Phyre2

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Description	P75820
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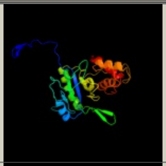
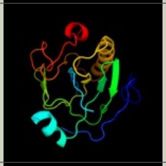
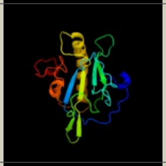
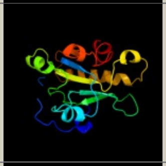
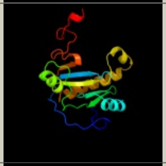
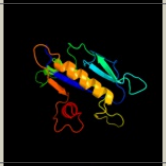
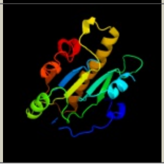
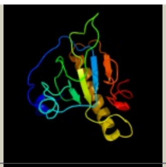
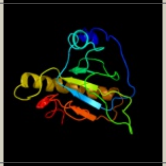
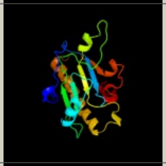
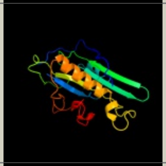
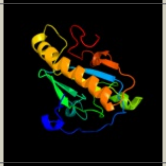
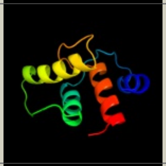
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bh7A_	Alignment		100.0	99	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
2	d2bgxa2	Alignment		100.0	100	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
3	d1j3ga_	Alignment		100.0	35	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
4	c3hmaA_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase xlya; **PDBTitle:** amidase from bacillus subtilis
5	d1yb0a1	Alignment		100.0	22	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
6	d1ycka1	Alignment		100.0	24	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
7	d2cb3a1	Alignment		100.0	15	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
8	d1sk4a_	Alignment		100.0	18	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
9	c2xz4A_	Alignment		99.9	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**peptidoglycan-recognition protein lf; **PDBTitle:** crystal structure of the lfz ectodomain of the2 peptidoglycan recognition protein lf
10	d1lbaa_	Alignment		99.9	27	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
11	c2rkqA_	Alignment		99.9	19	**PDB header:**immune system **Chain:** A: **PDB Molecule:**peptidoglycan-recognition protein-sd; **PDBTitle:** crystal structure of drosophila peptidoglycan recognition2 protein sd (pgrp-sd)

12	c1ohtA_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg14704 protein; **PDBTitle:** peptidoglycan recognition protein-lb
13	d1ohta_	Alignment		99.9	14	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
14	d2f2lx1	Alignment		99.9	20	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
15	d1sxra_	Alignment		99.9	16	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
16	c3latB_	Alignment		99.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bifunctional autolysin; **PDBTitle:** crystal structure of staphylococcus peptidoglycan hydrolase2 amie
17	c1s2jA_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan recognition protein sa cg11709-pa; **PDBTitle:** crystal structure of the drosophila pattern-recognition2 receptor pgrp-sa
18	d2f2la1	Alignment		99.9	12	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
19	d2bgxa1	Alignment		99.9	100	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
20	c3ep1B_	Alignment		99.9	19	**PDB header:**immune system **Chain:** B: **PDB Molecule:**pgrp-hd - peptidoglycan recognition protein **PDBTitle:** structure of the pgrp-hd from alvinella pompejana
21	c2xz8A_	Alignment	not modelled	99.2	13	**PDB header:**immune system **Chain:** A: **PDB Molecule:**peptidoglycan-recognition protein lf; **PDBTitle:** crystal structure of the lfw ectodomain of the2 peptidoglycan recognition protein lf
22	c3bkhA_	Alignment	not modelled	99.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
23	d1lbua1	Alignment	not modelled	98.9	14	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
24	c1lbuA_	Alignment	not modelled	98.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**muramoyl-pentapeptide carboxypeptidase; **PDBTitle:** hydrolase metallo (zn) dd-peptidase
25	d1eaka1	Alignment	not modelled	97.3	17	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
26	d1su3a1	Alignment	not modelled	96.5	21	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
27	d1slma1	Alignment	not modelled	96.4	22	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
28	d1l6ja1	Alignment	not modelled	96.3	24	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
						PDB header:hydrolase/hydrolase inhibitor

29	c1eakA_	Alignment	not modelled	96.3	17	**Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
30	c1l6jA_	Alignment	not modelled	95.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
31	c1gxdA_	Alignment	not modelled	92.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** prommp-2/timp-2 complex
32	c3ds8A_	Alignment	not modelled	64.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
33	c3d0kA_	Alignment	not modelled	55.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative poly(3-hydroxybutyrate) depolymerase lpqc; **PDBTitle:** crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
34	d2ikba1	Alignment	not modelled	55.4	14	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
35	c1cr6A_	Alignment	not modelled	40.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
36	d2nr7a1	Alignment	not modelled	39.4	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
37	c2zycA_	Alignment	not modelled	37.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj; **PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
38	c3so4C_	Alignment	not modelled	37.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**methionine-adenosyltransferase; **PDBTitle:** methionine-adenosyltransferase from entamoeba histolytica
39	c3fi7A_	Alignment	not modelled	35.5	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lmo1076 protein; **PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
40	c3imlB_	Alignment	not modelled	34.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from burkholderia2 pseudomallei
41	d2dsta1	Alignment	not modelled	34.9	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**TTHA1544-like
42	c3fleB_	Alignment	not modelled	34.6	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**se_1780 protein; **PDBTitle:** se_1780 protein of unknown function from staphylococcus epidermidis.
43	c2y96A_	Alignment	not modelled	34.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase dupd1; **PDBTitle:** structure of human dual-specificity phosphatase 27
44	d1mxaa3	Alignment	not modelled	32.4	29	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
45	c3mlcC_	Alignment	not modelled	31.5	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**fg41 malonate semialdehyde decarboxylase; **PDBTitle:** crystal structure of fg41msad inactivated by 3-chloropropiolate
46	d1hpla2	Alignment	not modelled	30.5	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
47	d3b5ea1	Alignment	not modelled	30.2	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/thioesterase 1
48	c3lyfB_	Alignment	not modelled	30.0	24	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**nucleocapsid protein; **PDBTitle:** crystal structure of the rift valley fever virus nucleocapsid protein
49	c3lp5A_	Alignment	not modelled	29.4	21	**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
50	c2vavL_	Alignment	not modelled	27.8	18	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
51	d1k8qa_	Alignment	not modelled	26.8	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
52	c2pplA_	Alignment	not modelled	24.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pancreatic lipase-related protein 1; **PDBTitle:** human pancreatic lipase-related protein 1
53	c1gplA_	Alignment	not modelled	23.9	20	**PDB header:**serine esterase **Chain:** A: **PDB Molecule:**rp2 lipase; **PDBTitle:** rp2 lipase
54	d1etha2	Alignment	not modelled	23.6	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
55	d2h1ia1	Alignment	not modelled	23.4	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases

						Family: Carboxylesterase/thioesterase 1
56	d1rp1a2	Alignment	not modelled	23.4	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
57	d1lpbb2	Alignment	not modelled	23.4	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
58	d1bu8a2	Alignment	not modelled	23.0	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
59	c2pvsB_	Alignment	not modelled	22.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pancreatic lipase-related protein 2; **PDBTitle:** structure of human pancreatic lipase related protein 22 mutant n336q
60	c1hplB_	Alignment	not modelled	21.1	16	**PDB header:**hydrolase(carboxylic esterase) **Chain:** B: **PDB Molecule:**lipase; **PDBTitle:** horse pancreatic lipase. the crystal structure at 2.32 angstroms resolution
61	c1rp1A_	Alignment	not modelled	20.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pancreatic lipase related protein 1; **PDBTitle:** dog pancreatic lipase related protein 1
62	c3abqA_	Alignment	not modelled	20.6	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ethanolamine ammonia-lyase heavy chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with cn-cbl and 2-amino-1-propanol
63	c3rv2B_	Alignment	not modelled	19.8	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum
64	c2zyiB_	Alignment	not modelled	19.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase, putative; **PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium
65	d1cvla_	Alignment	not modelled	19.6	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
66	d1gpla2	Alignment	not modelled	18.9	20	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
67	c3rgiA_	Alignment	not modelled	18.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**disd protein; **PDBTitle:** trans-acting transferase from disorazole synthase
68	c2qtsA_	Alignment	not modelled	18.5	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**acid-sensing ion channel; **PDBTitle:** structure of an acid-sensing ion channel 1 at 1.9 a resolution and low2 ph
69	d2aala1	Alignment	not modelled	18.3	13	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MSAD-like
70	c3im8A_	Alignment	not modelled	17.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyl acyl carrier protein transacylase; **PDBTitle:** crystal structure of mcat from streptococcus pneumoniae
71	d1ex9a_	Alignment	not modelled	17.2	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
72	c2q0xA_	Alignment	not modelled	15.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** alpha/beta hydrolase fold protein of unknown function
73	c3ezoA_	Alignment	not modelled	15.6	17	**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
74	c3og9A_	Alignment	not modelled	15.3	3	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein yahd a copper inducible hydrolase; **PDBTitle:** structure of yahd with malic acid
75	c1rg9D_	Alignment	not modelled	15.2	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**s-adenosylmethionine synthetase; **PDBTitle:** s-adenosylmethionine synthetase complexed with sam and ppnp
76	c2qezC_	Alignment	not modelled	15.2	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ethanolamine ammonia-lyase heavy chain; **PDBTitle:** crystal structure of ethanolamine ammonia-lyase heavy chain2 (yp_013784.1) from listeria monocytogenes 4b f2365 at 2.15 a3 resolution
77	c1xhoB_	Alignment	not modelled	15.2	7	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**chorismate mutase; **PDBTitle:** chorismate mutase from clostridium thermocellum cth-682
78	d1xhoa_	Alignment	not modelled	15.2	7	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
79	c2h1iA_	Alignment	not modelled	14.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylesterase; **PDBTitle:** crystal structure of the bacillus cereus carboxylesterase
80	d1ispa_	Alignment	not modelled	14.9	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
						PDB header:transferase **Chain:** A: **PDB Molecule:**malonyl coa-acyl carrier protein

81	c3g87A_	Alignment	not modelled	14.8	10	transacylase; **PDBTitle:** crystal structure of malonyl coa-acyl carrier protein transacylase2 from burkholderia pseudomallei using dried seaweed as nucleant or3 protease
82	c3i1iA_	Alignment	not modelled	14.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
83	d1vhra_	Alignment	not modelled	14.7	16	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
84	c2gwoC_	Alignment	not modelled	14.6	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dual specificity protein phosphatase 13; **PDBTitle:** crystal structure of tmdp
85	c1qgeD_	Alignment	not modelled	14.4	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
86	c3m6yA_	Alignment	not modelled	14.2	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
87	d1fnja_	Alignment	not modelled	13.9	37	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
88	c2qmqA_	Alignment	not modelled	13.9	8	**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
89	c3muxB_	Alignment	not modelled	13.9	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative 4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
90	d2gsta2	Alignment	not modelled	13.4	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
91	c3ptwA_	Alignment	not modelled	13.3	10	**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
92	c3ex7I_	Alignment	not modelled	13.1	22	**PDB header:**hydrolase/rna binding protein/rna **Chain:** I: **PDB Molecule:**protein casc3; **PDBTitle:** the crystal structure of ejc in its transition state
93	c3l80A_	Alignment	not modelled	12.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
94	c3doiA_	Alignment	not modelled	12.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a thermostable esterase complex with2 paraoxon
95	c2jfkD_	Alignment	not modelled	12.3	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**fatty acid synthase; **PDBTitle:** structure of the mat domain of human fas with malonyl-coa
96	d4lipd_	Alignment	not modelled	12.2	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
97	c3eenA_	Alignment	not modelled	12.2	21	**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
98	d1dbfa_	Alignment	not modelled	11.9	37	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
99	d1xw6a2	Alignment	not modelled	11.8	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain