

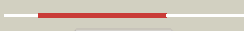








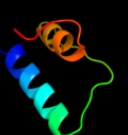



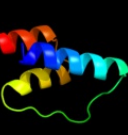



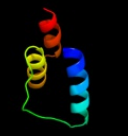



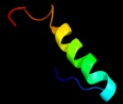

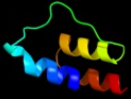

















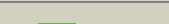






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dloxwa_	 Alignment		100.0	19	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Patatin
2	d1cya2	 Alignment		99.3	23	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: Lysophospholipase
3	c1cyaB_	 Alignment		98.2	24	PDB header: hydrolase Chain: B: PDB Molecule: protein (cytosolic phospholipase a2); PDBTitle: human cytosolic phospholipase a2
4	d1mlaa1	 Alignment		84.6	16	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
5	c3l4eA_	 Alignment		81.8	18	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
6	c3im8A_	 Alignment		79.5	21	PDB header: transferase Chain: A: PDB Molecule: malonyl acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from streptococcus pneumoniae
7	c3rgiA_	 Alignment		78.8	16	PDB header: transferase Chain: A: PDB Molecule: disd protein; PDBTitle: trans-acting transferase from disorazole synthase
8	c2jfkD_	 Alignment		78.2	18	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
9	c2drhD_	 Alignment		76.9	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
10	c3ptwA_	 Alignment		74.7	20	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
11	d1fyea_	 Alignment		71.9	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE

12	c3n5iC_	 Alignment		71.5	17	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
13	c2cuyA_	 Alignment		70.5	21	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
14	c3en0A_	 Alignment		70.2	18	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
15	c3tqeA_	 Alignment		69.3	16	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
16	c3eenA_	 Alignment		68.9	20	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
17	c2hunB_	 Alignment		68.4	21	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
18	d1nm2a1	 Alignment		67.5	14	Fold: FabD/lysophospholipase-like Superfamily: FabD/lysophospholipase-like Family: FabD-like
19	d1o6ca_	 Alignment		65.6	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
20	c3g87A_	 Alignment		61.6	18	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
21	c1e3hA_	 Alignment	not modelled	61.2	24	PDB header: polyribonucleotide transferase Chain: A: PDB Molecule: guanosine pentaphosphate synthetase; PDBTitle: semet derivative of streptomyces antibioticus pnpase/gpsi2 enzyme
22	d1b65a_	 Alignment	not modelled	60.2	8	Fold: DmpA/ArgJ-like Superfamily: DmpA/ArgJ-like Family: DmpA-like
23	c3cdiA_	 Alignment	not modelled	59.8	30	PDB header: transferase Chain: A: PDB Molecule: polynucleotide phosphorylase; PDBTitle: crystal structure of e. coli pnpase
24	c2qo3A_	 Alignment	not modelled	56.9	20	PDB header: transferase Chain: A: PDB Molecule: eryaii erythromycin polyketide synthase modules 3 and 4; PDBTitle: crystal structure of [ks3][at3] di domain from module 3 of 6-2 deoxyerthrionolide b synthase
25	c3l3bA_	 Alignment	not modelled	56.6	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
26	c2jlmH_	 Alignment	not modelled	54.0	29	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
27	c2h1yA_	 Alignment	not modelled	53.8	10	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
						PDB header: transferase

28	c3kwpA	Alignment	not modelled	52.8	17	Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
29	c2cdh9	Alignment	not modelled	52.7	26	PDB header: transferase Chain: 9: PDB Molecule: acetyl transferase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
30	c3qatB	Alignment	not modelled	52.2	21	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
31	c2g2oA	Alignment	not modelled	49.9	18	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: structure of e.coli fabd complexed with sulfate
32	c3ezwD	Alignment	not modelled	47.8	14	PDB header: transferase Chain: D: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
33	c3d3kD	Alignment	not modelled	47.4	11	PDB header: protein binding Chain: D: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
34	c2przB	Alignment	not modelled	47.1	14	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
35	c3e18A	Alignment	not modelled	46.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
36	c3mjdA	Alignment	not modelled	46.5	21	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
37	d2cdqa3	Alignment	not modelled	45.3	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
38	c2hg4A	Alignment	not modelled	45.2	22	PDB header: transferase Chain: A: PDB Molecule: 6-deoxyerythronlide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
39	c3lwbA	Alignment	not modelled	45.0	17	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
40	c3ot5D	Alignment	not modelled	43.3	16	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
41	c3e5nA	Alignment	not modelled	43.1	22	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
42	d1jzta	Alignment	not modelled	41.7	11	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
43	d1wyza1	Alignment	not modelled	40.4	15	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
44	c3hhdC	Alignment	not modelled	40.4	19	PDB header: transferase, hydrolase Chain: C: PDB Molecule: fatty acid synthase; PDBTitle: structure of the human fatty acid synthase ks-mat didomain2 as a framework for inhibitor design.
45	d2cdqa2	Alignment	not modelled	39.9	30	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
46	d1wdea	Alignment	not modelled	39.8	10	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
47	c2qj3B	Alignment	not modelled	39.0	21	PDB header: transferase Chain: B: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: mycobacterium tuberculosis fabd
48	c3iliA	Alignment	not modelled	38.4	28	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
49	c3nbmA	Alignment	not modelled	38.1	5	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
50	d2hmfa2	Alignment	not modelled	36.6	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
51	c3ezoA	Alignment	not modelled	36.3	20	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
52	c2iyaB	Alignment	not modelled	35.2	13	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering PDB header: lvase

53	c1qzuB_	Alignment	not modelled	34.8	21	Chain: B: PDB Molecule: hypothetical protein mds018; PDBTitle: crystal structure of human phosphopantothenoyl cysteine decarboxylase
54	c3krnB_	Alignment	not modelled	34.7	21	PDB header: hydrolase Chain: B: PDB Molecule: protein c14a4.5, confirmed by transcript evidence; PDBTitle: crystal structure of c. elegans cell-death-related nuclease 5(crn-5)
55	c3axgN_	Alignment	not modelled	34.0	35	PDB header: hydrolase Chain: N: PDB Molecule: endotype 6-aminohexanoat-oligomer hydrolase; PDBTitle: structure of 6-aminohexanoate-oligomer hydrolase
56	d2j0wa2	Alignment	not modelled	33.5	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
57	c2dg2D_	Alignment	not modelled	32.5	17	PDB header: protein binding Chain: D: PDB Molecule: apolipoprotein a-i binding protein; PDBTitle: crystal structure of mouse apolipoprotein a-i binding2 protein
58	d1vhva_	Alignment	not modelled	32.4	16	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
59	c3l6gA_	Alignment	not modelled	32.1	16	PDB header: glycine betaine-binding protein Chain: A: PDB Molecule: betaine abc transporter permease and substrate binding PDBTitle: crystal structure of lactococcal opuac in its open conformation
60	d1r88a_	Alignment	not modelled	31.4	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
61	c1kh2D_	Alignment	not modelled	31.0	50	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
62	d1dqza_	Alignment	not modelled	31.0	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
63	d2d81a1	Alignment	not modelled	30.5	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PHB depolymerase-like
64	c2vz8B_	Alignment	not modelled	30.4	22	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase
65	c3mcuF_	Alignment	not modelled	29.6	16	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
66	d1j20a1	Alignment	not modelled	29.1	50	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
67	d3c8da2	Alignment	not modelled	28.7	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
68	c2cwdA_	Alignment	not modelled	28.2	19	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight phosphotyrosine protein phosphatase; PDBTitle: crystal structure of tt1001 protein from thermus thermophilus hb8
69	c3d3jA_	Alignment	not modelled	27.6	11	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
70	c2e8bA_	Alignment	not modelled	27.4	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of the putative protein (aq1419) from aquifex2 aeolicus vf5
71	d1lh0a_	Alignment	not modelled	27.2	27	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
72	d2je6b2	Alignment	not modelled	26.8	3	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
73	c2x0dA_	Alignment	not modelled	26.8	8	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
74	c3cdjA_	Alignment	not modelled	26.4	30	PDB header: transferase Chain: A: PDB Molecule: polynucleotide phosphorylase; PDBTitle: crystal structure of the e. coli kh/s1 domain truncated2 pnpase
75	c3flaB_	Alignment	not modelled	25.9	24	PDB header: hydrolase Chain: B: PDB Molecule: rifr; PDBTitle: rifr - type ii thioesterase from rifamycin nrps/pks biosynthetic2 pathway - form 1
76	d1d1qa_	Alignment	not modelled	25.8	16	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
77	c2d4wA_	Alignment	not modelled	25.8	13	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
						PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase;

78	c3n2lA_	Alignment	not modelled	25.5	27	PDBTitle: 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961 PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
79	c2pvpB_	Alignment	not modelled	25.3	14	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
80	d1p3y1_	Alignment	not modelled	25.1	14	PDB header: hydrolase Chain: D: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
81	c1qgeD_	Alignment	not modelled	25.0	23	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
82	c3kcqA_	Alignment	not modelled	24.3	24	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
83	c3e4dD_	Alignment	not modelled	24.0	24	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
84	c2qmqa_	Alignment	not modelled	23.9	17	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
85	c3fcxA_	Alignment	not modelled	23.9	19	PDB header: ligase Chain: B: PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase
86	c1e4eB_	Alignment	not modelled	23.5	22	PDB header: transferase Chain: A: PDB Molecule: malonyl coa-acyl carrier protein transacylase; PDBTitle: crystal structure of mcat from staphylococcus aureus
87	c3im9A_	Alignment	not modelled	23.4	13	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
88	d1ve2a1	Alignment	not modelled	23.3	26	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
89	c3zquA_	Alignment	not modelled	23.0	17	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
90	c1vl2C_	Alignment	not modelled	22.6	25	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii
91	c3tqtB_	Alignment	not modelled	22.4	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
92	d1f0na_	Alignment	not modelled	22.3	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: O-acetyltransferase
93	d2vata1	Alignment	not modelled	22.0	24	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
94	d1sfra_	Alignment	not modelled	21.7	24	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
95	d2ax3a2	Alignment	not modelled	21.6	23	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
96	d1vhqa_	Alignment	not modelled	21.4	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
97	c2dnpB_	Alignment	not modelled	20.8	15	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
98	c3tqrA_	Alignment	not modelled	20.1	21	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
99	d1zh8a1	Alignment	not modelled	20.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain