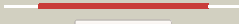



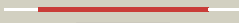




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0896_gltA_999475_1000770
Date	Fri Jul 26 01:50:48 BST 2019
Unique Job ID	cd9ad98e7b62ba04

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2h12C_	 Alignment		100.0	53	PDB header: transferase Chain: C: PDB Molecule: citrate synthase; PDBTitle: structure of acetobacter aceti citrate synthase complexed with2 oxaloacetate and carboxymethyldehia coenzyme a (cmx)
2	d1k3pa_	 Alignment		100.0	53	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
3	c3msuA_	 Alignment		100.0	47	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from francisella tularensis
4	c4tvmA_	 Alignment		100.0	98	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: structure of citrate synthase from mycobacterium tuberculosis
5	c4xghA_	 Alignment		100.0	54	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: x-ray crystal structure of citrate synthase from burkholderia2 thailandensis
6	c2ibpB_	 Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from pyrobaculum aerophilum
7	d1aj8a_	 Alignment		100.0	37	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
8	d1csca_	 Alignment		100.0	28	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
9	d1ioma_	 Alignment		100.0	35	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
10	c1vgmB_	 Alignment		100.0	36	PDB header: transferase Chain: B: PDB Molecule: 378aa long hypothetical citrate synthase; PDBTitle: crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaïi strain7
11	d1cscha_	 Alignment		100.0	29	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase

12	c1vgpA_	Alignment		100.0	39	PDB header: transferase Chain: A; PDB Molecule: 373aa long hypothetical citrate synthase; PDBTitle: crystal structure of an isozyme of citrate synthase from sulfolobus2 tokodaii strain7
13	c2r26C_	Alignment		100.0	32	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
14	d2ctsa_	Alignment		100.0	30	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
15	c6abxA_	Alignment		100.0	40	PDB header: transferase Chain: A; PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase (msed_1522) from metallosphaera2 sedula in complex with citrate
16	c3hwkE_	Alignment		100.0	32	PDB header: transferase Chain: E; PDB Molecule: methylcitrate synthase; PDBTitle: crystal structure of methylcitrate synthase from mycobacterium2 tuberculosis
17	d1a59a_	Alignment		100.0	37	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
18	d1o7xa_	Alignment		100.0	34	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
19	c2p2wA_	Alignment		100.0	40	PDB header: transferase Chain: A; PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from thermotoga maritima msb8
20	c3tqgA_	Alignment		100.0	32	PDB header: transferase Chain: A; PDB Molecule: 2-methylcitrate synthase; PDBTitle: structure of the 2-methylcitrate synthase (prpc) from coxiella2 burnetii
21	c2c6xA_	Alignment	not modelled	100.0	35	PDB header: transferase Chain: A; PDB Molecule: citrate synthase 1; PDBTitle: structure of bacillus subtilis citrate synthase
22	c3o8jH_	Alignment	not modelled	100.0	33	PDB header: transferase Chain: H; PDB Molecule: 2-methylcitrate synthase; PDBTitle: crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
23	c5uqqD_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: D; PDB Molecule: 2-methylcitrate synthase, mitochondrial; PDBTitle: crystal structure of 2-methylcitrate synthase from aspergillus2 fumigatus
24	c6hxpA_	Alignment	not modelled	100.0	25	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	27	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	27	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	c6hxD_	Alignment	not modelled	100.0	30	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	c6hxoH_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: H; 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)
29	c6qfbB_	Alignment	not modelled	100.0	31	PDB header: lyase 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	22	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	c3zeyl_	Alignment	not modelled	56.1	23	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s15, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
32	d1ehia1	Alignment	not modelled	48.0	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
33	c3j38P_	Alignment	not modelled	46.1	33	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein s15, isoform a; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
34	c2xzmS_	Alignment	not modelled	41.0	41	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
35	c3j20T_	Alignment	not modelled	35.9	38	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)
36	c5xyiP_	Alignment	not modelled	28.0	33	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein s19, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
37	c5xxuP_	Alignment	not modelled	25.9	29	PDB header: ribosome Chain: P: PDB Molecule: ribosomal protein us19; PDBTitle: small subunit of toxoplasma gondii ribosome
38	d1e4ea1	Alignment	not modelled	19.3	24	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
39	c6co6B_	Alignment	not modelled	18.3	14	PDB header: hydrolase Chain: B: PDB Molecule: probable coa-transferase beta subunit; PDBTitle: crystal structure of rhodococcus jostii rha1 ipdab
40	c2l0cA_	Alignment	not modelled	17.2	60	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
41	c2nx9B_	Alignment	not modelled	16.8	17	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
42	c3c65A_	Alignment	not modelled	16.2	13	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of bacillus stearothermophilus uvr c 5' endonuclease2 domain
43	d1kha2	Alignment	not modelled	15.9	20	Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Family: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
44	c3sukB_	Alignment	not modelled	15.8	24	PDB header: unknown function Chain: B: PDB Molecule: cerato-platanin-like protein; PDBTitle: crystal structure of cerato-platanin 2 from m. pernicioso (mpcp2)
45	c4pxuA_	Alignment	not modelled	15.7	16	PDB header: cell cycle Chain: A: PDB Molecule: bipolar kinesin krp-130; PDBTitle: structural basis for the assembly of the mitotic motor kinesin-5 into2 bipolar tetramers
46	c2e28A_	Alignment	not modelled	14.5	20	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
47	c3mesB_	Alignment	not modelled	14.5	16	PDB header: transferase Chain: B: PDB Molecule: choline kinase; PDBTitle: crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
48	c3fcgB_	Alignment	not modelled	14.0	9	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
49	c5lnk3_	Alignment	not modelled	12.9	11	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
50	c5xxuR_	Alignment	not modelled	12.7	21	PDB header: ribosome Chain: R: PDB Molecule: ribosomal protein es17; PDBTitle: small subunit of toxoplasma gondii ribosome
51	c5n02B_	Alignment	not modelled	12.5	21	PDB header: lyase Chain: B: PDB Molecule: glutaconate coa-transferase family, subunit b; PDBTitle: crystal structure of the decarboxylase aiba/aibb c56s variant
52	c2ckpB_	Alignment	not modelled	11.9	16	PDB header: transferase Chain: B: PDB Molecule: choline kinase alpha; PDBTitle: crystal structure of human choline kinase alpha-2 in2 complex with adp
						Fold: NagB/RpiA/CoA transferase-like

53	d1poib_	Alignment	not modelled	11.7	13	Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase beta subunit-like
54	c2i81B_	Alignment	not modelled	10.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-cys peroxiredoxin; PDBTitle: crystal structure of plasmodium vivax 2-cys peroxiredoxin,2 reduced
55	c3izbQ_	Alignment	not modelled	10.5	26	PDB header: ribosome Chain: Q: PDB Molecule: 40s ribosomal protein rps17 (s17e); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
56	c3t07D_	Alignment	not modelled	10.0	19	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
57	c3c5iD_	Alignment	not modelled	10.0	10	PDB header: transferase Chain: D: PDB Molecule: choline kinase; PDBTitle: crystal structure of plasmodium knowlesi choline kinase, pkh 134520
58	c5x6bF_	Alignment	not modelled	9.2	31	PDB header: rna binding protein/rna Chain: F: PDB Molecule: uncharacterized protein mj1481; PDBTitle: crystal structure of sepcyse-sepcyss in complex with trnacs from2 methanocaldococcus jannaschii
59	c3lmaC_	Alignment	not modelled	9.0	19	PDB header: membrane protein Chain: C: PDB Molecule: stage v sporulation protein ad (spovad); PDBTitle: crystal structure of the stage v sporulation protein ad (spovad) from2 bacillus licheniformis. northeast structural genomics consortium3 target bir6.
60	c3j3aR_	Alignment	not modelled	8.9	16	PDB header: ribosome Chain: R: PDB Molecule: 40s ribosomal protein s17; PDBTitle: structure of the human 40s ribosomal proteins
61	c3o30I_	Alignment	not modelled	8.6	24	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.
62	c1c4cA_	Alignment	not modelled	8.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (fe-only hydrogenase); PDBTitle: binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
63	c5xf9F_	Alignment	not modelled	8.6	13	PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
64	c2fugC_	Alignment	not modelled	8.5	7	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-quinone oxidoreductase chain 3; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
65	c3zu3A_	Alignment	not modelled	8.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative reductase ypo4104/y4119/yp_4011; PDBTitle: structure of the enoyl-acyl reductase fabv from yersinia pestis with2 the cofactor nadh (mr, cleaved histag)
66	c3kgkA_	Alignment	not modelled	8.3	31	PDB header: chaperone Chain: A: PDB Molecule: arsenical resistance operon trans-acting repressor arsd; PDBTitle: crystal structure of arsd
67	c6conF_	Alignment	not modelled	8.3	16	PDB header: hydrolase Chain: F: PDB Molecule: coa-transferase subunit beta; PDBTitle: crystal structure of mycobacterium tuberculosis ipdab
68	c2r9qD_	Alignment	not modelled	8.1	22	PDB header: hydrolase Chain: D: PDB Molecule: 2'-deoxycytidine 5'-triphosphate deaminase; PDBTitle: crystal structure of 2'-deoxycytidine 5'-triphosphate deaminase from2 agrobacterium tumefaciens
69	c3ktbD_	Alignment	not modelled	7.9	23	PDB header: transcription regulator Chain: D: PDB Molecule: arsenical resistance operon trans-acting repressor; PDBTitle: crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
70	c5t59D_	Alignment	not modelled	7.8	7	PDB header: cell cycle Chain: D: PDB Molecule: klla0f02343p; PDBTitle: structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
71	d1kbla2	Alignment	not modelled	7.8	42	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
72	c3w6gP_	Alignment	not modelled	7.6	25	PDB header: oxidoreductase Chain: P: PDB Molecule: probable peroxiredoxin; PDBTitle: structure of peroxiredoxin from anaerobic hyperthermophilic archaeon2 pyrococcus horikoshii
73	c4rvga_	Alignment	not modelled	7.5	21	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
74	c3j3bF_	Alignment	not modelled	7.3	20	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the human 60s ribosomal proteins
75	c1tlla_	Alignment	not modelled	7.1	18	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.
76	c1fcta_	Alignment	not modelled	7.1	43	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
77	d1m1ha1	Alignment	not modelled	7.1	26	Fold: N-utilization substance G protein NusG, insert domain Superfamily: N-utilization substance G protein NusG, insert domain Family: N-utilization substance G protein NusG, insert domain

78	c1ynmA	Alignment	not modelled	7.0	33	PDB header: hydrolase Chain: A: PDB Molecule: r.hinp1i restriction endonuclease; PDBTitle: crystal structure of restriction endonuclease hinp1i
79	c5vylA	Alignment	not modelled	6.9	11	PDB header: viral protein Chain: A: PDB Molecule: inner tegument protein; PDBTitle: crystal structure of n-terminal half of herpes simplex virus type 12 ul37 protein
80	c4c92B	Alignment	not modelled	6.9	19	PDB header: transcription Chain: B: PDB Molecule: u6 snrna-associated sm-like protein lsm2; PDBTitle: crystal structure of the yeast lsm1-7 complex
81	d1f0la3	Alignment	not modelled	6.8	23	Fold: Toxins' membrane translocation domains Superfamily: Diphtheria toxin, middle domain Family: Diphtheria toxin, middle domain
82	d1mula	Alignment	not modelled	6.8	16	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
83	c5foeA	Alignment	not modelled	6.7	24	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
84	c3ajvD	Alignment	not modelled	6.6	43	PDB header: hydrolase Chain: D: PDB Molecule: trna-splicing endonuclease; PDBTitle: splicing endonuclease from aeropyrum pernix
85	c3sulA	Alignment	not modelled	6.6	22	PDB header: unknown function Chain: A: PDB Molecule: cerato-platanin-like protein; PDBTitle: crystal structure of cerato-platanin 3 from m. perniciosa (mpcp3)
86	c3j39F	Alignment	not modelled	6.6	25	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
87	c5zteA	Alignment	not modelled	6.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-cys peroxiredoxin bas1, chloroplastic; PDBTitle: crystal structure of prxa c119s mutant from arabidopsis thaliana
88	c6hu9u	Alignment	not modelled	6.4	7	PDB header: oxidoreductase/electron transport Chain: U: PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
89	c2qg7A	Alignment	not modelled	6.4	18	PDB header: transferase Chain: A: PDB Molecule: ethanolamine kinase pv091845; PDBTitle: plasmodium vivax ethanolamine kinase pv091845
90	c5ovqL	Alignment	not modelled	6.3	24	PDB header: oxidoreductase Chain: L: PDB Molecule: peroxiredoxin; PDBTitle: crystal structure of the peroxiredoxin (ahpc2) from the2 hyperthermophilic bacteria aquifex aeolicus vf
91	c2rf4A	Alignment	not modelled	6.2	6	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase i subunit rpa4; PDBTitle: crystal structure of the rna polymerase i subcomplex a14/43
92	c2yzjB	Alignment	not modelled	5.9	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 167aa long hypothetical dutpase; PDBTitle: crystal structure of dctp deaminase from sulfolobus tokodaii
93	c2lmcA	Alignment	not modelled	5.9	10	PDB header: transcription Chain: A: PDB Molecule: bacterial rna polymerase inhibitor; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
94	c2wnmA	Alignment	not modelled	5.9	10	PDB header: hydrolase Chain: A: PDB Molecule: gene 2; PDBTitle: solution structure of gp2
95	c2rilA	Alignment	not modelled	5.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
96	c5nd1A	Alignment	not modelled	5.8	29	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
97	d1b8za	Alignment	not modelled	5.8	20	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
98	d1ioka2	Alignment	not modelled	5.8	41	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
99	d2huec1	Alignment	not modelled	5.7	25	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones