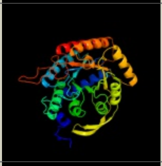
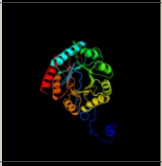
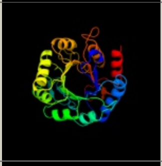
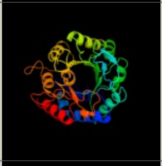
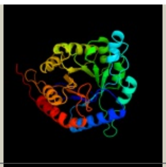
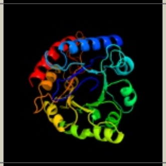
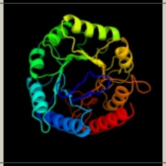
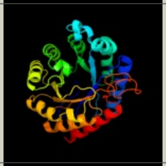
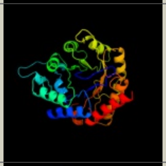
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P00888
Date	Thu Jan 5 10:56:59 GMT 2012
Unique Job ID	cfc2e7f9f51b6dff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1n8fa_	Alignment		100.0	54	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
2	c3tqkA_	Alignment		100.0	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** structure of phospho-2-dehydro-3-deoxyheptonate aldolase from2 francisella tularensis schu s4
3	d1of8a_	Alignment		100.0	52	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
4	c1ofaB_	Alignment		100.0	52	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** crystal structure of the tyrosine-regulated2 3-deoxy-d-arabino-heptulosonate-7-phosphate synthase3 from saccharomyces cerevisiae in complex with4 phosphoenolpyruvate and cobalt(ii)
5	d1vr6a1	Alignment		100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
6	c1vs1B_	Alignment		100.0	23	**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
7	c1zcoA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase; **PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
8	d2a21a1	Alignment		100.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
9	c3nvtA_	Alignment		100.0	24	**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
10	c3stgA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** 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
11	c3fs2A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate2 aldolase from bruciella melitensis at 1.85a resolution

12	d1d9ea_	Alignment		100.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
13	d1o60a_	Alignment		100.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
14	c3t4cD_	Alignment		100.0	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 1; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
15	c3sz8D_	Alignment		100.0	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
16	c3pg8B_	Alignment		100.0	21	**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
17	d2zdra2	Alignment		99.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
18	d1vlia2	Alignment		99.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
19	c1xuzA_	Alignment		99.0	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
20	c1vliA_	Alignment		98.8	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
21	d2b7oa1	Alignment	not modelled	98.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
22	c3g8rA_	Alignment	not modelled	98.3	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
23	d1ad1a_	Alignment	not modelled	94.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
24	d1ajza_	Alignment	not modelled	92.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
25	c3eb2A_	Alignment	not modelled	87.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
26	c2y5sA_	Alignment	not modelled	86.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
27	c2bmbA_	Alignment	not modelled	82.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**folic acid synthesis protein fol1; **PDBTitle:** x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
28	d1dxha1	Alignment	not modelled	80.7	28	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase

						Family: Aspartate/ornithine carbamoyltransferase
29	c2otcA_	Alignment	not modelled	80.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
30	c1ortD_	Alignment	not modelled	78.6	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
31	d1tx2a_	Alignment	not modelled	77.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
32	c1tx2A_	Alignment	not modelled	77.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
33	d1duvg1	Alignment	not modelled	67.1	23	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
34	c3updA_	Alignment	not modelled	63.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
35	d1eyea_	Alignment	not modelled	63.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
36	c3e5bB_	Alignment	not modelled	62.7	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
37	d1sq5a_	Alignment	not modelled	60.3	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
38	d1f74a_	Alignment	not modelled	57.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
39	c3fa4D_	Alignment	not modelled	57.4	15	**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
40	c2hjpA_	Alignment	not modelled	56.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
41	c1a1sA_	Alignment	not modelled	56.2	26	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus
42	d1vlva1	Alignment	not modelled	56.1	22	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
43	d1o5ka_	Alignment	not modelled	55.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
44	c2p2gD_	Alignment	not modelled	54.1	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
45	c2ehhE_	Alignment	not modelled	53.5	18	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
46	c3d6nB_	Alignment	not modelled	53.2	19	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
47	c1vlvA_	Alignment	not modelled	52.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
48	c3grfA_	Alignment	not modelled	52.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
49	c3si9B_	Alignment	not modelled	51.3	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
50	c3gd5D_	Alignment	not modelled	50.8	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
51	c3noeA_	Alignment	not modelled	50.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
52	c2e3zB_	Alignment	not modelled	47.4	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of intracellular family 1 beta-2 glucosidase bgl1a from the basidiomycete phanerochaete3 chrysosporium in substrate-free form
53	c3tqcB_	Alignment	not modelled	46.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the pantothenate kinase (coaa) from coxiella burnetii
						PDB header:lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase;

54	c3pueA_	Alignment	not modelled	46.0	21	**PDBTitle:** crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
55	c2v9dB_	Alignment	not modelled	45.8	17	**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
56	d1pvva1	Alignment	not modelled	45.7	26	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
57	c2ze3A_	Alignment	not modelled	44.2	15	**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
58	c2w37A_	Alignment	not modelled	42.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
59	c3b4uB_	Alignment	not modelled	42.5	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
60	d1muma_	Alignment	not modelled	40.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
61	c3bi8A_	Alignment	not modelled	39.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
62	c1fvoB_	Alignment	not modelled	39.7	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
63	c3igxA_	Alignment	not modelled	39.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of transaldolase b (tala)2 from francisella tularensis.
64	c2vqqA_	Alignment	not modelled	38.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 4; **PDBTitle:** structure of hdac4 catalytic domain (a double cysteine-to-2 alanine mutant) bound to a trifluoromethylketone inhbitor
65	c2ef0A_	Alignment	not modelled	38.1	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
66	c2ze5A_	Alignment	not modelled	37.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl transferase; **PDBTitle:** crystal structure of adenosine phosphate-isopentenyltransferase
67	d2v3za1	Alignment	not modelled	36.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
68	c2yxgD_	Alignment	not modelled	36.8	23	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
69	c3ptkB_	Alignment	not modelled	36.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase os4bglu12; **PDBTitle:** the crystal structure of rice (oryza sativa l.) os4bglu12
70	d1igwa_	Alignment	not modelled	36.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
71	c2qw5B_	Alignment	not modelled	34.1	14	**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
72	d1pffa_	Alignment	not modelled	34.0	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
73	c3g0sA_	Alignment	not modelled	33.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
74	c3cprB_	Alignment	not modelled	31.9	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
75	c3a8tA_	Alignment	not modelled	31.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate isopentenyltransferase; **PDBTitle:** plant adenylate isopentenyltransferase in complex with atp
76	c3daqB_	Alignment	not modelled	31.6	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
77	c3oixA_	Alignment	not modelled	31.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative dihydroorotate dehydrogenase; dihydroorotate **PDBTitle:** crystal structure of the putative dihydroorotate dehydrogenase from2 streptococcus mutans
78	c2p2sA_	Alignment	not modelled	30.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
						PDB header:isomerase

79	c1f9cA_	Alignment	not modelled	29.8	14	**Chain:** A: **PDB Molecule:**protein (muconate cycloisomerase i); **PDBTitle:** crystal structure of mle d178n variant
80	c3fluD_	Alignment	not modelled	29.4	16	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
81	d2a6na1	Alignment	not modelled	27.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
82	c3na8A_	Alignment	not modelled	27.5	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
83	c3ahyD_	Alignment	not modelled	27.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of beta-glucosidase 2 from fungus trichoderma reesei2 in complex with tris
84	d1f05a_	Alignment	not modelled	26.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
85	d2e1da1	Alignment	not modelled	26.5	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
86	c2wamB_	Alignment	not modelled	26.4	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical alanine and leucine rich **PDBTitle:** crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
87	c2dzaA_	Alignment	not modelled	25.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
88	c3s5oA_	Alignment	not modelled	25.7	13	**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
89	c2gqnB_	Alignment	not modelled	25.3	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cystathionine beta-lyase; **PDBTitle:** cystathionine beta-lyase (cbl) from escherichia coli in complex with2 n-hydrazinocarbonylmethyl-2-nitro-benzamide
90	d1e5ea_	Alignment	not modelled	25.3	27	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
91	c3m16A_	Alignment	not modelled	25.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase; **PDBTitle:** structure of a transaldolase from oleispira antarctica
92	d1piia2	Alignment	not modelled	24.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
93	c2cb1A_	Alignment	not modelled	24.5	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**o-acetyl homoserine sulfhydrylase; **PDBTitle:** crystal structure of o-actetyl homoserine sulfhydrylase2 from thermus thermophilus hb8,oah2.
94	d1tuga1	Alignment	not modelled	24.1	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
95	c2nmpC_	Alignment	not modelled	23.5	24	**PDB header:**lyase **Chain:** C: **PDB Molecule:**cystathionine gamma-lyase; **PDBTitle:** crystal structure of human cystathionine gamma lyase
96	d1n8pa_	Alignment	not modelled	23.4	35	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
97	c3d3qB_	Alignment	not modelled	23.3	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
98	c3exaD_	Alignment	not modelled	22.6	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of the full-length trna2 isopentenylpyrophosphate transferase (bh2366) from3 bacillus halodurans, northeast structural genomics4 consortium target bhr41.
99	c3gndC_	Alignment	not modelled	22.2	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
100	d1qgna_	Alignment	not modelled	22.1	29	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
101	c2rgwD_	Alignment	not modelled	22.0	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
102	d1ujqa_	Alignment	not modelled	21.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
103	c3tr9A_	Alignment	not modelled	21.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
						Fold:lambda repressor-like DNA-binding domains

104	d2auwa1	Alignment	not modelled	21.4	63	**Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
105	c2jf7B_	Alignment	not modelled	21.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**strictosidine-o-beta-d-glucosidase; **PDBTitle:** structure of strictosidine glucosidase
106	c2vc6A_	Alignment	not modelled	20.2	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound