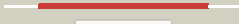



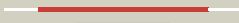




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2458_(mmuM)_2759789_2760697
Date	Wed Aug 7 12:50:08 BST 2019
Unique Job ID	3a12a22c2c975434

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3bofa2	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
2	c3bolB_	 Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
3	c4cczA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of human 5-methyltetrahydrofolate-homocysteine2 methyltransferase, the homocysteine and folate binding domains
4	d1umya_	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
5	c5dmnA_	 Alignment		100.0	47	PDB header: transferase Chain: A: PDB Molecule: homocysteine s-methyltransferase; PDBTitle: crystal structure of the homocysteine methyltransferase mmum from2 escherichia coli, apo form
6	d1lt7a_	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
7	c5ks8D_	 Alignment		96.0	13	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
8	c4mwaA_	 Alignment		95.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
9	c3igsB_	 Alignment		94.8	19	PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
10	c2nx9B_	 Alignment		94.7	11	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
11	d1muma_	 Alignment		93.5	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like

12	c3eooL_	Alignment		91.9	21	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
13	c2dwuA_	Alignment		91.9	15	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
14	c3vndD_	Alignment		91.6	12	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
15	c2ekcA_	Alignment		90.5	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
16	c1zfaA_	Alignment		90.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
17	d2fdsa1	Alignment		90.3	8	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
18	c2fdsA_	Alignment		90.3	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: orotidine-monophosphate-decarboxylase; PDBTitle: crystal structure of plasmodium berghei orotidine 5'-monophosphate2 decarboxylase (ortholog of plasmodium falciparum pf10_0225)
19	d2ffca1	Alignment		89.7	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
20	c1rr2A_	Alignment		88.7	11	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
21	c2infB_	Alignment	not modelled	88.2	22	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
22	d1j93a_	Alignment	not modelled	88.0	22	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
23	c5ey5A_	Alignment	not modelled	87.9	19	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
24	c3cyvA_	Alignment	not modelled	87.4	24	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 shigella flexneri: new insights into its catalytic3 mechanism
25	c3ih1A_	Alignment	not modelled	87.3	17	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
26	c3hfrA_	Alignment	not modelled	87.1	16	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes
27	c3n2xB_	Alignment	not modelled	87.1	16	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
28	c5xzoA_	Alignment	not modelled	86.9	11	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylanase; PDBTitle: crystal structure of gh10 xylanase xyl10c from bispora. sp mey-1

29	d1wbha1	Alignment	not modelled	86.8	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
30	c5zknA	Alignment	not modelled	86.6	17	PDB header: isomerase Chain: A: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
31	c1zlpA	Alignment	not modelled	86.5	16	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
32	d1a3xa2	Alignment	not modelled	86.2	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
33	c4zr8B	Alignment	not modelled	86.0	24	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
34	c4mg4G	Alignment	not modelled	85.9	18	PDB header: unknown function Chain: G: PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
35	c4axkB	Alignment	not modelled	85.9	14	PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens
36	c4i7vD	Alignment	not modelled	85.7	19	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhps with pyruvate
37	c3q58A	Alignment	not modelled	85.5	22	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
38	c4jn6C	Alignment	not modelled	84.8	19	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
39	d1xcfa	Alignment	not modelled	84.2	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
40	c3pm6B	Alignment	not modelled	84.0	12	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
41	c3lyeA	Alignment	not modelled	83.8	18	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
42	c3fa4D	Alignment	not modelled	83.8	19	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
43	c4x2rA	Alignment	not modelled	83.7	16	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis
44	c3r89A	Alignment	not modelled	83.5	7	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548
45	d2q8za1	Alignment	not modelled	83.5	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
46	d1m3ua	Alignment	not modelled	83.3	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
47	c3fkkA	Alignment	not modelled	83.1	14	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
48	c4exqA	Alignment	not modelled	81.7	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
49	c2ze3A	Alignment	not modelled	81.2	14	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
50	c3b8iF	Alignment	not modelled	81.0	21	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+.
51	d1gvfa	Alignment	not modelled	80.4	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
52	c2jfoB	Alignment	not modelled	78.8	10	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
53	c4fxsA	Alignment	not modelled	78.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid

54	d1rqba2	Alignment	not modelled	77.4	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
55	c3qz6A	Alignment	not modelled	77.4	10	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
56	d1ujqa	Alignment	not modelled	76.8	24	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
57	c5zjnB	Alignment	not modelled	76.5	19	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
58	d1qopa	Alignment	not modelled	76.3	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
59	c4uxdC	Alignment	not modelled	76.0	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
60	c1zh8B	Alignment	not modelled	75.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
61	d1pkla2	Alignment	not modelled	74.2	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
62	c2gzmb	Alignment	not modelled	74.2	13	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of the glutamate racemase from bacillus anthracis
63	c3ez4B	Alignment	not modelled	74.0	21	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
64	c3s5oA	Alignment	not modelled	74.0	14	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; PDBTitle: crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
65	d1xlma	Alignment	not modelled	73.4	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
66	c5ks8F	Alignment	not modelled	71.9	14	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
67	d1ur4a	Alignment	not modelled	71.9	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
68	c3pg8B	Alignment	not modelled	71.6	18	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
69	c2y0fD	Alignment	not modelled	71.6	21	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
70	d2a6na1	Alignment	not modelled	71.0	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
71	c2qiwa	Alignment	not modelled	69.8	16	PDB header: transferase Chain: A: PDB Molecule: pep phosphonomutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
72	d1pv8a	Alignment	not modelled	69.3	42	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
73	c6daoB	Alignment	not modelled	69.1	12	PDB header: lyase Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine
74	c4fxjB	Alignment	not modelled	68.8	13	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes m1/m2; PDBTitle: structure of m2 pyruvate kinase in complex with phenylalanine
75	c3gr7A	Alignment	not modelled	68.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
76	c3tsmB	Alignment	not modelled	67.8	15	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
77	c5ud6B	Alignment	not modelled	67.5	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhds from cyanidioschyzon merolae with lysine2 bound
78	c5d9a	Alignment	not modelled	67.2	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted protease of the collagenase

78	c3u6a	Alignment	not modelled	67.2	14	family; PDB header: lyase Chain: A; PDB Molecule: isocitrate lyase; PDBTitle: the structure of the u32 peptidase mk0906
79	c3i4eA	Alignment	not modelled	66.4	13	Chain: A; PDB Molecule: isocitrate lyase; PDBTitle: crystal structure of isocitrate lyase from burkholderia2 pseudomallei
80	d1muwa	Alignment	not modelled	65.7	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
81	c1jpkA	Alignment	not modelled	65.5	20	PDB header: lyase Chain: A; PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
82	d1r3sa	Alignment	not modelled	65.2	20	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
83	c3nvtA	Alignment	not modelled	65.0	16	PDB header: transferase/isomerase Chain: A; PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
84	c5x8aA	Alignment	not modelled	64.9	23	PDB header: oxidoreductase Chain: A; PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
85	c4ph6A	Alignment	not modelled	64.2	16	PDB header: lyase Chain: A; PDB Molecule: 3-dehydroquininate dehydratase; PDBTitle: structure of 3-dehydroquininate dehydratase from enterococcus faecalis
86	c5lzlH	Alignment	not modelled	64.0	38	PDB header: lyase Chain: H; PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: pyrobaculum caldifontis 5-aminolevulinic acid dehydratase
87	c3noyA	Alignment	not modelled	63.9	20	PDB header: oxidoreductase Chain: A; PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
88	c2r94B	Alignment	not modelled	63.9	14	PDB header: lyase Chain: B; PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
89	d2c1ha1	Alignment	not modelled	63.3	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: 5-aminolaevulinic acid dehydratase, ALAD (porphobilinogen synthase)
90	d1o5ka	Alignment	not modelled	63.3	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
91	c4lrtC	Alignment	not modelled	63.2	17	PDB header: lyase/oxidoreductase 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
92	c2yw3E	Alignment	not modelled	63.2	17	PDB header: lyase Chain: E; PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxyphosphogluconate aldolase from tthb1
93	d1d3ga	Alignment	not modelled	63.1	20	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
94	c6oviA	Alignment	not modelled	62.9	16	PDB header: lyase Chain: A; PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
95	d1ps9a1	Alignment	not modelled	62.9	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
96	c1vs1B	Alignment	not modelled	62.8	24	PDB header: transferase Chain: B; PDB Molecule: 3-deoxy-7-phosphoheptulonate synthase; PDBTitle: crystal structure of 3-deoxy-d-arabino-heptulosonate-7-2 phosphate synthase (dahp synthase) from aeropyrum pernix3 in complex with mn2+ and pep
97	d1o66a	Alignment	not modelled	62.2	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
98	c4b5sB	Alignment	not modelled	62.2	13	PDB header: lyase Chain: B; PDB Molecule: 4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; PDBTitle: crystal structures of divalent metal dependent pyruvate aldolase,2 hpai, in complex with pyruvate
99	c3lciA	Alignment	not modelled	61.9	19	PDB header: lyase Chain: A; PDB Molecule: n-acetylneuraminic acid lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
100	c3navB	Alignment	not modelled	61.9	14	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
101	d2a0ma1	Alignment	not modelled	61.6	12	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
						Fold: TIM beta/alpha-barrel

102	d1w3ia_	Alignment	not modelled	61.5	17	Superfamily: Aldolase Family: Class I aldolase
103	c4ay8B_	Alignment	not modelled	60.7	21	PDB header: transferase Chain: B: PDB Molecule: methylcobalamin); coenzyme m methyltransferase; PDBTitle: semet-derivative of a methyltransferase from m. mazei
104	d1ajza_	Alignment	not modelled	60.6	16	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
105	d1rvga_	Alignment	not modelled	60.2	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
106	c5kzmA_	Alignment	not modelled	59.9	9	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
107	d1dvja_	Alignment	not modelled	59.4	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
108	c2c3za_	Alignment	not modelled	59.4	16	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
109	c1jvnB_	Alignment	not modelled	58.8	21	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
110	c2fglA_	Alignment	not modelled	58.8	18	PDB header: hydrolase Chain: A: PDB Molecule: alkaline thermostable endoxylanase; PDBTitle: an alkali thermostable f/10 xylanase from alkalophilic bacillus sp.2 ng-27
111	d2glka1	Alignment	not modelled	58.7	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
112	c2vwtA_	Alignment	not modelled	58.5	14	PDB header: lyase Chain: A: PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
113	c1zuwA_	Alignment	not modelled	57.5	13	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase 1; PDBTitle: crystal structure of b.subtilis glutamate racemase (race) with d-glu
114	c3l2iB_	Alignment	not modelled	57.3	22	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: 1.85 angstrom crystal structure of the 3-dehydroquinat dehydratase2 (arod) from salmonella typhimurium lt2.
115	c2r8wB_	Alignment	not modelled	56.5	22	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
116	c2ejaB_	Alignment	not modelled	56.4	13	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 aquifex aeolicus
117	c5uncB_	Alignment	not modelled	56.1	16	PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
118	c6b8sB_	Alignment	not modelled	55.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroorotate dehydrogenase (quinone); PDBTitle: crystal structure of dihydroorotate dehydrogenase from helicobacter2 pylori with bound fmn
119	c4gmfD_	Alignment	not modelled	55.8	11	PDB header: oxidoreductase Chain: D: PDB Molecule: yersiniabactin biosynthetic protein ybtu; PDBTitle: apo structure of a thiazolanyl imine reductase from yersinia2 enterocolitica (irp3)
120	c2qygC_	Alignment	not modelled	54.1	19	PDB header: unknown function Chain: C: PDB Molecule: ribulose bisphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris