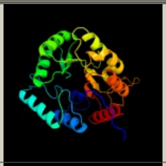
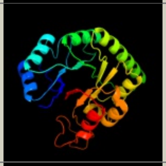
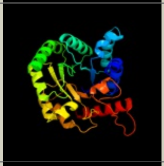
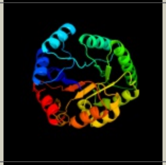
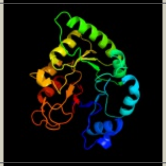
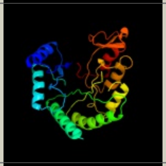
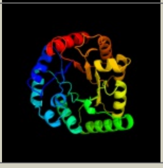
Phyre^{2}

Email	l.a.kelley@imperial.ac.uk
Description	P32134
Date	Thu Jan 5 11:49:19 GMT 2012
Unique Job ID	84d11eed840072ee

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lmzA_	Alignment		100.0	18	**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
2	c3dx5A_	Alignment		100.0	16	**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
3	c2hk1D_	Alignment		100.0	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
4	c3p6lA_	Alignment		100.0	19	**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
5	d1i60a_	Alignment		100.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
6	c3obeB_	Alignment		100.0	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
7	c3l23A_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
8	c2ou4C_	Alignment		100.0	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
9	c3cnyA_	Alignment		100.0	17	**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 wcfs1 at 1.85 a3 resolution
10	d2g0wa1	Alignment		100.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
11	c2zdsB_	Alignment		100.0	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of sco6571 from streptomyces coelicolor2 a3(2)

12	c2qw5B_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
13	c3cqkB_	Alignment		100.0	16	**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
14	c3kwsB_	Alignment		100.0	14	**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
15	c3qxbB_	Alignment		100.0	13	**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
16	d1tz9a_	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
17	d1yx1a1	Alignment		100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
18	d1k77a_	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Hypothetical protein YgbM (EC1530)
19	c3ju2A_	Alignment		100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
20	c2zvrA_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**uncharacterized protein tm_0416; **PDBTitle:** crystal structure of a d-tagatose 3-epimerase-related2 protein from thermotoga maritima
21	d2q02a1	Alignment	not modelled	100.0	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
22	d1xp3a1	Alignment	not modelled	100.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
23	c3ngfA_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family 2; **PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis
24	c3ktcB_	Alignment	not modelled	100.0	15	**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
25	c3bdkB_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
26	d1qtwa_	Alignment	not modelled	99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Endonuclease IV
27	d1bxca_	Alignment	not modelled	99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
28	d1muwa_	Alignment	not modelled	99.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
29	c2x7vA_	Alignment	not modelled	99.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable endonuclease 4;

29	c2x7vA_	Alignment	not modelled	99.9	12	**PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
30	d1bxba_	Alignment	not modelled	99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
31	d1qt1a_	Alignment	not modelled	99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
32	d2glka1	Alignment	not modelled	99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
33	d1xima_	Alignment	not modelled	99.9	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
34	c3aamA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease iv; **PDBTitle:** crystal structure of endonuclease iv from thermus thermophilus hb8
35	d1xlma_	Alignment	not modelled	99.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
36	c2i56A_	Alignment	not modelled	99.5	12	**PDB header:**isomerase, metal-binding protein **Chain:** A: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase from pseudomonas2 stutzeri with l-rhamnose
37	d1a0ea_	Alignment	not modelled	99.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
38	d1a0ca_	Alignment	not modelled	99.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
39	d1a0da_	Alignment	not modelled	99.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
40	c3bzjA_	Alignment	not modelled	99.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
41	c3bwwA_	Alignment	not modelled	98.4	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein of unknown function duf692/cog3220; **PDBTitle:** crystal structure of a duf692 family protein (hs_1138) from2 haemophilus somnus 129pt at 2.20 a resolution
42	c2v9dB_	Alignment	not modelled	97.5	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
43	c3si9B_	Alignment	not modelled	97.4	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
44	c3na8A_	Alignment	not modelled	97.3	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
45	d1d8wa_	Alignment	not modelled	97.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**L-rhamnose isomerase
46	c3lciA_	Alignment	not modelled	97.2	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
47	c3lerA_	Alignment	not modelled	97.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
48	c3dz1A_	Alignment	not modelled	97.2	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
49	c2zq0B_	Alignment	not modelled	97.2	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb); **PDBTitle:** crystal structure of susb complexed with acarbose
50	d1rpxa_	Alignment	not modelled	97.2	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
51	c3cprB_	Alignment	not modelled	97.1	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
52	c3pueA_	Alignment	not modelled	97.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
53	c3noeA_	Alignment	not modelled	97.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
54	c3p14C_	Alignment	not modelled	97.1	10	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-rhamnose isomerase; **PDBTitle:** crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
						PDB header:lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase,

55	c3s5oA_	Alignment	not modelled	97.0	14	mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
56	d1w3ia_	Alignment	not modelled	96.9	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
57	c3fkkA_	Alignment	not modelled	96.9	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
58	c3b4uB_	Alignment	not modelled	96.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
59	c3fluD_	Alignment	not modelled	96.8	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
60	c3a24A_	Alignment	not modelled	96.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of bt1871 retaining glycosidase
61	c3h5dD_	Alignment	not modelled	96.8	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
62	c2yxgD_	Alignment	not modelled	96.8	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
63	c3eb2A_	Alignment	not modelled	96.8	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
64	d2a6na1	Alignment	not modelled	96.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
65	d1hl2a_	Alignment	not modelled	96.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
66	c3g0sA_	Alignment	not modelled	96.7	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
67	c2r8wB_	Alignment	not modelled	96.6	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**agr_c_1641p; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
68	d1o5ka_	Alignment	not modelled	96.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
69	d1xxxa1	Alignment	not modelled	96.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
70	c3qc3B_	Alignment	not modelled	96.6	10	**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
71	c2hmcA_	Alignment	not modelled	96.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
72	c2nuxB_	Alignment	not modelled	96.6	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
73	c2bdqA_	Alignment	not modelled	96.5	12	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**copper homeostasis protein cutc; **PDBTitle:** crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
74	c3n2xB_	Alignment	not modelled	96.5	20	**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
75	d1xkya1	Alignment	not modelled	96.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
76	c2vc6A_	Alignment	not modelled	96.5	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
77	c3inpA_	Alignment	not modelled	96.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
78	c2r94B_	Alignment	not modelled	96.4	12	**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
79	c2ehhE_	Alignment	not modelled	96.3	13	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
80	d1f74a_	Alignment	not modelled	96.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase

81	c2rfgB_	Alignment	not modelled	96.1	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
82	c3e96B_	Alignment	not modelled	95.8	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
83	c3ct7E_	Alignment	not modelled	95.5	7	**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
84	c3qfeB_	Alignment	not modelled	95.4	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative dihydrodipicolinate synthase family protein; **PDBTitle:** crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
85	c3bi8A_	Alignment	not modelled	95.4	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
86	d1tqja_	Alignment	not modelled	95.2	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
87	c3gk0H_	Alignment	not modelled	95.1	14	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
88	d2flia1	Alignment	not modelled	95.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
89	c3daqB_	Alignment	not modelled	94.9	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
90	c3m0zD_	Alignment	not modelled	94.6	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of putative aldolase from klebsiella2 pneumoniae.
91	d1uuqa_	Alignment	not modelled	94.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
92	c1uz4A_	Alignment	not modelled	94.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**man5a; **PDBTitle:** common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 intineraries for glucoside and mannoside hydrolysis
93	c3d0cB_	Alignment	not modelled	94.5	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
94	d1tqxa_	Alignment	not modelled	94.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
95	c3ou8B_	Alignment	not modelled	94.3	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
96	c2h9aB_	Alignment	not modelled	94.3	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase, iron- **PDBTitle:** corrinoid iron-sulfur protein
97	d3bofa1	Alignment	not modelled	94.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
98	d1ub3a_	Alignment	not modelled	94.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
99	c3ivuB_	Alignment	not modelled	93.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
100	d1h1ya_	Alignment	not modelled	93.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
101	c3mznA_	Alignment	not modelled	93.5	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glucarate dehydratase; **PDBTitle:** crystal structure of probable glucarate dehydratase from2 chromohalobacter salexigens dsm 3043
102	c3ou8A_	Alignment	not modelled	93.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase; **PDBTitle:** the crystal structure of adenosine deaminase from pseudomonas2 aeruginosa
103	d1qwga_	Alignment	not modelled	93.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
104	d1m5wa_	Alignment	not modelled	93.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
105	c2ftpA_	Alignment	not modelled	93.3	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
106	d1ad1a_	Alignment	not modelled	93.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase

107	c3ngjC_	Alignment	not modelled	93.1	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
108	d1o0ya_	Alignment	not modelled	93.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
109	c1ydoC_	Alignment	not modelled	92.8	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
110	d1u83a_	Alignment	not modelled	92.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
111	c1u83A_	Alignment	not modelled	92.5	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
112	c3gndC_	Alignment	not modelled	92.4	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
113	c2vg2C_	Alignment	not modelled	92.1	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
114	c2h90A_	Alignment	not modelled	91.8	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
115	c3oa3A_	Alignment	not modelled	91.7	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
116	c3bleA_	Alignment	not modelled	91.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**citramalate synthase from leptospira interrogans; **PDBTitle:** crystal structure of the catalytic domain of licms in2 complexed with malonate
117	c3jugA_	Alignment	not modelled	91.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-mannanase; **PDBTitle:** crystal structure of endo-beta-1,4-mannanase from the alkaliphilic2 bacillus sp. n16-5
118	c1nvmG_	Alignment	not modelled	91.0	13	**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
119	c3iwpK_	Alignment	not modelled	90.9	13	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
120	d1i4na_	Alignment	not modelled	90.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes