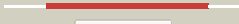



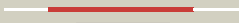




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2578c_(-)_2902519_2903541
Date	Wed Aug 7 12:50:21 BST 2019
Unique Job ID	0460848364aceda4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fheA_	 Alignment		100.0	17	PDB header: lyase Chain: A: PDB Molecule: spore photoproduct lyase; PDBTitle: spore photoproduct lyase c140a mutant
2	c4jc0B_	 Alignment		100.0	12	PDB header: transferase Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
3	c6fd2B_	 Alignment		99.9	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: putative apramycin biosynthetic oxidoreductase 4; PDBTitle: radical sam 1,2-diol dehydratase aprd4 in complex with its substrate2 paromamine
4	d1olta_	 Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
5	c517jA_	 Alignment		99.9	16	PDB header: translation Chain: A: PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
6	c5ul4A_	 Alignment		99.9	12	PDB header: metal binding protein Chain: A: PDB Molecule: oxsb protein; PDBTitle: structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
7	c6qk7C_	 Alignment		99.9	15	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
8	c3cixA_	 Alignment		99.9	17	PDB header: adomet binding protein Chain: A: PDB Molecule: feFe-hydrogenase maturase; PDBTitle: x-ray structure of the [FeFe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
9	c2qqaF_	 Alignment		99.9	10	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: protein tm_1862; PDBTitle: crystal structure of tm_1862 from thermotoga maritima. northeast2 structural genomics consortium target vr77
10	c3t7vA_	 Alignment		99.8	13	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
11	c5v1tA_	 Alignment		99.8	17	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua

12	c5exkG	Alignment		99.8	19	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
13	c1r30A	Alignment		99.8	17	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
14	d1r30a	Alignment		99.8	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
15	c6iazA	Alignment		99.8	15	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase, elp3 family; PDBTitle: the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
16	c3rfaA	Alignment		99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
17	c3rfaB	Alignment		99.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
18	c6fz6B	Alignment		99.7	13	PDB header: transferase Chain: B: PDB Molecule: probable dual-specificity rna methyltransferase rlmn; PDBTitle: crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
19	d1tv8a	Alignment		99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
20	c2yx0A	Alignment		99.7	19	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
21	c6efnA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
22	c4u0pB	Alignment	not modelled	99.7	13	PDB header: transferase Chain: B: PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
23	c3c8fA	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate formate-lyase 1-activating enzyme; PDBTitle: 4fe-4s-pyruvate formate-lyase activating enzyme with partially2 disordered adomet
24	c4wxcC	Alignment	not modelled	99.5	14	PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
25	c4k39A	Alignment	not modelled	99.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmece with bound adomet and cp18cys peptide
26	c2a5hC	Alignment	not modelled	99.5	14	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldime form of pyridoxal-5'-phosphate).
27	c5vslB	Alignment	not modelled	99.5	12	PDB header: antiviral protein Chain: B: PDB Molecule: radical s-adenosyl methionine domain-containing protein 2; PDBTitle: crystal structure of viperin with bound [4fe-4s] cluster and s-2 adenosylhomocysteine (sah)

28	c5wggA	Alignment	not modelled	99.5	10	PDB header: peptide binding protein Chain: A: PDB Molecule: radical sam domain protein; PDBTitle: structural insights into thioether bond formation in the biosynthesis2 of sactipeptides
29	c4rtbA	Alignment	not modelled	99.4	17	PDB header: lyase Chain: A: PDB Molecule: hydrg protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydrg from2 carboxydotherrnus hydrogenoformans
30	c6b4cH	Alignment	not modelled	99.4	10	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
31	c5th5C	Alignment	not modelled	99.4	13	PDB header: lyase Chain: C: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
32	c4r33A	Alignment	not modelled	99.1	17	PDB header: lyase Chain: A: PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
33	c6nhlB	Alignment	not modelled	99.0	15	PDB header: lyase Chain: B: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from escherichia coli
34	c4m7tA	Alignment	not modelled	98.9	16	PDB header: metal binding protein Chain: A: PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doia
35	c3canA	Alignment	not modelled	98.8	11	PDB header: lyase activator Chain: A: PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
36	c2z2uA	Alignment	not modelled	98.7	14	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
37	c4njkA	Alignment	not modelled	98.4	17	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from burkholderia multivorans in complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
38	c6c8vA	Alignment	not modelled	98.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
39	c5kzmA	Alignment	not modelled	93.0	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
40	c2y5sA	Alignment	not modelled	92.1	18	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
41	c3vndD	Alignment	not modelled	92.1	24	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
42	d1qopa	Alignment	not modelled	91.4	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
43	c5tchG	Alignment	not modelled	90.8	19	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
44	d2p10a1	Alignment	not modelled	90.7	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MIl9387-like
45	c6omzA	Alignment	not modelled	89.0	21	PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
46	c5k9xA	Alignment	not modelled	88.1	14	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
47	c2ekcA	Alignment	not modelled	87.7	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
48	c3lmzA	Alignment	not modelled	87.3	9	PDB header: isomerase Chain: A: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
49	c3p6lA	Alignment	not modelled	86.6	8	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
50	c3navB	Alignment	not modelled	86.5	16	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
51	c2dzaA	Alignment	not modelled	86.5	22	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
52	d1x7fa2	Alignment	not modelled	86.0	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain

53	d1bxbA	Alignment	not modelled	85.9	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
54	c5ey5A	Alignment	not modelled	85.9	15	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
55	c2zdsB	Alignment	not modelled	85.2	10	PDB header: dna binding protein Chain: B: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from streptomyces coelicolor a3(2)
56	c3bleA	Alignment	not modelled	84.6	10	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
57	d1l6wa	Alignment	not modelled	82.6	22	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
58	c3rmjB	Alignment	not modelled	82.4	15	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
59	c5ks8D	Alignment	not modelled	82.3	10	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
60	d1j0ha3	Alignment	not modelled	81.7	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
61	c4ovxA	Alignment	not modelled	81.6	7	PDB header: isomerase Chain: A: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
62	c2z1kA	Alignment	not modelled	81.5	20	PDB header: hydrolase Chain: A: PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of ttha1563 from thermus thermophilus hb8
63	c6e1jB	Alignment	not modelled	81.3	13	PDB header: plant protein Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
64	c3s1vD	Alignment	not modelled	80.9	20	PDB header: transferase Chain: D: PDB Molecule: probable transaldolase; PDBTitle: transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
65	c1x7fA	Alignment	not modelled	80.7	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein
66	d1wx0a1	Alignment	not modelled	80.6	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
67	d1ea9c3	Alignment	not modelled	80.6	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
68	c3vm7A	Alignment	not modelled	80.1	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of an alpha-amylase from malbranchea cinnamomea
69	d1qt1a	Alignment	not modelled	80.1	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
70	c3ewbX	Alignment	not modelled	79.8	13	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
71	c3cqkB	Alignment	not modelled	79.5	17	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
72	c5ud6B	Alignment	not modelled	79.5	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhbps from cyanidioschyzon merolae with lysine2 bound
73	c1ydnA	Alignment	not modelled	79.4	15	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
74	c2bdqA	Alignment	not modelled	79.0	12	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast structural genomics target sar15.
75	d1pkla2	Alignment	not modelled	78.7	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
76	c2ftpA	Alignment	not modelled	78.7	14	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
77	d1ajza	Alignment	not modelled	78.4	12	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
						PDB header: hydrolase,oxidoreductase Chain: A: PDB Molecule: protein regulated by acid ph;

78	c5vrvA_	Alignment	not modelled	78.3	16	PDBTitle: 2.05 angstrom resolution crystal structure of c-terminal domain2 (duf2156) of putative lysylphosphatidylglycerol synthetase from3 agrobacterium fabrum.
79	d2q02a1	Alignment	not modelled	77.8	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
80	d1muma_	Alignment	not modelled	77.6	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
81	d1vpxa_	Alignment	not modelled	77.5	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
82	c1ea9D_	Alignment	not modelled	77.2	23	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltodextrinase; PDBTitle: cyclomaltodextrinase
83	d1ujga_	Alignment	not modelled	76.8	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
84	d1yx1a1	Alignment	not modelled	76.8	23	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
85	c3qbuD_	Alignment	not modelled	76.5	12	PDB header: hydrolase Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of putative peptidoglycan deactelyase (hp0310) from2 helicobacter pylori
86	d2aaaa2	Alignment	not modelled	76.3	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
87	c3khdC_	Alignment	not modelled	76.3	8	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
88	c3thaB_	Alignment	not modelled	76.1	12	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
89	c3bdkB_	Alignment	not modelled	74.6	16	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
90	c3kwsB_	Alignment	not modelled	74.2	10	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
91	c3d0cB_	Alignment	not modelled	73.1	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
92	d1a3xa2	Alignment	not modelled	72.8	12	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
93	c3dx5A_	Alignment	not modelled	72.7	8	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
94	d1gvia3	Alignment	not modelled	72.6	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	c3r8rj_	Alignment	not modelled	72.5	22	PDB header: transferase Chain: J: PDB Molecule: transaldolase; PDBTitle: transaldolase from bacillus subtilis
96	c2p10D_	Alignment	not modelled	72.1	17	PDB header: hydrolase Chain: D: PDB Molecule: mlI9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
97	c5afdA_	Alignment	not modelled	71.9	9	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: native structure of n-acetylneuraminatase lyase (sialic acid aldolase)2 from aliivibrio salmonicida
98	c4k3zA_	Alignment	not modelled	71.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: d-erythrulose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrulose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
99	d1djqa1	Alignment	not modelled	71.6	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
100	d1twda_	Alignment	not modelled	71.1	16	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like
101	c3c52B_	Alignment	not modelled	70.5	9	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolohydroxamic acid, a competitive3 inhibitor
102	d1f74a_	Alignment	not modelled	70.0	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
103	c3e96B_	Alignment	not modelled	70.0	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii

104	c2cw6B_	Alignment	not modelled	69.7	11	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
105	c4ah7C_	Alignment	not modelled	69.6	12	PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: structure of wild type staphylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
106	d1ad1a_	Alignment	not modelled	69.3	12	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
107	c5dlcC_	Alignment	not modelled	68.5	23	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
108	c5kinC_	Alignment	not modelled	67.6	15	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
109	c3iwpK_	Alignment	not modelled	67.5	16	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
110	d2gjp2	Alignment	not modelled	67.2	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
111	d1bxca_	Alignment	not modelled	67.1	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
112	d3dhpa2	Alignment	not modelled	66.5	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
113	c2hmcA_	Alignment	not modelled	66.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
114	c4nq1B_	Alignment	not modelled	66.0	14	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
115	c3na8A_	Alignment	not modelled	65.9	11	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
116	c4ur7B_	Alignment	not modelled	65.7	11	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
117	c3rxzA_	Alignment	not modelled	65.7	14	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
118	c4uxdC_	Alignment	not modelled	65.7	9	PDB header: lyase Chain: C: PDB Molecule: 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from picrophilus torridus
119	c3gk0H_	Alignment	not modelled	65.6	23	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
120	c3b8iF_	Alignment	not modelled	65.5	13	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.