Phyre^2

Email	l.a.kelley@imperial.ac.uk
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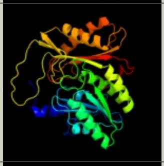
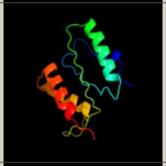
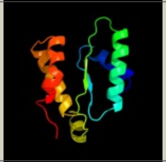
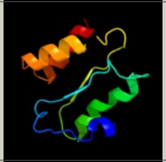
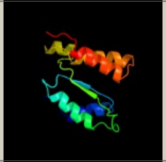
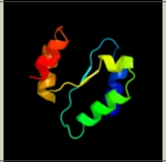
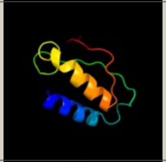
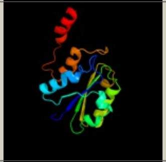
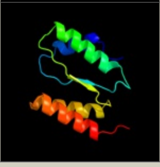
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1oi2a_	Alignment		100.0	100	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
2	d1un8a4	Alignment		100.0	32	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
3	c1un9B_	Alignment		100.0	32	**PDB header:**kinase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
4	c3ct4B_	Alignment		100.0	46	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts-dependent dihydroxyacetone kinase, **PDBTitle:** structure of dha-kinase subunit dhak from l. lactis
5	c2iu6B_	Alignment		100.0	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** regulation of the dha operon of lactococcus lactis
6	c3pl5A_	Alignment		95.3	16	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** fatty acid binding protein
7	c3jr7A_	Alignment		94.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized egv family protein cog1307; **PDBTitle:** the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149
8	d1pzxa_	Alignment		93.3	14	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
9	c1mgpA_	Alignment		93.2	16	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm841; **PDBTitle:** hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
10	d1mgpa_	Alignment		93.2	16	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
11	d3ct6a1	Alignment		92.7	16	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like

12	d2bz1a1	Alignment		91.9	27	**Fold:**RibA-like **Superfamily:**RibA-like **Family:**RibA-like
13	c3nyiA_	Alignment		91.4	16	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fat acid-binding protein; **PDBTitle:** the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
14	c3fdjA_	Alignment		88.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** the structure of a degv family protein from eubacterium eligens.
15	c3gdwA_	Alignment		86.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
16	c2dt8A_	Alignment		86.8	21	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** fatty acid binding of a degv family protein from thermus thermophilus
17	d3b48a1	Alignment		82.3	22	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
18	d1hf2a2	Alignment		69.5	18	**Fold:**Cell-division inhibitor MinC, N-terminal domain **Superfamily:**Cell-division inhibitor MinC, N-terminal domain **Family:**Cell-division inhibitor MinC, N-terminal domain
19	c3c3jA_	Alignment		65.5	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative tagatose-6-phosphate ketose/aldose isomerase; **PDBTitle:** crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
20	c2g7zB_	Alignment		64.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein spy1493; **PDBTitle:** conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
21	c3lupA_	Alignment	not modelled	61.5	11	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
22	c3h7aC_	Alignment	not modelled	57.8	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of short-chain dehydrogenase from2 rhodopseudomonas palustris
23	c3gndC_	Alignment	not modelled	54.2	26	**PDB header:**lyase **Chain:** C: **PDB Molecule:**aldolase lsrf; **PDBTitle:** crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
24	c3t4xA_	Alignment	not modelled	51.9	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** short chain dehydrogenase/reductase family oxidoreductase from2 bacillus anthracis str. ames ancestor
25	c3rd5A_	Alignment	not modelled	47.4	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mypaa.01249.c; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
26	c3i1jB_	Alignment	not modelled	45.7	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, short chain **PDBTitle:** structure of a putative short chain dehydrogenase from2 pseudomonas syringae
27	d2o23a1	Alignment	not modelled	45.0	54	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
28	c3uxyC_	Alignment	not modelled	44.9	54	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** the crystal structure of short chain dehydrogenase from

						rhodobacter2 sphaeroides
29	c3pxxE_	Alignment	not modelled	44.7	46	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carveol dehydrogenase; **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nicotinamide adenine dinucleotide
30	c3s55F_	Alignment	not modelled	42.2	54	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of a putative short-chain dehydrogenase/reductase2 from mycobacterium abscessus bound to nad
31	c3qivA_	Alignment	not modelled	41.8	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase or 3-oxoacyl-[acyl-carrier- **PDBTitle:** crystal structure of a putative short-chain dehydrogenase or 3-2 oxoacyl-[acyl-carrier-protein] reductase from mycobacterium3 paratuberculosis atcc baa-968 / k-10
32	c3bmrA_	Alignment	not modelled	40.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pteridine reductase; **PDBTitle:** structure of pteridine reductase 1 (ptr1) from trypanosoma2 brucei in ternary complex with cofactor (nadp+) and3 inhibitor (compound ax6)
33	c3sc4A_	Alignment	not modelled	40.6	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase (a0qtm2 homolog); **PDBTitle:** crystal structure of a short chain dehydrogenase (a0qtm2 homolog)2 mycobacterium thermoresistibile
34	c3oidA_	Alignment	not modelled	40.3	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadph]; **PDBTitle:** crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
35	c3ftpD_	Alignment	not modelled	40.1	29	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein)2 reductase from burkholderia pseudomallei at 2.05 a3 resolution
36	d1vl8a_	Alignment	not modelled	40.0	54	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
37	c3sx2F_	Alignment	not modelled	39.1	46	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative 3-ketoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of a putative 3-ketoacyl-(acyl-carrier-protein)2 reductase from mycobacterium paratuberculosis in complex with nad
38	c3uveC_	Alignment	not modelled	39.0	46	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carveol dehydrogenase ((+)-trans-carveol dehydrogenase); **PDBTitle:** crystal structure of carveol dehydrogenase ((+)-trans-carveol2 dehydrogenase) from mycobacterium avium
39	c2ntnB_	Alignment	not modelled	38.9	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of maba-c60v/g139a/s144l
40	d2ag5a1	Alignment	not modelled	38.7	38	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
41	c3un1D_	Alignment	not modelled	38.7	31	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**probable oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from sinorhizobium meliloti2 1021
42	d1e6wa_	Alignment	not modelled	37.8	54	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
43	c3gx1A_	Alignment	not modelled	37.8	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1832 protein; **PDBTitle:** crystal structure of a domain of lin1832 from listeria innocua
44	c3kvoB_	Alignment	not modelled	37.7	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hydroxysteroid dehydrogenase-like protein 2; **PDBTitle:** crystal structure of the catalytic domain of human hydroxysteroid2 dehydrogenase like 2 (hsdl2)
45	d1ae1a_	Alignment	not modelled	37.6	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
46	c2pd6D_	Alignment	not modelled	37.6	46	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**estradiol 17-beta-dehydrogenase 8; **PDBTitle:** structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
47	c1w4zA_	Alignment	not modelled	37.5	40	**PDB header:**antibiotic biosynthesis **Chain:** A: **PDB Molecule:**ketoacyl reductase; **PDBTitle:** structure of actinorhodin polyketide (actiii) reductase
48	c3gafF_	Alignment	not modelled	37.2	31	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**7-alpha-hydroxysteroid dehydrogenase; **PDBTitle:** 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
49	d1xkqa_	Alignment	not modelled	36.9	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
50	c2ekqB_	Alignment	not modelled	36.9	42	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-deoxy-d-gluconate 3-dehydrogenase; **PDBTitle:** structure of tt0495 protein from thermus thermophilus
51	c3lf2B_	Alignment	not modelled	36.6	46	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain oxidoreductase q9hya2; **PDBTitle:** nadph bound structure of the short chain oxidoreductase q9hya2 from2 pseudomonas aeruginosa pao1 containing an

						atypical catalytic center
52	d1q7ba_	Alignment	not modelled	36.5	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
53	d2a4ka1	Alignment	not modelled	36.4	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
54	c3nywD_	Alignment	not modelled	36.2	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a betaketoacyl-[acp] reductase (fabg) from2 bacteroides thetaiotaomicron
55	d1p33a_	Alignment	not modelled	36.1	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
56	c2q2qG_	Alignment	not modelled	36.0	54	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**beta-d-hydroxybutyrate dehydrogenase; **PDBTitle:** structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
57	d1o5ia_	Alignment	not modelled	36.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
58	c3t7cC_	Alignment	not modelled	35.9	46	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carveol dehydrogenase; **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium avium2 bound to nad
59	d1h5qa_	Alignment	not modelled	35.7	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
60	c3rkuC_	Alignment	not modelled	35.6	38	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase ymr226c; **PDBTitle:** substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+
61	c2nq8B_	Alignment	not modelled	35.5	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** malarial enoyl acyl acp reductase bound with inh-nad adduct
62	c2foiB_	Alignment	not modelled	35.5	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** synthesis, biological activity, and x-ray crystal structural analysis2 of diaryl ether inhibitors of malarial enoyl acp reductase.
63	c3r3sD_	Alignment	not modelled	35.5	46	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase; **PDBTitle:** structure of the ygha oxidoreductase from salmonella enterica
64	d1cyda_	Alignment	not modelled	35.2	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
65	c2fwmX_	Alignment	not modelled	35.2	38	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase; **PDBTitle:** crystal structure of e. coli enta, a 2,3-dihydrodihydroxy benzoate2 dehydrogenase
66	c3nugA_	Alignment	not modelled	35.1	54	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
67	c3f5sA_	Alignment	not modelled	34.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of putatitve short chain dehydrogenase from shigella2 flexneri 2a str. 301
68	d1uaya_	Alignment	not modelled	34.9	50	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
69	c3diiB_	Alignment	not modelled	34.8	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a carbohydrate specific scor enzyme2 from clostridium thermocellum, ligand-free form
70	d1oaaa_	Alignment	not modelled	34.7	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
71	c3ioyB_	Alignment	not modelled	34.6	46	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** structure of putative short-chain dehydrogenase (saro_0793)2 from novosphingobium aromaticivorans
72	c2wdzD_	Alignment	not modelled	34.6	46	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
73	c2ptgA_	Alignment	not modelled	34.3	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** crystal structure of eimeria tenella enoyl reductase
74	d2gdza1	Alignment	not modelled	34.2	54	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
75	d1ulsa_	Alignment	not modelled	33.8	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
76	d1xq1a_	Alignment	not modelled	33.6	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

						Family: Tyrosine-dependent oxidoreductases
77	d1g0oa_	Alignment	not modelled	33.6	62	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
78	d2ew8a1	Alignment	not modelled	33.5	38	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
79	d1xg5a_	Alignment	not modelled	33.5	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
80	c3a28H_	Alignment	not modelled	33.4	50	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**l-2.3-butanediol dehydrogenase; **PDBTitle:** crystal structure of l-2,3-butanediol dehydrogenase
81	d1tqha_	Alignment	not modelled	33.4	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/lipase
82	c3e9nB_	Alignment	not modelled	33.3	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of a putative short-chain2 dehydrogenase/reductase from corynebacterium glutamicum
83	c3o38D_	Alignment	not modelled	32.9	46	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
84	c2p68A_	Alignment	not modelled	32.9	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of aq_1716 from aquifex aeolicus vf5
85	d2d1ya1	Alignment	not modelled	32.6	54	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
86	c3toxG_	Alignment	not modelled	32.5	46	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
87	d1e7wa_	Alignment	not modelled	32.5	36	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	c3e03C_	Alignment	not modelled	32.3	31	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a putative dehydrogenase from2 xanthomonas campestris
89	c2zatC_	Alignment	not modelled	32.2	38	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase/reductase sdr family member 4; **PDBTitle:** crystal structure of a mammalian reductase
90	c3oecA_	Alignment	not modelled	32.2	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carveol dehydrogenase (mytha.01326.c, a0r518 homolog); **PDBTitle:** crystal structure of carveol dehydrogenase from mycobacterium2 thermoresistibile
91	d1k2wa_	Alignment	not modelled	32.0	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
92	c3pgxB_	Alignment	not modelled	31.8	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**carveol dehydrogenase; **PDBTitle:** crystal structure of a putative carveol dehydrogenase from2 mycobacterium paratuberculosis bound to nicotinamide adenine3 dinucleotide
93	c2hq1A_	Alignment	not modelled	31.8	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** crystal structure of orf 1438 a putative glucose/ribitol2 dehydrogenase from clostridium thermocellum
94	d1pr9a_	Alignment	not modelled	31.8	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
95	c3shoA_	Alignment	not modelled	31.7	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
96	d1d7oa_	Alignment	not modelled	31.6	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
97	d1gz6a_	Alignment	not modelled	31.3	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	d1nffa_	Alignment	not modelled	31.3	69	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
99	c2jahB_	Alignment	not modelled	31.2	62	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**clavulanic acid dehydrogenase; **PDBTitle:** biochemical and structural analysis of the clavulanic acid2 dehydeogenase (cad) from streptomyces clavuligerus
100	d1ydea1	Alignment	not modelled	31.2	62	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
101	d1bdba_	Alignment	not modelled	31.2	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
102	c3ctmH_	Alignment	not modelled	31.1	46	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of a carbonyl reductase from candida2

						parapsilosis with anti-prelog stereo-specificity
103	c3ijrF_	Alignment	not modelled	31.1	54	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
104	c3qljB_	Alignment	not modelled	30.9	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 avium
105	d1uzma1	Alignment	not modelled	30.8	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
106	d1zk4a1	Alignment	not modelled	30.7	54	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
107	d1spxa_	Alignment	not modelled	30.6	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
108	d2rhca1	Alignment	not modelled	30.5	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
109	c3fysA_	Alignment	not modelled	30.5	7	**PDB header:**fatty acid-binding protein **Chain:** A: **PDB Molecule:**protein degv; **PDBTitle:** crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis
110	c3r1iB_	Alignment	not modelled	30.4	46	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
111	c3gvcB_	Alignment	not modelled	30.4	62	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable short-chain type **PDBTitle:** crystal structure of probable short-chain dehydrogenase-2 reductase from mycobacterium tuberculosis
112	c3uf0A_	Alignment	not modelled	30.3	54	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
113	d2fr1a1	Alignment	not modelled	30.2	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
114	c3ppiA_	Alignment	not modelled	30.2	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase type-2; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
115	d2bd0a1	Alignment	not modelled	30.1	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
116	c3afnC_	Alignment	not modelled	30.0	38	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of aldose reductase a1-r complexed with nadp
117	c3emkA_	Alignment	not modelled	30.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
118	c1yb1B_	Alignment	not modelled	30.0	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**17-beta-hydroxysteroid dehydrogenase type xi; **PDBTitle:** crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi
119	c2z1nA_	Alignment	not modelled	29.6	41	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
120	d2ae2a_	Alignment	not modelled	29.6	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases