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Description	Q46803
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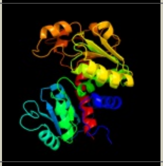
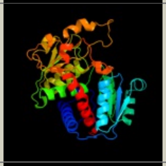
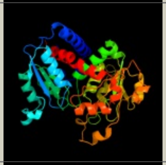
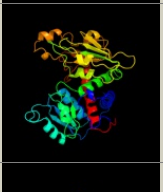
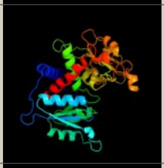
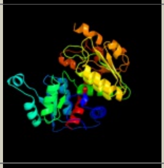
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3q98A_	Alignment		100.0	96	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
2	c2otcA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
3	c3updA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
4	c2w37A_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
5	c1ortD_	Alignment		100.0	26	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
6	c1fvoB_	Alignment		100.0	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
7	c1a1sA_	Alignment		100.0	27	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus
8	c1vlvA_	Alignment		100.0	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
9	c1ml4A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
10	c1zq2A_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
11	d1tuga1	Alignment		100.0	22	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase

12	c3sdsA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
13	c2p2gD_	Alignment		100.0	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
14	c3tpfF_	Alignment		100.0	27	**PDB header:**transferase **Chain:** F: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
15	c1js1Z_	Alignment		100.0	26	**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
16	c1pg5A_	Alignment		100.0	18	**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
17	c2rgwD_	Alignment		100.0	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
18	c2ef0A_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
19	c3gd5D_	Alignment		100.0	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
20	c3grfA_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
21	c2at2B_	Alignment	not modelled	100.0	24	**PDB header:** **PDB COMPND:**
22	c3d6nB_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
23	c3lxmC_	Alignment	not modelled	100.0	24	**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
24	d1ml4a1	Alignment	not modelled	100.0	25	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
25	d1vlva1	Alignment	not modelled	100.0	26	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
26	d1pvva1	Alignment	not modelled	100.0	28	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
27	d1duvg1	Alignment	not modelled	100.0	30	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
28	d1dxha1	Alignment	not modelled	100.0	27	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
29	d1otha1	Alignment	not modelled	100.0	28	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase

						Family: Aspartate/ornithine carbamoyltransferase
30	d1ekxa1	Alignment	not modelled	100.0	31	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
31	d1dxha2	Alignment	not modelled	100.0	24	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
32	d2at2a1	Alignment	not modelled	100.0	27	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
33	d1duvg2	Alignment	not modelled	100.0	21	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
34	d1otha2	Alignment	not modelled	100.0	24	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
35	d1pg5a1	Alignment	not modelled	100.0	22	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
36	d1pvva2	Alignment	not modelled	100.0	28	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
37	d1js1x1	Alignment	not modelled	100.0	23	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
38	d1vlva2	Alignment	not modelled	100.0	34	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
39	d1js1x2	Alignment	not modelled	100.0	30	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
40	d1ml4a2	Alignment	not modelled	100.0	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
41	d1ekxa2	Alignment	not modelled	100.0	15	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
42	d1pg5a2	Alignment	not modelled	100.0	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
43	d2at2a2	Alignment	not modelled	100.0	21	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
44	d2atca2	Alignment	not modelled	100.0	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
45	c3gvpB_	Alignment	not modelled	97.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
46	c3l07B_	Alignment	not modelled	97.8	16	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
47	c3d4oA_	Alignment	not modelled	97.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
48	c4a26B_	Alignment	not modelled	97.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
49	c3d64A_	Alignment	not modelled	97.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
50	c1b0aA_	Alignment	not modelled	97.6	18	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
51	c1gpjA_	Alignment	not modelled	97.5	20	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
52	c3oneA_	Alignment	not modelled	97.5	25	**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
53	c3p2oB_	Alignment	not modelled	97.5	16	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
54	c3n58D_	Alignment	not modelled	97.5	25	**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
55	c1d4fD_	Alignment	not modelled	97.4	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant

						s-2 adenosylhomocysteine hydrolase
56	c3p2oA_	Alignment	not modelled	97.3	16	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
57	c2rirA_	Alignment	not modelled	97.3	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
58	d1a4ia1	Alignment	not modelled	97.2	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
59	c4a5oB_	Alignment	not modelled	97.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
60	d1gpja2	Alignment	not modelled	97.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
61	c3nglA_	Alignment	not modelled	96.9	12	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
62	d1b0aa1	Alignment	not modelled	96.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
63	c3n7uD_	Alignment	not modelled	96.3	17	**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
64	d1pjca1	Alignment	not modelled	96.3	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
65	c2eezG_	Alignment	not modelled	96.3	20	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase from themus thermophilus
66	d2naca1	Alignment	not modelled	96.3	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
67	c1v8bA_	Alignment	not modelled	96.3	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
68	c1vjtA_	Alignment	not modelled	96.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
69	d1l7da1	Alignment	not modelled	96.1	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
70	c2nacA_	Alignment	not modelled	96.1	21	**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
71	c1pjcA_	Alignment	not modelled	96.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (l-alanine dehydrogenase); **PDBTitle:** l-alanine dehydrogenase complexed with nad
72	c2dbqA_	Alignment	not modelled	96.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
73	c2c2xB_	Alignment	not modelled	96.1	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
74	d1mx3a1	Alignment	not modelled	96.1	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
75	c2j6iC_	Alignment	not modelled	96.0	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
76	c1u8xX_	Alignment	not modelled	96.0	27	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**maltose-6'-phosphate glucosidase; **PDBTitle:** crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
77	c1l7eC_	Alignment	not modelled	96.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinamide nucleotide transhydrogenase, **PDBTitle:** crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
78	c3p2yA_	Alignment	not modelled	96.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
79	c3dhyC_	Alignment	not modelled	96.0	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
80	c1gdhA_	Alignment	not modelled	95.8	13	**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
81	c1a4iB_	Alignment	not modelled	95.8	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
82	c2omeA_	Alignment	not modelled	95.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**c-terminal-binding protein 2; **PDBTitle:** crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
83	c3kboB_	Alignment	not modelled	95.7	10	**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
84	d1li4a1	Alignment	not modelled	95.6	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
85	d1gdha1	Alignment	not modelled	95.5	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
86	c2gcgB_	Alignment	not modelled	95.5	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
87	c1wwkA_	Alignment	not modelled	95.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
88	c1obbB_	Alignment	not modelled	95.4	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
89	d1pjqa1	Alignment	not modelled	95.3	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
90	c2qm3A_	Alignment	not modelled	95.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**predicted methyltransferase; **PDBTitle:** crystal structure of a predicted methyltransferase from pyrococcus2 furiosus
91	c1j4aA_	Alignment	not modelled	95.3	17	**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
92	c3bazA_	Alignment	not modelled	95.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyphenylpyruvate reductase; **PDBTitle:** structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
93	d1vjta1	Alignment	not modelled	95.3	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
94	c2cukC_	Alignment	not modelled	95.3	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
95	c3oj0A_	Alignment	not modelled	95.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
96	c2eklA_	Alignment	not modelled	95.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
97	d1v8ba1	Alignment	not modelled	95.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
98	c2g76A_	Alignment	not modelled	95.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
99	d1pzga1	Alignment	not modelled	95.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
100	c3gg2B_	Alignment	not modelled	95.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sugar dehydrogenase, udp-glucose/gdp-mannose **PDBTitle:** crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
101	c2bruB_	Alignment	not modelled	94.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase subunit alpha; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
102	c3evtA_	Alignment	not modelled	94.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
103	c1ybaC_	Alignment	not modelled	94.9	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
104	d1j4aa1	Alignment	not modelled	94.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
105	c1m75B_	Alignment	not modelled	94.8	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa

106	c3oetF_	Alignment	not modelled	94.8	29	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad
107	d2dlda1	Alignment	not modelled	94.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
108	c3gg9C_	Alignment	not modelled	94.7	24	**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
109	c3dfzB_	Alignment	not modelled	94.7	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
110	c3k5pA_	Alignment	not modelled	94.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
111	c1xdwA_	Alignment	not modelled	94.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad+-dependent (r)-2-hydroxyglutarate **PDBTitle:** nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
112	c1np3B_	Alignment	not modelled	94.6	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
113	d1x7da_	Alignment	not modelled	94.6	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Ornithine cyclodeaminase-like
114	c2pi1C_	Alignment	not modelled	94.5	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
115	c2hjrK_	Alignment	not modelled	94.5	16	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of cryptosporidium parvum malate2 dehydrogenase
116	d1np3a2	Alignment	not modelled	94.4	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
117	c3c7cB_	Alignment	not modelled	94.3	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**octopine dehydrogenase; **PDBTitle:** a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
118	d1qp8a1	Alignment	not modelled	94.3	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
119	d1ygya1	Alignment	not modelled	94.3	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
120	c3k96B_	Alignment	not modelled	94.1	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii