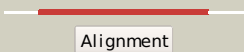

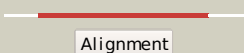

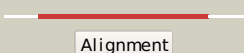

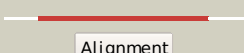



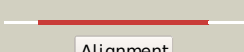

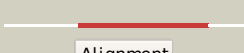

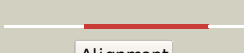















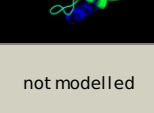


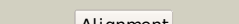
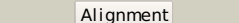

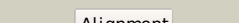






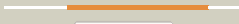
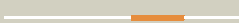
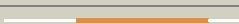







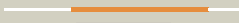



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cyvA_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uoporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uoporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
2	<a href="#">dlr3sa_</a>	 Alignment		100.0	46	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uoporphyrinogen decarboxylase, UROD
3	<a href="#">cljpkA_</a>	 Alignment		100.0	46	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uoporphyrinogen decarboxylase; <b>PDBTitle:</b> gly156asp mutant of human urod, human uoporphyrinogen iii2 decarboxylase
4	<a href="#">c2infB_</a>	 Alignment		100.0	40	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uoporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uoporphyrinogen decarboxylase from2 bacillus subtilis
5	<a href="#">dlj93a_</a>	 Alignment		100.0	41	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uoporphyrinogen decarboxylase, UROD
6	<a href="#">c2ejaB_</a>	 Alignment		100.0	39	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uoporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uoporphyrinogen decarboxylase from2 aquifex aeolicus
7	<a href="#">c3rpdB_</a>	 Alignment		99.4	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methionine synthase (b12-independent); <b>PDBTitle:</b> the structure of a b12-independent methionine synthase from shewanella2 sp. w3-18-1 in complex with selenomethionine.
8	<a href="#">dlu1ha2</a>	 Alignment		99.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Cobalamin-independent methionine synthase
9	<a href="#">c1u22A_</a>	 Alignment		99.3	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyl triglutamate-- <b>PDBTitle:</b> a. thaliana cobalamin independent methionine synthase
10	<a href="#">c1t7IA_</a>	 Alignment		99.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyl triglutamate-- <b>PDBTitle:</b> crystal structure of cobalamin-independent methionine2 synthase from t. maritima
11	<a href="#">c2nq5A_</a>	 Alignment		99.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyl triglutamate-- <b>PDBTitle:</b> crystal structure of methyltransferase from streptococcus2 mutans

12	<a href="#">c3l7sA_</a>	Alignment		99.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 5-methyltetrahydropteroyltriglutamate--homocysteine <b>PDBTitle:</b> crystal structure of mete coordinated with zinc from streptococcus2 mutans
13	<a href="#">c1ypxA_</a>	Alignment		99.2	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative vitamin-b12 independent methionine synthase family <b>PDBTitle:</b> crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
14	<a href="#">dlu1ha1</a>	Alignment		98.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MeTE-like <b>Family:</b> Cobalamin-independent methionine synthase
15	<a href="#">dltx2a_</a>	Alignment		96.1	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
16	<a href="#">cltx2A_</a>	Alignment		96.1	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dhps, dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
17	<a href="#">clpiiA_</a>	Alignment		95.7	18	<b>PDB header:</b> bifunctional(isomerase and synthase) <b>Chain:</b> A: <b>PDB Molecule:</b> n-(5' phosphoribosyl)anthranilate isomerase; <b>PDBTitle:</b> three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
18	<a href="#">c3lciA_</a>	Alignment		95.7	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> the d-sialic acid aldolase mutant v251w
19	<a href="#">c3bg3B_</a>	Alignment		95.2	20	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of human pyruvate carboxylase (missing2 the biotin carboxylase domain at the n-terminus)
20	<a href="#">c3bi8A_</a>	Alignment		95.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of dihydrodipicolinate synthase from clostridium2 botulinum
21	<a href="#">c3d0cB_</a>	Alignment	not modelled	94.9	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
22	<a href="#">c3daqB_</a>	Alignment	not modelled	94.8	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
23	<a href="#">dlqopa_</a>	Alignment	not modelled	94.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
24	<a href="#">c3n2xB_</a>	Alignment	not modelled	94.8	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
25	<a href="#">c3h5dD_</a>	Alignment	not modelled	94.5	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
26	<a href="#">c3qfwB_</a>	Alignment	not modelled	94.5	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose-1,5-bisphosphate carboxylase/oxygenase large <b>PDBTitle:</b> crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
27	<a href="#">dlxkya1</a>	Alignment	not modelled	94.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
28	<a href="#">c2v9dB_</a>	Alignment	not modelled	94.4	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12

29	<a href="#">c3noeA</a>	Alignment	not modelled	94.2	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
30	<a href="#">d1ad1a</a>	Alignment	not modelled	93.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
31	<a href="#">c2ehhE</a>	Alignment	not modelled	93.7	16	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
32	<a href="#">c3pueA</a>	Alignment	not modelled	93.5	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
33	<a href="#">c2h9aB</a>	Alignment	not modelled	93.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase, iron- <b>PDBTitle:</b> corrinoid iron-sulfur protein
34	<a href="#">c2y5sA</a>	Alignment	not modelled	93.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
35	<a href="#">c2r8wB</a>	Alignment	not modelled	93.3	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> agr_c_1641p; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
36	<a href="#">c2bmbA</a>	Alignment	not modelled	93.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> folic acid synthesis protein fol1; <b>PDBTitle:</b> x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
37	<a href="#">c3lerA</a>	Alignment	not modelled	93.2	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
38	<a href="#">d1hl2a</a>	Alignment	not modelled	93.2	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
39	<a href="#">c3bg5C</a>	Alignment	not modelled	93.1	15	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus pyruvate2 carboxylase
40	<a href="#">c2rfgB</a>	Alignment	not modelled	93.1	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
41	<a href="#">d1d9ea</a>	Alignment	not modelled	92.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
42	<a href="#">d1vlia2</a>	Alignment	not modelled	92.9	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
43	<a href="#">c2h90A</a>	Alignment	not modelled	92.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xenobiotic reductase a; <b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin
44	<a href="#">d1o5ka</a>	Alignment	not modelled	91.7	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
45	<a href="#">d2a6na1</a>	Alignment	not modelled	91.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
46	<a href="#">c2vc6A</a>	Alignment	not modelled	91.5	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of mosa from s. meliloti with pyruvate bound
47	<a href="#">c3eb2A</a>	Alignment	not modelled	91.5	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
48	<a href="#">c2qygC</a>	Alignment	not modelled	91.5	13	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> ribulose biphosphate carboxylase-like protein 2; <b>PDBTitle:</b> crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
49	<a href="#">d1xxa1</a>	Alignment	not modelled	91.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
50	<a href="#">c1rr2A</a>	Alignment	not modelled	91.2	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcarboxylase 5s subunit; <b>PDBTitle:</b> propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
51	<a href="#">c3f4wA</a>	Alignment	not modelled	91.2	15	<b>PDB header:</b> synthase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hexulose 6 phosphate synthase; <b>PDBTitle:</b> the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
52	<a href="#">c3g0sA</a>	Alignment	not modelled	91.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from salmonella typhimurium lt2
53	<a href="#">c3gr7A</a>	Alignment	not modelled	90.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
54	<a href="#">d1ps9a1</a>	Alignment	not modelled	90.6	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases

					<b>Family:</b> FMN-linked oxidoreductases
55	<a href="#">c2d69B_</a>	 Alignment	not modelled	90.2	15 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose biphosphate carboxylase; <b>PDBTitle:</b> crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
56	<a href="#">c3stgA_</a>	 Alignment	not modelled	90.2	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase; <b>PDBTitle:</b> crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
57	<a href="#">c3fluD_</a>	 Alignment	not modelled	90.1	18 <b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
58	<a href="#">c3cprB_</a>	 Alignment	not modelled	90.1	14 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthetase; <b>PDBTitle:</b> the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
59	<a href="#">d1ajza_</a>	 Alignment	not modelled	90.0	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
60	<a href="#">c3sz8D_</a>	 Alignment	not modelled	90.0	16 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase 2; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
61	<a href="#">c2vefB_</a>	 Alignment	not modelled	89.8	17 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> dihydropteroate synthase from streptococcus pneumoniae
62	<a href="#">c3s5oA_</a>	 Alignment	not modelled	89.7	11 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; <b>PDBTitle:</b> crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
63	<a href="#">d1piia1</a>	 Alignment	not modelled	89.7	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
64	<a href="#">d2d69a1</a>	 Alignment	not modelled	89.7	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
65	<a href="#">c3na8A_</a>	 Alignment	not modelled	89.2	15 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
66	<a href="#">c3dz1A_</a>	 Alignment	not modelled	89.1	14 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
67	<a href="#">c1telA_</a>	 Alignment	not modelled	89.0	13 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose biphosphate carboxylase, large subunit; <b>PDBTitle:</b> crystal structure of a rubisco-like protein from chlorobium2 tepidum
68	<a href="#">c2nx9B_</a>	 Alignment	not modelled	88.5	16 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> oxaloacetate decarboxylase 2, subunit alpha; <b>PDBTitle:</b> crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
69	<a href="#">c3si9B_</a>	 Alignment	not modelled	88.5	15 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
70	<a href="#">c3e96B_</a>	 Alignment	not modelled	88.4	13 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
71	<a href="#">d1r74a_</a>	 Alignment	not modelled	88.3	19 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase
72	<a href="#">c2vp8A_</a>	 Alignment	not modelled	88.3	11 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase 2; <b>PDBTitle:</b> structure of mycobacterium tuberculosis rv1207
73	<a href="#">c2yxd_</a>	 Alignment	not modelled	88.2	14 <b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase (dapa)
74	<a href="#">d1q6oa_</a>	 Alignment	not modelled	87.0	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Decarboxylase
75	<a href="#">c1x7fA_</a>	 Alignment	not modelled	86.9	22 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> outer surface protein; <b>PDBTitle:</b> crystal structure of an uncharacterized b. cereus protein
76	<a href="#">d1o60a_</a>	 Alignment	not modelled	86.9	14 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
77	<a href="#">c3bolB_</a>	 Alignment	not modelled	86.4	17 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-methyltetrahydrofolate s-homocysteine <b>PDBTitle:</b> cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
78	<a href="#">d1xvaa_</a>	 Alignment	not modelled	85.8	22 <b>Fold:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Superfamily:</b> S-adenosyl-L-methionine-dependent methyltransferases <b>Family:</b> Glycine N-methyltransferase <b>PDB header:</b> lyase

79	<a href="#">c1zcoA</a>	Alignment	not modelled	85.7	13	<b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphoheptonate aldolase; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
80	<a href="#">d1eyea</a>	Alignment	not modelled	85.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Dihydropteroate synthetase
81	<a href="#">d1f74a</a>	Alignment	not modelled	85.6	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
82	<a href="#">c2yciX</a>	Alignment	not modelled	85.5	12	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> 5-methyltetrahydrofolate corrinoid/iron sulfur protein <b>PDBTitle:</b> methyltransferase native
83	<a href="#">c1nmvG</a>	Alignment	not modelled	85.3	13	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> 4-hydroxy-2-oxovalerate aldolase; <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
84	<a href="#">c3mcnA</a>	Alignment	not modelled	85.2	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-amino-4-hydroxy-6-hydroxymethyl dihydropteridine <b>PDBTitle:</b> crystal structure of the 6-hydroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis
85	<a href="#">d1x7fa2</a>	Alignment	not modelled	84.5	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Outer surface protein, N-terminal domain
86	<a href="#">c3hf3A</a>	Alignment	not modelled	83.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from thermus scotoductus sa-01
87	<a href="#">c2ze3A</a>	Alignment	not modelled	83.0	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dfa0005; <b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
88	<a href="#">c1xuzA</a>	Alignment	not modelled	82.9	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> polysialic acid capsule biosynthesis protein siac; <b>PDBTitle:</b> crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
89	<a href="#">c3gkaB</a>	Alignment	not modelled	82.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
90	<a href="#">c3q94B</a>	Alignment	not modelled	82.7	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> fructose-bisphosphate aldolase, class ii; <b>PDBTitle:</b> the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
91	<a href="#">c3qfeB</a>	Alignment	not modelled	82.5	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dihydrodipicolinate synthase family protein; <b>PDBTitle:</b> crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
92	<a href="#">c3gndC</a>	Alignment	not modelled	82.1	16	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> aldolase lsrf; <b>PDBTitle:</b> crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
93	<a href="#">c3b4uB</a>	Alignment	not modelled	81.7	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
94	<a href="#">d1ccwa</a>	Alignment	not modelled	81.2	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
95	<a href="#">c2r94B</a>	Alignment	not modelled	81.2	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; <b>PDBTitle:</b> crystal structure of kd(p)ga from t.tenax
96	<a href="#">d1vjia</a>	Alignment	not modelled	81.0	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
97	<a href="#">c3t4cD</a>	Alignment	not modelled	80.8	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase 1; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
98	<a href="#">c3bleA</a>	Alignment	not modelled	80.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> citramalate synthase from leptospira interrogans; <b>PDBTitle:</b> crystal structure of the catalytic domain of licms in2 complexed with malonate
99	<a href="#">c3fkkA</a>	Alignment	not modelled	80.2	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-keto-3-deoxyarabonate dehydratase; <b>PDBTitle:</b> structure of l-2-keto-3-deoxyarabonate dehydratase
100	<a href="#">d1nvma2</a>	Alignment	not modelled	80.1	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> HMGL-like
101	<a href="#">d3bofa1</a>	Alignment	not modelled	79.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
102	<a href="#">d1rbla1</a>	Alignment	not modelled	79.9	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
103	<a href="#">d1olta</a>	Alignment	not modelled	79.6	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Radical SAM enzymes



						<b>Family:</b> Oxygen-independent coproporphyrinogen III oxidase HemN
104	<a href="#">c3igsB_</a>	Alignment	not modelled	78.6	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmannosamine-6-phosphate 2-epimerase 2; <b>PDBTitle:</b> structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
105	<a href="#">d1w3ia_</a>	Alignment	not modelled	78.1	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
106	<a href="#">d2zdra2</a>	Alignment	not modelled	78.1	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> NeuB-like
107	<a href="#">d3bofa2</a>	Alignment	not modelled	78.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Homocysteine S-methyltransferase <b>Family:</b> Homocysteine S-methyltransferase
108	<a href="#">d1f6ya_</a>	Alignment	not modelled	77.9	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Dihydropteroate synthetase-like <b>Family:</b> Methyltetrahydrofolate-utilizing methyltransferases
109	<a href="#">d1rvga_</a>	Alignment	not modelled	77.4	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
110	<a href="#">d1icpa_</a>	Alignment	not modelled	76.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
111	<a href="#">d1gvfa_</a>	Alignment	not modelled	76.8	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
112	<a href="#">d7reqa2</a>	Alignment	not modelled	76.5	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
113	<a href="#">c2hmcA_</a>	Alignment	not modelled	76.2	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
114	<a href="#">c3b8iF_</a>	Alignment	not modelled	76.2	21	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.
115	<a href="#">c3tr9A_</a>	Alignment	not modelled	75.9	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydropteroate synthase; <b>PDBTitle:</b> structure of a dihydropteroate synthase (folp) in complex with pteroi2 acid from coxiella burnetii
116	<a href="#">c1vliA_</a>	Alignment	not modelled	75.8	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> spore coat polysaccharide biosynthesis protein spse; <b>PDBTitle:</b> crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
117	<a href="#">c3f4cA_</a>	Alignment	not modelled	75.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> organophosphorus hydrolase; <b>PDBTitle:</b> crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
118	<a href="#">d1gwja_</a>	Alignment	not modelled	75.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
119	<a href="#">d1xrsb1</a>	Alignment	not modelled	73.8	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
120	<a href="#">c2nuxB_</a>	Alignment	not modelled	73.0	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate <b>PDBTitle:</b> 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution