Phyre2

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Description	P39407
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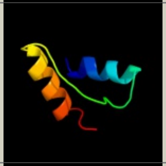
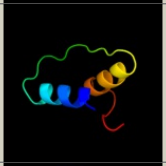
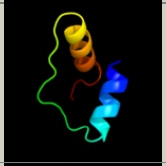
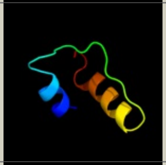
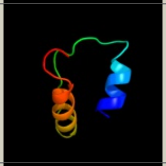
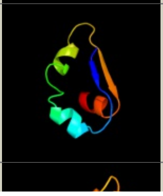
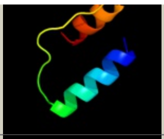
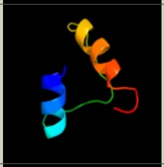
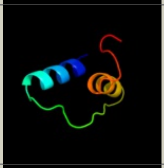
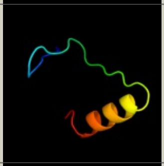
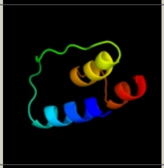
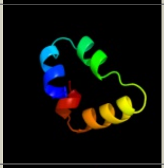
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1oxwa_	Alignment		100.0	17	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Patatin
2	d1cjya2	Alignment		99.0	15	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Lysophospholipase
3	c1cjyB_	Alignment		98.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (cytosolic phospholipase a2); **PDBTitle:** human cytosolic phospholipase a2
4	c3l4eA_	Alignment		83.3	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
5	c3i1iA_	Alignment		79.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
6	d1mlaa1	Alignment		74.7	10	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like
7	d2b61a1	Alignment		72.6	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
8	c3rgiA_	Alignment		72.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**disd protein; **PDBTitle:** trans-acting transferase from disorazole synthase
9	d2pl5a1	Alignment		71.9	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
10	d2vata1	Alignment		71.4	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
11	d1fyea_	Alignment		67.5	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE

12	c3ptwA_	Alignment		67.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from clostridium perfringens atcc 13124
13	c3en0A_	Alignment		64.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
14	c2vavL_	Alignment		63.5	8	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
15	c3im8A_	Alignment		62.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl acyl carrier protein transacylase; **PDBTitle:** crystal structure of mcat from streptococcus pneumoniae
16	c3lp5A_	Alignment		59.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cell surface hydrolase; **PDBTitle:** the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
17	c2jfkD_	Alignment		58.2	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the mat domain of human fas with malonyl-coa
18	c1znnF_	Alignment		56.9	9	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
19	c2zyiB_	Alignment		56.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase, putative; **PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium
20	c2qo3A_	Alignment		54.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**eryaii erythromycin polyketide synthase modules 3 and 4; **PDBTitle:** crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerthronolide b synthase
21	d1znna1	Alignment	not modelled	53.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
22	c3ffsC_	Alignment	not modelled	52.6	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
23	d1vcfa1	Alignment	not modelled	52.5	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
24	c2a7nA_	Alignment	not modelled	51.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l(+)-mandelate dehydrogenase; **PDBTitle:** crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
25	c2cu0B_	Alignment	not modelled	50.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine-5'-monophosphate dehydrogenase from2 pyrococcus horikoshii ot3
26	c3tqeA_	Alignment	not modelled	49.5	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl-coa-[acyl-carrier-protein] transacylase; **PDBTitle:** structure of the malonyl coa-acyl carrier protein transacylase (fabd)2 from coxiella burnetii
27	c3khjE_	Alignment	not modelled	48.7	27	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
						PDB header:oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase

28	c1jcnA_	Alignment	not modelled	47.8	35	i; **PDBTitle:** binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
29	d1jcna1	Alignment	not modelled	47.5	35	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
30	c2e77B_	Alignment	not modelled	47.2	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate oxidase; **PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex
31	d2cu0a1	Alignment	not modelled	47.2	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
32	c1kbiB_	Alignment	not modelled	46.6	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome b2; **PDBTitle:** crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
33	d1eepa_	Alignment	not modelled	46.5	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
34	d1kbia1	Alignment	not modelled	46.3	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
35	d1p4ca_	Alignment	not modelled	46.2	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
36	c3g87A_	Alignment	not modelled	45.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
37	c2drhD_	Alignment	not modelled	45.7	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**361aa long hypothetical d-aminopeptidase; **PDBTitle:** crystal structure of the ph0078 protein from pyrococcus horikoshii ot3
38	d1ufoa_	Alignment	not modelled	45.3	26	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein TT1662
39	c3r2gA_	Alignment	not modelled	44.3	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
40	c1e3hA_	Alignment	not modelled	44.1	12	**PDB header:**polyribonucleotide transferase **Chain:** A: **PDB Molecule:**guanosine pentaphosphate synthetase; **PDBTitle:** semet derivative of streptomyces antibioticus pnpase/gpsi2 enzyme
41	d1p0ka_	Alignment	not modelled	43.5	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
42	d1jr1a1	Alignment	not modelled	42.9	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
43	c2hg4A_	Alignment	not modelled	42.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-deoxyerythronolide b synthase; **PDBTitle:** structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
44	d1uh5a_	Alignment	not modelled	42.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
45	c3opyB_	Alignment	not modelled	41.8	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
46	c3opyH_	Alignment	not modelled	41.8	20	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
47	c1me9A_	Alignment	not modelled	41.6	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
48	d1qo2a_	Alignment	not modelled	41.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
49	d1tb3a1	Alignment	not modelled	41.3	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
50	c2zrvC_	Alignment	not modelled	41.2	22	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase; **PDBTitle:** crystal structure of sulfolobus shibatae isopentenyl2 diphosphate isomerase in complex with reduced fmn.
51	d1pvna1	Alignment	not modelled	41.1	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
52	c1cr6A_	Alignment	not modelled	40.9	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
						PDB header:oxidoreductase

53	c1vrdA_	Alignment	not modelled	40.8	31	**Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
54	d1vrda1	Alignment	not modelled	40.6	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
55	c2rduA_	Alignment	not modelled	40.6	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyacid oxidase 1; **PDBTitle:** crystal structure of human glycolate oxidase in complex with2 glyoxylate
56	d1goxa_	Alignment	not modelled	40.2	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
57	c2a7rD_	Alignment	not modelled	39.9	31	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
58	c1ypfB_	Alignment	not modelled	39.8	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
59	c3cdiA_	Alignment	not modelled	39.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide phosphorylase; **PDBTitle:** crystal structure of e. coli pnpase
60	c2ywjA_	Alignment	not modelled	39.7	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
61	c2qr6A_	Alignment	not modelled	39.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**imp dehydrogenase/gmp reductase; **PDBTitle:** crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
62	c3eenA_	Alignment	not modelled	38.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acp transacylase; **PDBTitle:** crystal structure of malonyl-coa:acyl carrier protein transacylase2 (fabd), xoo0880, from xanthomonas oryzae pv. oryzae kacc10331
63	c2qruA_	Alignment	not modelled	38.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
64	c3n5iC_	Alignment	not modelled	37.6	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-peptidyl aminopeptidase; **PDBTitle:** crystal structure of the precursor (s250a mutant) of the n-terminal2 beta-aminopeptidase bapa
65	c1zfjA_	Alignment	not modelled	37.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase; **PDBTitle:** inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
66	d1zfja1	Alignment	not modelled	37.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
67	d2cdqa2	Alignment	not modelled	36.2	27	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
68	d1r88a_	Alignment	not modelled	34.9	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
69	c2cuyA_	Alignment	not modelled	34.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-[acyl carrier protein] transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from thermus thermophilus hb8
70	c3ezoA_	Alignment	not modelled	33.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein s-2 malonyltransferase from burkholderia pseudomallei 1710b
71	c3fijD_	Alignment	not modelled	33.0	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
72	d1b65a_	Alignment	not modelled	32.7	8	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**DmpA-like
73	d2j0wa2	Alignment	not modelled	32.4	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
74	d1s1ma1	Alignment	not modelled	32.3	27	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
75	c2w7tA_	Alignment	not modelled	32.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative cytidine triphosphate synthase; **PDBTitle:** trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
76	d1dqza_	Alignment	not modelled	31.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
77	d2dsta1	Alignment	not modelled	31.8	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**TTHA1544-like
						Fold:TIM beta/alpha-barrel

78	d1vqta1	Alignment	not modelled	31.8	26	**Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
79	d1k8qa_	Alignment	not modelled	31.7	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
80	c2h1yA_	Alignment	not modelled	30.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coenzyme a-acyl carrier protein transacylase; **PDBTitle:** crystal structure of malonyl-coa:acyl carrier protein transacylase2 (mcat) from helicobacter pylori
81	d1vzwa1	Alignment	not modelled	29.5	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
82	c2ptgA_	Alignment	not modelled	29.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** crystal structure of eimeria tenella enoyl reductase
83	c2d4wA_	Alignment	not modelled	29.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
84	c2qmqA_	Alignment	not modelled	29.1	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein ndrg2; **PDBTitle:** crystal structure of a n-myc downstream regulated 2 protein (ndrg2,2 syld, ndr2, ai182517, au040374) from mus musculus at 1.70 a3 resolution
85	d1juba_	Alignment	not modelled	29.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
86	d1hlga_	Alignment	not modelled	28.8	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
87	d1xm3a_	Alignment	not modelled	28.8	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
88	c3gg4B_	Alignment	not modelled	28.6	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
89	c2dpnB_	Alignment	not modelled	28.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
90	c3flaB_	Alignment	not modelled	28.2	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rifr; **PDBTitle:** rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
91	d1rd5a_	Alignment	not modelled	28.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
92	c3l80A_	Alignment	not modelled	27.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
93	c2cdh1_	Alignment	not modelled	27.5	31	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
94	d2hmfa2	Alignment	not modelled	27.3	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
95	c2o2sA_	Alignment	not modelled	27.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan
96	d1sfra_	Alignment	not modelled	26.7	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
97	d2h7ma1	Alignment	not modelled	26.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	c3fcxA_	Alignment	not modelled	26.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**s-formylglutathione hydrolase; **PDBTitle:** crystal structure of human esterase d
99	d1thfd_	Alignment	not modelled	26.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
100	c3k31B_	Alignment	not modelled	25.8	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of eonyl-(acyl-carrier-protein) reductase from2 anaplasma phagocytophilum in complex with nad at 1.9a resolution
101	c3g25B_	Alignment	not modelled	25.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
102	c2nq8B_	Alignment	not modelled	25.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** malarial enoyl acyl acp reductase bound with inh-nad adduct
103	d1d7oa_	Alignment	not modelled	25.6	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						PDB header:hydrolase

104	c1pjaA_	Alignment	not modelled	25.5	11	**Chain:** A: **PDB Molecule:**palmitoyl-protein thioesterase 2 precursor; **PDBTitle:** the crystal structure of palmitoyl protein thioesterase-2 reveals the2 basis for divergent substrate specificities of the two lysosomal3 thioesterases (ppt1 and ppt2)
105	d1pjaa_	Alignment	not modelled	25.5	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
106	c3fleB_	Alignment	not modelled	25.2	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**se_1780 protein; **PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis.
107	d1nm2a1	Alignment	not modelled	25.2	19	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like
108	d3c8da2	Alignment	not modelled	25.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase
109	c2htmB_	Alignment	not modelled	25.0	20	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiazole biosynthesis protein thig; **PDBTitle:** crystal structure of ttha0676 from thermus thermophilus hb8
110	c2w40C_	Alignment	not modelled	24.7	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
111	c1qgeD_	Alignment	not modelled	24.1	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
112	c3ds8A_	Alignment	not modelled	23.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
113	d1h5ya_	Alignment	not modelled	23.7	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
114	c3e4dD_	Alignment	not modelled	23.6	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**esterase d; **PDBTitle:** structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
115	d1y0ea_	Alignment	not modelled	23.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
116	c3qjaA_	Alignment	not modelled	23.5	35	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
117	c2foiB_	Alignment	not modelled	23.4	19	**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.
118	c3dcjA_	Alignment	not modelled	23.4	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
119	d1lh0a_	Alignment	not modelled	23.1	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
120	c3jr2D_	Alignment	not modelled	22.8	18	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**hexulose-6-phosphate synthase sgbh; **PDBTitle:** x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961