Phyre^{2}

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Description	P30138
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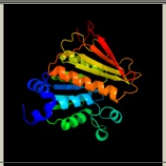
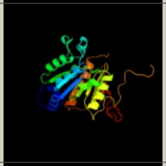
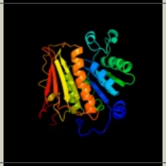
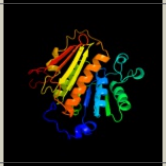
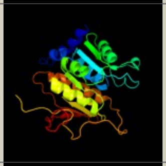
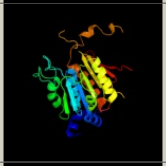
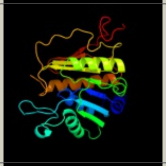
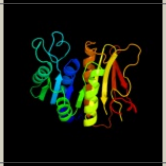
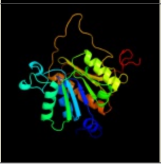
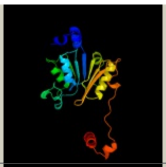
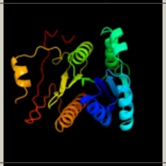
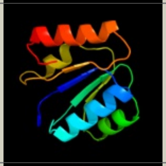
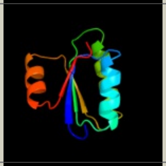
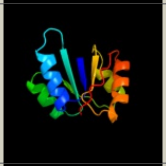
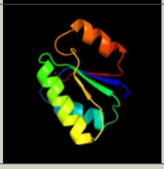
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zfnA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylyltransferase thif; **PDBTitle:** structural analysis of escherichia coli thif
2	d1jw9b_	Alignment		100.0	46	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Molybdenum cofactor biosynthesis protein MoeB
3	c3h9gA_	Alignment		100.0	27	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**mccb protein; **PDBTitle:** crystal structure of e. coli mccb + mcca-n7isoasn
4	d1yovb1	Alignment		100.0	27	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Ubiquitin activating enzymes (UBA)
5	c3gznB_	Alignment		100.0	25	**PDB header:**protein binding/ligase **Chain:** B: **PDB Molecule:**nedd8-activating enzyme e1 catalytic subunit; **PDBTitle:** structure of nedd8-activating enzyme in complex with nedd82 and mln4924
6	c3vh3A_	Alignment		100.0	21	**PDB header:**metal binding protein/protein transport **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of atg7ctd-atg8 complex
7	c1y8qA_	Alignment		100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-like 1 activating enzyme e1a; **PDBTitle:** sumo e1 activating enzyme sae1-sae2-mg-atp complex
8	c2nvuB_	Alignment		100.0	30	**PDB header:**protein turnover, ligase **Chain:** B: **PDB Molecule:**maltose binding protein/nedd8-activating enzyme **PDBTitle:** structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
9	c3kydB_	Alignment		100.0	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**sumo-activating enzyme subunit 2; **PDBTitle:** human sumo e1~sumo1-amp tetrahedral intermediate mimic
10	c3vh1A_	Alignment		100.0	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of saccharomyces cerevisiae atg7 (1-595)
11	c1y8qD_	Alignment		100.0	25	**PDB header:**ligase **Chain:** D: **PDB Molecule:**ubiquitin-like 2 activating enzyme e1b; **PDBTitle:** sumo e1 activating enzyme sae1-sae2-mg-atp complex

12	c3cmmA_	Alignment		100.0	27	**PDB header:**ligase/protein binding **Chain:** A: **PDB Molecule:**ubiquitin-activating enzyme e1 1; **PDBTitle:** crystal structure of the uba1-ubiquitin complex
13	c3gucB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ubiquitin-like modifier-activating enzyme 5; **PDBTitle:** human ubiquitin-activating enzyme 5 in complex with amppnp
14	d1yova1	Alignment		100.0	19	**Fold:**Activating enzymes of the ubiquitin-like proteins **Superfamily:**Activating enzymes of the ubiquitin-like proteins **Family:**Ubiquitin activating enzymes (UBA)
15	c1e5lA_	Alignment		98.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
16	d1pjqa1	Alignment		98.1	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
17	c2axqA_	Alignment		98.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
18	d1vi2a1	Alignment		98.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
19	c3ic5A_	Alignment		97.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
20	c2nloA_	Alignment		97.8	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
21	c1vi2B_	Alignment	not modelled	97.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad
22	d1pzga1	Alignment	not modelled	97.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
23	c3tozA_	Alignment	not modelled	97.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
24	c2hjrK_	Alignment	not modelled	97.7	24	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of cryptosporidium parvum malate2 dehydrogenase
25	c1pjtB_	Alignment	not modelled	97.7	21	**PDB header:**transferase/oxidoreductase/lyase **Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
26	d1e5qa1	Alignment	not modelled	97.6	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
27	c2z2vA_	Alignment	not modelled	97.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
28	c1gpjA_	Alignment	not modelled	97.6	30	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri

29	d9ldta1	Alignment	not modelled	97.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
30	d1np3a2	Alignment	not modelled	97.5	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
31	c3pgjB_	Alignment	not modelled	97.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
32	c1u4sA_	Alignment	not modelled	97.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
33	c2fnzA_	Alignment	not modelled	97.5	22	**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)
34	c2eggA_	Alignment	not modelled	97.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
35	c1pzfD_	Alignment	not modelled	97.4	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** t.gondii ldh1 ternary complex with apad+ and oxalate
36	d1uxja1	Alignment	not modelled	97.4	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
37	d1t2da1	Alignment	not modelled	97.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
38	d1i0za1	Alignment	not modelled	97.4	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
39	c1bg6A_	Alignment	not modelled	97.4	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; **PDBTitle:** crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
40	c3o8qB_	Alignment	not modelled	97.4	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase i alpha; **PDBTitle:** 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
41	c1ur5C_	Alignment	not modelled	97.4	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** stabilization of a tetrameric malate dehydrogenase by2 introduction of a disulfide bridge at the dimer/dimer3 interface
42	d1gpja2	Alignment	not modelled	97.4	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
43	c2g1uA_	Alignment	not modelled	97.4	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical protein tm1088a; **PDBTitle:** crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
44	c2d0iC_	Alignment	not modelled	97.4	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
45	c3u62A_	Alignment	not modelled	97.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from thermotoga maritima
46	c2ew2B_	Alignment	not modelled	97.3	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase, putative; **PDBTitle:** crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
47	c3d1lB_	Alignment	not modelled	97.3	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
48	c3dfzB_	Alignment	not modelled	97.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
49	d1lssa_	Alignment	not modelled	97.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
50	c3n7uD_	Alignment	not modelled	97.3	16	**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
51	c3donA_	Alignment	not modelled	97.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
52	d1kyqa1	Alignment	not modelled	97.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
53	c3eywA_	Alignment	not modelled	97.2	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
						Fold:NAD(P)-binding Rossmann-fold domains

54	d1pjca1	Alignment	not modelled	97.2	32	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
55	c1np3B_	Alignment	not modelled	97.2	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
56	c1z82A_	Alignment	not modelled	97.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from2 thermotoga maritima at 2.00 a resolution
57	c3gviB_	Alignment	not modelled	97.2	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp
58	c1m67A_	Alignment	not modelled	97.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
59	d5ldha1	Alignment	not modelled	97.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
60	c3k96B_	Alignment	not modelled	97.2	17	**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
61	d2pgda2	Alignment	not modelled	97.2	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
62	d1nvta1	Alignment	not modelled	97.1	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
63	d1ldna1	Alignment	not modelled	97.1	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
64	d1i10a1	Alignment	not modelled	97.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
65	c3pwzA_	Alignment	not modelled	97.1	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase 3; **PDBTitle:** crystal structure of an ael1 enzyme from pseudomonas putida
66	c1ldbA_	Alignment	not modelled	97.1	22	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**apo-l-lactate dehydrogenase; **PDBTitle:** structure determination and refinement of bacillus2 stearothermophilus lactate dehydrogenase
67	c1wpqB_	Alignment	not modelled	97.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad+], **PDBTitle:** ternary complex of glycerol 3-phosphate dehydrogenase 12 with nad and dihydroxyactone
68	d1n1ea2	Alignment	not modelled	97.1	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
69	c3llvA_	Alignment	not modelled	97.1	14	**PDB header:**nad(p) binding protein **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
70	d1bg6a2	Alignment	not modelled	97.1	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
71	d2hmva1	Alignment	not modelled	97.1	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
72	d2ldxa1	Alignment	not modelled	97.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
73	c1wwkA_	Alignment	not modelled	97.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
74	c3nzoB_	Alignment	not modelled	97.0	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**udp-n-acetylglucosamine 4,6-dehydratase; **PDBTitle:** udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri.
75	c2d4aC_	Alignment	not modelled	97.0	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of the malate dehydrogenase from aeropyrum pernix
76	c1hyhA_	Alignment	not modelled	97.0	27	**PDB header:**oxidoreductase (choh(d)-nad+(a)) **Chain:** A: **PDB Molecule:**l-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
77	c1gv1D_	Alignment	not modelled	97.0	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
78	c8ldhA_	Alignment	not modelled	97.0	14	**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
						PDB header:oxidoreductase

79	c3cumA_	Alignment	not modelled	97.0	31	**Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
80	c1kyqC_	Alignment	not modelled	97.0	16	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
81	c2dfdD_	Alignment	not modelled	97.0	34	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of human malate dehydrogenase type 2
82	c3pqeD_	Alignment	not modelled	97.0	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
83	c2ldxA_	Alignment	not modelled	96.9	22	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**apo-lactate dehydrogenase; **PDBTitle:** characterization of the antigenic sites on the refined 3-2 angstroms resolution structure of mouse testicular lactate3 dehydrogenase c4
84	c3k6jA_	Alignment	not modelled	96.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence; **PDBTitle:** crystal structure of the dehydrogenase part of multifuctional enzyme 12 from c.elegans
85	c2ph5A_	Alignment	not modelled	96.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
86	c1pgqA_	Alignment	not modelled	96.9	9	**PDB header:**oxidoreductase (choh(d)-nadp+(a)) **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
87	c1txgA_	Alignment	not modelled	96.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
88	c2nacA_	Alignment	not modelled	96.9	14	**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
89	d1llda1	Alignment	not modelled	96.9	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
90	c3hwrA_	Alignment	not modelled	96.9	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution
91	d1obba1	Alignment	not modelled	96.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
92	c2ofpB_	Alignment	not modelled	96.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketopantoate reductase; **PDBTitle:** crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
93	d1hyha1	Alignment	not modelled	96.9	32	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
94	c3evtA_	Alignment	not modelled	96.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
95	c3djeA_	Alignment	not modelled	96.9	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fructosyl amine: oxygen oxidoreductase; **PDBTitle:** crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
96	c1a5zA_	Alignment	not modelled	96.9	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** lactate dehydrogenase from thermotoga maritima (tmldh)
97	d1s6ya1	Alignment	not modelled	96.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
98	c1ojuA_	Alignment	not modelled	96.9	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.
99	c2gcgB_	Alignment	not modelled	96.9	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
100	d1gtea4	Alignment	not modelled	96.8	8	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
101	d1u8xx1	Alignment	not modelled	96.8	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
102	c3d0oA_	Alignment	not modelled	96.8	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase 1; **PDBTitle:** crystal structure of lactate dehydrogenase from2 staphylococcus aureus
						PDB header:oxidoreductase

103	c1pj6A_	Alignment	not modelled	96.8	27	**Chain:** A: **PDB Molecule:**n,n-dimethylglycine oxidase; **PDBTitle:** crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
104	c2dbqA_	Alignment	not modelled	96.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
105	c1nvtA_	Alignment	not modelled	96.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5'-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
106	c2e37B_	Alignment	not modelled	96.8	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** structure of tt0471 protein from thermus thermophilus
107	c2v65A_	Alignment	not modelled	96.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase a chain; **PDBTitle:** apo ldh from the psychrophile c. gunnari
108	d1txga2	Alignment	not modelled	96.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
109	c1mldA_	Alignment	not modelled	96.8	33	**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
110	d1ojua1	Alignment	not modelled	96.8	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
111	c3fi9B_	Alignment	not modelled	96.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from porphyromonas2 gingivalis
112	c2g76A_	Alignment	not modelled	96.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
113	c3qhaB_	Alignment	not modelled	96.7	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
114	c2cukC_	Alignment	not modelled	96.7	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
115	d1ldma1	Alignment	not modelled	96.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
116	c1lldA_	Alignment	not modelled	96.7	18	**PDB header:**oxidoreductase(choh (d)-nad (a)) **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** molecular basis of allosteric activation of bacterial l-lactate2 dehydrogenase
117	c1ks9A_	Alignment	not modelled	96.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** ketopantoate reductase from escherichia coli
118	d2jfga1	Alignment	not modelled	96.7	20	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
119	c1pgjA_	Alignment	not modelled	96.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
120	c2iz1C_	Alignment	not modelled	96.7	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data