



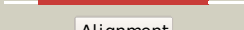

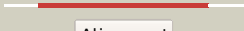









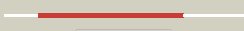
















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1efvb_	 Alignment		100.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
2	d1efpb_	 Alignment		100.0	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
3	d3clsc1	 Alignment		100.0	23	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
4	d1o94c_	 Alignment		100.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
5	c1o94D_	 Alignment		99.9	11	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
6	d3clsd1	 Alignment		99.9	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
7	c3ih5A_	 Alignment		99.8	9	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: crystal structure of electron transfer flavoprotein alpha-2 subunit from bacteroides thetaiotaomicron
8	d1efva1	 Alignment		99.6	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
9	c1t9gR_	 Alignment		99.5	16	PDB header: oxidoreductase, electron transport Chain: R: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: structure of the human mcad:etf complex
10	d1efpa1	 Alignment		99.0	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
11	c1efpC_	 Alignment		99.0	17	PDB header: electron transport Chain: C: PDB Molecule: protein (electron transfer flavoprotein); PDBTitle: electron transfer flavoprotein (etf) from paracoccus2 denitrificans

12	c3feta_	Alignment		98.7	12	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein subunit alpha related PDBTitle: crystal structure of the electron transfer flavoprotein subunit alpha2 related protein ta0212 from thermoplasma acidophilum
13	c3mt0A_	Alignment		90.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1789; PDBTitle: the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
14	c1dkrB_	Alignment		88.8	13	PDB header: transferase Chain: B: PDB Molecule: phosphoribosyl pyrophosphate synthetase; PDBTitle: crystal structures of bacillus subtilis phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
15	d1tq8a_	Alignment		86.9	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
16	d2z3va1	Alignment		85.6	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
17	c1w96B_	Alignment		84.5	8	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
18	d1uana_	Alignment		84.4	16	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
19	c3lpnB_	Alignment		83.1	11	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
20	c3fh0A_	Alignment		82.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative universal stress protein kpn_01444; PDBTitle: crystal structure of putative universal stress protein kpn_01444 -2 atpase
21	d1iowa1	Alignment	not modelled	81.8	15	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
22	c2c4kD_	Alignment	not modelled	81.4	10	PDB header: regulatory protein Chain: D: PDB Molecule: phosphoribosyl pyrophosphate synthetase- PDBTitle: crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
23	c3efhB_	Alignment	not modelled	81.0	13	PDB header: transferase Chain: B: PDB Molecule: ribose-phosphate pyrophosphokinase 1; PDBTitle: crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
24	c2ixdB_	Alignment	not modelled	80.8	16	PDB header: hydrolase Chain: B: PDB Molecule: lmbE-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from2 bacillus cereus
25	c3fg9B_	Alignment	not modelled	79.3	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
26	c3hgmD_	Alignment	not modelled	78.2	19	PDB header: signaling protein Chain: D: PDB Molecule: universal stress protein tead; PDBTitle: universal stress protein tead from the trap transporter2 teaabc of halomonas elongata
27	d2ji7a1	Alignment	not modelled	77.8	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
						Fold: DHS-like NAD/FAD-binding domain

28	dlozha1	Alignment	not modelled	75.7	11	Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
29	dlq77a_	Alignment	not modelled	74.0	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
30	c2vu2D_	Alignment	not modelled	73.0	12	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: biosynthetic thiolase from z. ramigera. complex with s-2 pantetheine-11-pivalate.
31	c2pfsA_	Alignment	not modelled	69.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
32	c2v4wB_	Alignment	not modelled	68.5	13	PDB header: transferase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa synthase, PDBTitle: crystal structure of human mitochondrial 3-hydroxy-3-2 methylglutaryl-coenzyme a synthase 2 (hmgcs2)
33	c2dy0A_	Alignment	not modelled	68.2	13	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli
34	d2djia1	Alignment	not modelled	65.6	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
35	c1u9yD_	Alignment	not modelled	65.4	12	PDB header: transferase Chain: D: PDB Molecule: ribose-phosphate pyrophosphokinase; PDBTitle: crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
36	c2ebdB_	Alignment	not modelled	64.9	16	PDB header: transferase Chain: B: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase iii2 from aquifex aeolicus vf5
37	dlu1la_	Alignment	not modelled	64.4	21	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
38	c2fw9A_	Alignment	not modelled	64.4	22	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
39	dlxmpa_	Alignment	not modelled	63.3	19	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
40	c1kh2D_	Alignment	not modelled	61.8	14	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
41	c1zq1B_	Alignment	not modelled	61.3	15	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
42	dlw0ma_	Alignment	not modelled	61.0	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
43	c2is8A_	Alignment	not modelled	60.7	18	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
44	c3loqA_	Alignment	not modelled	60.5	14	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: the crystal structure of a universal stress protein from2 archaeoglobus fulgidus dsm 4304
45	c3ss6B_	Alignment	not modelled	60.2	13	PDB header: transferase Chain: B: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
46	c2iikA_	Alignment	not modelled	59.2	9	PDB header: transferase Chain: A: PDB Molecule: 3-ketoacyl-coa thiolase, peroxisomal; PDBTitle: crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)
47	dljlja_	Alignment	not modelled	56.4	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
48	dlybha1	Alignment	not modelled	56.3	9	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
49	c3il5D_	Alignment	not modelled	56.0	8	PDB header: transferase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: structure of e. faecalis fabh in complex with 2-(4-bromo-3-2 [(diethylamino)sulfonyl]benzoyl)amino)benzoic acid
50	c3lp6D_	Alignment	not modelled	55.5	17	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
51	dlrqba2	Alignment	not modelled	55.3	17	Fold: TIM beta/alpha-barrel Superfamily: Al dolase Family: HMGL-like
						PDB header: transferase

52	c3cwcB_	Alignment	not modelled	52.8	24	Chain: B; PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella typhimurium lt2
53	dlznnal	Alignment	not modelled	52.5	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
54	clznnF_	Alignment	not modelled	52.5	20	PDB header: biosynthetic protein Chain: F; PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
55	c3trhl_	Alignment	not modelled	52.5	11	PDB header: lyase Chain: I; PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
56	c2qnxA_	Alignment	not modelled	52.2	14	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: crystal structure of the complex between the mycobacterium beta-2 ketoacyl-acyl carrier protein synthase iii (fabh) and 11-3 [(decyloxy carbonyl) dithio]-undecanoic acid
57	dlwv2a_	Alignment	not modelled	51.4	26	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
58	dlo4va_	Alignment	not modelled	51.2	16	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
59	c2yvwA_	Alignment	not modelled	49.9	21	PDB header: lyase Chain: A; PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
60	clrr2A_	Alignment	not modelled	49.8	16	PDB header: transferase Chain: A; PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
61	c2x3eA_	Alignment	not modelled	49.4	13	PDB header: transferase Chain: A; PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: crystal structure of 3-oxoacyl-(acyl carrier protein)2 synthase iii, fabh from pseudomonas aeruginosa pao1
62	dlmiob_	Alignment	not modelled	49.2	18	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
63	dlzpdal	Alignment	not modelled	48.6	10	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
64	dlqcza_	Alignment	not modelled	48.5	16	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
65	dlidi6a_	Alignment	not modelled	47.4	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
66	c2z6jB_	Alignment	not modelled	47.2	15	PDB header: oxidoreductase Chain: B; PDB Molecule: trans-2-enoyl-acp reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
67	c3orsD_	Alignment	not modelled	46.9	15	PDB header: isomerase,biosynthetic protein Chain: D; PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
68	dlilqa_	Alignment	not modelled	46.3	10	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
69	d2ihtal	Alignment	not modelled	46.1	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
70	dly0ba1	Alignment	not modelled	44.6	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
71	c3dloC_	Alignment	not modelled	44.4	16	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus
72	dlvcfa1	Alignment	not modelled	43.8	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
73	dlo57a2	Alignment	not modelled	42.9	17	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
74	clo57A_	Alignment	not modelled	42.9	15	PDB header: dna binding protein Chain: A; PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
75	c3lyhB_	Alignment	not modelled	42.7	4	PDB header: lyase Chain: B; PDB Molecule: cobalamin (vitamin b12) biosynthesis cbix protein; PDBTitle: crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution PDB header: protein binding

76	c3pdiG_	Alignment	not modelled	42.2	16	Chain: G: PDB Molecule: nitrogenase mofe cofactor biosynthesis protein nife; PDBTitle: precursor bound nifen
77	c1ub7A_	Alignment	not modelled	42.2	13	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] synthase; PDBTitle: the crystal analysis of beta-keroacyl-[acyl carrier protein] synthase2 iii (fabh)from thermus thermophilus.
78	c2p8uB_	Alignment	not modelled	41.8	9	PDB header: transferase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa synthase, cytoplasmic; PDBTitle: crystal structure of human 3-hydroxy-3-methylglutaryl coa synthase i
79	d1jcna1	Alignment	not modelled	41.4	12	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
80	d2ez9a1	Alignment	not modelled	41.1	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
81	d1g2qa_	Alignment	not modelled	40.7	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
82	c1mzjB_	Alignment	not modelled	40.5	11	PDB header: transferase Chain: B: PDB Molecule: beta-ketoacylsynthase iii; PDBTitle: crystal structure of the priming beta-ketosynthase from the2 r1128 polyketide biosynthetic pathway
83	d1qh8a_	Alignment	not modelled	39.7	19	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
84	c2htmB_	Alignment	not modelled	39.4	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
85	d1ovma1	Alignment	not modelled	38.8	2	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
86	c3s29C_	Alignment	not modelled	37.7	28	PDB header: transferase Chain: C: PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
87	c2ibyD_	Alignment	not modelled	37.3	11	PDB header: transferase Chain: D: PDB Molecule: acetyl-coa acetyltransferase; PDBTitle: crystallographic and kinetic studies of human mitochondrial2 acetoacetyl-coa thiolase (t2): the importance of potassium and3 chloride for its structure and function
88	d1q6za1	Alignment	not modelled	37.3	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
89	d1xm3a_	Alignment	not modelled	37.3	22	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
90	d1q74a_	Alignment	not modelled	36.7	18	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
91	c2pjka_	Alignment	not modelled	36.4	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: 178aa long hypothetical molybdenum cofactor PDBTitle: structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
92	d1zn7a1	Alignment	not modelled	35.9	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
93	c1kbiB_	Alignment	not modelled	35.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
94	c1olsB_	Alignment	not modelled	35.1	9	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoisovalerate dehydrogenase beta subunit; PDBTitle: roles of his291-alpha and his146-beta' in the reductive2 acylation reaction catalyzed by human branched-chain3 alpha-ketoacid dehydrogenase
95	d1kbia1	Alignment	not modelled	34.8	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
96	c2nrrA_	Alignment	not modelled	34.7	15	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal rnaseh endonuclease2 domain of uvrC
97	d1hc7a1	Alignment	not modelled	34.4	13	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
98	d1v4va_	Alignment	not modelled	34.1	17	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
99	d1uuya_	Alignment	not modelled	34.1	17	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
100	d1hg3a_	Alignment	not modelled	32.5	13	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
101	d1jq5a_	Alignment	not modelled	32.2	9	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like

					Family: Iron-containing alcohol dehydrogenase
102	c1wl5A_	Alignment	not modelled	32.0	12 PDB header: transferase Chain: A: PDB Molecule: acetyl-coenzyme a acetyltransferase 2; PDBTitle: human cytosolic acetoacetyl-coa thiolase
103	d2gm3a1	Alignment	not modelled	32.0	18 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
104	c3rggD_	Alignment	not modelled	30.9	15 PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase, pure protein; PDBTitle: crystal structure of treponema denticola pure bound to air
105	c3fiuD_	Alignment	not modelled	30.8	16 PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
106	c1zfjA_	Alignment	not modelled	30.1	14 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
107	c3qjaA_	Alignment	not modelled	30.1	14 PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
108	d1hnja1	Alignment	not modelled	29.7	13 Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
109	c2vbgB_	Alignment	not modelled	29.2	15 PDB header: lyase Chain: B: PDB Molecule: branched-chain alpha-ketoacid decarboxylase; PDBTitle: the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
110	c3s3tD_	Alignment	not modelled	29.0	11 PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
111	c3gidB_	Alignment	not modelled	28.8	11 PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: the biotin carboxylase (bc) domain of human acetyl-coa2 carboxylase 2 (acc2) in complex with soraphen a
112	c3gwaA_	Alignment	not modelled	28.7	16 PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) synthase iii; PDBTitle: 1.6 angstrom crystal structure of 3-oxoacyl-(acyl-carrier-protein)2 synthase iii
113	c3bo9B_	Alignment	not modelled	28.5	20 PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
114	c2f9aA_	Alignment	not modelled	28.1	9 PDB header: transferase Chain: A: PDB Molecule: 3-hydroxy-3-methylglutaryl coenzyme a synthase 1; PDBTitle: hmg-coa synthase from brassica juncea in complex with f-244
115	d1e0ta2	Alignment	not modelled	27.5	8 Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
116	c1dl5A_	Alignment	not modelled	27.4	15 PDB header: transferase Chain: A: PDB Molecule: protein-l-isoaspartate o-methyltransferase; PDBTitle: protein-l-isoaspartate o-methyltransferase
117	d1lbqa_	Alignment	not modelled	27.2	9 Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
118	d2c4ka1	Alignment	not modelled	27.1	12 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosylpyrophosphate synthetase-like
119	d1tqxa_	Alignment	not modelled	26.1	7 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
120	d1vdma1	Alignment	not modelled	26.0	17 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)