB header: toxin Chain: A: PDB Molecule: antitoxin hicb3; PDBTitle: antitoxin hicb3 crystal structure
58	c5d6hB_	Alignment	not modelled	8.9	42	PDB header: chaperone/protein transport Chain: B: PDB Molecule: csua/b; PDBTitle: crystal structure of csuc-csua/b chaperone-major subunit pre-assembly2 complex from csu biofilm-mediating pili of acinetobacter baumannii
59	c2daoA_	Alignment	not modelled	8.8	13	PDB header: dna binding protein Chain: A: PDB Molecule: transcription factor etv6; PDBTitle: solution structure of ets domain transcriptional factor2 etv6 protein
60	c4n58A_	Alignment	not modelled	8.6	26	PDB header: hydrolase Chain: A: PDB Molecule: pectocin m2; PDBTitle: crystal structure of pectocin m2 at 1.86 angstroms
61	d1flia_	Alignment	not modelled	8.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ets domain
62	c2aexA_	Alignment	not modelled	8.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: coproporphyrinogen iii oxidase, mitochondrial; PDBTitle: the 1.58a crystal structure of human coproporphyrinogen oxidase2 reveals the structural basis of hereditary coproporphyrin
63	d1awca_	Alignment	not modelled	8.4	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ets domain
64	c5e5bA_	Alignment	not modelled	8.2	6	PDB header: transcription Chain: A: PDB Molecule: fact complex subunit spt16; PDBTitle: crystal structure of human spt16 n-terminal domain
65	c2rf4B_	Alignment	not modelled	8.2	20	PDB header: transferase Chain: B: PDB Molecule: dna-directed rna polymerase i subunit rpa4; PDBTitle: crystal structure of the rna polymerase i subcomplex a14/43
66	d1puee_	Alignment	not modelled	8.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ets domain
67	d1f37b_	Alignment	not modelled	8.1	29	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioredoxin-like 2Fe-2S ferredoxin
68	c5c3qB_	Alignment	not modelled	8.1	8	PDB header: oxidoreductase Chain: B: PDB Molecule: thymine dioxygenase; PDBTitle: crystal structure of the full-length neurospora crassa t7h in complex2 with alpha-kg and thymine (t)
69	c3ooxA_	Alignment	not modelled	8.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2og-fe(ii) oxygenase family protein; PDBTitle: crystal structure of a putative 2og-fe(ii) oxygenase family protein2 (cc_0200) from caulobacter crescentus at 1.44 a resolution
70	c4g76A_	Alignment	not modelled	8.0	31	PDB header: hydrolase Chain: A: PDB Molecule: phosphodiesterase; PDBTitle: structure of paem, a colicin m-like bacteriocin produced by2 pseudomonas aeruginosa
71	c6fxaF_	Alignment	not modelled	7.9	25	PDB header: viral protein Chain: F: PDB Molecule: ci; PDBTitle: dimerization domain of tp901-1 ci repressor
72	c6fxaA_	Alignment	not modelled	7.9	25	PDB header: viral protein Chain: A: PDB Molecule: ci; PDBTitle: dimerization domain of tp901-1 ci repressor
73	c6fxaB_	Alignment	not modelled	7.9	25	PDB header: viral protein Chain: B: PDB Molecule: ci; PDBTitle: dimerization domain of tp901-1 ci repressor
74	d1k78b_	Alignment	not modelled	7.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ets domain
75	c3jtgA_	Alignment	not modelled	7.9	21	PDB header: transcription Chain: A: PDB Molecule: ets-related transcription factor elf-3; PDBTitle: crystal structure of mouse elf3 c-terminal dna-binding domain in2 complex with type ii tgf-beta receptor promoter dna
76	c5lunC_	Alignment	not modelled	7.9	11	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate-dependent ethylene/succinate-forming enzyme; PDBTitle: ethylene forming enzyme from pseudomonas syringae pv. phaseolicola -2 p1 ultra-high resolution crystal form in complex with iron, n-3 oxalylglycine and arginine
77	d1duxc_	Alignment	not modelled	7.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ets domain
78	c3zqjF_	Alignment	not modelled	7.9	13	PDB header: dna binding protein Chain: F: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
79	c4avnD_	Alignment	not modelled	7.8	21	PDB header: transcription Chain: D: PDB Molecule: ets translocation variant 1;

79	c4vvpD	Alignment	not modelled	7.8	41	PDBTitle: crystal structure of the dna-binding domain of human etv1. PDB header: dna binding protein, cell cycle
80	c5h68B	Alignment	not modelled	7.8	8	Chain: B; PDB Molecule: chromosome partition protein smc; PDBTitle: crystal structure of an engaged dimer of the geobacillus2 stearothermophilus smc head domain
81	d1umdb2	Alignment	not modelled	7.8	20	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
82	d2stta	Alignment	not modelled	7.7	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ets domain
83	c2nnyA	Alignment	not modelled	7.7	21	PDB header: transcription/dna Chain: A; PDB Molecule: c-ets-1 protein; PDBTitle: crystal structure of the ets1 dimer dna complex.
84	c3zgxA	Alignment	not modelled	7.4	8	PDB header: cell cycle Chain: A; PDB Molecule: chromosome partition protein smc; PDBTitle: crystal structure of the kleisin-n smc interface in2 prokaryotic condensin
85	c3b1bA	Alignment	not modelled	7.4	20	PDB header: lyase Chain: A; PDB Molecule: carbonic anhydrase 1; PDBTitle: the unique structure of wild type carbonic anhydrase alpha-ca1 from2 chlamydomonas reinhardtii
86	c6fxaC	Alignment	not modelled	7.4	25	PDB header: viral protein Chain: C; PDB Molecule: ci; PDBTitle: dimerization domain of tp901-1 ci repressor
87	c6fxaE	Alignment	not modelled	7.4	25	PDB header: viral protein Chain: E; PDB Molecule: ci; PDBTitle: dimerization domain of tp901-1 ci repressor
88	c4egeA	Alignment	not modelled	7.3	27	PDB header: hydrolase Chain: A; PDB Molecule: dipeptidase pepe; PDBTitle: crystal structure of dipeptidase pepe from mycobacterium ulcerans
89	d1gvja	Alignment	not modelled	7.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ets domain
90	d2id1a1	Alignment	not modelled	7.2	23	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: lojap/YbeB-like
91	c2p09A	Alignment	not modelled	7.2	18	PDB header: de novo protein Chain: A; PDB Molecule: a non-biological atp binding protein with two mutations PDBTitle: structural insights into the evolution of a non-biological protein
92	c4p3xA	Alignment	not modelled	7.2	4	PDB header: transferase Chain: A; PDB Molecule: quinolinate synthase a; PDBTitle: structure of the fe4s4 quinolinate synthase nada from thermotoga2 maritima
93	d1rrza	Alignment	not modelled	7.2	22	Fold: Spectrin repeat-like Superfamily: Glycogen synthesis protein GlgS Family: Glycogen synthesis protein GlgS
94	c1rrzA	Alignment	not modelled	7.2	22	PDB header: structural genomics,biosynthetic protein Chain: A; PDB Molecule: glycogen synthesis protein glgs; PDBTitle: solution structure of glgs protein from e. coli
95	d1bc8c	Alignment	not modelled	7.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ets domain
96	c1olsB	Alignment	not modelled	7.0	19	PDB header: oxidoreductase Chain: B; PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: roles of his291-alpha and his146-beta' in the reductive acylation2 reaction catalyzed by human branched-chain alpha-ketoacid3 dehydrogenase
97	c3zqjC	Alignment	not modelled	7.0	13	PDB header: dna binding protein Chain: C; PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
98	d1otja	Alignment	not modelled	6.8	5	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: TauD/TfdA-like
99	c1w7vD	Alignment	not modelled	6.7	25	PDB header: hydrolase Chain: D; PDB Molecule: xaa-pro aminopeptidase; PDBTitle: znmg substituted aminopeptidase p from e. coli