Phyre^2

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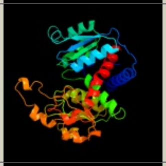
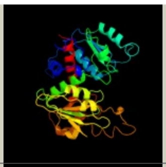
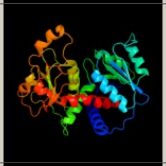
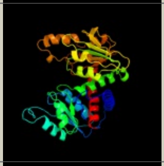
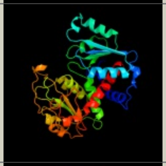
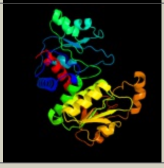
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2otcA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
2	c3updA_	Alignment		100.0	67	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
3	c1ortD_	Alignment		100.0	58	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
4	c2w37A_	Alignment		100.0	48	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
5	c1vlvA_	Alignment		100.0	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
6	c1a1sA_	Alignment		100.0	42	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus
7	c1fvoB_	Alignment		100.0	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
8	c1ml4A_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
9	c2p2gD_	Alignment		100.0	40	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
10	c1zq2A_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
11	c3tpfF_	Alignment		100.0	36	**PDB header:**transferase **Chain:** F: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168

12	d1tuga1	Alignment		100.0	27	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
13	c3grfA_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
14	c3sdsA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
15	c1pg5A_	Alignment		100.0	24	**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
16	c2rgwD_	Alignment		100.0	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
17	c2ef0A_	Alignment		100.0	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
18	c3gd5D_	Alignment		100.0	41	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
19	c1js1Z_	Alignment		100.0	29	**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
20	c3q98A_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
21	c3d6nB_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
22	c2at2B_	Alignment	not modelled	100.0	29	**PDB header:** **PDB COMPND:**
23	c3lxmC_	Alignment	not modelled	100.0	31	**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	d1duvg2	Alignment	not modelled	100.0	100	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
25	d1dxha2	Alignment	not modelled	100.0	54	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
26	d1duvg1	Alignment	not modelled	100.0	100	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
27	d1vlva1	Alignment	not modelled	100.0	49	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
28	d1pvva1	Alignment	not modelled	100.0	43	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
						Fold:ATC-like

29	d1dxha1	Alignment	not modelled	100.0	64	**Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
30	d1ml4a1	Alignment	not modelled	100.0	31	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
31	d1otha1	Alignment	not modelled	100.0	42	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
32	d1otha2	Alignment	not modelled	100.0	38	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
33	d1ekxa1	Alignment	not modelled	100.0	37	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
34	d1pvva2	Alignment	not modelled	100.0	39	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
35	d1vlva2	Alignment	not modelled	100.0	44	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
36	d2at2a1	Alignment	not modelled	100.0	38	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
37	d1pg5a1	Alignment	not modelled	100.0	34	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
38	d1ml4a2	Alignment	not modelled	100.0	23	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
39	d1js1x1	Alignment	not modelled	100.0	28	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
40	d1ekxa2	Alignment	not modelled	100.0	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
41	d1pg5a2	Alignment	not modelled	100.0	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
42	d1js1x2	Alignment	not modelled	100.0	30	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
43	d2at2a2	Alignment	not modelled	100.0	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
44	d2atca2	Alignment	not modelled	100.0	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
45	c3oneA_	Alignment	not modelled	98.7	18	**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
46	c3n58D_	Alignment	not modelled	98.5	14	**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
47	c3dhyC_	Alignment	not modelled	98.5	20	**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
48	c3gvpB_	Alignment	not modelled	98.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
49	c1d4fD_	Alignment	not modelled	98.4	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
50	c1v8bA_	Alignment	not modelled	98.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
51	c3d64A_	Alignment	not modelled	98.1	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
52	c2j6iC_	Alignment	not modelled	98.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
53	c1xdwA_	Alignment	not modelled	97.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad+-dependent (r)-2-hydroxyglutarate **PDBTitle:** nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
54	c3d4oA_	Alignment	not modelled	97.8	13	**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
55	c3n7uD_	Alignment	not modelled	97.8	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
56	c1ybaC_	Alignment	not modelled	97.7	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
57	c3k5pA_	Alignment	not modelled	97.6	16	**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
58	c2omeA_	Alignment	not modelled	97.6	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**c-terminal-binding protein 2; **PDBTitle:** crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
59	c2gcgB_	Alignment	not modelled	97.5	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
60	c2dbqA_	Alignment	not modelled	97.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
61	c1gdhA_	Alignment	not modelled	97.5	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
62	c3l07B_	Alignment	not modelled	97.5	12	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
63	d1mx3a1	Alignment	not modelled	97.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
64	c1j4aA_	Alignment	not modelled	97.4	12	**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
65	c3evtA_	Alignment	not modelled	97.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
66	c4a26B_	Alignment	not modelled	97.4	14	**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
67	c3bazA_	Alignment	not modelled	97.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyphenylpyruvate reductase; **PDBTitle:** structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
68	c1ygyA_	Alignment	not modelled	97.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
69	c3oetF_	Alignment	not modelled	97.3	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad
70	c2o4cB_	Alignment	not modelled	97.3	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
71	d2naca1	Alignment	not modelled	97.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
72	c2cukC_	Alignment	not modelled	97.3	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
73	c2eklA_	Alignment	not modelled	97.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
74	c1b0aA_	Alignment	not modelled	97.3	18	**PDB header:**oxidoreductase,hydrolase **Chain:** A: **PDB Molecule:**protein (fold bifunctional protein); **PDBTitle:** 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
75	c1dxyA_	Alignment	not modelled	97.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** structure of d-2-hydroxyisocaproate dehydrogenase
76	c2w2kB_	Alignment	not modelled	97.3	14	**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.
77	c2rirA_	Alignment	not modelled	97.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
78	c2nacA_	Alignment	not modelled	97.2	15	**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
79	c3gg9C_	Alignment	not modelled	97.1	17	**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

80	d1gdha1	Alignment	not modelled	97.1	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
81	c3nglA_	Alignment	not modelled	97.1	10	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
82	c2g76A_	Alignment	not modelled	97.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
83	c2pi1C_	Alignment	not modelled	97.1	19	**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
84	c1qp8A_	Alignment	not modelled	97.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
85	c3gvxA_	Alignment	not modelled	97.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerate dehydrogenase related protein; **PDBTitle:** crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
86	d1sc6a1	Alignment	not modelled	96.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
87	d2dlda1	Alignment	not modelled	96.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
88	c3hg7A_	Alignment	not modelled	96.9	18	**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
89	c1wwkA_	Alignment	not modelled	96.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
90	d1qp8a1	Alignment	not modelled	96.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
91	d1j4aa1	Alignment	not modelled	96.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
92	c3kboB_	Alignment	not modelled	96.8	18	**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
93	c4a5oB_	Alignment	not modelled	96.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
94	d1dxya1	Alignment	not modelled	96.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
95	c3p2oA_	Alignment	not modelled	96.5	18	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
96	c2d0iC_	Alignment	not modelled	96.5	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
97	d1li4a1	Alignment	not modelled	96.5	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
98	d1a4ia1	Alignment	not modelled	96.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
99	d1gpja2	Alignment	not modelled	96.4	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
100	c1u8xX_	Alignment	not modelled	96.4	14	**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
101	d1ygya1	Alignment	not modelled	96.4	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
102	c3g79A_	Alignment	not modelled	96.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; **PDBTitle:** crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1
103	d1civa1	Alignment	not modelled	96.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
104	c1gpjA_	Alignment	not modelled	96.3	17	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
105	c1vitA	Alignment	not modelled	96.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase;

105	c1vjtA_	Alignment	not modelled	96.2	17	**PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
106	d1b0aa1	Alignment	not modelled	96.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
107	d7mdha1	Alignment	not modelled	96.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
108	d1pjca1	Alignment	not modelled	96.2	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
109	c7mdhA_	Alignment	not modelled	96.1	16	**PDB header:**chloroplastic malate dehydrogenase **Chain:** A: **PDB Molecule:**protein (malate dehydrogenase); **PDBTitle:** structural basis for light acitvation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
110	c1obbB_	Alignment	not modelled	95.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
111	d1b8pa1	Alignment	not modelled	95.8	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
112	d1y7ta1	Alignment	not modelled	95.8	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
113	c3p2oB_	Alignment	not modelled	95.7	20	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
114	c3prjB_	Alignment	not modelled	95.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
115	d1vjta1	Alignment	not modelled	95.5	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
116	d1v8ba1	Alignment	not modelled	95.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
117	d1l7da1	Alignment	not modelled	95.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
118	c2c2xB_	Alignment	not modelled	95.4	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
119	c1b8vA_	Alignment	not modelled	95.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (malate dehydrogenase); **PDBTitle:** malate dehydrogenase from aquaspirillum arcticum
120	d5mdha1	Alignment	not modelled	95.3	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like