Phyre2

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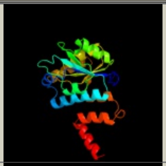
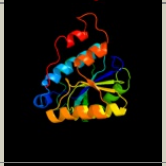
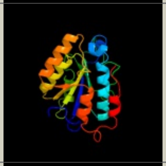
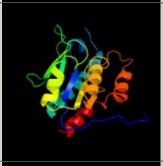
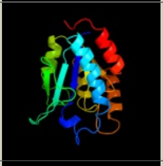
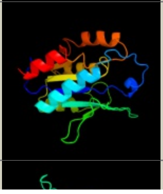
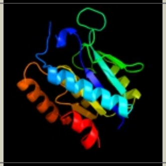
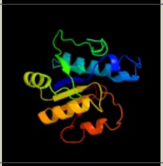
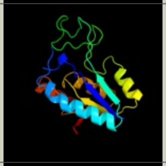
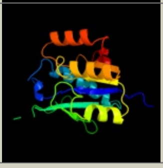
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yaca_	Alignment		100.0	98	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
2	c2b34C_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
3	c1yzvA_	Alignment		100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from trypanosoma cruzi
4	d1x9ga_	Alignment		100.0	17	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
5	c2fq1A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
6	c3irvA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysteine hydrolase; **PDBTitle:** crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
7	d1j2ra_	Alignment		100.0	17	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
8	d1nbaa_	Alignment		100.0	15	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
9	d1nf9a_	Alignment		100.0	22	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
10	c3kl2K_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase from streptomyces2 avermitilis
11	c3mcwA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution

12	c3oqpA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
13	c3oqpB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
14	c3hu5B_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
15	c3ot4F_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative isochorismatase; **PDBTitle:** structure and catalytic mechanism of bordetella bronchiseptica nicf
16	c3eefA_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-carbamoylsarcosine amidase related protein; **PDBTitle:** crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum
17	c3hb7G_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**isochorismatase hydrolase; **PDBTitle:** the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
18	d1im5a_	Alignment		100.0	21	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
19	c3r2jC_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta-hydrolase-like protein; **PDBTitle:** crystal structure of pnc1 from l. infantum in complex with nicotinate
20	c3lqyA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase hydrolase; **PDBTitle:** crystal structure of putative isochorismatase hydrolase from2 oleispira antarctica
21	c3o93A_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
22	c2wtaA_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** acinetobacter baumanii nicotinamidase pyrazinamidease
23	c2a67C_	Alignment	not modelled	100.0	21	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein
24	c3gbcA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrazinamidase/nicotinamidas pnca; **PDBTitle:** determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
25	c2h0rD_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
26	d1cmwa2	Alignment	not modelled	84.6	24	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
27	c3o26A_	Alignment	not modelled	82.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**salutaridine reductase; **PDBTitle:** the structure of salutaridine reductase from papaver somniferum.
28	d2ae2a_	Alignment	not modelled	81.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						Fold: Pyruvate kinase C-terminal domain-like

29	d1vp8a_	Alignment	not modelled	79.4	27	**Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
30	d1xdpa3	Alignment	not modelled	75.8	21	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
31	d1a9xa3	Alignment	not modelled	75.7	33	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
32	c3toxG_	Alignment	not modelled	75.5	25	**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
33	d1ae1a_	Alignment	not modelled	73.2	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
34	c3ldaA_	Alignment	not modelled	73.0	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
35	d1gega_	Alignment	not modelled	72.2	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
36	d1xg5a_	Alignment	not modelled	71.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
37	d1xsea_	Alignment	not modelled	67.2	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
38	d1xq1a_	Alignment	not modelled	66.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
39	c3nugA_	Alignment	not modelled	64.4	20	**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
40	c2c07A_	Alignment	not modelled	63.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** oxoacyl-acp reductase of plasmodium falciparum
41	d2c07a1	Alignment	not modelled	63.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
42	d1pv8a_	Alignment	not modelled	62.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
43	c2nwqA_	Alignment	not modelled	62.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable short-chain dehydrogenase; **PDBTitle:** short chain dehydrogenase from pseudomonas aeruginosa
44	c3sjuA_	Alignment	not modelled	62.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**keto reductase; **PDBTitle:** hedamycin polyketide ketoreductase bound to nadph
45	c3ijrF_	Alignment	not modelled	62.2	15	**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+
46	c2ihnA_	Alignment	not modelled	61.9	10	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
47	c2cfcB_	Alignment	not modelled	61.3	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-(r)-hydroxypropyl-com dehydrogenase; **PDBTitle:** structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
48	d1tfra2	Alignment	not modelled	61.0	10	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
49	c2pd6D_	Alignment	not modelled	60.7	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**estradiol 17-beta-dehydrogenase 8; **PDBTitle:** structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
50	c2vyeA_	Alignment	not modelled	60.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
51	c2qq5A_	Alignment	not modelled	60.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase/reductase sdr family member 1; **PDBTitle:** crystal structure of human sdr family member 1
52	d1xu9a_	Alignment	not modelled	60.3	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
53	c3imfA_	Alignment	not modelled	60.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
54	c3bh0A_	Alignment	not modelled	58.9	12	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
						Fold:NAD(P)-binding Rossmann-fold domains

55	d1wmaa1	Alignment	not modelled	58.0	17	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
56	d1f2da_	Alignment	not modelled	57.6	13	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
57	c1xdoB_	Alignment	not modelled	56.1	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase
58	d1xkqa_	Alignment	not modelled	55.6	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
59	d1xhla_	Alignment	not modelled	55.0	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
60	c3iccA_	Alignment	not modelled	54.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 3-oxoacyl-(acyl carrier protein) reductase; **PDBTitle:** crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
61	c1x1qA_	Alignment	not modelled	54.4	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
62	d1qwga_	Alignment	not modelled	54.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
63	c2nm0B_	Alignment	not modelled	53.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 3-oxacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2)
64	c2b4qB_	Alignment	not modelled	52.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rhamnolipids biosynthesis 3-oxoacyl-[acyl- **PDBTitle:** pseudomonas aeruginosa rhlg/nadp active-site complex
65	c3svtA_	Alignment	not modelled	51.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** structure of a short-chain type dehydrogenase/reductase from2 mycobacterium ulcerans
66	d1qsga_	Alignment	not modelled	51.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
67	c3cxtA_	Alignment	not modelled	50.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
68	c2uvdE_	Alignment	not modelled	50.0	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**3-oxoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** the crystal structure of a 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis (ba3989)
69	d1tyza_	Alignment	not modelled	49.9	13	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
70	c1f8sA_	Alignment	not modelled	49.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
71	c3rd5A_	Alignment	not modelled	49.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mypaa.01249.c; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
72	c3tfoD_	Alignment	not modelled	49.1	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative 3-oxoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of a putative 3-oxoacyl-(acyl-carrier-protein)2 reductase from sinorhizobium meliloti
73	c3t4xA_	Alignment	not modelled	49.0	17	**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
74	c3ak4C_	Alignment	not modelled	48.8	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-dependent quinuclidinone reductase; **PDBTitle:** crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
75	d2zdra2	Alignment	not modelled	48.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
76	c3lylB_	Alignment	not modelled	48.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-(acyl-carrier-protein) reductase; **PDBTitle:** structure of 3-oxoacyl-acylcarrier protein reductase, fabg2 from francisella tularensis
77	c3bgwD_	Alignment	not modelled	48.3	12	**PDB header:**replication **Chain:** D: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase

78	c3pk0B_	Alignment	not modelled	47.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
79	d1w7ab4	Alignment	not modelled	47.4	21	**Fold:**MutS N-terminal domain-like **Superfamily:**DNA repair protein MutS, domain I **Family:**DNA repair protein MutS, domain I
80	c3ai3A_	Alignment	not modelled	46.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-sorbose reductase; **PDBTitle:** the crystal structure of l-sorbose reductase from gluconobacter2 frateurii complexed with nadph and l-sorbose
81	d1ulsa_	Alignment	not modelled	46.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
82	d1d7oa_	Alignment	not modelled	46.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
83	c2zatC_	Alignment	not modelled	46.2	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase/reductase sdr family member 4; **PDBTitle:** crystal structure of a mammalian reductase
84	c1cmwA_	Alignment	not modelled	46.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
85	c3lf2B_	Alignment	not modelled	44.5	15	**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
86	d1t57a_	Alignment	not modelled	43.1	20	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
87	d1w6ua_	Alignment	not modelled	42.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	d1y5ma1	Alignment	not modelled	42.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
89	d1zema1	Alignment	not modelled	41.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
90	c3gafF_	Alignment	not modelled	41.5	19	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**7-alpha-hydroxysteroid dehydrogenase; **PDBTitle:** 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
91	c2p68A_	Alignment	not modelled	41.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of aq_1716 from aquifex aeolicus vf5
92	c1yb1B_	Alignment	not modelled	41.2	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**17-beta-hydroxysteroid dehydrogenase type xi; **PDBTitle:** crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi
93	c2jahB_	Alignment	not modelled	40.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**clavulanic acid dehydrogenase; **PDBTitle:** biochemical and structural analysis of the clavulanic acid2 dehydeogenase (cad) from streptomyces clavuligerus
94	c3oidA_	Alignment	not modelled	40.3	13	**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)
95	d1pr9a_	Alignment	not modelled	39.7	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
96	d1qopb_	Alignment	not modelled	39.6	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
97	d1q7ba_	Alignment	not modelled	39.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	d1ooea_	Alignment	not modelled	39.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
99	c3o38D_	Alignment	not modelled	39.3	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from mycobacterium2 smegmatis
100	d1a9xa4	Alignment	not modelled	38.9	21	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
101	d2rhca1	Alignment	not modelled	38.7	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
102	d1edoa_	Alignment	not modelled	38.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						PDB header:oxidoreductase

103	c3r1iB_	Alignment	not modelled	38.3	25	**Chain:** B: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
104	c2wdzD_	Alignment	not modelled	38.3	12	**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
105	c3rkrC_	Alignment	not modelled	37.8	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain oxidoreductase; **PDBTitle:** crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp
106	d1x1ta1	Alignment	not modelled	37.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
107	c3ctmH_	Alignment	not modelled	37.4	17	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
108	c2ztsB_	Alignment	not modelled	37.3	20	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein ph0186; **PDBTitle:** crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
109	c3g8rA_	Alignment	not modelled	37.2	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
110	d1vlia2	Alignment	not modelled	37.0	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
111	d1yxma1	Alignment	not modelled	37.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
112	c3m1aF_	Alignment	not modelled	36.4	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** the crystal structure of a short-chain dehydrogenase from2 streptomyces avermitilis to 2a
113	c3ioyB_	Alignment	not modelled	36.4	14	**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
114	d1onfa2	Alignment	not modelled	36.2	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
115	d1hdca_	Alignment	not modelled	36.1	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
116	d1nffa_	Alignment	not modelled	36.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
117	c2dy0A_	Alignment	not modelled	35.9	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
118	c3kvoB_	Alignment	not modelled	35.7	20	**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)
119	c2ptgA_	Alignment	not modelled	35.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** crystal structure of eimeria tenella enoyl reductase
120	d2a4ka1	Alignment	not modelled	35.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases