Phyre2

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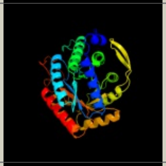
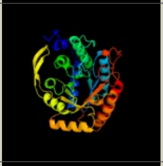
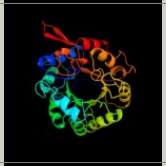
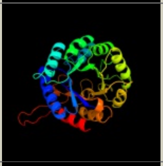
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1n8fa_	Alignment		100.0	57	**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	51	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
4	c1ofaB_	Alignment		100.0	51	**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	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
6	c1vs1B_	Alignment		100.0	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
7	c1zcoA_	Alignment		100.0	24	**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	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
9	c3nvtA_	Alignment		100.0	19	**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	16	**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	22	**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	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
13	d1o60a_	Alignment		100.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
14	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
15	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
16	c3pg8B_	Alignment		100.0	24	**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		99.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
18	d1vlia2	Alignment		99.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
19	c1xuzA_	Alignment		98.7	15	**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	d2b7oa1	Alignment		98.1	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase
21	c1vliA_	Alignment	not modelled	98.0	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
22	c3g8rA_	Alignment	not modelled	97.5	13	**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	d1ajza_	Alignment	not modelled	93.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
24	d1ad1a_	Alignment	not modelled	93.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
25	c2y5sA_	Alignment	not modelled	86.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
26	c3eb2A_	Alignment	not modelled	84.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
27	d1dxha1	Alignment	not modelled	82.5	22	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
						PDB header:transferase

28	c2otcA_	Alignment	not modelled	79.8	18	**Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
29	c3tr9A_	Alignment	not modelled	79.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
30	c1ortD_	Alignment	not modelled	76.3	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
31	c1tx2A_	Alignment	not modelled	74.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
32	d1tx2a_	Alignment	not modelled	74.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
33	c1ml4A_	Alignment	not modelled	71.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
34	d1sq5a_	Alignment	not modelled	70.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
35	c3updA_	Alignment	not modelled	69.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
36	d1duvg1	Alignment	not modelled	69.0	22	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
37	c2vqqA_	Alignment	not modelled	64.7	18	**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
38	d1eyea_	Alignment	not modelled	64.6	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
39	c3d6nB_	Alignment	not modelled	63.8	20	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
40	c3tqcB_	Alignment	not modelled	60.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the pantothenate kinase (coaa) from coxiella burnetii
41	c3e5bB_	Alignment	not modelled	59.6	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
42	d1vlva1	Alignment	not modelled	57.9	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
43	d1f74a_	Alignment	not modelled	57.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
44	d1ml4a1	Alignment	not modelled	56.8	24	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
45	d1otha1	Alignment	not modelled	56.3	22	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
46	c2p2gD_	Alignment	not modelled	56.2	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
47	c2e3zB_	Alignment	not modelled	56.1	16	**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
48	c3gd5D_	Alignment	not modelled	54.3	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
49	c1a1sA_	Alignment	not modelled	52.5	21	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus
50	c3si9B_	Alignment	not modelled	50.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
51	d1o5ka_	Alignment	not modelled	49.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
52	d1pvva1	Alignment	not modelled	49.7	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
53	c3grfA_	Alignment	not modelled	47.8	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
						PDB header:transferase

54	c1vlvA_	Alignment	not modelled	47.2	15	**Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
55	c2ze5A_	Alignment	not modelled	47.1	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl transferase; **PDBTitle:** crystal structure of adenosine phosphate-isopentenyltransferase
56	c3bi8A_	Alignment	not modelled	47.0	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
57	c3ptkB_	Alignment	not modelled	46.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-glucosidase os4bglu12; **PDBTitle:** the crystal structure of rice (oryza sativa l.) os4bglu12
58	c2w37A_	Alignment	not modelled	45.5	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
59	c3pueA_	Alignment	not modelled	44.8	18	**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
60	c1fvoB_	Alignment	not modelled	44.5	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
61	d1tuga1	Alignment	not modelled	43.8	19	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
62	c2ef0A_	Alignment	not modelled	41.3	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
63	c2hjpA_	Alignment	not modelled	40.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphonopyruvate hydrolase; **PDBTitle:** crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
64	d2e1da1	Alignment	not modelled	38.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
65	c2p2sA_	Alignment	not modelled	38.1	22	**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
66	c3a8tA_	Alignment	not modelled	37.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate isopentenyltransferase; **PDBTitle:** plant adenylate isopentenyltransferase in complex with atp
67	c3ahyD_	Alignment	not modelled	36.9	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-glucosidase; **PDBTitle:** crystal structure of beta-glucosidase 2 from fungus trichoderma reesei2 in complex with tris
68	c2ehhE_	Alignment	not modelled	36.3	19	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
69	c3noeA_	Alignment	not modelled	36.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
70	c3daqB_	Alignment	not modelled	35.3	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
71	c2bmbA_	Alignment	not modelled	35.1	15	**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
72	c3cprB_	Alignment	not modelled	33.6	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
73	d2v3za1	Alignment	not modelled	33.4	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
74	d1u1ia1	Alignment	not modelled	33.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	d1igwa_	Alignment	not modelled	33.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
76	c3b4uB_	Alignment	not modelled	32.0	7	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
77	d2v89a1	Alignment	not modelled	31.5	21	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
78	c3d3qB_	Alignment	not modelled	29.1	28	**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

79	d1pffa_	Alignment	not modelled	29.1	25	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
80	c2jf7B_	Alignment	not modelled	28.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**strictosidine-o-beta-d-glucosidase; **PDBTitle:** structure of strictosidine glucosidase
81	c2yxgD_	Alignment	not modelled	28.3	19	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
82	d1ulza3	Alignment	not modelled	28.3	11	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
83	c3u57A_	Alignment	not modelled	28.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**raucaffricine-o-beta-d-glucosidase; **PDBTitle:** structures of alkaloid biosynthetic glucosidases decode substrate2 specificity
84	c1h6dL_	Alignment	not modelled	27.8	18	**PDB header:**protein translocation **Chain:** L: **PDB Molecule:**precursor form of glucose-fructose **PDBTitle:** oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
85	c3exaD_	Alignment	not modelled	27.1	28	**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.
86	c2qt7B_	Alignment	not modelled	26.9	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**receptor-type tyrosine-protein phosphatase-like **PDBTitle:** crystallographic structure of the mature ectodomain of the2 human receptor-type protein-tyrosine phosphatase ia-2 at3 1.30 angstroms
87	c1v02F_	Alignment	not modelled	26.8	21	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**dhurrinase; **PDBTitle:** crystal structure of the sorghum bicolor dhurrinase 1
88	d1v02a_	Alignment	not modelled	26.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
89	c3fluD_	Alignment	not modelled	26.6	18	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
90	c3oqbF_	Alignment	not modelled	26.0	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
91	c3na8A_	Alignment	not modelled	25.4	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
92	c2ixaA_	Alignment	not modelled	24.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
93	d2auwa1	Alignment	not modelled	24.4	75	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
94	c2h9aA_	Alignment	not modelled	24.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron- **PDBTitle:** corrinoid iron-sulfur protein
95	c1ofgF_	Alignment	not modelled	24.3	19	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
96	c3btuD_	Alignment	not modelled	23.0	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
97	c2wamB_	Alignment	not modelled	22.6	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
98	c2auwB_	Alignment	not modelled	22.5	75	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
99	d1ryda1	Alignment	not modelled	21.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
100	c3crqA_	Alignment	not modelled	21.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** structure of trna dimethylallyltransferase: rna2 modification through a channel
101	c3cdzB_	Alignment	not modelled	21.7	10	**PDB header:**blood clotting **Chain:** B: **PDB Molecule:**coagulation factor viii light chain; **PDBTitle:** crystal structure of human factor viii
102	c3g0sA_	Alignment	not modelled	21.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
103	c3fhlC_	Alignment	not modelled	21.4	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343

104	c3fa4D_	Alignment	not modelled	21.4	13	**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
105	d1ydwa1	Alignment	not modelled	21.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
106	c3fozB_	Alignment	not modelled	21.1	20	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate transferase; **PDBTitle:** structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
107	d1f05a_	Alignment	not modelled	20.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
108	c3m16A_	Alignment	not modelled	20.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase; **PDBTitle:** structure of a transaldolase from oleispira antarctica