Phyre^2

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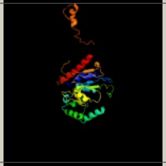
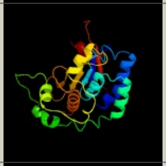
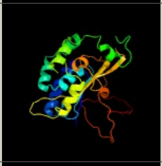
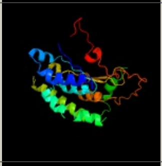
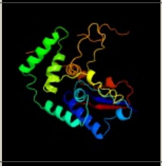
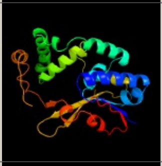
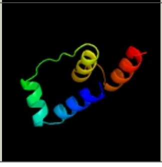
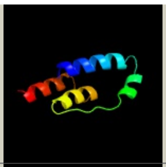
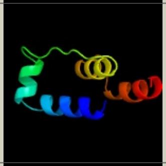
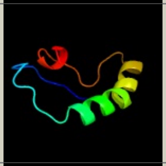
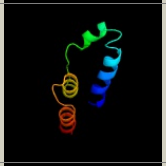
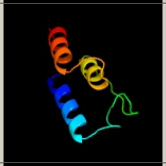
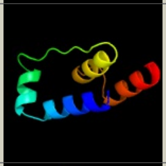
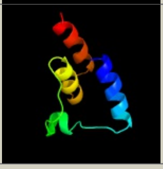
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5fyaA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**patatin-like protein, plpd; **PDBTitle:** cubic crystal of the native plpd
2	c4akfA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vipd; **PDBTitle:** crystal structure of vipd from legionella pneumophila
3	c4qmkB_	Alignment		100.0	19	**PDB header:**toxin **Chain:** B: **PDB Molecule:**type iii secretion system effector protein exou; **PDBTitle:** crystal structure of type iii effector protein exou (exou)
4	c3tu3B_	Alignment		100.0	22	**PDB header:**toxin/toxin chaperone **Chain:** B: **PDB Molecule:**exou; **PDBTitle:** 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
5	c4akxB_	Alignment		100.0	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**exou; **PDBTitle:** structure of the heterodimeric complex exou-spcu from the type iii2 secretion system (t3ss) of pseudomonas aeruginosa
6	d1oxwa_	Alignment		100.0	22	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Patatin
7	c6aunB_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pla2g6, ipla2beta; **PDBTitle:** calcium-independent phospholipase a2 beta
8	d1cjya2	Alignment		99.4	13	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Lysophospholipase
9	c5izrC_	Alignment		99.2	12	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**cytosolic phospholipase a2 delta; **PDBTitle:** human givd cytosolic phospholipase a2 in complex with methyl gamma-2 linolenyl fluorophosphonate inhibitor and terbium chloride
10	c1cjyB_	Alignment		98.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (cytosolic phospholipase a2); **PDBTitle:** human cytosolic phospholipase a2
11	d1mlaa1	Alignment		86.3	12	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like

12	c2jfkD_	Alignment		82.8	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the mat domain of human fas with malonyl-coa
13	c5ydmA_	Alignment		82.5	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pks; **PDBTitle:** the crystal structure of the acyl transferase domain of spnd complex2 with benzylmalonyl
14	c6a4tB_	Alignment		82.2	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase e; **PDBTitle:** crystal structure of peptidase e from deinococcus radiodurans r1
15	c6iytA_	Alignment		81.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type i modular polyketide synthase; **PDBTitle:** crystal structure of the acyltransferase domain from second module 142 of salinomycin polyketide synthase
16	c4ammA_	Alignment		81.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dyne8; **PDBTitle:** crystal structure of the acyltransferase domain of the2 iterative polyketide synthase in enediyne biosynthesis3 reveals the molecular basis of substrate specificity
17	c4rr5A_	Alignment		79.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** the crystal structure of synechocystis sp. pcc 6803 malonyl-coa: acp2 transacylase
18	c3im8A_	Alignment		78.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl acyl carrier protein transacylase; **PDBTitle:** crystal structure of mcat from streptococcus pneumoniae
19	c3l4eA_	Alignment		76.8	24	**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
20	c3ptwA_	Alignment		74.7	15	**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
21	c5dz7A_	Alignment	not modelled	74.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyketide biosynthesis protein pkse; **PDBTitle:** structural basis of acyl transfer in a trans-at polyketide synthase
22	c4qbuA_	Alignment	not modelled	74.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**zmaa; **PDBTitle:** structure of the acyl transferase domain of zmaa
23	c3tzzA_	Alignment	not modelled	73.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyketide synthase pks13; **PDBTitle:** crystal structure of a fragment containing the acyltransferase domain2 of pks13 from mycobacterium tuberculosis in the carboxypalmitoylated3 form at 2.5 a
24	c2bklB_	Alignment	not modelled	72.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
25	c3rgiA_	Alignment	not modelled	72.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**disd protein; **PDBTitle:** trans-acting transferase from disorazole synthase
26	c6iyrA_	Alignment	not modelled	72.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type i modular polyketide synthase; **PDBTitle:** crystal structure of the acyltransferase domain from module 8 of the2 salinomycin polyketide synthase
27	c5uzwD_	Alignment	not modelled	72.2	25	**PDB header:**lyase **Chain:** D: **PDB Molecule:**peptide cyclase 1; **PDBTitle:** pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
28	c3tqeA_	Alignment	not modelled	72.0	13	**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
29	c4rl1A_	Alignment	not modelled	71.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type i polyketide synthase aves 1; **PDBTitle:** structural and functional analysis of a loading acyltransferase from2 the avermectin modular polyketide synthase
30	c5bp1A_	Alignment	not modelled	70.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mycocerosic acid synthase; **PDBTitle:** condensing di-domain (ks-at) of a mycocerosic acid synthase-like (mas-2 like) pks
31	c5dz6A_	Alignment	not modelled	69.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyketide biosynthesis malonyl coa-acyl carrier protein **PDBTitle:** acyl transferase from bacillaene pks
32	c2qo3A_	Alignment	not modelled	65.7	16	**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
33	c4mz0B_	Alignment	not modelled	64.3	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**curl; **PDBTitle:** structure of a ketosynthase-acyltransferase di-domain from module curl2 of the curacin a polyketide synthase
34	c3eenA_	Alignment	not modelled	64.1	17	**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
35	c4uzqA_	Alignment	not modelled	63.1	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein notum homolog; **PDBTitle:** structure of the wnt deacylase notum in complex with2 o-palmitoleoyl serine - crystal form ix - 1.5a
36	c2cuyA_	Alignment	not modelled	60.1	13	**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
37	d1hdoa_	Alignment	not modelled	59.6	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
38	c2g2oA_	Alignment	not modelled	59.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** structure of e.coli fabd complexed with sulfate
39	d1fyea_	Alignment	not modelled	58.3	32	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
40	c1yr2A_	Alignment	not modelled	58.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
41	c5czcA_	Alignment	not modelled	58.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl-coa-[acyl-carrier-protein] transacylase; **PDBTitle:** the structure of vink
42	c3g87A_	Alignment	not modelled	57.9	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
43	c3en0A_	Alignment	not modelled	56.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
44	c3iumA_	Alignment	not modelled	55.2	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** appep_wtx opened state
45	c6dntA_	Alignment	not modelled	54.7	19	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** udp-n-acetylglucosamine 4-epimerase from methanobrevibacter2 ruminantium m1 in complex with udp-n-acetylmuramic acid
46	c3lu1C_	Alignment	not modelled	53.8	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**wbgu; **PDBTitle:** crystal structure analysis of wbgu: a udp-galnac 4-epimerase
47	c6c9uA_	Alignment	not modelled	53.7	16	**PDB header:**transferase/immune system **Chain:** A: **PDB Molecule:**6-deoxyerythronolide-b synthase erya2, modules 3 and 4; **PDBTitle:** crystal structure of [ks3][at3] didomain from module 3 of 6-2 deoxyerythronolide b synthase in complex with antibody fragment (fab)
48	c3hhdC_	Alignment	not modelled	52.5	13	**PDB header:**transferase, hydrolase **Chain:** C: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the human fatty acid synthase ks-mat didomain as a2 framework for inhibitor design.
49	c6iyoA_	Alignment	not modelled	51.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type i modular polyketide synthase; **PDBTitle:** crystal structure of the acyltransferase domain from the second module2 of the salinomycin polyketide synthase
50	c4hvtA_	Alignment	not modelled	51.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**post-proline cleaving enzyme; **PDBTitle:** structure of a post-proline cleaving enzyme from rickettsia typhi
51	d2bkaa1	Alignment	not modelled	50.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
						PDB header:transferase

52	c3i1iA_	Alignment	not modelled	50.1	35	**Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
53	c3qatB_	Alignment	not modelled	48.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein-s-malonyltransferase from2 bartonella henselae
54	d2fmua1	Alignment	not modelled	48.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
55	c2hg4A_	Alignment	not modelled	47.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-deoxyerythronolide b synthase; **PDBTitle:** structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
56	c3s3uB_	Alignment	not modelled	46.3	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cysteine transferase; **PDBTitle:** crystal structure of uncleaved thnt t282c
57	c3sc6F_	Alignment	not modelled	45.6	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase; **PDBTitle:** 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
58	c4r1sB_	Alignment	not modelled	43.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cinnamoyl coa reductase; **PDBTitle:** crystal structure of petunia hydrida cinnamoyl-coa reductase
59	c4fleA_	Alignment	not modelled	43.5	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of the esterase yqia (ye3661) from yersinia2 enterocolitica, northeast structural genomics consortium target yer85
60	c2drhD_	Alignment	not modelled	42.6	23	**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
61	c5n4dA_	Alignment	not modelled	42.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
62	d1ek6a_	Alignment	not modelled	41.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
63	d1nm2a1	Alignment	not modelled	41.2	11	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**FabD-like
64	c3n5iC_	Alignment	not modelled	40.0	18	**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	c4qloA_	Alignment	not modelled	39.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
66	c3enkB_	Alignment	not modelled	39.2	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from burkholderia2 pseudomallei
67	d1b65a_	Alignment	not modelled	38.3	20	**Fold:**DmpA/ArgJ-like **Superfamily:**DmpA/ArgJ-like **Family:**DmpA-like
68	c2q1uA_	Alignment	not modelled	37.9	12	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative nucleotide sugar epimerase/dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
69	c2h1yA_	Alignment	not modelled	35.9	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
70	c4uzjB_	Alignment	not modelled	35.3	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**notum; **PDBTitle:** structure of the wnt deacylase notum from drosophila -2 crystal form i - 2.4a
71	c3sxpD_	Alignment	not modelled	35.2	15	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**adp-l-glycero-d-mannoheptose-6-epimerase; **PDBTitle:** crystal structure of helicobacter pylori adp-l-glycero-d-manno-2 heptose-6-epimerase (rfad, hp0859)
72	c5jkjA_	Alignment	not modelled	35.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase e22; **PDBTitle:** crystal structure of esterase e22 l374d mutant
73	c6d2vA_	Alignment	not modelled	33.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**terb oxidoreductase; **PDBTitle:** apo structure of terb, an nadp dependent oxidoreductase in the2 terfestatin biosynthesis pathway
74	c2cdh9_	Alignment	not modelled	33.4	12	**PDB header:**transferase **Chain:** 9: **PDB Molecule:**acetyl transferase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
75	c5ypvA_	Alignment	not modelled	32.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of fabd from acinetobacter baumannii
76	c5w8pA_	Alignment	not modelled	30.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** homoserine transacetylase meta from mycobacterium

						abscessus
77	c5uzhA_	Alignment	not modelled	30.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nafoa.00085.b; **PDBTitle:** crystal structure of a gdp-mannose dehydratase from naegleria fowleri
78	c2qj3B_	Alignment	not modelled	30.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** mycobacterium tuberculosis fabd
79	c3ezoA_	Alignment	not modelled	29.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein transacylase; **PDBTitle:** crystal structure of acyl-carrier-protein s-malonyltransferase from2 burkholderia pseudomallei 1710b
80	c1qfmA_	Alignment	not modelled	29.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (prolyl oligopeptidase); **PDBTitle:** prolyl oligopeptidase from porcine muscle
81	c4nbqB_	Alignment	not modelled	29.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyribonucleotide nucleotidyltransferase; **PDBTitle:** structure of the polynucleotide phosphorylase (cbu_0852) from coxiella2 burnetii
82	d1db3a_	Alignment	not modelled	28.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
83	c5n2pA_	Alignment	not modelled	27.7	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** sulfolobus solfataricus tryptophan synthase a
84	c3tdnB_	Alignment	not modelled	27.1	20	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**flr symmetric alpha-beta tim barrel; **PDBTitle:** computationally designed two-fold symmetric tim-barrel protein, flr
85	c4j0dB_	Alignment	not modelled	26.6	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tannase; **PDBTitle:** tannin acyl hydrolase from lactobacillus plantarum (cadmium)
86	c3vthA_	Alignment	not modelled	26.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydrogenase maturation factor; **PDBTitle:** crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
87	d2vata1	Alignment	not modelled	26.4	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
88	c5d6oB_	Alignment	not modelled	26.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** orthorhombic crystal structure of an acetylester hydrolase from2 corynebacterium glutamicum
89	c5t88B_	Alignment	not modelled	25.9	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**prolyl endopeptidase; **PDBTitle:** prolyl oligopeptidase from pyrococcus furiosus
90	c5bjuA_	Alignment	not modelled	25.8	21	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**wlal protein; **PDBTitle:** x-ray structure of the pglf dehydratase from campylobacter jejuni in2 complex with udp and nad(h)
91	c2dlnA_	Alignment	not modelled	25.7	26	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine ligase at 2.32 angstroms resolution
92	d1dqza_	Alignment	not modelled	25.6	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
93	d1z45a2	Alignment	not modelled	25.6	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
94	c2o2sA_	Alignment	not modelled	25.5	17	**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
95	c4wpgA_	Alignment	not modelled	25.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase; **PDBTitle:** group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmld)
96	c4x2rA_	Alignment	not modelled	25.1	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) **PDBTitle:** crystal structure of pria from actinomyces urogenitalis
97	d2b61a1	Alignment	not modelled	24.8	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
98	d1uh5a_	Alignment	not modelled	24.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
99	c2hunB_	Alignment	not modelled	24.3	26	**PDB header:**lyase **Chain:** B: **PDB Molecule:**336aa long hypothetical dtdp-glucose 4,6-dehydratase; **PDBTitle:** crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
100	c1pjaA_	Alignment	not modelled	22.7	25	**PDB header:**hydrolase **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)
101	d1pjaa_	Alignment	not modelled	22.7	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
102	c4alnE	Alignment	not modelled	22.7	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase

102	c4alnE_	Alignment	not modelled	22.7	19	[nadph]; **PDBTitle:** crystal structure of s. aureus fabi (p32)
103	c1cr6A_	Alignment	not modelled	22.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
104	c2ptgA_	Alignment	not modelled	22.5	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** crystal structure of eimeria tenella enoyl reductase
105	d1r88a_	Alignment	not modelled	22.5	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Mycobacterial antigens
106	c6dvhF_	Alignment	not modelled	22.4	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**lactate 2-monooxygenase; **PDBTitle:** lactate monooxygenase from mycobacterium smegmatis - c203a mutant
107	c1fcbA_	Alignment	not modelled	22.4	26	**PDB header:**oxidoreductase (ch-oh(d)-cytochrome(a)) **Chain:** A: **PDB Molecule:**flavocytochrome b2; **PDBTitle:** molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
108	c2vz8A_	Alignment	not modelled	22.0	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fatty acid synthase; **PDBTitle:** crystal structure of mammalian fatty acid synthase
109	c4lw8B_	Alignment	not modelled	21.4	30	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative epimerase; **PDBTitle:** crystal structure of a putative epimerase from burkholderia2 cenocepacia j2315
110	c1e3hA_	Alignment	not modelled	21.0	18	**PDB header:**polyribonucleotide transferase **Chain:** A: **PDB Molecule:**guanosine pentaphosphate synthetase; **PDBTitle:** semet derivative of streptomyces antibioticus pnpase/gpsi enzyme
111	c5lnkd_	Alignment	not modelled	20.9	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:** **PDBTitle:** entire ovine respiratory complex i
112	c3vvlA_	Alignment	not modelled	20.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway