Phyre^2

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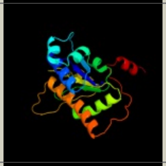
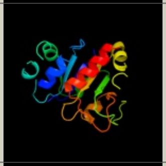
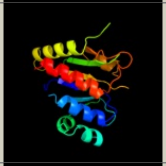
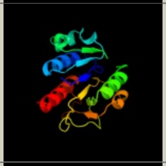
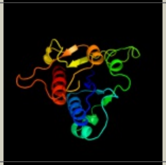
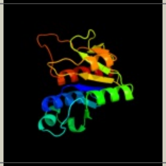
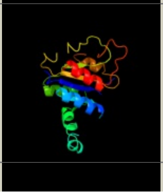
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ilkB_	Alignment		100.0	54	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized trna/rrna methyltransferase hi0380; **PDBTitle:** the structure of a probable methylase family protein from haemophilus2 influenzae rd kw20
2	c3ic6A_	Alignment		100.0	41	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative methylase family protein; **PDBTitle:** crystal structure of putative methylase family protein from neisseria2 gonorrhoeae
3	c3onpA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna/rrna methyltransferase (spou); **PDBTitle:** crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
4	c1zjrA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanosine-2'-o-)-methyltransferase; **PDBTitle:** crystal structure of a. aeolicus trmh/spou trna modifying enzyme
5	c3ktyA_	Alignment		100.0	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable methyltransferase; **PDBTitle:** crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
6	d1v2xa_	Alignment		100.0	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
7	c2ha8A_	Alignment		100.0	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**tar (hiv-1) rna loop binding protein; **PDBTitle:** methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
8	d1gz0a1	Alignment		100.0	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
9	c1gz0G_	Alignment		100.0	19	**PDB header:**transferase **Chain:** G: **PDB Molecule:**hypothetical trna/rrna methyltransferase yjfh; **PDBTitle:** 23s ribosomal rna g2251 2'o-methyltransferase rlmb
10	c1ipaA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna 2'-o-ribose methyltransferase; **PDBTitle:** crystal structure of rna 2'-o ribose methyltransferase
11	c3dcmX_	Alignment		100.0	17	**PDB header:**transferase **Chain:** X: **PDB Molecule:**uncharacterized protein tm_1570; **PDBTitle:** crystal structure of the thermotoga maritima spout family2 rna-methyltransferase protein tm1570 in complex with s-3 adenosyl-l-methionine

12	c1x7pB_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna methyltransferase; **PDBTitle:** crystal structure of the spou methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
13	d1ipaa1	Alignment		100.0	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
14	c2i6dA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna methyltransferase, trmh family; **PDBTitle:** the structure of a putative rna methyltransferase of the trmh family2 from porphyromonas gingivalis.
15	d1mxia_	Alignment		100.0	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
16	c3gyqB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna (adenosine-2'-o-)-methyltransferase; **PDBTitle:** structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
17	c3l8uA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
18	c3e5yB_	Alignment		100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trmh family rna methyltransferase; **PDBTitle:** crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
19	c1vhkA_	Alignment		95.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
20	d1vhka2	Alignment		95.2	11	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
21	d1duvg2	Alignment	not modelled	95.0	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
22	c2egwB_	Alignment	not modelled	94.9	17	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
23	d1pvva2	Alignment	not modelled	94.8	19	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
24	d1otha2	Alignment	not modelled	94.7	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
25	d1dxha2	Alignment	not modelled	94.3	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
26	d1vlva2	Alignment	not modelled	93.9	26	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
27	c2w37A_	Alignment	not modelled	93.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
28	d1ml4a2	Alignment	not modelled	93.7	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
29	c1a1sA_	Alignment	not modelled	93.7	19	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus

						furiosus
30	d1nxza2	Alignment	not modelled	93.6	12	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
31	c1vhyB_	Alignment	not modelled	93.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein hi0303; **PDBTitle:** crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
32	d1ekxa2	Alignment	not modelled	92.9	15	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
33	c2otcA_	Alignment	not modelled	92.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
34	d1v6za2	Alignment	not modelled	92.4	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
35	c3updA_	Alignment	not modelled	92.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
36	c1vlvA_	Alignment	not modelled	92.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
37	c2p2gD_	Alignment	not modelled	92.0	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
38	c1ortD_	Alignment	not modelled	91.5	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
39	d1pg5a2	Alignment	not modelled	91.3	12	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
40	d1tuga1	Alignment	not modelled	90.0	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
41	c3d6nB_	Alignment	not modelled	90.0	13	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
42	c3kw2A_	Alignment	not modelled	89.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
43	c1fvoB_	Alignment	not modelled	89.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
44	c2cx8B_	Alignment	not modelled	89.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyl transferase; **PDBTitle:** crystal structure of methyltransferase with ligand(sah)
45	c2yy8B_	Alignment	not modelled	89.1	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0106 protein ph0461; **PDBTitle:** crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
46	c1pg5A_	Alignment	not modelled	88.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius
47	c2rgwD_	Alignment	not modelled	88.6	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
48	d1js1x2	Alignment	not modelled	87.1	22	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
49	c3grfA_	Alignment	not modelled	85.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
50	c1ml4A_	Alignment	not modelled	85.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
51	d2o3aa1	Alignment	not modelled	83.8	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
52	c3q98A_	Alignment	not modelled	82.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
53	c3gd5D_	Alignment	not modelled	82.8	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
54	c2ef0A_	Alignment	not modelled	82.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
55	d2at2a2	Alignment	not modelled	79.8	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase

						Family: Aspartate/ornithine carbamoyltransferase
56	c3n7uD_	Alignment	not modelled	74.1	31	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
57	c3sdsA_	Alignment	not modelled	72.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
58	c3lxmC_	Alignment	not modelled	72.2	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** 2.00 angstrom resolution crystal structure of a catalytic2 subunit of an aspartate carbamoyltransferase (pyrb) from3 yersinia pestis co92
59	d2naca1	Alignment	not modelled	72.1	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
60	c1js1Z_	Alignment	not modelled	71.9	22	**PDB header:**transferase **Chain:** Z: **PDB Molecule:**transcarbamylase; **PDBTitle:** crystal structure of a new transcarbamylase from the2 anaerobic bacterium bacteroides fragilis at 2.0 a3 resolution
61	d2qmma1	Alignment	not modelled	71.7	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
62	c1zq2A_	Alignment	not modelled	70.5	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
63	c3gg9C_	Alignment	not modelled	69.2	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase oxidoreductase protein; **PDBTitle:** crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
64	d1ygya1	Alignment	not modelled	68.2	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
65	c2omeA_	Alignment	not modelled	68.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**c-terminal-binding protein 2; **PDBTitle:** crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
66	c3ijpA_	Alignment	not modelled	67.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
67	d1qp8a1	Alignment	not modelled	65.8	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
68	c1k3rA_	Alignment	not modelled	65.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mt0001; **PDBTitle:** crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
69	c2nacA_	Alignment	not modelled	65.1	23	**PDB header:**oxidoreductase(aldehyde(d),nad+(a)) **Chain:** A: **PDB Molecule:**nad-dependent formate dehydrogenase; **PDBTitle:** high resolution structures of holo and apo formate dehydrogenase
70	c2j6iC_	Alignment	not modelled	64.4	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
71	c1d4fD_	Alignment	not modelled	63.0	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
72	d1mx3a1	Alignment	not modelled	62.3	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
73	c1gdhA_	Alignment	not modelled	60.7	17	**PDB header:**oxidoreductase(choh (d)-nad(p)+ (a)) **Chain:** A: **PDB Molecule:**d-glycerate dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
74	c2g76A_	Alignment	not modelled	60.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
75	c3evtA_	Alignment	not modelled	59.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
76	d1k3ra2	Alignment	not modelled	58.3	16	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
77	c3gvpB_	Alignment	not modelled	57.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
78	c3dhyC_	Alignment	not modelled	57.3	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
79	d1gdha1	Alignment	not modelled	56.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
80	c1j4aA_	Alignment	not modelled	54.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3

						bulgaricus
81	d1sc6a1	Alignment	not modelled	54.2	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
82	c1qp8A_	Alignment	not modelled	52.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
83	c2w2kB_	Alignment	not modelled	51.3	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-mandelate dehydrogenase; **PDBTitle:** crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
84	d1vh0a_	Alignment	not modelled	51.1	22	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
85	c1mldA_	Alignment	not modelled	50.3	22	**PDB header:**oxidoreductase(nad(a)-choh(d)) **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
86	c3oneA_	Alignment	not modelled	49.9	22	**PDB header:**hydrolase/hydrolase substrate **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
87	d1o6da_	Alignment	not modelled	49.2	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
88	c2a9fB_	Alignment	not modelled	48.4	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative malic enzyme ((s)-malate:nad+ **PDBTitle:** crystal structure of a putative malic enzyme ((s)-2 malate:nad+ oxidoreductase (decarboxylating))
89	d2atca2	Alignment	not modelled	48.0	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
90	c3tpfF_	Alignment	not modelled	47.9	14	**PDB header:**transferase **Chain:** F: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
91	c2at2B_	Alignment	not modelled	47.6	15	**PDB header:** **PDB COMPND:**
92	d1oi7a1	Alignment	not modelled	47.5	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
93	c3hg7A_	Alignment	not modelled	47.1	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-isomer specific 2-hydroxyacid dehydrogenase family **PDBTitle:** crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from aeromonas salmonicida subsp. salmonicida a449
94	c2gcgB_	Alignment	not modelled	47.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
95	c3pqeD_	Alignment	not modelled	46.9	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
96	d1diha1	Alignment	not modelled	46.8	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	c2pi1C_	Alignment	not modelled	45.8	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
98	d1ns5a_	Alignment	not modelled	45.7	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
99	c2dbqA_	Alignment	not modelled	45.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
100	c3bazA_	Alignment	not modelled	44.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyphenylpyruvate reductase; **PDBTitle:** structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
101	c1wwkA_	Alignment	not modelled	43.3	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
102	c3ktdC_	Alignment	not modelled	42.9	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
103	c1drwA_	Alignment	not modelled	42.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
104	c1gpjA_	Alignment	not modelled	42.3	21	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
105	c3n58D_	Alignment	not modelled	42.0	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase

						from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
106	c3d0oA_	Alignment	not modelled	42.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase 1; **PDBTitle:** crystal structure of lactate dehydrogenase from2 staphylococcus aureus
107	c1z85B_	Alignment	not modelled	40.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein tm1380; **PDBTitle:** crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
108	d1to0a_	Alignment	not modelled	40.7	13	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
109	c1v8bA_	Alignment	not modelled	40.2	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
110	c1ybaC_	Alignment	not modelled	39.9	25	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
111	c1dxyA_	Alignment	not modelled	39.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** structure of d-2-hydroxyisocaproate dehydrogenase
112	d7reqb2	Alignment	not modelled	37.6	23	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
113	d1gpja2	Alignment	not modelled	37.1	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
114	c2d4aC_	Alignment	not modelled	36.1	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of the malate dehydrogenase from aeropyrum pernix
115	c2d0iC_	Alignment	not modelled	35.7	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
116	c2eklA_	Alignment	not modelled	35.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
117	c3oirA_	Alignment	not modelled	34.5	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter sulfate transporter family protein; **PDBTitle:** crystal structure of sulfate transporter family protein from wolinella2 succinogenes
118	c2fnzA_	Alignment	not modelled	32.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
119	c2cukC_	Alignment	not modelled	32.6	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
120	c1xdwA_	Alignment	not modelled	32.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad+-dependent (r)-2-hydroxyglutarate **PDBTitle:** nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans