Phyre^2

Email	l.a.kelley@imperial.ac.uk
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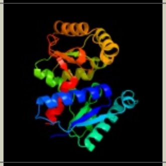
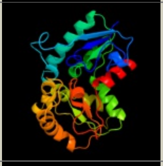
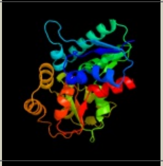
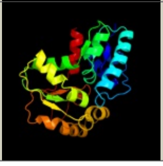
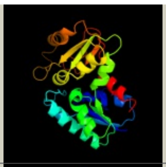
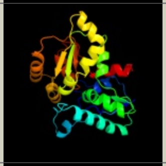
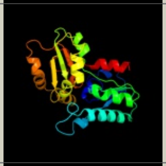
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ojcD_	Alignment		100.0	57	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative aspartate/glutamate racemase; **PDBTitle:** crystal structure of a putative asp/glu racemase from yersinia pestis
2	c2dx7B_	Alignment		100.0	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
3	c2zskA_	Alignment		100.0	34	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
4	c3s81A_	Alignment		100.0	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
5	c1zuwA_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
6	c3hfrA_	Alignment		100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from listeria monocytogenes
7	c2gzmB_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of the glutamate racemase from bacillus2 anthracis
8	c2dwuA_	Alignment		100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
9	c2jfoB_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
10	c2jfqA_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
11	c3outC_	Alignment		100.0	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.

12	c1b74A_	Alignment		100.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
13	c2jfzB_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of helicobacter pylori glutamate racemase2 in complex with d-glutamate and an inhibitor
14	c2jfnA_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
15	c2ohoA_	Alignment		100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** structural basis for glutamate racemase inhibitor
16	d1jfla1	Alignment		100.0	23	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
17	d1jfla2	Alignment		99.9	25	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
18	c2eq5D_	Alignment		99.9	19	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**228aa long hypothetical hydantoin racemase; **PDBTitle:** crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
19	d2dx7a1	Alignment		99.9	23	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
20	c3qvjB_	Alignment		99.9	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae
21	c2vlbC_	Alignment	not modelled	99.9	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
22	d1b74a2	Alignment	not modelled	99.8	18	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
23	c2dgdD_	Alignment	not modelled	99.7	8	**PDB header:**lyase **Chain:** D: **PDB Molecule:**223aa long hypothetical arylmalonate decarboxylase; **PDBTitle:** crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
24	d1b74a1	Alignment	not modelled	99.7	20	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
25	c2xecD_	Alignment	not modelled	98.8	16	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
26	d1m3ua_	Alignment	not modelled	95.8	35	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
27	c2q5cA_	Alignment	not modelled	95.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
28	d1oy0a_	Alignment	not modelled	94.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
						PDB header:transferase

29	c3ez4B_	Alignment	not modelled	94.5	30	**Chain:** B: **PDB Molecule:**3-methyl-2-oxobutanoate hydroxymethyltransferase; **PDBTitle:** crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
30	d1o66a_	Alignment	not modelled	94.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
31	d2pjua1	Alignment	not modelled	94.4	14	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
32	c2pjuD_	Alignment	not modelled	93.4	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
33	c2iksA_	Alignment	not modelled	92.7	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding transcriptional dual regulator; **PDBTitle:** crystal structure of n-terminal truncated dna-binding transcriptional2 dual regulator from escherichia coli k12
34	c1dkrB_	Alignment	not modelled	92.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
35	c3eooL_	Alignment	not modelled	91.7	15	**PDB header:**lyase **Chain:** L: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
36	c3dahB_	Alignment	not modelled	91.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
37	d1muma_	Alignment	not modelled	91.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
38	d2pv7a2	Alignment	not modelled	90.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
39	d1dbqa_	Alignment	not modelled	90.7	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
40	c3i09A_	Alignment	not modelled	90.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic branched-chain amino acid-binding protein; **PDBTitle:** crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
41	c2qiwA_	Alignment	not modelled	90.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
42	c3ih1A_	Alignment	not modelled	89.6	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
43	c3h5oB_	Alignment	not modelled	89.5	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
44	c3noyA_	Alignment	not modelled	89.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** crystal structure of ispg (gcpe)
45	c3sg0A_	Alignment	not modelled	88.0	8	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
46	c2iswB_	Alignment	not modelled	87.3	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative fructose-1,6-bisphosphate aldolase; **PDBTitle:** structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
47	c1u9yD_	Alignment	not modelled	87.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
48	c2ze3A_	Alignment	not modelled	86.6	12	**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
49	d1pqua1	Alignment	not modelled	86.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	c3d8uA_	Alignment	not modelled	86.3	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**purr transcriptional regulator; **PDBTitle:** the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
51	c3kwlA_	Alignment	not modelled	86.1	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a hypothetical protein from helicobacter pylori
52	c3brqA_	Alignment	not modelled	85.9	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg; **PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg

53	c3lftA_	Alignment	not modelled	84.7	15	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of the abc domain in complex with l-trp from2 streptococcus pneumonia to 1.35a
54	d1ujqa_	Alignment	not modelled	84.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
55	c3oa2B_	Alignment	not modelled	83.7	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**wbpb; **PDBTitle:** crystal structure of the wlba (wbpb) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
56	c2c4kD_	Alignment	not modelled	82.6	14	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
57	c2rgyA_	Alignment	not modelled	82.5	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
58	c1zlpA_	Alignment	not modelled	81.9	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**petal death protein; **PDBTitle:** petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
59	d1twda_	Alignment	not modelled	81.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**CutC-like **Family:**CutC-like
60	c3snrA_	Alignment	not modelled	80.2	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
61	c3mizB_	Alignment	not modelled	79.8	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator protein, laci **PDBTitle:** crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli
62	c3orsD_	Alignment	not modelled	78.4	13	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
63	c1xeaD_	Alignment	not modelled	78.0	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
64	d1ydwa1	Alignment	not modelled	77.3	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	d1o7ja_	Alignment	not modelled	76.9	14	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
66	d4pgaa_	Alignment	not modelled	76.9	16	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
67	c3kc2A_	Alignment	not modelled	76.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w; **PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
68	c3efhB_	Alignment	not modelled	75.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
69	c3k9cA_	Alignment	not modelled	75.1	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
70	c1i36A_	Alignment	not modelled	74.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein mth1747; **PDBTitle:** structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
71	c1ps9A_	Alignment	not modelled	74.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
72	c3ic5A_	Alignment	not modelled	74.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
73	c3hf3A_	Alignment	not modelled	74.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
74	d1gvfa_	Alignment	not modelled	74.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class II FBP aldolase
75	c3iwpK_	Alignment	not modelled	73.5	33	**PDB header:**metal binding protein **Chain:** K: **PDB Molecule:**copper homeostasis protein cutc homolog; **PDBTitle:** crystal structure of human copper homeostasis protein cutc
76	c3b8iF_	Alignment	not modelled	73.3	18	**PDB header:**lyase **Chain:** F: **PDB Molecule:**pa4872 oxaloacetate decarboxylase; **PDBTitle:** crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+.

77	c3h5lB_	Alignment	not modelled	72.4	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative branched-chain amino acid abc **PDBTitle:** crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi
78	c3zu0A_	Alignment	not modelled	70.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nad nucleotidase; **PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn)
79	c2pv7B_	Alignment	not modelled	70.8	13	**PDB header:**isomerase, oxidoreductase **Chain:** B: **PDB Molecule:**t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) **PDBTitle:** crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
80	c2o48X_	Alignment	not modelled	70.6	16	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
81	c3kg2A_	Alignment	not modelled	70.6	14	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**glutamate receptor 2; **PDBTitle:** ampa subtype ionotropic glutamate receptor in complex with competitive2 antagonist zk 200775
82	d1vyra_	Alignment	not modelled	70.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
83	d1byka_	Alignment	not modelled	69.9	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
84	c3m2tA_	Alignment	not modelled	69.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
85	c1zq1B_	Alignment	not modelled	68.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
86	d1xeaa1	Alignment	not modelled	68.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
87	c2fqxA_	Alignment	not modelled	67.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**membrane lipoprotein tmpc; **PDBTitle:** pnra from treponema pallidum complexed with guanosine
88	c3fefB_	Alignment	not modelled	67.8	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glucosidase lpld; **PDBTitle:** crystal structure of putative glucosidase lpld from2 bacillus subtilis
89	c2y0fD_	Alignment	not modelled	67.3	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
90	c3d6nB_	Alignment	not modelled	67.0	10	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
91	c3e61A_	Alignment	not modelled	66.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional repressor of ribose operon; **PDBTitle:** crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
92	d1mx3a1	Alignment	not modelled	66.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
93	d1jaya_	Alignment	not modelled	66.1	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
94	c1drwA_	Alignment	not modelled	65.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
95	c2q4eB_	Alignment	not modelled	64.6	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable oxidoreductase at4g09670; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
96	c3gr7A_	Alignment	not modelled	64.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph dehydrogenase; **PDBTitle:** structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
97	c3c52B_	Alignment	not modelled	64.5	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** class ii fructose-1,6-bisphosphate aldolase from2 helicobacter pylori in complex with3 phosphoglycolohydroxamic acid, a competitive inhibitor
98	c3egcF_	Alignment	not modelled	62.9	13	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative ribose operon repressor; **PDBTitle:** crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
99	c3q94B_	Alignment	not modelled	62.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase, class ii; **PDBTitle:** the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
100	c3jy6B_	Alignment	not modelled	61.9	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci transcriptional regulator from lactobacillus2 brevis
101	d1jkxa_	Alignment	not modelled	61.6	20	**Fold:**Formyltransferase **Superfamily:**Formyltransferase

						Family: Formyltransferase
102	d2d6fa2	Alignment	not modelled	61.6	16	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
103	c3hskB_	Alignment	not modelled	61.6	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
104	c3qk7C_	Alignment	not modelled	61.3	13	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
105	d1i36a2	Alignment	not modelled	60.5	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
106	c3c3kA_	Alignment	not modelled	60.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of an uncharacterized protein from actinobacillus2 succinogenes
107	d2liva_	Alignment	not modelled	59.3	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
108	d4pfka_	Alignment	not modelled	59.1	18	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
109	d1cb0a_	Alignment	not modelled	58.3	50	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
110	d1vc4a_	Alignment	not modelled	58.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
111	c2ywrA_	Alignment	not modelled	57.8	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex2 aeolicus
112	d1n1ea2	Alignment	not modelled	57.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
113	c1kjjA_	Alignment	not modelled	56.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
114	d1deka_	Alignment	not modelled	56.6	45	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
115	c3e3mA_	Alignment	not modelled	56.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
116	c3kkeA_	Alignment	not modelled	56.5	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**laci family transcriptional regulator; **PDBTitle:** crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
117	c3fd8A_	Alignment	not modelled	55.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
118	c3etjB_	Alignment	not modelled	54.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
119	c3fa4D_	Alignment	not modelled	54.1	16	**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
120	d1qcza_	Alignment	not modelled	53.4	17	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)