



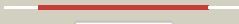

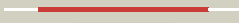


























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1j3ga_</a>	 Alignment		100.0	87	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
2	<a href="#">c2bh7A_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmuramoyl-L-alanine amidase; <b>PDBTitle:</b> crystal structure of a semet derivative of amid at 2.22 angstroms
3	<a href="#">d2bgxa2</a>	 Alignment		100.0	33	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
4	<a href="#">c3hmaA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmuramoyl-L-alanine amidase xlyA; <b>PDBTitle:</b> amidase from bacillus subtilis
5	<a href="#">d1yb0a1</a>	 Alignment		100.0	21	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
6	<a href="#">d1ycka1</a>	 Alignment		100.0	16	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
7	<a href="#">d2cb3a1</a>	 Alignment		100.0	14	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
8	<a href="#">c2xz4A_</a>	 Alignment		100.0	16	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan-recognition protein If; <b>PDBTitle:</b> crystal structure of the Ifz ectodomain of the2 peptidoglycan recognition protein If
9	<a href="#">c2rkqA_</a>	 Alignment		100.0	15	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan-recognition protein-sd; <b>PDBTitle:</b> crystal structure of drosophila peptidoglycan recognition2 protein sd (pgpr-sd)
10	<a href="#">d1ohta_</a>	 Alignment		100.0	17	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
11	<a href="#">c1ohtA_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg14704 protein; <b>PDBTitle:</b> peptidoglycan recognition protein-lb

12	<a href="#">d2f2lx1</a>	Alignment		100.0	14	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
13	<a href="#">d1sk4a_</a>	Alignment		100.0	14	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
14	<a href="#">d1lbaa_</a>	Alignment		100.0	28	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
15	<a href="#">c3latB_</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional autolysin; <b>PDBTitle:</b> crystal structure of staphylococcus peptidoglycan hydrolase2 amie
16	<a href="#">c1s2jA_</a>	Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan recognition protein sa cg11709-pa; <b>PDBTitle:</b> crystal structure of the drosophila pattern-recognition2 receptor pgrp-sa
17	<a href="#">d1sxra_</a>	Alignment		100.0	14	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
18	<a href="#">d2f2la1</a>	Alignment		100.0	11	<b>Fold:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Superfamily:</b> N-acetylmuramoyl-L-alanine amidase-like <b>Family:</b> N-acetylmuramoyl-L-alanine amidase-like
19	<a href="#">c3ep1B_</a>	Alignment		100.0	11	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> pgrp-hd - peptidoglycan recognition protein <b>PDBTitle:</b> structure of the pgrp-hd from alvinella pompejana
20	<a href="#">c2xz8A_</a>	Alignment		99.7	7	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan-recognition protein If; <b>PDBTitle:</b> crystal structure of the Ifw ectodomain of the2 peptidoglycan recognition protein If
21	<a href="#">d2dsta1</a>	Alignment	not modelled	50.7	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> TTHA1544-like
22	<a href="#">c3ds8A_</a>	Alignment	not modelled	40.9	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2722 protein; <b>PDBTitle:</b> the crysatl structure of the gene lin2722 products from listeria2 innocua
23	<a href="#">c3pohA_</a>	Alignment	not modelled	36.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-beta-n-acetylglucosaminidase f1; <b>PDBTitle:</b> crystal structure of an endo-beta-n-acetylglucosaminidase (bt_3987)2 from bacteroides thetaiotaomicron vpi-5482 at 1.55 a resolution
24	<a href="#">c1cr6A_</a>	Alignment	not modelled	28.1	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase; <b>PDBTitle:</b> crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
25	<a href="#">c3d8mA_</a>	Alignment	not modelled	23.7	36	<b>PDB header:</b> virus/viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> baseplate protein, receptor binding protein; <b>PDBTitle:</b> crystal structure of a chimeric receptor binding protein from2 lactococcal phages subspecies tp901-1 and p2
26	<a href="#">d1hpla2</a>	Alignment	not modelled	23.1	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
27	<a href="#">d1zrua1</a>	Alignment	not modelled	22.1	36	<b>Fold:</b> Virus attachment protein globular domain <b>Superfamily:</b> Virus attachment protein globular domain <b>Family:</b> Lactophage receptor-binding protein head domain
28	<a href="#">c3da0C_</a>	Alignment	not modelled	21.9	36	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> cleaved chimeric receptor binding protein from

28	<a href="#">c3uavC</a>	Alignment	not modelled	21.9	30	<b>PDBTitle:</b> crystal structure of a cleaved form of a chimeric receptor binding2 protein from lactococcal phages subspecies tp901-1 and p2
29	<a href="#">c2y96A</a>	Alignment	not modelled	21.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity phosphatase dupd1; <b>PDBTitle:</b> structure of human dual-specificity phosphatase 27
30	<a href="#">c2pplA</a>	Alignment	not modelled	19.4	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pancreatic lipase-related protein 1; <b>PDBTitle:</b> human pancreatic lipase-related protein 1
31	<a href="#">c1hplB</a>	Alignment	not modelled	18.6	16	<b>PDB header:</b> hydrolase(carboxylic esterase) <b>Chain:</b> B: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> horse pancreatic lipase. the crystal structure at 2.32 angstroms resolution
32	<a href="#">d1etha2</a>	Alignment	not modelled	18.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
33	<a href="#">c2pvsB</a>	Alignment	not modelled	17.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> pancreatic lipase-related protein 2; <b>PDBTitle:</b> structure of human pancreatic lipase related protein 22 mutant n336q
34	<a href="#">d1bu8a2</a>	Alignment	not modelled	16.3	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
35	<a href="#">d1rp1a2</a>	Alignment	not modelled	16.1	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
36	<a href="#">c1rp1A</a>	Alignment	not modelled	16.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pancreatic lipase related protein 1; <b>PDBTitle:</b> dog pancreatic lipase related protein 1
37	<a href="#">c1gplA</a>	Alignment	not modelled	15.6	16	<b>PDB header:</b> serine esterase <b>Chain:</b> A: <b>PDB Molecule:</b> rp2 lipase; <b>PDBTitle:</b> rp2 lipase
38	<a href="#">d1lpbb2</a>	Alignment	not modelled	15.3	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
39	<a href="#">d1xw8a</a>	Alignment	not modelled	13.3	15	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
40	<a href="#">c3mlcC</a>	Alignment	not modelled	12.5	11	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> fg41 malonate semialdehyde decarboxylase; <b>PDBTitle:</b> crystal structure of fg41msad inactivated by 3-chloropropionate
41	<a href="#">d1gpla2</a>	Alignment	not modelled	11.4	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Pancreatic lipase, N-terminal domain
42	<a href="#">c2zycA</a>	Alignment	not modelled	10.5	4	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan hydrolase flgJ; <b>PDBTitle:</b> crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
43	<a href="#">c3lp5A</a>	Alignment	not modelled	10.4	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell surface hydrolase; <b>PDBTitle:</b> the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
44	<a href="#">c2gwoC</a>	Alignment	not modelled	10.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dual specificity protein phosphatase 13; <b>PDBTitle:</b> crystal structure of tmdp
45	<a href="#">c3lcrA</a>	Alignment	not modelled	10.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tautomycetin biosynthetic pks; <b>PDBTitle:</b> thioesterase from tautomycetin biosynthetic pathway
46	<a href="#">d1jmx1</a>	Alignment	not modelled	9.5	15	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
47	<a href="#">d1vhra</a>	Alignment	not modelled	8.4	17	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Dual specificity phosphatase-like
48	<a href="#">c2x5eA</a>	Alignment	not modelled	8.3	13	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0271 protein pa4511; <b>PDBTitle:</b> crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
49	<a href="#">d1v6ta</a>	Alignment	not modelled	8.2	11	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
50	<a href="#">d2dfaa1</a>	Alignment	not modelled	7.9	10	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> Glycoside hydrolase/deacetylase <b>Family:</b> LamB/YcsF-like
51	<a href="#">d2acya</a>	Alignment	not modelled	7.8	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> Acylphosphatase-like
52	<a href="#">c2r37A</a>	Alignment	not modelled	7.7	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione peroxidase 3; <b>PDBTitle:</b> crystal structure of human glutathione peroxidase 3 (selenocysteine to2 glycine mutant)
53	<a href="#">d2ccaa2</a>	Alignment	not modelled	7.7	15	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
54	<a href="#">c3eurA</a>	Alignment	not modelled	7.1	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the c-terminal domain of uncharacterized protein2 from bacteroides fragilis nctc 9343

55	<a href="#">d1cvla_</a>	Alignment	not modelled	7.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Bacterial lipase
56	<a href="#">c3fleB_</a>	Alignment	not modelled	6.9	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> se_1780 protein; <b>PDBTitle:</b> se_1780 protein of unknown function from staphylococcus epidermidis.
57	<a href="#">d1mwwa_</a>	Alignment	not modelled	6.5	14	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> Hypothetical protein HI1388.1
58	<a href="#">d3b5ea1</a>	Alignment	not modelled	6.4	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
59	<a href="#">d1pbya1</a>	Alignment	not modelled	6.4	21	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
60	<a href="#">d1gpla_</a>	Alignment	not modelled	6.3	36	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
61	<a href="#">d2ccaa1</a>	Alignment	not modelled	6.2	16	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> Catalase-peroxidase KatG
62	<a href="#">c2p04B_</a>	Alignment	not modelled	6.1	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> signal transduction histidine kinase; <b>PDBTitle:</b> 2.1 ang structure of the dimerized pas domain of signal transduction2 histidine kinase from nostoc punctiforme pcc 73102 with homology to3 the h-noxa/h-noba domain of the soluble guanylyl cyclase
63	<a href="#">d1jfua_</a>	Alignment	not modelled	6.0	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
64	<a href="#">d1otfa_</a>	Alignment	not modelled	5.9	17	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
65	<a href="#">d3buxb3</a>	Alignment	not modelled	5.9	38	<b>Fold:</b> SH2-like <b>Superfamily:</b> SH2 domain <b>Family:</b> SH2 domain
66	<a href="#">d1xhoa_</a>	Alignment	not modelled	5.8	4	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> Chorismate mutase
67	<a href="#">c1xhoB_</a>	Alignment	not modelled	5.8	4	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> chorismate mutase; <b>PDBTitle:</b> chorismate mutase from clostridium thermocellum cth-682
68	<a href="#">d1yt3a2</a>	Alignment	not modelled	5.8	6	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> HRDC-like <b>Family:</b> RNase D C-terminal domains
69	<a href="#">d1rbli_</a>	Alignment	not modelled	5.7	14	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
70	<a href="#">c3fi7A_</a>	Alignment	not modelled	5.7	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo1076 protein; <b>PDBTitle:</b> crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
71	<a href="#">c1itkB_</a>	Alignment	not modelled	5.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> catalase-peroxidase; <b>PDBTitle:</b> crystal structure of catalase-peroxidase from haloarcula2 marismortui
72	<a href="#">c3dwvB_</a>	Alignment	not modelled	5.6	55	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione peroxidase-like protein; <b>PDBTitle:</b> glutathione peroxidase-type trypanredoxin peroxidase,2 oxidized form
73	<a href="#">d2choa2</a>	Alignment	not modelled	5.6	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> alpha-D-glucuronidase/Hyaluronidase catalytic domain
74	<a href="#">c2zyiB_</a>	Alignment	not modelled	5.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase, putative; <b>PDBTitle:</b> a. fulgidus lipase with fatty acid fragment and calcium
75	<a href="#">c2op8A_</a>	Alignment	not modelled	5.5	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> probable tautomerase ywhb; <b>PDBTitle:</b> crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
76	<a href="#">d2h1ia1</a>	Alignment	not modelled	5.4	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase/thioesterase 1
77	<a href="#">c2e0tA_</a>	Alignment	not modelled	5.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dual specificity phosphatase 26; <b>PDBTitle:</b> crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
78	<a href="#">d1svdm1</a>	Alignment	not modelled	5.1	24	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
79	<a href="#">d1uzhc1</a>	Alignment	not modelled	5.1	10	<b>Fold:</b> RuBisCO, small subunit <b>Superfamily:</b> RuBisCO, small subunit <b>Family:</b> RuBisCO, small subunit
80	<a href="#">d2f8aa1</a>	Alignment	not modelled	5.1	27	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> Glutathione peroxidase-like
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional p-450/nadph-p450

81	<a href="#">c3hf2A_</a>	Alignment	not modelled	5.1	13	reductase; <b>PDBTitle:</b> crystal structure of the i401p mutant of cytochrome p450 bm3
82	<a href="#">c1qgeD_</a>	Alignment	not modelled	5.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (triacylglycerol hydrolase); <b>PDBTitle:</b> new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
83	<a href="#">c2obiA_</a>	Alignment	not modelled	5.1	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipid hydroperoxide glutathione mutant2 of human phospholipid hydroperoxide glutathione peroxidase3 (gpx4) <b>PDBTitle:</b> crystal structure of the selenocysteine to cysteine