Phyre^2

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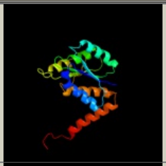
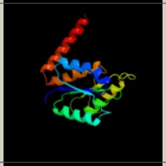
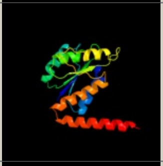
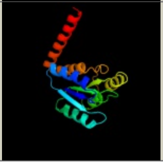
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qcza_	Alignment		100.0	98	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
2	c3lp6D_	Alignment		100.0	49	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
3	c3trhI_	Alignment		100.0	47	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
4	c2fw9A_	Alignment		100.0	59	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
5	d1u11a_	Alignment		100.0	60	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
6	c3orsD_	Alignment		100.0	49	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
7	d1o4va_	Alignment		100.0	52	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
8	d1xmpa_	Alignment		100.0	60	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
9	c3rggD_	Alignment		100.0	27	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
10	c2h31A_	Alignment		100.0	23	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
11	c2ywxA_	Alignment		100.0	42	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii

12	d1jq5a_	Alignment		98.0	12	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
13	c1ta9A_	Alignment		97.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
14	c3ce9A_	Alignment		97.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol dehydrogenase; **PDBTitle:** crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
15	d1o2da_	Alignment		97.4	18	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
16	c3ox4D_	Alignment		97.3	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
17	d1vlja_	Alignment		97.2	17	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
18	c3bfjK_	Alignment		97.2	13	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**1,3-propanediol oxidoreductase; **PDBTitle:** crystal structure analysis of 1,3-propanediol oxidoreductase
19	c3jzdA_	Alignment		97.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
20	c3okfA_	Alignment		97.1	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** 2.5 angstrom resolution crystal structure of 3-dehydroquinate synthase2 (arob) from vibrio cholerae
21	d1rrma_	Alignment	not modelled	97.1	16	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
22	c3hl0B_	Alignment	not modelled	96.9	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maleylacetate reductase; **PDBTitle:** crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
23	c3uhjE_	Alignment	not modelled	96.9	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**probable glycerol dehydrogenase; **PDBTitle:** crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
24	c3iv7B_	Alignment	not modelled	96.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alcohol dehydrogenase iv; **PDBTitle:** crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
25	c2gruB_	Alignment	not modelled	95.9	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-deoxy-scyllo-inosose synthase; **PDBTitle:** crystal structure of 2-deoxy-scyllo-inosose synthase2 complexed with carbaglucose-6-phosphate, nad+ and co2+
26	d1oj7a_	Alignment	not modelled	95.9	20	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
27	d2pjua1	Alignment	not modelled	95.9	11	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
28	d1sg6a_	Alignment	not modelled	95.7	16	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS

29	d1kq3a_	Alignment	not modelled	95.7	18	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
30	c3clhA_	Alignment	not modelled	95.6	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of 3-dehydroquinate synthase (dhqs)from2 helicobacter pylori
31	c2q5cA_	Alignment	not modelled	95.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
32	c3rf7A_	Alignment	not modelled	94.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
33	c2bonB_	Alignment	not modelled	94.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipid kinase; **PDBTitle:** structure of an escherichia coli lipid kinase (yegs)
34	c1xahA_	Alignment	not modelled	94.5	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of staphlyococcus aureus 3-dehydroquinate2 synthase (dhqs) in complex with zn2+ and nad+
35	c3lftA_	Alignment	not modelled	93.9	10	**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
36	c2pjuD_	Alignment	not modelled	92.8	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
37	d2bona1	Alignment	not modelled	92.7	19	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
38	d1ujna_	Alignment	not modelled	92.5	18	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Dehydroquinate synthase, DHQS
39	d1guda_	Alignment	not modelled	91.8	11	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
40	d2p1ra1	Alignment	not modelled	91.5	16	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
41	c2qv7A_	Alignment	not modelled	91.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**diacylglycerol kinase dgkb; **PDBTitle:** crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
42	c3s99A_	Alignment	not modelled	91.2	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**basic membrane lipoprotein; **PDBTitle:** crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
43	d2qv7a1	Alignment	not modelled	90.5	20	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
44	c3h8qB_	Alignment	not modelled	90.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 3; **PDBTitle:** crystal structure of glutaredoxin domain of human thioredoxin2 reductase 3
45	c3rotA_	Alignment	not modelled	88.8	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc sugar transporter, periplasmic sugar binding protein; **PDBTitle:** crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
46	c2e7pC_	Alignment	not modelled	88.0	16	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
47	c2iy3A_	Alignment	not modelled	86.9	19	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
48	c2ht9A_	Alignment	not modelled	86.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-2; **PDBTitle:** the structure of dimeric human glutaredoxin 2
49	d2gm3a1	Alignment	not modelled	86.6	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
50	c2qh8A_	Alignment	not modelled	85.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961
51	c2klxA_	Alignment	not modelled	84.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from bartonella henselae str.2 houston
52	d2jgra1	Alignment	not modelled	83.7	20	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
53	c2f59B_	Alignment	not modelled	83.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase 1; **PDBTitle:** lumazine synthase ribh1 from brucella abortus (gene bruab1_0785,2 swiss-prot entry q57dy1) complexed with inhibitor 5-nitro-6-(d-3 ribitylamino)-2,4(1h,3h) pyrimidinedione
						PDB header:transport protein

54	c2fqxA_	Alignment	not modelled	83.5	12	**Chain:** A: **PDB Molecule:**membrane lipoprotein tmpc; **PDBTitle:** pnra from treponema pallidum complexed with guanosine
55	d1nm3a1	Alignment	not modelled	82.8	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
56	c3fysA_	Alignment	not modelled	81.8	11	**PDB header:**fatty acid-binding protein **Chain:** A: **PDB Molecule:**protein degv; **PDBTitle:** crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis
57	d1gega_	Alignment	not modelled	81.5	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
58	c3fzaA_	Alignment	not modelled	81.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of poplar glutaredoxin s12 in complex with2 glutathione and beta-mercaptoethanol
59	c3ak4C_	Alignment	not modelled	81.1	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-dependent quinuclidinone reductase; **PDBTitle:** crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
60	d2f7wa1	Alignment	not modelled	80.0	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
61	d1fova_	Alignment	not modelled	79.7	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
62	c2dwuA_	Alignment	not modelled	79.7	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis
63	d1gcaa_	Alignment	not modelled	79.3	11	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
64	c3s40C_	Alignment	not modelled	79.0	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
65	c3ksmA_	Alignment	not modelled	78.4	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system, periplasmic component; **PDBTitle:** crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
66	c1tvmA_	Alignment	not modelled	78.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
67	c3opyB_	Alignment	not modelled	77.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
68	c3opyH_	Alignment	not modelled	77.6	16	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
69	c3k2qA_	Alignment	not modelled	77.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase; **PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
70	c1zuwA_	Alignment	not modelled	77.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
71	d1wika_	Alignment	not modelled	77.1	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
72	d1ejba_	Alignment	not modelled	76.2	18	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
73	d1pfka_	Alignment	not modelled	76.2	17	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
74	d1c2ya_	Alignment	not modelled	75.5	22	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
75	c2fn9A_	Alignment	not modelled	75.5	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**ribose abc transporter, periplasmic ribose-binding protein; **PDBTitle:** thermotoga maritima ribose binding protein unliganded form
76	c1b74A_	Alignment	not modelled	75.2	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
77	c3dm5A_	Alignment	not modelled	75.1	13	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
78	d1rvv1_	Alignment	not modelled	74.2	23	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase

79	d1nqua_	Alignment	not modelled	74.2	16	**Fold:**Lumazine synthase **Superfamily:**Lumazine synthase **Family:**Lumazine synthase
80	c3brsA_	Alignment	not modelled	73.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein/laci transcriptional regulator; **PDBTitle:** crystal structure of sugar transporter from clostridium2 phytofermentans
81	c2jfzB_	Alignment	not modelled	73.8	11	**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
82	d1obba1	Alignment	not modelled	73.4	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
83	d1di6a_	Alignment	not modelled	72.8	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
84	c1zxxA_	Alignment	not modelled	72.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
85	c1ykaA_	Alignment	not modelled	72.1	5	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**monothiol glutaredoxin ydhd; **PDBTitle:** solution structure of grx4, a monothiol glutaredoxin from2 e. coli.
86	d4pfka_	Alignment	not modelled	71.7	19	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
87	d1xi8a3	Alignment	not modelled	71.2	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
88	c1x60A_	Alignment	not modelled	71.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sporulation-specific n-acetylmuramoyl-l-alanine **PDBTitle:** solution structure of the peptidoglycan binding domain of2 b. subtilis cell wall lytic enzyme cwlc
89	d1a4ia2	Alignment	not modelled	70.8	11	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
90	c2khpA_	Alignment	not modelled	69.2	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**glutaredoxin; **PDBTitle:** solution structure of glutaredoxin from brucella melitensis
91	c3hcwB_	Alignment	not modelled	69.1	7	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**maltose operon transcriptional repressor; **PDBTitle:** crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus areus
92	c3h75A_	Alignment	not modelled	69.1	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**periplasmic sugar-binding domain protein; **PDBTitle:** crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
93	c1k0nB_	Alignment	not modelled	68.7	15	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 1; **PDBTitle:** chloride intracellular channel 1 (clic1) complexed with glutathione
94	d1jhba_	Alignment	not modelled	68.6	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
95	c3toxG_	Alignment	not modelled	68.2	22	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
96	d1o6ca_	Alignment	not modelled	68.1	19	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
97	c3mk3L_	Alignment	not modelled	67.3	22	**PDB header:**transferase **Chain:** L: **PDB Molecule:**6,7-dimethyl-8-ribityllumazine synthase; **PDBTitle:** crystal structure of lumazine synthase from salmonella typhimurium lt2
98	d1um0a_	Alignment	not modelled	66.8	15	**Fold:**Chorismate synthase, AroC **Superfamily:**Chorismate synthase, AroC **Family:**Chorismate synthase, AroC
99	c3l49D_	Alignment	not modelled	66.6	15	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc sugar (ribose) transporter, periplasmic **PDBTitle:** crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1
100	c2vk2A_	Alignment	not modelled	66.5	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
101	d1u0ta_	Alignment	not modelled	66.1	22	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
102	c2jfoB_	Alignment	not modelled	65.6	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
103	d3eeqa2	Alignment	not modelled	65.6	11	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like **Family:**CbiG N-terminal domain-like
						PDB header:transport protein **Chain:** C: **PDB Molecule:**sugar abc transporter, periplasmic

104	c2qvcC_	Alignment	not modelled	65.5	12	sugar-binding **PDBTitle:** crystal structure of a periplasmic sugar abc transporter2 from thermotoga maritima
105	c2h1fB_	Alignment	not modelled	64.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
106	c2jahB_	Alignment	not modelled	64.2	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**clavulanic acid dehydrogenase; **PDBTitle:** biochemical and structural analysis of the clavulanic acid2 dehydeogenase (cad) from streptomyces clavuligerus
107	c3p2oB_	Alignment	not modelled	64.1	11	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
108	c3rfqC_	Alignment	not modelled	64.0	12	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
109	c3fy7B_	Alignment	not modelled	63.8	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**chloride intracellular channel protein 3; **PDBTitle:** crystal structure of homo sapiens clic3
110	c3p2oA_	Alignment	not modelled	63.6	12	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
111	d1ktea_	Alignment	not modelled	63.6	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
112	c2pd6D_	Alignment	not modelled	63.1	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**estradiol 17-beta-dehydrogenase 8; **PDBTitle:** structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
113	d1pq4a_	Alignment	not modelled	62.9	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
114	c2hzfA_	Alignment	not modelled	62.9	9	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes
115	c2higA_	Alignment	not modelled	62.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
116	c3se7A_	Alignment	not modelled	62.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**vana; **PDBTitle:** ancient vana
117	c2yhsA_	Alignment	not modelled	61.0	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
118	d1zema1	Alignment	not modelled	60.9	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
119	c1z0zC_	Alignment	not modelled	60.1	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**probable inorganic polyphosphate/atp-nad kinase; **PDBTitle:** crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
120	d1z0sa1	Alignment	not modelled	60.1	19	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like