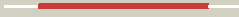
















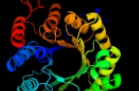















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3710_(leuA)_4153918_4155852
Date	Fri Aug 9 18:20:40 BST 2019
Unique Job ID	67c0699bce43aee0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1sr9A_	Alignment 		100.0	98	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leuA from mycobacterium tuberculosis
2	c3hpxB_	Alignment 		100.0	100	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of mycobacterium tuberculosis leuA active site2 domain 1-425 (truncation mutant delta:426-644)
3	c6e1jB_	Alignment 		100.0	25	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
4	c4ov9A_	Alignment 		100.0	27	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
5	c3jvuB_	Alignment 		100.0	20	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
6	c3a9iA_	Alignment 		100.0	23	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
7	c2zyfA_	Alignment 		100.0	24	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
8	c3rmjB_	Alignment 		100.0	26	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
9	d1sr9a2	Alignment 		100.0	98	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
10	c3bleA_	Alignment 		100.0	20	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
11	c4jn6C_	Alignment 		100.0	18	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
						PDB header: lyase/oxidoreductase

12	c4lrtC	Alignment		100.0	15	Chain: C; PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
13	c1nvmG	Alignment		100.0	17	PDB header: lyase/oxidoreductase Chain: G; PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
14	c1ydoC	Alignment		100.0	17	PDB header: lyase Chain: C; PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
15	c2ftpA	Alignment		100.0	17	PDB header: lyase Chain: A; PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
16	c4qslE	Alignment		100.0	16	PDB header: ligase Chain: E; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
17	c2cw6B	Alignment		100.0	17	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
18	c3ewbX	Alignment		100.0	25	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
19	c3bg5C	Alignment		100.0	16	PDB header: ligase Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
20	c3eegB	Alignment		100.0	26	PDB header: transferase Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
21	c3bg3A	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
22	d1nvma2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
23	d1rqba2	Alignment	not modelled	100.0	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
24	c1ydnA	Alignment	not modelled	100.0	17	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.
25	c5ks8F	Alignment	not modelled	100.0	14	PDB header: ligase Chain: F; PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
26	c1rr2A	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A; PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
27	c5ks8D	Alignment	not modelled	100.0	17	PDB header: ligase Chain: D; PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
28	c3bg3B	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
						PDB header: lyase Chain: B; PDB Molecule: oxaloacetate decarboxylase 2, subunit

29	c2nx9B_	Alignment	not modelled	100.0	16	alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
30	c3dxiB_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative aldolase; PDBTitle: crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
31	c4qslC_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
32	c4qskB_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
33	c2qf7A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
34	c4hnbV_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
35	c3bg5B_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
36	c5vz0D_	Alignment	not modelled	100.0	13	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
37	c3tw6B_	Alignment	not modelled	100.0	17	PDB header: ligase/activator Chain: B: PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
38	c3hblA_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
39	d1sr9a3	Alignment	not modelled	99.9	100	Fold: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Superfamily: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain Family: 2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
40	c3f6hA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: alpha-isopropylmalate synthase; PDBTitle: crystal structure of the regulatory domain of licms in2 complexed with isoleucine - type iii
41	d1xcfa_	Alignment	not modelled	98.2	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
42	d1sr9a1	Alignment	not modelled	98.0	96	Fold: RuvA C-terminal domain-like Superfamily: post-HMGL domain-like Family: DmpG/LeuA communication domain-like
43	c5n2pA_	Alignment	not modelled	97.6	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
44	c5kzmA_	Alignment	not modelled	97.4	19	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
45	c3thaB_	Alignment	not modelled	97.2	11	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
46	c2ekcA_	Alignment	not modelled	97.2	12	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
47	c3t7vA_	Alignment	not modelled	97.2	13	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
48	c3vndD_	Alignment	not modelled	97.0	21	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
49	c3vy1B_	Alignment	not modelled	96.8	17	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose 3-epimerase; PDBTitle: structure of l-ribulose 3-epimerase
50	c3navB_	Alignment	not modelled	96.7	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	d1qopa_	Alignment	not modelled	96.7	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
52	c2zvrA_	Alignment	not modelled	96.6	16	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related protein from2 thermotoga maritima
53	c3ajxA_	Alignment	not modelled	96.6	13	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
54	c3f4wA_	Alignment	not modelled	96.4	16	PDB header: synthase, lyase Chain: A: PDB Molecule: putative hexulose 6 phosphate synthase; PDBTitle: the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium

55	c5k9xA	Alignment	not modelled	96.2	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
56	c3exsB	Alignment	not modelled	96.1	10	PDB header: lyase Chain: B: PDB Molecule: rrmpd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
57	c3wqoB	Alignment	not modelled	96.1	12	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein mj1311; PDBTitle: crystal structure of d-tagatose 3-epimerase-like protein
58	c3ktcB	Alignment	not modelled	95.8	10	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
59	c5ey5A	Alignment	not modelled	95.7	19	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
60	d1rd5a	Alignment	not modelled	95.7	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
61	d1geqa	Alignment	not modelled	95.7	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
62	c3qc3B	Alignment	not modelled	95.7	14	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
63	c4nu7C	Alignment	not modelled	95.2	14	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
64	d1q6oa	Alignment	not modelled	95.1	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
65	c1tx2A	Alignment	not modelled	95.1	14	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
66	d1tx2a	Alignment	not modelled	95.1	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
67	d1ajza	Alignment	not modelled	95.1	22	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
68	c2zdsB	Alignment	not modelled	94.7	14	PDB header: dna binding protein Chain: B: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from streptomyces coelicolor a3(2)
69	c6oviA	Alignment	not modelled	94.7	13	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
70	c3jr2D	Alignment	not modelled	94.7	17	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbh; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
71	c5kinC	Alignment	not modelled	94.7	15	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
72	d1tqxa	Alignment	not modelled	94.4	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
73	c4muza	Alignment	not modelled	94.4	13	PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 archaeoglobus fulgidus complexed with inhibitor bmp
74	c4e38A	Alignment	not modelled	94.1	15	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156)
75	c3kruC	Alignment	not modelled	93.9	12	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
76	c5tnvA	Alignment	not modelled	93.7	13	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family protein 2; PDBTitle: crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
77	c5uurA	Alignment	not modelled	93.7	19	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid
78	c4ot7A	Alignment	not modelled	92.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
79	c3cixA	Alignment	not modelled	92.8	14	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

80	c3dx5A	Alignment	not modelled	92.7	13	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
81	d1k77a	Alignment	not modelled	92.7	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Hypothetical protein YgbM (EC1530)
82	c5hmqE	Alignment	not modelled	92.7	11	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
83	c5zfsA	Alignment	not modelled	92.2	15	PDB header: isomerase Chain: A: PDB Molecule: d-allulose-3-epimerase; PDBTitle: crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
84	d1vyra	Alignment	not modelled	92.1	13	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
85	c2ou4C	Alignment	not modelled	92.1	15	PDB header: isomerase Chain: C: PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
86	d1bxca	Alignment	not modelled	92.0	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
87	c3tr9A	Alignment	not modelled	91.7	15	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroi2 acid from coxiella burnetii
88	c3gr7A	Alignment	not modelled	91.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
89	d1h1ya	Alignment	not modelled	91.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
90	d1wbha1	Alignment	not modelled	91.2	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
91	c3cqkB	Alignment	not modelled	91.1	16	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
92	c3aytA	Alignment	not modelled	91.0	13	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein tthb071; PDBTitle: tthb071 protein from thermus thermophilus hb8
93	d2q02a1	Alignment	not modelled	90.6	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
94	d1i60a	Alignment	not modelled	90.1	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
95	c3qxbB	Alignment	not modelled	90.1	12	PDB header: isomerase Chain: B: PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
96	c5tchG	Alignment	not modelled	90.0	28	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
97	c6nkeA	Alignment	not modelled	89.9	18	PDB header: transferase Chain: A: PDB Molecule: geranylgeranylglyceryl phosphate synthase; PDBTitle: wild-type gggps from thermoplasma volcanium
98	c2hk1D	Alignment	not modelled	89.6	16	PDB header: isomerase Chain: D: PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
99	c4k3zA	Alignment	not modelled	89.5	13	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
100	c3ct7E	Alignment	not modelled	89.2	17	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
101	c5dbul	Alignment	not modelled	89.0	13	PDB header: lyase Chain: I: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis
102	d1rpxa	Alignment	not modelled	88.6	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
103	d1r30a	Alignment	not modelled	88.4	11	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
104	c1r30A	Alignment	not modelled	88.4	11	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
105	c5vooB	Alignment	not modelled	88.2	14	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate homocysteine s-methyltransferase; PDBTitle: methionine synthase folate-binding domain with

						methyltetrahydrofolate2 from thermus thermophilus hb8
106	d2flia1	Alignment	not modelled	87.8	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
107	d1xima_	Alignment	not modelled	86.6	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
108	d2czda1	Alignment	not modelled	86.5	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
109	d1tqja_	Alignment	not modelled	86.3	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
110	c4xbsA_	Alignment	not modelled	85.9	15	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
111	c5exkG_	Alignment	not modelled	85.7	9	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
112	c1ps9A_	Alignment	not modelled	85.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
113	c3cnyA_	Alignment	not modelled	84.8	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a3 resolution
114	d1muwa_	Alignment	not modelled	84.8	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
115	c3w01A_	Alignment	not modelled	84.4	11	PDB header: transferase Chain: A: PDB Molecule: heptaprenylglyceryl phosphate synthase; PDBTitle: crystal structure of pcrb complexed with peg from staphylococcus2 aureus subsp. aureus mu3
116	c4eacC_	Alignment	not modelled	84.0	20	PDB header: lyase Chain: C: PDB Molecule: mannonate dehydratase; PDBTitle: crystal structure of mannonate dehydratase from escherichia coli2 strain k12
117	d1mxsa_	Alignment	not modelled	83.9	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
118	c4rtbA_	Alignment	not modelled	83.7	12	PDB header: lyase Chain: A: PDB Molecule: hydG protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydG from2 carboxydotherrmus hydrogenoformans
119	c4jejA_	Alignment	not modelled	83.4	12	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl glyceryl phosphate synthase; PDBTitle: ggpps from flavobacterium johnsoniae
120	d1yx1a1	Alignment	not modelled	82.9	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like