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1	c3ilkB_	 Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized trna/rna methyltransferase hi0380; PDBTitle: the structure of a probable methylase family protein from haemophilus2 influenzae rd kw20
2	c3ic6A_	 Alignment		100.0	35	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	37	PDB header: transferase Chain: A: PDB Molecule: trna/rna methyltransferase (spou); PDBTitle: crystal structure of trna/rna methyltransferase spou from rhodobacter2 sphaeroides
4	c1zjrA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: trna (guanosine-2'-o-)-methyltransferase; PDBTitle: crystal structure of a. aeolicus trmh/spou trna modifying enzyme
5	d1v2xa_	 Alignment		100.0	23	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
6	c3ktyA_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: probable methyltransferase; PDBTitle: crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
7	c2ha8A_	 Alignment		100.0	16	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	18	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
9	c1gz0G_	 Alignment		100.0	18	PDB header: transferase Chain: G: PDB Molecule: hypothetical trna/rna methyltransferase yjfh; PDBTitle: 23s ribosomal rna g2251 2'-o-methyltransferase rlmb
10	c2i6dA_	 Alignment		100.0	19	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.
11	c1ipaA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: rna 2'-o-ribose methyltransferase; PDBTitle: crystal structure of rna 2'-o ribose methyltransferase

12	c1x7pB	<div><div></div><div>Alignment</div></div>		100.0	21	PDB header: transferase Chain: B: PDB Molecule: rrna methyltransferase; PDBTitle: crystal structure of the spoU methyltransferase avirB from <i>Streptomyces viridochromogenes</i> in complex with the cofactor adomet
13	d1mxia	<div><div></div><div>Alignment</div></div>		100.0	19	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
14	d1ipaa	<div><div></div><div>Alignment</div></div>		100.0	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: SpoU-like RNA 2'-O ribose methyltransferase
15	c3gyqB	<div><div></div><div>Alignment</div></div>		100.0	19	PDB header: transferase Chain: B: PDB Molecule: rrna (adenosine-2'-o)-methyltransferase; PDBTitle: structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
16	c3dcmX	<div><div></div><div>Alignment</div></div>		100.0	14	PDB header: transferase Chain: X: PDB Molecule: uncharacterized protein tm_1570; PDBTitle: crystal structure of the thermotoga maritima spoU family2 rna-methyltransferase protein tm1570 in complex with s-3 adenosyl-l-methionine
17	c3e5yB	<div><div></div><div>Alignment</div></div>		100.0	18	PDB header: transferase Chain: B: PDB Molecule: trmH family rna methyltransferase; PDBTitle: crystal structure of trmH family rna methyltransferase from <i>Streptococcus pseudomallei</i>
18	c3l8uA	<div><div></div><div>Alignment</div></div>		100.0	20	PDB header: transferase Chain: A: PDB Molecule: putative rRNA methylase; PDBTitle: crystal structure of smu.1707c, a putative rRNA methyltransferase from <i>Streptococcus mutans</i> ua159
19	c1vhkA	<div><div></div><div>Alignment</div></div>		97.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yqeU; PDBTitle: crystal structure of an hypothetical protein
20	d1vhka2	<div><div></div><div>Alignment</div></div>		96.8	13	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
21	d1nxza2	<div><div></div><div>Alignment</div></div>	not modelled	96.4	15	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
22	c2egwB	<div><div></div><div>Alignment</div></div>	not modelled	95.7	13	PDB header: rrna methyltransferase Chain: B: PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rRNA methyltransferase with sah ligand
23	c3kw2A	<div><div></div><div>Alignment</div></div>	not modelled	95.7	17	PDB header: transferase Chain: A: PDB Molecule: probable rRNA methyltransferase; PDBTitle: crystal structure of probable rRNA-methyltransferase from <i>Porphyromonas gingivalis</i>
24	c1vhyB	<div><div></div><div>Alignment</div></div>	not modelled	95.5	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein hi0303; PDBTitle: crystal structure of Haemophilus influenzae protein hi0303, pfam2_duf558
25	d1v6za2	<div><div></div><div>Alignment</div></div>	not modelled	95.2	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
26	c2yy8B	<div><div></div><div>Alignment</div></div>	not modelled	94.7	17	PDB header: transferase Chain: B: PDB Molecule: upf0106 protein ph0461; PDBTitle: crystal structure of archaeal tRNA-methylase for position 256 (atm56) from <i>Pyrococcus horikoshii</i> , complexed with s-3 adenosyl-l-methionine
27	c2cx8B	<div><div></div><div>Alignment</div></div>	not modelled	94.6	18	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
28	d2o3aa1	<div><div></div><div>Alignment</div></div>	not modelled	93.6	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: AF0751-like
		<div><div></div><div></div></div>				Fold: ATC-like

29	d1duvg2	Alignment	not modelled	85.0	20	Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
30	d1otha2	Alignment	not modelled	84.4	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
31	d1pvva2	Alignment	not modelled	84.1	11	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
32	c3d6nB	Alignment	not modelled	82.6	9	PDB header: hydrolase/transferase Chain: B: PDB Molecule: aspartate carbamoyltransferase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
33	d1js1x2	Alignment	not modelled	81.9	16	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
34	c1a1sA	Alignment	not modelled	81.2	11	PDB header: transcarbamylase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine carbamoyltransferase from pyrococcus furiosus
35	d1dxha2	Alignment	not modelled	80.3	13	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
36	d1ml4a2	Alignment	not modelled	80.2	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
37	d1pg5a2	Alignment	not modelled	78.2	12	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
38	c2otcA	Alignment	not modelled	77.5	21	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
39	c2w37A	Alignment	not modelled	76.2	12	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
40	c1z85B	Alignment	not modelled	74.4	13	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein tm1380; PDBTitle: crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msh8 at 2.12 a resolution
41	d1ekxa2	Alignment	not modelled	74.0	15	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
42	d1vlva2	Alignment	not modelled	72.3	9	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
43	c1pg5A	Alignment	not modelled	72.1	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
44	c2p2gD	Alignment	not modelled	69.8	18	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
45	c1vlvA	Alignment	not modelled	66.8	11	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
46	c1k3rA	Alignment	not modelled	64.0	27	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
47	c3updA	Alignment	not modelled	63.7	20	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
48	c1a5zA	Alignment	not modelled	62.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: lactate dehydrogenase from thermotoga maritima (tml dh)
49	d1up7a1	Alignment	not modelled	62.2	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
50	c2omeA	Alignment	not modelled	61.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
51	c1fvoB	Alignment	not modelled	60.4	14	PDB header: transferase Chain: B: PDB Molecule: ornithine transcarbamylase; PDBTitle: crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
52	c1ortD	Alignment	not modelled	60.3	16	PDB header: transferase Chain: D: PDB Molecule: ornithine transcarbamoylase; PDBTitle: ornithine transcarbamoylase from pseudomonas aeruginosa
53	d1ygya1	Alignment	not modelled	59.3	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
54	c1ml4A	Alignment	not modelled	59.0	14	PDB header: transferase Chain: A: PDB Molecule: aspartate transcarbamoylase; PDBTitle: the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
55	c2gawD	Alignment	not modelled	59.0	15	PDB header: transferase Chain: D: PDB Molecule: aspartate carbamoyltransferase;

55	c2zgWb	Alignment	not modelled	59.0	15	PDBTitle: catalytic subunit of m. jannaschii aspartate2 transcarbamoylase PDB header: oxidoreductase
56	c3n7uD	Alignment	not modelled	58.9	23	Chain: D: PDB Molecule: formate dehydrogenase; PDBTitle: nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide PDB header: oxidoreductase
57	c2v6bB	Alignment	not modelled	58.8	19	Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form) PDB header: oxidoreductase
58	c2g76A	Alignment	not modelled	58.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
59	d1k3ra2	Alignment	not modelled	56.8	27	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
60	c3gg9C	Alignment	not modelled	56.6	16	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 PDB header: oxidoreductase(aldehyde(d), nad+(a))
61	c2nacA	Alignment	not modelled	56.0	19	Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: high resolution structures of holo and apo formate dehydrogenase
62	d1obba1	Alignment	not modelled	55.4	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
63	c3grfA	Alignment	not modelled	55.3	15	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
64	c3evtA	Alignment	not modelled	53.8	22	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
65	d2naca1	Alignment	not modelled	53.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
66	c3bazA	Alignment	not modelled	53.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
67	d1qp8a1	Alignment	not modelled	53.1	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
68	d1sc6a1	Alignment	not modelled	51.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
69	d1mx3a1	Alignment	not modelled	51.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
70	c1js1Z	Alignment	not modelled	49.6	13	PDB header: transferase Chain: Z: PDB Molecule: transcarbamylase; PDBTitle: crystal structure of a new transcarbamylase fromthe2 anaerobic bacterium bacteroides fragilis at 2.0 a3 resolution
71	c1d4fD	Alignment	not modelled	48.6	17	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
72	c1j4aA	Alignment	not modelled	47.7	16	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
73	c1zq2A	Alignment	not modelled	45.3	17	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
74	c3jipA	Alignment	not modelled	45.1	9	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
75	d1gdha1	Alignment	not modelled	44.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
76	c3gvpB	Alignment	not modelled	42.1	19	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
77	c1qp8A	Alignment	not modelled	40.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
78	c2pwzG	Alignment	not modelled	40.1	18	PDB header: oxidoreductase Chain: G: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of the apo form of e.coli malate dehydrogenase
79	c3gd5D	Alignment	not modelled	40.0	8	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
80	c1gdhA	Alignment	not modelled	39.8	15	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
						Fold: ATC-like

81	d2at2a2	Alignment	not modelled	39.7	8	Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
82	c1wwkA	Alignment	not modelled	39.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
83	d1a5za1	Alignment	not modelled	39.4	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
84	d1u8xx1	Alignment	not modelled	38.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
85	d2cmda1	Alignment	not modelled	38.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
86	d1gpja2	Alignment	not modelled	38.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
87	d1j4aa1	Alignment	not modelled	37.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
88	c3q98A	Alignment	not modelled	35.7	10	PDB header: transferase Chain: A: PDB Molecule: transcarbamylase; PDBTitle: structure of ygew encoded protein from e. coli
89	c2gcgB	Alignment	not modelled	35.2	24	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
90	c3hg7A	Alignment	not modelled	34.4	24	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
91	d7reqb2	Alignment	not modelled	31.4	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
92	c2j6iC	Alignment	not modelled	31.4	23	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
93	d1tuga1	Alignment	not modelled	30.9	10	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
94	c2pi1C	Alignment	not modelled	30.9	20	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
95	d1s6ya1	Alignment	not modelled	30.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
96	c1mldA	Alignment	not modelled	29.8	20	PDB header: oxidoreductase(nad(a)-chod(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
97	c2d0iC	Alignment	not modelled	29.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase; PDBTitle: crystal structure ph0520 protein from pyrococcus horikoshii ot3
98	d1diha1	Alignment	not modelled	28.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
99	c2dbqA	Alignment	not modelled	28.8	22	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	c2y0fD	Alignment	not modelled	28.0	24	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
101	c3lxmC	Alignment	not modelled	27.9	19	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
102	c3sdsA	Alignment	not modelled	27.9	18	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, mitochondrial; PDBTitle: crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
103	c3dhyC	Alignment	not modelled	27.9	22	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
104	c1ybaC	Alignment	not modelled	27.3	23	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
105	c2w2kB	Alignment	not modelled	26.2	17	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. PDB header: oxidoreductase

106	c2cukC_	Alignment	not modelled	25.7	24	Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
107	d2dlad1	Alignment	not modelled	25.5	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
108	c1dxyA_	Alignment	not modelled	25.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyisocaproate dehydrogenase; PDBTitle: structure of d-2-hydroxyisocaproate dehydrogenase
109	c2eklA_	Alignment	not modelled	24.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
110	c8ldhA_	Alignment	not modelled	24.5	18	PDB header: oxidoreductase(choh(d)-nad(a)) Chain: A: PDB Molecule: m4 apo-lactate dehydrogenase; PDBTitle: refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
111	c3ckyA_	Alignment	not modelled	23.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
112	c1xdwA_	Alignment	not modelled	23.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
113	d1o94c_	Alignment	not modelled	21.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
114	c3oirA_	Alignment	not modelled	21.4	15	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter sulfate transporter family protein; PDBTitle: crystal structure of sulfate transporter family protein from wolinetella2 succinogenes
115	c2v3ja_	Alignment	not modelled	21.4	18	PDB header: ribosomal protein Chain: A: PDB Molecule: essential for mitotic growth 1; PDBTitle: the yeast ribosome synthesis factor emg1 alpha beta knot2 fold methyltransferase
116	c3kboB_	Alignment	not modelled	20.9	22	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate/hydroxypyruvate reductase a; PDBTitle: 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex with nadp
117	c3n58D_	Alignment	not modelled	20.8	17	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