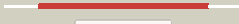







Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3687c_(rsfB)_4129501_4129869
 Date Fri Aug 9 18:20:38 BST 2019
 Unique Job ID deced81d8eb4543e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4hylB_	 Alignment		99.9	18	PDB header: transcription regulator Chain: B: PDB Molecule: stage ii sporulation protein; PDBTitle: the crystal structure of an anti-sigma-factor antagonist from <i>Haliangium ochraceum</i> DSM 14365
2	d1th8b_	 Alignment		99.9	24	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
3	c3t6oA_	 Alignment		99.9	21	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: the structure of an anti-sigma-factor antagonist (stas) domain protein2 from <i>Planctomyces limnophilus</i> .
4	c3f43A_	 Alignment		99.9	19	PDB header: transcription Chain: A: PDB Molecule: putative anti-sigma factor antagonist tm1081; PDBTitle: crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from <i>Thermotoga maritima</i> at 1.59 Å resolution
5	d1lauza_	 Alignment		99.9	22	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
6	d1vc1a_	 Alignment		99.9	22	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
7	c4xs5D_	 Alignment		99.9	13	PDB header: transport protein Chain: D: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: crystal structure of sulfate transporter/antisigma-factor antagonist2 stas from <i>Dyadobacter fermentans</i> DSM 18053
8	d1h4xa_	 Alignment		99.8	15	Fold: Spollaa-like Superfamily: Spollaa-like Family: Anti-sigma factor antagonist Spollaa
9	c3ny7A_	 Alignment		99.8	17	PDB header: membrane protein Chain: A: PDB Molecule: sulfate transporter; PDBTitle: stas domain of ychm bound to acp
10	c2klnA_	 Alignment		99.8	16	PDB header: transport protein Chain: A: PDB Molecule: probable sulphate-transport transmembrane protein, cog0659; PDBTitle: solution structure of stas domain of rv1739c from <i>M. tuberculosis</i>
11	c2vy9A_	 Alignment		99.8	17	PDB header: gene regulation Chain: A: PDB Molecule: anti-sigma-factor antagonist; PDBTitle: molecular architecture of the stressosome, a signal2 integration and transduction hub

12	c3mg1A_	Alignment		99.8	19	PDB header: transport protein Chain: A: PDB Molecule: sulfate permease family protein; PDBTitle: crystal structure of permease family protein from vibrio cholerae
13	c5ezbB_	Alignment		99.8	18	PDB header: transport protein Chain: B: PDB Molecule: chicken prestin stas domain,chicken prestin stas domain; PDBTitle: chicken prestin stas domain
14	c3oirA_	Alignment		99.8	17	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolinnella2 succinogenes
15	c3lloA_	Alignment		99.7	20	PDB header: motor protein Chain: A: PDB Molecule: prestin; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
16	c6rtfA_	Alignment		99.6	20	PDB header: membrane protein Chain: A: PDB Molecule: solute carrier family 26 member 9,solute carrier family 26 PDBTitle: structure of murine solute carrier 26 family member a9 (slc26a9) anion2 transporter in an intermediate state
17	c6ic4K_	Alignment		99.6	19	PDB header: protein transport Chain: K: PDB Molecule: ttg2e; PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
18	c3lk1B_	Alignment		99.5	10	PDB header: transport protein Chain: B: PDB Molecule: antisigma-factor antagonist stas; PDBTitle: crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
19	c5da0A_	Alignment		99.2	14	PDB header: transport protein Chain: A: PDB Molecule: sulphate transporter; PDBTitle: structure of the the slc26 transporter slc26dg in complex with a2 nanobody
20	d2q31a1	Alignment		95.3	13	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
21	c3bl4B_	Alignment	not modelled	94.6	16	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function (arth_0117) from2 arthrobacter sp. fb24 at 2.20 a resolution
22	c3ih9A_	Alignment	not modelled	92.6	24	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure analysis of mglu in its tris form
23	d2ooka1	Alignment	not modelled	78.2	8	Fold: Spollaa-like Superfamily: Spollaa-like Family: Sfri0576-like
24	c2deoA_	Alignment	not modelled	76.2	33	PDB header: hydrolase Chain: A: PDB Molecule: 441aa long hypothetical nfed protein; PDBTitle: 1510-n membrane protease specific for a stomatin homolog from2 pyrococcus horikoshii
25	c3qmjA_	Alignment	not modelled	72.4	24	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase, echa8_6; PDBTitle: crystal structure of enoyl-coa hydratase echa8_6 from mycobacterium2 marinum
26	c3bezC_	Alignment	not modelled	65.5	16	PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
27	c2k1cA_	Alignment	not modelled	60.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr solution structure of human ubiquitin-like domain of ubiquilin 1,2 northeast structural genomics consortium (nesg) target ht5a
28	c6iqsD_	Alignment	not modelled	55.8	20	PDB header: hydrolase Chain: D: PDB Molecule: tail-specific protease; PDBTitle: crystal structure of prc with I245a and I340g mutations in complex2 with nlpi

29	c6k4fU_	Alignment	not modelled	54.6	21	PDB header: biosynthetic protein Chain: U: PDB Molecule: duf1987 domain-containing protein; PDBTitle: siac of pseudomonas aeruginosa
30	c5wybB_	Alignment	not modelled	50.4	22	PDB header: isomerase Chain: B: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: structure of pseudomonas aeruginosa dspi
31	c4oIQD_	Alignment	not modelled	46.5	13	PDB header: lyase Chain: D: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of a putative enoyl-coa hydratase/isomerase family2 protein from hyphomonas neptunium
32	c3isaA_	Alignment	not modelled	41.5	13	PDB header: hydrolase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
33	c2qtdA_	Alignment	not modelled	35.2	4	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein mj0327; PDBTitle: crystal structure of a putative dinitrogenase (mj0327) from2 methanocaldococcus jannaschii dsm at 1.70 a resolution
34	d1sg4a1	Alignment	not modelled	34.7	21	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
35	c2pr7A_	Alignment	not modelled	34.6	10	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
36	c6emsA_	Alignment	not modelled	33.8	17	PDB header: rna binding protein Chain: A: PDB Molecule: trna (guanine(9)-/adenine(9)-n1)-methyltransferase; PDBTitle: crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis.
37	c2yuiA_	Alignment	not modelled	33.7	17	PDB header: apoptosis Chain: A: PDB Molecule: anamorsin; PDBTitle: solution structure of the n-terminal domain in human2 cytokine-induced apoptosis inhibitor anamorsin
38	c4og1A_	Alignment	not modelled	33.5	14	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a putative enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444
39	c2qq3F_	Alignment	not modelled	31.2	7	PDB header: lyase Chain: F: PDB Molecule: enoyl-coa hydratase subunit i; PDBTitle: crystal structure of enoyl-coa hydrates subunit i (gk_2039)2 other form from geobacillus kaustophilus hta426
40	c3rstH_	Alignment	not modelled	30.9	16	PDB header: hydrolase Chain: H: PDB Molecule: signal peptide peptidase sppa; PDBTitle: crystal structure of bacillus subtilis signal peptide peptidase a
41	d2csua3	Alignment	not modelled	30.1	7	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
42	c5wqlC_	Alignment	not modelled	29.9	19	PDB header: protein binding/signaling protein/hydrol Chain: C: PDB Molecule: tail-specific protease; PDBTitle: structure of a pdz-protease bound to a substrate-binding adaptor
43	c2f6qA_	Alignment	not modelled	29.0	14	PDB header: isomerase Chain: A: PDB Molecule: peroxisomal 3,2-trans-enoyl-coa isomerase; PDBTitle: the crystal structure of human peroxisomal delta3, delta2 enoyl coa2 isomerase (peci)
44	d1t3va_	Alignment	not modelled	27.6	13	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
45	c5zaiB_	Alignment	not modelled	27.4	11	PDB header: hydrolase Chain: B: PDB Molecule: 3-hydroxypropionyl-coenzyme a dehydratase; PDBTitle: crystal structure of 3-hydroxypropionyl-coa dehydratase from2 metallosphaera sedula
46	c2yx6C_	Alignment	not modelled	26.7	13	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein ph0822; PDBTitle: crystal structure of ph0822
47	c4fmwA_	Alignment	not modelled	24.2	12	PDB header: transferase Chain: A: PDB Molecule: rna (guanine-9)-methyltransferase domain-containing PDBTitle: crystal structure of methyltransferase domain of human rna (guanine-9-2) methyltransferase domain containing protein 2
48	d1yqba1	Alignment	not modelled	23.7	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
49	c3fwnB_	Alignment	not modelled	23.2	10	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
50	d1o13a_	Alignment	not modelled	22.0	10	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
51	d1fmfa_	Alignment	not modelled	21.7	12	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
52	c3i47A_	Alignment	not modelled	21.4	9	PDB header: lyase Chain: A: PDB Molecule: enoyl coa hydratase/isomerase (crotonase); PDBTitle: crystal structure of putative enoyl coa hydratase/isomerase2 (crotonase) from legionella pneumophila

						subsp. pneumophila str.3 philadelphia 1 PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
53	c2iz1C_	Alignment	not modelled	20.8	12	PDB header: lyase, isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of enoyl-coa hydratase from pseudomonas2 aeruginosa pa01
54	c3laoA_	Alignment	not modelled	20.7	16	PDB header: isomerase Chain: A: PDB Molecule: putative enoyl-coa hydratase/isomerase; PDBTitle: the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
55	c3rsiA_	Alignment	not modelled	19.7	16	PDB header: lyase Chain: F: PDB Molecule: enoyl-coa hydratase; PDBTitle: structure of acryloyl-coa hydratase acuh from roseovarius nubinhibens2 ism
56	c5xzdF_	Alignment	not modelled	19.6	14	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
57	d1ef8a_	Alignment	not modelled	19.3	20	PDB header: cell cycle Chain: A: PDB Molecule: septum site-determining protein minc; PDBTitle: crystal structure of the septum site-determining protein minc from2 salmonella typhimurium
58	c3ghfA_	Alignment	not modelled	19.1	20	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of enoyl-coa hydratase/isomerase from cupriavidus2 metallidurans ch34
59	c4jcsA_	Alignment	not modelled	18.8	18	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a enoyl-coa hydratase from polaromonas sp. js666
60	c4jfcA_	Alignment	not modelled	18.6	16	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
61	d1rdua_	Alignment	not modelled	18.6	13	PDB header: isomerase Chain: A: PDB Molecule: probable enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
62	c3trrA_	Alignment	not modelled	18.6	15	PDB header: isomerase Chain: B: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a putative enoyl-coa hydratase/isomerase from2 novosphingobium aromaticivorans
63	c4wczB_	Alignment	not modelled	18.5	20	PDB header: hydrolase Chain: A: PDB Molecule: salt-tolerant glutaminase; PDBTitle: crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
64	c2dfwA_	Alignment	not modelled	18.0	23	PDB header: lyase Chain: F: PDB Molecule: p-hydroxycinnamoyl coa hydratase/lyase; PDBTitle: crystal structure of hydroxycinnamoyl-coa hydratase-lyase
65	c2j5fF_	Alignment	not modelled	17.3	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
66	d1wx7a1	Alignment	not modelled	17.3	25	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase echa17; PDBTitle: crystal structure of enoyl-coa hydratase echa17 from mycobacterium2 marinum
67	c4di1A_	Alignment	not modelled	17.0	19	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of csx1 of pyrococcus furiosus
68	c4eogA_	Alignment	not modelled	17.0	18	PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase family protein; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase family member,2 nysgrc target 028282
69	c4mouA_	Alignment	not modelled	16.8	24	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
70	d2cbya1	Alignment	not modelled	16.8	17	PDB header: ligase Chain: A: PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
71	c4yajA_	Alignment	not modelled	16.7	14	PDB header: hydrolase Chain: A: PDB Molecule: carboxy-terminal processing protease; PDBTitle: structure of c. trachomatis ct441
72	c4ql6A_	Alignment	not modelled	16.4	16	PDB header: isomerase,lyase Chain: J: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase/isomerase from2 pseudoalteromonas atlantica t6c at 2.3 a resolution.
73	c5ve2J_	Alignment	not modelled	16.2	25	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
74	d1r5ja_	Alignment	not modelled	16.1	15	PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of enoyl-coa hydratase from thermoplasma volcanium2 gss1
75	c4jylE_	Alignment	not modelled	16.0	19	PDB header: isomerase Chain: A: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of a enoyl-coa hydratase/isomerase from burkholderia2 graminis c4d1m
76	c4kd6A_	Alignment	not modelled	15.7	23	PDB header: lyase Chain: A: PDB Molecule: enoyl-coa hydratase echa1; PDBTitle: crystal structure of enoyl-coa hydratase echa1 from mycobacterium2 marinum
77	c3qxiA_	Alignment	not modelled	15.6	20	PDB header: hydrolase/peptide Chain: C: PDB Molecule: carboxy-terminal processing protease
78	c4c2dC_	Alignment	not modelled	15.4	25	

78	c4zuc_	Alignment	not modelled	13.4	23	ctpb; PDBTitle: crystal structure of the protease ctpb in an active state
79	d1izca_	Alignment	not modelled	15.2	10	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: HpcH/Hpal aldolase
80	c1izcA_	Alignment	not modelled	15.2	10	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
81	d1eola_	Alignment	not modelled	14.0	15	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
82	c4jvwA_	Alignment	not modelled	13.5	20	PDB header: lyase Chain: A: PDB Molecule: short chain enoyl-coa hydratase; PDBTitle: crystal structure of putative short chain enoyl-coa hydratase from2 novosphingobium aromaticivorans dsm 12444
83	c2mwgB_	Alignment	not modelled	13.3	12	PDB header: protein binding Chain: B: PDB Molecule: blue-light photoreceptor; PDBTitle: full-length solution structure of ytva, a lov-photoreceptor protein2 and regulator of bacterial stress response
84	c3tlf_	Alignment	not modelled	13.1	16	PDB header: isomerase Chain: F: PDB Molecule: enoyl-coa hydratase/isomerase; PDBTitle: crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
85	d1ptma_	Alignment	not modelled	13.0	24	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
86	d1nzya_	Alignment	not modelled	12.8	16	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
87	d2f6qa1	Alignment	not modelled	12.8	16	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
88	c3omeE_	Alignment	not modelled	12.5	16	PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
89	d1xcoa_	Alignment	not modelled	12.3	18	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
90	c2e58D_	Alignment	not modelled	12.1	14	PDB header: transferase Chain: D: PDB Molecule: mnmc2; PDBTitle: crystal structure of mnmc2 from aquifex aeolicus
91	c1yb2A_	Alignment	not modelled	12.1	2	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ta0852; PDBTitle: structure of a putative methyltransferase from thermoplasma2 acidophilum.
92	d1yb2a1	Alignment	not modelled	12.1	2	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: tRNA(1-methyladenosine) methyltransferase-like
93	c6emvA_	Alignment	not modelled	12.0	14	PDB header: rna binding protein Chain: A: PDB Molecule: trna (guanine(9)-adenine(9)-n1)-methyltransferase; PDBTitle: crystal structure of dual specific trm10 construct from thermococcus2 kodakaraensis.
94	c4zu2A_	Alignment	not modelled	11.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative isohexenylglutaconyl-coa hydratase; PDBTitle: pseudomonas aeruginosa atue
95	d1q52a_	Alignment	not modelled	11.8	12	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Crotonase-like
96	d1yg6a1	Alignment	not modelled	11.7	15	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
97	d2f6ia1	Alignment	not modelled	11.6	20	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Clp protease, ClpP subunit
98	c5z7rA_	Alignment	not modelled	11.4	25	PDB header: lyase Chain: A: PDB Molecule: short-chain-enoyl-coa hydratase; PDBTitle: crystal strcture of crotonase from clostridium acetobutylicum
99	c2iz6A_	Alignment	not modelled	11.4	7	PDB header: metal transport Chain: A: PDB Molecule: molybdenum cofactor carrier protein; PDBTitle: structure of the chlamydomonas reinhardtii moco carrier2 protein