
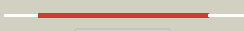









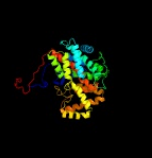



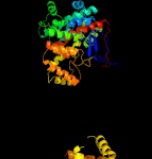
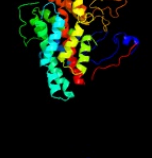
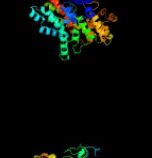
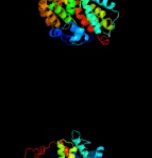
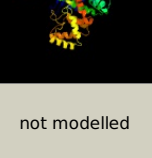


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0889c_(citA)_988743_989864
Date	Fri Jul 26 01:50:48 BST 2019
Unique Job ID	438251d813eedd17

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2h12C_	 Alignment		100.0	27	PDB header: transferase Chain: C: PDB Molecule: citrate synthase; PDBTitle: structure of acetobacter aceti citrate synthase complexed with2 oxaloacetate and carboxymethyldeithia coenzyme a (cmx)
2	d1k3pa_	 Alignment		100.0	29	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
3	c3msuA_	 Alignment		100.0	28	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from francisella tularensis
4	d1aj8a_	 Alignment		100.0	28	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
5	c2ibpB_	 Alignment		100.0	28	PDB header: transferase Chain: B: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from pyrobaculum aerophilum
6	c1vgpA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: 373aa long hypothetical citrate synthase; PDBTitle: crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7
7	c2r26C_	 Alignment		100.0	25	PDB header: transferase Chain: C: PDB Molecule: citrate synthase; PDBTitle: the structure of the ternary complex of carboxymethyl2 coenzyme a and oxalateacetate with citrate synthase from3 the thermophilic archaeonthermoplasma acidophilum
8	d1ioma_	 Alignment		100.0	31	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
9	c6abxA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase (msed_1522) from metallospheara2 sedula in complex with citrate
10	c1vgmB_	 Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: 378aa long hypothetical citrate synthase; PDBTitle: crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7
11	c2c6xA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: citrate synthase 1; PDBTitle: structure of bacillus subtilis citrate synthase

12	c3hwkE_	Alignment		100.0	30	PDB header: transferase Chain: E: PDB Molecule: methylcitrate synthase; PDBTitle: crystal structure of methylcitrate synthase from mycobacterium2 tuberculosis
13	d1cscha_	Alignment		100.0	21	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
14	c2p2wA_	Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from thermotoga maritima msb8
15	d2ctsa_	Alignment		100.0	22	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
16	d1a59a_	Alignment		100.0	30	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
17	d1csca_	Alignment		100.0	22	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
18	c3tqgA_	Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: 2-methylcitrate synthase; PDBTitle: structure of the 2-methylcitrate synthase (prpc) from coxiella2 burnetii
19	d1o7xa_	Alignment		100.0	28	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
20	c3o8jH_	Alignment		100.0	31	PDB header: transferase Chain: H: PDB Molecule: 2-methylcitrate synthase; PDBTitle: crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
21	c5uqqD_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: D: PDB Molecule: 2-methylcitrate synthase, mitochondrial; PDBTitle: crystal structure of 2-methylcitrate synthase from aspergillus2 fumigatus
22	c4tvmA_	Alignment	not modelled	100.0	32	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: structure of citrate synthase from mycobacterium tuberculosis
23	c4xghA_	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: x-ray crystal structure of citrate synthase from burkholderia2 thailandensis
24	c6hxpA_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: A: PDB Molecule: citryl-coa lyase; PDBTitle: structure of citryl-coa lyase from hydrogenobacter thermophilus
25	c6hxjB_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: B: PDB Molecule: atp-citrate lyase alpha-subunit; PDBTitle: structure of atp citrate lyase from chlorobium limicola in complex2 with citrate and coenzyme a.
26	c6hxiD_	Alignment	not modelled	100.0	25	PDB header: lyase Chain: D: PDB Molecule: succinyl-coa ligase (adp-forming) subunit alpha; PDBTitle: structure of atp citrate lyase from methanotrix soehngenii in complex2 with citrate and coenzyme a
27	c6hxiD_	Alignment	not modelled	100.0	26	PDB header: lyase Chain: D: PDB Molecule: atp-citrate synthase; PDBTitle: structure of the citryl-coa lyase core module of human atp citrate2 lyase in complex with citrate and coash (space group p21)
28	c6hxpH_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: H: PDB Molecule: atp-citrate lyase alpha-subunit;

28	c0tkv1L	Alignment	not modelled	100.0	24	PDBTitle: structure of the citryl-coa lyase core module of chlorobium limicola2 atp citrate lyase (space group p21) PDB header: lyase
29	c6qfbB	Alignment	not modelled	100.0	25	Chain: B: PDB Molecule: atp-citrate synthase; PDBTitle: structure of the human atp citrate lyase holoenzyme in complex with2 citrate, coenzyme a and mg.adp
30	c6hxoE	Alignment	not modelled	100.0	23	PDB header: lyase Chain: E: PDB Molecule: atp-citrate lyase alpha-subunit; PDBTitle: structure of the citryl-coa lyase core module of chlorobium limicola2 atp citrate lyase (space group p21)
31	c3j38P	Alignment	not modelled	56.1	33	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein s15, isoform a; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
32	c3zeyI	Alignment	not modelled	56.1	38	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s15, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
33	c3j20T	Alignment	not modelled	45.7	29	PDB header: ribosome Chain: T: PDB Molecule: 30s ribosomal protein s19p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
34	d1khd2	Alignment	not modelled	39.3	34	Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Family: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
35	c5xyiP	Alignment	not modelled	38.3	38	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein s19, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
36	c2xzmS	Alignment	not modelled	37.7	26	PDB header: ribosome Chain: S: PDB Molecule: rps15e; 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 1
37	c5xxuP	Alignment	not modelled	37.6	33	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein us19; PDBTitle: small subunit of toxoplasma gondii ribosome
38	c4jhlA	Alignment	not modelled	24.6	12	PDB header: hydrolase Chain: A: PDB Molecule: acetyl xylan esterase; PDBTitle: crystal structure of of axe2, an acetylxylan esterase from geobacillus2 stearothermophilus
39	c3t5qA	Alignment	not modelled	21.5	23	PDB header: viral protein/rna Chain: A: PDB Molecule: nucleoprotein; PDBTitle: 3a structure of lassa virus nucleoprotein in complex with ssrna
40	c3j20S	Alignment	not modelled	18.4	32	PDB header: ribosome Chain: S: PDB Molecule: 30s ribosomal protein s17e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
41	c5xxuR	Alignment	not modelled	17.0	29	PDB header: ribosome Chain: R: PDB Molecule: ribosomal protein es17; PDBTitle: small subunit of toxoplasma gondii ribosome
42	c2ly8A	Alignment	not modelled	15.4	35	PDB header: chaperone Chain: A: PDB Molecule: budding yeast chaperone scm3; PDBTitle: the budding yeast chaperone scm3 recognizes the partially unfolded2 dimer of the centromere-specific cse4/h4 histone variant
43	c4gyxB	Alignment	not modelled	15.2	67	PDB header: structural protein, blood clotting Chain: B: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
44	c4gyxA	Alignment	not modelled	15.2	67	PDB header: structural protein, blood clotting Chain: A: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
45	c4ay8B	Alignment	not modelled	14.9	12	PDB header: transferase Chain: B: PDB Molecule: methylcobalamin): coenzyme m methyltransferase; PDBTitle: semet-derivative of a methyltransferase from m. mazei
46	c3o30I	Alignment	not modelled	14.5	43	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s15; PDBTitle: yeast 80s ribosome. this entry consists of the 40s subunit of the2 second 80s in the asymmetric unit.
47	c5t59D	Alignment	not modelled	14.5	13	PDB header: cell cycle Chain: D: PDB Molecule: klla0f02343p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
48	c4dmtA	Alignment	not modelled	14.4	67	PDB header: structural protein Chain: A: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
49	c4dmtC	Alignment	not modelled	14.4	67	PDB header: structural protein Chain: C: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
50	c4dmtB	Alignment	not modelled	14.4	67	PDB header: structural protein Chain: B: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
51	c4gtnA	Alignment	not modelled	14.3	23	PDB header: transferase Chain: A: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: structure of anthranilate phosphoribosyl transferase from2 acinetobacter baylyi
52	d2huec1	Alignment	not modelled	14.1	25	Fold: Histone-fold Superfamily: Histone-fold

						Family: Nucleosome core histones
53	c2v53D_	Alignment	not modelled	14.1	67	PDB header: cell adhesion Chain: D: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of a sparccollagen complex
54	c2v53C_	Alignment	not modelled	14.1	67	PDB header: cell adhesion Chain: C: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of a sparccollagen complex
55	c2v53B_	Alignment	not modelled	14.1	67	PDB header: cell adhesion Chain: B: PDB Molecule: collagen alpha-1(iii) chain; PDBTitle: crystal structure of a sparccollagen complex
56	d2elca2	Alignment	not modelled	13.7	31	Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Family: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
57	c1j9zB_	Alignment	not modelled	13.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-cytochrome p450 reductase; PDBTitle: cypor-w677g
58	c3mx2A_	Alignment	not modelled	12.9	23	PDB header: nuclear protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: lassa fever virus nucleoprotein complexed with dttp
59	c3c3iA_	Alignment	not modelled	12.6	15	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
60	c3j3aR_	Alignment	not modelled	12.6	24	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s17; PDBTitle: structure of the human 40s ribosomal proteins
61	c4gyxC_	Alignment	not modelled	12.3	67	PDB header: structural protein, blood clotting Chain: C: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
62	d1zy3a1	Alignment	not modelled	11.9	16	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
63	c5b02C_	Alignment	not modelled	11.3	17	PDB header: transferase, dna binding protein Chain: C: PDB Molecule: moen5,dna-binding protein 7d; PDBTitle: structure of the prenyltransferase moen5 with a fusion protein tag of2 sso7d
64	c1fctA_	Alignment	not modelled	10.8	86	PDB header: transit peptide Chain: A: PDB Molecule: ferredoxin chloroplastic transit peptide PDBTitle: nmr structures of ferredoxin chloroplastic transit peptide2 from chlamydomonas reinhardtii promoted by3 trifluoroethanol in aqueous solution
65	c5nd1A_	Alignment	not modelled	10.6	24	PDB header: virus Chain: A: PDB Molecule: capsid protein; PDBTitle: viral evolution results in multiple, surface-allocated enzymatic2 activities in a fungal double-stranded rna virus
66	d1r3sa_	Alignment	not modelled	10.6	20	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
67	d1kx5b_	Alignment	not modelled	10.5	26	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
68	d1brwa2	Alignment	not modelled	10.5	19	Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Family: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
69	c5foeA_	Alignment	not modelled	10.4	38	PDB header: transferase Chain: A: PDB Molecule: gdp-fucose protein o-fucosyltransferase 2,thrombospondin-1; PDBTitle: crystal structure of the c. elegans protein o-fucosyltransferase 22 (cepofut2) double mutant (r298k-r299k) in complex with gdp and the3 human tsr1 from thrombospondin 1
70	c1tllA_	Alignment	not modelled	10.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase, brain; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
71	c5b0mB_	Alignment	not modelled	10.1	17	PDB header: transferase, dna binding protein Chain: B: PDB Molecule: moen5,dna-binding protein 7d; PDBTitle: structure of moen5-sso7d fusion protein in complex with beta-dodecyl2 maltoside
72	c5jd3A_	Alignment	not modelled	9.7	18	PDB header: hydrolase Chain: A: PDB Molecule: lae5; PDBTitle: crystal structure of lae5, an alpha/beta hydrolase enzyme from the2 metagenome of lake arreo, spain
73	d1b8za_	Alignment	not modelled	9.6	29	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-binding protein
74	c2l0cA_	Alignment	not modelled	9.5	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative membrane protein; PDBTitle: solution nmr structure of protein sty4237 (residues 36-120) from2 salmonella enterica, northeast structural genomics consortium target3 slr115
75	d1id3b_	Alignment	not modelled	9.5	23	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
76	c2bpqB_	Alignment	not modelled	9.5	24	PDB header: transferase Chain: B: PDB Molecule: anthranilate phosphoribosyltransferase; PDBTitle: anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)

77	c3fcgB	Alignment	not modelled	9.0	14	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: f1 capsule-anchoring protein; PDBTitle: crystal structure analysis of the middle domain of the2 caf1a usher
78	c6nmiE	Alignment	not modelled	8.9	14	PDB header: transcription Chain: E: PDB Molecule: general transcription factor iih subunit 2, p44; PDBTitle: cryo-em structure of the human tfiih core complex
79	c2d4nA	Alignment	not modelled	8.5	18	PDB header: hydrolase Chain: A: PDB Molecule: du; PDBTitle: crystal structure of m-pmv dutpase complexed with dupnpp, substrate2 analogue
80	d1vyqa1	Alignment	not modelled	8.3	17	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
81	d1uoua2	Alignment	not modelled	8.2	16	Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Family: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
82	d2incb1	Alignment	not modelled	8.2	14	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
83	d1mula	Alignment	not modelled	8.1	19	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
84	c6hc2L	Alignment	not modelled	7.8	38	PDB header: cell cycle Chain: L: PDB Molecule: nuclear mitotic apparatus protein 1; PDBTitle: crystal structure of numa/Ign hetero-hexamers
85	c3cxnB	Alignment	not modelled	7.7	12	PDB header: chaperone Chain: B: PDB Molecule: urease accessory protein uref; PDBTitle: structure of the urease accessory protein uref from helicobacter2 pylori
86	c3ajvD	Alignment	not modelled	7.7	14	PDB header: hydrolase Chain: D: PDB Molecule: trna-splicing endonuclease; PDBTitle: splicing endonuclease from aeropyrum pernix
87	c3h1nA	Alignment	not modelled	7.7	15	PDB header: transferase Chain: A: PDB Molecule: probable glutathione s-transferase; PDBTitle: crystal structure of probable glutathione s-transferase from2 bordetella bronchiseptica rb50
88	c5t58A	Alignment	not modelled	7.5	13	PDB header: cell cycle Chain: A: PDB Molecule: klla0f02343p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
89	c5wwlM	Alignment	not modelled	7.4	21	PDB header: cell cycle Chain: M: PDB Molecule: centromere protein mis12; PDBTitle: crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
90	c2l5aA	Alignment	not modelled	7.4	35	PDB header: nuclear protein Chain: A: PDB Molecule: histone h3-like centromeric protein cse4, protein scm3, PDBTitle: structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
91	c4e2i3	Alignment	not modelled	7.3	19	PDB header: hydrolase/dna binding protein Chain: 3: PDB Molecule: dna polymerase alpha subunit b; PDBTitle: the complex structure of the sv40 helicase large t antigen and p682 subunit of dna polymerase alpha-primase
92	c2kebA	Alignment	not modelled	7.3	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase subunit alpha b; PDBTitle: nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
93	c5xyiR	Alignment	not modelled	7.3	24	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s17-b, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
94	d1ja1a2	Alignment	not modelled	7.3	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
95	c2a5yA	Alignment	not modelled	7.2	11	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator ced-9; PDBTitle: structure of a ced-4/ced-9 complex
96	c2p9oB	Alignment	not modelled	7.2	17	PDB header: hydrolase Chain: B: PDB Molecule: dutp pyrophosphatase-like protein; PDBTitle: structure of dutpase from arabidopsis thaliana
97	d1hiod	Alignment	not modelled	7.0	40	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
98	c2xzmV	Alignment	not modelled	7.0	24	PDB header: ribosome Chain: V: PDB Molecule: rps17e; 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 1
99	c2yzjB	Alignment	not modelled	7.0	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 167aa long hypothetical dutpase; PDBTitle: crystal structure of dctp deaminase from sulfolobus tokodaii