Phyre2

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Description	P21177
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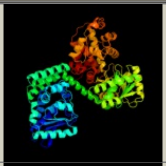
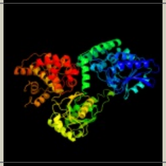
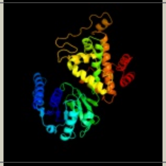
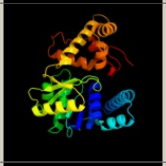
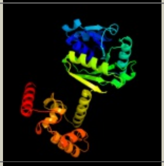
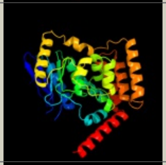
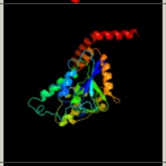
Unique Job ID	00f82ac27212aff5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d3tB_	Alignment		100.0	56	**PDB header:**lyase, oxidoreductase/transferase **Chain:** B: **PDB Molecule:**fatty oxidation complex alpha subunit; **PDBTitle:** fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
2	c2x58B_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** the crystal structure of mfe1 liganded with coa
3	c2wtbA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fatty acid multifunctional protein (atmfp2); **PDBTitle:** arabidopsis thaliana multifuctional protein, mfp2
4	c1zcjA_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase
5	c3k6jA_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence; **PDBTitle:** crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
6	c3mogA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxybutyryl-coa dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
7	c1m75B_	Alignment		100.0	36	**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
8	c1zejA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of the 3-hydroxyacyl-coa dehydrogenase (hbd-9,2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution
9	d1wdka4	Alignment		100.0	51	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
10	c2ep9A_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-gulonate 3-dehydrogenase; **PDBTitle:** crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
11	c3bptA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyryl-coa hydrolase; **PDBTitle:** crystal structure of human beta-hydroxyisobutyryl-coa hydrolase in2 complex with quercetin

12	d1nzya_	Alignment		100.0	20	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
13	c3moyA_	Alignment		100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of probable enoyl-coa hydratase from mycobacterium2 smegmatis
14	c3g64A_	Alignment		100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from streptomyces2 coelicolor a3(2)
15	c3hinA_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative 3-hydroxybutyryl-coa dehydratase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase from2 rhodopseudomonas palustris cga009
16	c3i47A_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl coa hydratase/isomerase (crotonase); **PDBTitle:** crystal structure of putative enoyl coa hydratase/isomerase2 (crotonase) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1
17	d1dcia_	Alignment		100.0	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
18	c3ju1A_	Alignment		100.0	15	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of enoyl-coa hydratase/isomerase family protein
19	c2qq3F_	Alignment		100.0	28	**PDB header:**lyase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase subunit i; **PDBTitle:** crystal structure of enoyl-coa hydrates subunit i (gk_2039)2 other form from geobacillus kaustophilus hta426
20	d1uiya_	Alignment		100.0	25	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
21	c2hw5F_	Alignment	not modelled	100.0	26	**PDB header:**lyase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** the crystal structure of human enoyl-coenzyme a (coa) hydratase short2 chain 1, echs1
22	c3kqfC_	Alignment	not modelled	100.0	29	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** 1.8 angstrom resolution crystal structure of enoyl-coa hydratase from2 bacillus anthracis.
23	c3h81A_	Alignment	not modelled	100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase echa8; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
24	c3hrxD_	Alignment	not modelled	100.0	29	**PDB header:**lyase **Chain:** D: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of phenylacetic acid degradation protein paag
25	d1wz8a1	Alignment	not modelled	100.0	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
26	c2vx2D_	Alignment	not modelled	100.0	24	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**enoyl-coa hydratase domain-containing protein 3; **PDBTitle:** crystal structure of human enoyl coenzyme a hydratase2 domain-containing protein 3 (echdc3)
27	c2ej5B_	Alignment	not modelled	100.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase subunit ii; **PDBTitle:** crystal structure of gk2038 protein (enoyl-coa hydratase subunit ii)2 from geobacillus kaustophilus
28	c3mybA_	Alignment	not modelled	100.0	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase mycobacterium

						smegmatis
29	c2iexA_	Alignment	not modelled	100.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxynapthoic acid synthetase; **PDBTitle:** crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
30	c2ppyE_	Alignment	not modelled	100.0	27	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydrates (gk_1992) from geobacillus2 kaustophilus hta426
31	d1hzda_	Alignment	not modelled	100.0	29	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
32	c3rsiA_	Alignment	not modelled	100.0	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** the structure of a putative enoyl-coa hydratase/isomerase from2 mycobacterium abscessus atcc 19977 / dsm 44196
33	d2fw2a1	Alignment	not modelled	100.0	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
34	c3p5mB_	Alignment	not modelled	100.0	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium avium
35	c3trrA_	Alignment	not modelled	100.0	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
36	c3r0oA_	Alignment	not modelled	100.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carnitinyl-coa dehydratase; **PDBTitle:** crystal structure of carnitinyl-coa hydratase from mycobacterium avium
37	c3peaD_	Alignment	not modelled	100.0	29	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of enoyl-coa hydratase from bacillus anthracis str.2 'ames ancestor'
38	d1mj3a_	Alignment	not modelled	100.0	29	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
39	c3swxB_	Alignment	not modelled	100.0	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
40	c3qxzA_	Alignment	not modelled	100.0	24	**PDB header:**lyase,isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
41	d1xx4a_	Alignment	not modelled	100.0	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
42	c3njbA_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium smegmatis,2 iodide soak
43	c3sllC_	Alignment	not modelled	100.0	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**probable enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase/isomerase from2 mycobacterium abscessus
44	d1q52a_	Alignment	not modelled	100.0	20	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
45	c3qxiA_	Alignment	not modelled	100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase echa1; **PDBTitle:** crystal structure of enoyl-coa hydratase echa1 from mycobacterium2 marinum
46	c3lkeA_	Alignment	not modelled	100.0	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from bacillus2 halodurans
47	c3rrvC_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase from2 mycobacterium paratuberculosis
48	c3gkbA_	Alignment	not modelled	100.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase from streptomyces2 avermitilis
49	d1ef8a_	Alignment	not modelled	100.0	19	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
50	c2q35A_	Alignment	not modelled	100.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**curf; **PDBTitle:** crystal structure of the y82f variant of ech2 decarboxylase domain of2 curf from lyngbya majuscula
51	c3q1tB_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium avium
52	d2f6qa1	Alignment	not modelled	100.0	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
53	c2fbmB_	Alignment	not modelled	100.0	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**y chromosome chromodomain protein 1, telomeric isoform b; **PDBTitle:** acetyltransferase domain of cdy1
54	c3h0uB_	Alignment	not modelled	100.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative enoyl-coa hydratase;

54	c3h0uB_	Alignment	not modelled	100.0	24	**PDBTitle:** crystal structure of a putative enoyl-coa hydratase from2 streptomyces avermitilis
55	c2f6qA_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peroxisomal 3,2-trans-enoyl-coa isomerase; **PDBTitle:** the crystal structure of human peroxisomal delta3, delta2 enoyl coa2 isomerase (peci)
56	c2w3pB_	Alignment	not modelled	100.0	26	**PDB header:**lyase **Chain:** B: **PDB Molecule:**benzoyl-coa-dihydrodiol lyase; **PDBTitle:** boxc crystal structure
57	c3oc7A_	Alignment	not modelled	100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of an enoyl-coa hydratase from mycobacterium avium
58	c3l3sF_	Alignment	not modelled	100.0	24	**PDB header:**isomerase **Chain:** F: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of an enoyl-coa hydrotase/isomerase family2 protein from silicibacter pomeroyi
59	c3he2C_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enoyl-coa hydratase echa6; **PDBTitle:** crystal structure of enoyl-coa hydratase from mycobacterium2 tuberculosis
60	d1sg4a1	Alignment	not modelled	100.0	24	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
61	d1pjha_	Alignment	not modelled	100.0	18	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
62	c2j5iF_	Alignment	not modelled	100.0	24	**PDB header:**lyase **Chain:** F: **PDB Molecule:**p-hydroxycinnamoyl coa hydratase/lyase; **PDBTitle:** crystal structure of hydroxycinnamoyl-coa hydratase-lyase
63	c3r6hA_	Alignment	not modelled	100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase, echa3; **PDBTitle:** crystal structure of an enoyl-coa hydratase (echa3) from mycobacterium2 marinum
64	c3m6nA_	Alignment	not modelled	100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rpff protein; **PDBTitle:** crystal structure of rpff
65	c3qkaB_	Alignment	not modelled	100.0	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enoyl-coa hydratase, echa5; **PDBTitle:** crystal structure of enoyl-coa hydratase echa5 from mycobacterium2 marinum
66	c2pg8C_	Alignment	not modelled	100.0	23	**PDB header:**ligand binding protein **Chain:** C: **PDB Molecule:**dpgc; **PDBTitle:** crystal structure of r254k mutanat of dpgc with bound substrate analog
67	c3ot6A_	Alignment	not modelled	100.0	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase family protein; **PDBTitle:** crystal structure of an enoyl-coa hydratase/isomerase family protein2 from psudomonas syringae
68	c3isaA_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of putative enoyl-coa hydratase/isomerase from2 bordetella parapertussis
69	c3hp0B_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative polyketide biosynthesis enoyl-coa **PDBTitle:** crystal structure of a putative polyketide biosynthesis2 enoyl-coa hydratase (pksh) from bacillus subtilis
70	c3p85A_	Alignment	not modelled	100.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure enoyl-coa hydratase from mycobacterium avium
71	d2a7ka1	Alignment	not modelled	100.0	23	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
72	c3h02F_	Alignment	not modelled	100.0	24	**PDB header:**lyase **Chain:** F: **PDB Molecule:**naphthoate synthase; **PDBTitle:** 2.15 angstrom resolution crystal structure of naphthoate synthase from2 salmonella typhimurium.
73	c3fduF_	Alignment	not modelled	100.0	28	**PDB header:**isomerase **Chain:** F: **PDB Molecule:**putative enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of a putative enoyl-coa hydratase/isomerase from2 acinetobacter baumannii
74	c3laoA_	Alignment	not modelled	100.0	24	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase/isomerase; **PDBTitle:** crystal structure of enoyl-coa hydratase from pseudomonas2 aeruginosa pa01
75	c3omeE_	Alignment	not modelled	100.0	22	**PDB header:**lyase **Chain:** E: **PDB Molecule:**enoyl-coa hydratase; **PDBTitle:** crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
76	d1szoa_	Alignment	not modelled	100.0	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
77	c1rjnC_	Alignment	not modelled	100.0	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**menb; **PDBTitle:** the crystal structure of menb (rv0548c) from mycobacterium2 tuberculosis in complex with the coa portion of naphthoyl coa
78	d1rjma_	Alignment	not modelled	100.0	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
79	c3greA_	Alignment	not modelled	100.0	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase, echa12_1;

79	c3qreA_	Alignment	not modelled	100.0	27	**PDBTitle:** crystal structure of an enoyl-coa hydratase echa12_1 from2 mycobacterium marinum
80	c2j5gL_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**alr4455 protein; **PDBTitle:** the native structure of a beta-diketone hydrolase from the2 cyanobacterium anabaena sp. pcc 7120
81	c3qmjA_	Alignment	not modelled	100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enoyl-coa hydratase, echa8_6; **PDBTitle:** crystal structure of enoyl-coa hydratase echa8_6 from mycobacterium2 marinum
82	d1wdka3	Alignment	not modelled	100.0	67	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
83	d1f0ya2	Alignment	not modelled	100.0	36	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
84	d1wdka1	Alignment	not modelled	100.0	59	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
85	d1f0ya1	Alignment	not modelled	99.9	37	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
86	d3hdha1	Alignment	not modelled	99.9	39	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
87	d1wdka2	Alignment	not modelled	99.9	49	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
88	c1vpdA_	Alignment	not modelled	99.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
89	d1dlja2	Alignment	not modelled	99.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
90	c3d1lB_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
91	c3pduF_	Alignment	not modelled	99.8	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase family protein; **PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
92	d1ez4a1	Alignment	not modelled	99.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
93	c3pefA_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, nad-binding; **PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
94	c3ckyA_	Alignment	not modelled	99.7	18	**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
95	c3ggpA_	Alignment	not modelled	99.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
96	c3dzbA_	Alignment	not modelled	99.7	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
97	c2g5cD_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
98	d1uxja1	Alignment	not modelled	99.7	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
99	c1np3B_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
100	c2pv7B_	Alignment	not modelled	99.7	14	**PDB header:**isomerase, oxidoreductase **Chain:** B: **PDB Molecule:**t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) **PDBTitle:** crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
101	c3ctvA_	Alignment	not modelled	99.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of central domain of 3-hydroxyacyl-coa2 dehydrogenase from archaeoglobus fulgidus
102	d2g5ca2	Alignment	not modelled	99.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
103	c2uyyD_	Alignment	not modelled	99.6	14	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein;

						PDBTitle: structure of the cytokine-like nuclear factor n-pac
104	d1ldma1	Alignment	not modelled	99.6	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
105	c3l6dB_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
106	c3b1fA_	Alignment	not modelled	99.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 mutans
107	d1ojua1	Alignment	not modelled	99.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
108	d2b0ja2	Alignment	not modelled	99.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
109	d2f1ka2	Alignment	not modelled	99.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
110	c3dojA_	Alignment	not modelled	99.6	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase-like protein; **PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
111	c2gf2B_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of human hydroxyisobutyrate dehydrogenase
112	c2i76B_	Alignment	not modelled	99.6	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein tm1727 from thermotoga maritima
113	d2ahra2	Alignment	not modelled	99.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
114	c3cumA_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
115	d1guza1	Alignment	not modelled	99.6	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
116	c2ahrB_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative pyrroline carboxylate reductase; **PDBTitle:** crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
117	d1yqga2	Alignment	not modelled	99.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
118	d1ldna1	Alignment	not modelled	99.6	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
119	d1llca1	Alignment	not modelled	99.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
120	c2f1kD_	Alignment	not modelled	99.6	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase