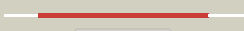
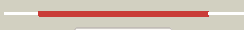
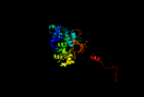


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qovD_	 Alignment		100.0	24	PDB header: ligase Chain: D: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of a hypothetical acyl-coa ligase (bt_0428) from2 bacteroides thetaiotaomicron vpi-5482 at 2.20 a resolution
2	c2y27B_	 Alignment		100.0	23	PDB header: ligase Chain: B: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak1 in complex with atp from2 burkholderia cenocepacia
3	c2vsqA_	 Alignment		100.0	12	PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
4	c2y4oA_	 Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: crystal structure of paak2 in complex with phenylacetyl adenylate
5	d1pg4a_	 Alignment		100.0	16	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
6	c4wd1A_	 Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: acetoacetate-coa ligase; PDBTitle: acetoacetyl-coa synthetase from streptomyces lividans
7	d1ry2a_	 Alignment		100.0	17	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
8	c3tsyA_	 Alignment		100.0	13	PDB header: ligase, transferase Chain: A: PDB Molecule: fusion protein 4-coumarate--coa ligase 1, resveratrol PDBTitle: 4-coumaroyl-coa ligase::stilbene synthase fusion protein
9	c3etcb_	 Alignment		100.0	14	PDB header: ligase Chain: B: PDB Molecule: amp-binding protein; PDBTitle: 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
10	c3e7wA_	 Alignment		100.0	13	PDB header: ligase Chain: A: PDB Molecule: d-alanine--poly(phosphoribitol) ligase subunit 1; PDBTitle: crystal structure of dlta: implications for the reaction2 mechanism of non-ribosomal peptide synthetase (nrps)3 adenylation domains
11	c4r0mB_	 Alignment		100.0	12	PDB header: ligase Chain: B: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate

12	d3cw9a1	Alignment		100.0	15	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
13	c3gqwB_	Alignment		100.0	11	PDB header: ligase Chain: B: PDB Molecule: fatty acid amp ligase; PDBTitle: crystal structure of a fatty acid amp ligase from e. coli with an acyl2 adenylate product bound
14	d1mdba_	Alignment		100.0	13	Fold: Acetyl-CoA synthetase-like Superfamily: Acetyl-CoA synthetase-like Family: Acetyl-CoA synthetase-like
15	c3vngA_	Alignment		100.0	13	PDB header: ligase Chain: A: PDB Molecule: nrps adenylation protein cytc1; PDBTitle: co-crystal structure of nrps adenylation protein cytc1 with atp from2 streptomyces
16	c4gr5B_	Alignment		100.0	15	PDB header: ligase Chain: B: PDB Molecule: non-ribosomal peptide synthetase; PDBTitle: crystal structure of slgn1deltaasub in complex with ampcpp
17	c3ni2A_	Alignment		100.0	13	PDB header: ligase Chain: A: PDB Molecule: 4-coumarate:coa ligase; PDBTitle: crystal structures and enzymatic mechanisms of a populus tomentosa 4-2 coumarate:coa ligase
18	c4dg9A_	Alignment		100.0	14	PDB header: ligase/inhibitor Chain: A: PDB Molecule: pa1221; PDBTitle: structure of holo-pa1221, an nrps protein containing adenylation and2 pcp domains bound to vinylsulfonamide inhibitor
19	c3kxwA_	Alignment		100.0	11	PDB header: ligase Chain: A: PDB Molecule: saframycin mx1 synthetase b; PDBTitle: the crystal structure of fatty acid amp ligase from legionella2 pneumophila
20	c3rg2H_	Alignment		100.0	13	PDB header: ligase Chain: H: PDB Molecule: enterobactin synthase component e (ente), 2,3-dihydro-2,3- PDBTitle: structure of a two-domain nrps fusion protein containing the ente2 adenylation domain and entb aryl-carrier protein from enterobactin3 biosynthesis
21	c4dg8A_	Alignment	not modelled	100.0	12	PDB header: ligase Chain: A: PDB Molecule: pa1221; PDBTitle: structure of pa1221, an nrps protein containing adenylation and pcp2 domains
22	c4r0mA_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: mcyg protein; PDBTitle: structure of mcyg a-pcp complexed with phenylalanyl-adenylate
23	c4eatB_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structure of a benzoate coenzyme a ligase
24	c3iteB_	Alignment	not modelled	100.0	13	PDB header: ligase Chain: B: PDB Molecule: sidn siderophore synthetase; PDBTitle: the third adenylation domain of the fungal sidn non-ribosomal peptide2 synthetase
25	c3eynB_	Alignment	not modelled	100.0	11	PDB header: ligase Chain: B: PDB Molecule: acyl-coenzyme a synthetase acsm2a; PDBTitle: crystal structure of human acyl-coa synthetase medium-chain2 family member 2a (l64p mutation) in a complex with coa
26	c3iplB_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: B: PDB Molecule: 2-succinylbenzoate--coa ligase; PDBTitle: crystal structure of o-succinylbenzoic acid-coa ligase from2 staphylococcus aureus subsp. aureus mu50
27	c2v7bB_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: B: PDB Molecule: benzoate-coenzyme a ligase; PDBTitle: crystal structures of a benzoate coa ligase from2 burkholderia xenovorans lb400
28	c4ir7A_	Alignment	not modelled	100.0	11	PDB header: transferase Chain: A: PDB Molecule: long chain fatty acid coa ligase fadd10; PDBTitle: crystal structure of mtb fadd10 in complex with dodecanoyl-amp

53	c3laxA_	Alignment	not modelled	99.5	19	Chain: A: PDB Molecule: phenylacetate-coenzyme a ligase; PDBTitle: the crystal structure of a domain of phenylacetate-coenzyme2 a ligase from bacteroides vulgatus atcc 8482
54	c4ewvB_	Alignment	not modelled	99.5	16	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
55	c3whpA_	Alignment	not modelled	70.0	16	PDB header: gene regulation Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
56	c2i2xD_	Alignment	not modelled	65.1	13	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
57	c3ezxA_	Alignment	not modelled	59.9	15	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
58	d3bula2	Alignment	not modelled	59.8	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
59	c1bmtB_	Alignment	not modelled	57.1	11	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
60	c1y80A_	Alignment	not modelled	54.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
61	c1k98A_	Alignment	not modelled	46.3	11	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
62	d1f06a2	Alignment	not modelled	45.6	20	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
63	c2zztA_	Alignment	not modelled	43.4	13	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
64	c4v195_	Alignment	not modelled	43.3	20	PDB header: ribosome Chain: 5: PDB Molecule: mitoribosomal protein bl32m, mrpl32; PDBTitle: structure of the large subunit of the mammalian2 mitochondrial ribosome, part 1 of 2
65	c4jgiB_	Alignment	not modelled	35.7	12	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
66	c3h7fB_	Alignment	not modelled	32.8	13	PDB header: transferase Chain: B: PDB Molecule: serine hydroxymethyltransferase 1; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 mycobacterium tuberculosis
67	d2hiya1	Alignment	not modelled	30.8	5	Fold: SP0830-like Superfamily: SP0830-like Family: SP0830-like
68	d7reqa2	Alignment	not modelled	27.8	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
69	c1xrsB_	Alignment	not modelled	25.7	17	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
70	c2wh7A_	Alignment	not modelled	25.3	45	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronidase-phage associated; PDBTitle: the partial structure of a group a streptococcal phage-2 encoded tail fibre hyaluronate lyase hylp2
71	d1mwwa_	Alignment	not modelled	23.7	18	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: Hypothetical protein HI1388.1
72	d1whua_	Alignment	not modelled	22.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 Family: Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3
73	c4lkbA_	Alignment	not modelled	21.5	16	PDB header: isomerase Chain: A: PDB Molecule: hypothetical protein alr4568/putative 4-oxalocrotonate PDBTitle: crystal structure of a putative 4-oxalocrotonate tautomerase from2 nostoc sp. pcc 7120
74	c1yj7A_	Alignment	not modelled	20.5	13	PDB header: protein transport Chain: A: PDB Molecule: escj; PDBTitle: crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
75	d1bjpa_	Alignment	not modelled	20.2	12	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
76	c3j1zP_	Alignment	not modelled	20.0	4	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
77	d2trcp_	Alignment	not modelled	19.3	30	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Phosducin
78	c2ormA_	Alignment	not modelled	17.9	7	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase hp0924; PDBTitle: crystal structure of the 4-oxalocrotonate tautomerase homologue dmpi2 from helicobacter pylori.

79	d3bzka3	Alignment	not modelled	17.6	12	Fold: Tex N-terminal region-like Superfamily: Tex N-terminal region-like Family: Tex N-terminal region-like
80	c2yxbA	Alignment	not modelled	16.1	12	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
81	d1ccwa	Alignment	not modelled	14.5	8	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
82	d2c3fa1	Alignment	not modelled	12.9	45	Fold: Triple-stranded beta-helix Superfamily: Phage fibre proteins Family: HylP-like
83	c2c3fA	Alignment	not modelled	12.9	45	PDB header: lyase Chain: A: PDB Molecule: hyaluronidase, phage associated; PDBTitle: the structure of a group a streptococcal phage-encoded2 tail-fibre showing hyaluronan lyase activity.
84	c3n4dF	Alignment	not modelled	12.4	18	PDB header: hydrolase Chain: F: PDB Molecule: putative tautomerase; PDBTitle: crystal structure of cg10062 inactivated by(r)-oxirane-2-carboxylate
85	c3wdoA	Alignment	not modelled	12.0	5	PDB header: transport protein Chain: A: PDB Molecule: mfs transporter; PDBTitle: a structure of protein.
86	d1otfa	Alignment	not modelled	11.9	10	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
87	c2qfiB	Alignment	not modelled	11.3	15	PDB header: transport protein Chain: B: PDB Molecule: ferrous-iron efflux pump fief; PDBTitle: structure of the zinc transporter yiiP
88	c2oceA	Alignment	not modelled	11.3	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pa5201; PDBTitle: crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
89	d1q6za2	Alignment	not modelled	11.2	9	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
90	c2op8A	Alignment	not modelled	11.1	10	PDB header: isomerase Chain: A: PDB Molecule: probable tautomerase ywhb; PDBTitle: crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
91	c3pplB	Alignment	not modelled	10.6	14	PDB header: transferase Chain: B: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
92	c3mb2G	Alignment	not modelled	10.0	12	PDB header: isomerase Chain: G: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - alpha subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
93	c3ziaT	Alignment	not modelled	9.3	50	PDB header: hydrolase Chain: T: PDB Molecule: atpase inhibitor, mitochondrial; PDBTitle: the structure of f1-atpase from saccharomyces cerevisiae2 inhibited by its regulatory protein if1
94	c3ziaI	Alignment	not modelled	9.3	50	PDB header: hydrolase Chain: J: PDB Molecule: atpase inhibitor, mitochondrial; PDBTitle: the structure of f1-atpase from saccharomyces cerevisiae2 inhibited by its regulatory protein if1
95	c3abfB	Alignment	not modelled	9.2	22	PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase; PDBTitle: crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
96	d1uzva	Alignment	not modelled	9.2	44	Fold: Calcium-mediated lectin Superfamily: Calcium-mediated lectin Family: Calcium-mediated lectin
97	c3d6kB	Alignment	not modelled	8.8	11	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
98	c1x4rA	Alignment	not modelled	8.7	57	PDB header: apoptosis Chain: A: PDB Molecule: parp14 protein; PDBTitle: solution structure of wwe domain in parp14 protein
99	d1a0rp	Alignment	not modelled	8.6	30	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Phosducin