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Description	P60566
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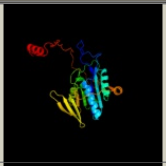
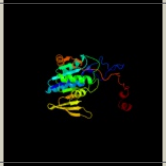
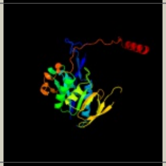
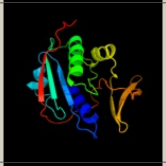
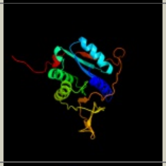
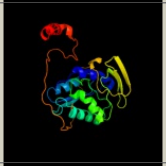
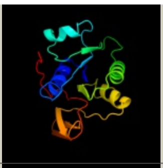
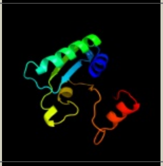
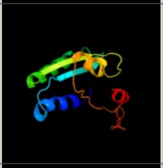
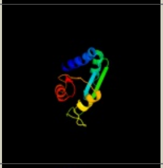
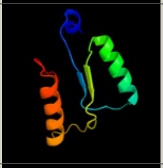
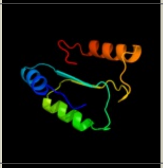
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1efvb_	Alignment		100.0	29	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
2	d1efpb_	Alignment		100.0	27	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
3	d3clsc1	Alignment		100.0	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
4	d1o94c_	Alignment		100.0	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
5	c1o94D_	Alignment		99.9	16	**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	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
7	c3ih5A_	Alignment		99.9	16	**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		99.9	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
9	c1t9gR_	Alignment		99.8	20	**PDB header:**oxidoreductase, electron transport **Chain:** R: **PDB Molecule:**electron transfer flavoprotein alpha-subunit, **PDBTitle:** structure of the human mcad:etf complex
10	c1efpC_	Alignment		99.8	17	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**protein (electron transfer flavoprotein); **PDBTitle:** electron transfer flavoprotein (etf) from paracoccus2 denitrificans
11	d1efpa1	Alignment		99.7	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits

12	c3fetA_	Alignment		99.5	8	**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	d1tq8a_	Alignment		94.7	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
14	c3mt0A_	Alignment		94.3	16	**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
15	c3fh0A_	Alignment		94.1	15	**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
16	c3fg9B_	Alignment		93.6	14	**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
17	c2ixdB_	Alignment		92.6	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmbe-related protein; **PDBTitle:** crystal structure of the putative deacetylase bc1534 from2 bacilus cereus
18	d1uana_	Alignment		92.5	14	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
19	d1q77a_	Alignment		92.5	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
20	c2pfsA_	Alignment		92.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
21	d2z3va1	Alignment	not modelled	90.2	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
22	c3hgmD_	Alignment	not modelled	89.8	21	**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
23	c3loqA_	Alignment	not modelled	89.7	15	**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
24	d1miob_	Alignment	not modelled	84.4	19	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
25	c3lpnB_	Alignment	not modelled	83.8	10	**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).
26	d1w0ma_	Alignment	not modelled	83.1	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
27	c1dkrB_	Alignment	not modelled	82.9	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.
28	c3dloC_	Alignment	not modelled	81.1	11	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein;

28		Alignment	not modelled	81.1	11	**PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
29	d1jmva_	Alignment	not modelled	75.7	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
30	c1zq1B_	Alignment	not modelled	75.1	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit d; **PDBTitle:** structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
31	d1v4va_	Alignment	not modelled	75.0	24	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
32	c3s3tD_	Alignment	not modelled	74.8	21	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**nucleotide-binding protein, universal stress protein uspa **PDBTitle:** universal stress protein uspa from lactobacillus plantarum
33	c3iupB_	Alignment	not modelled	74.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadph:quinone oxidoreductase; **PDBTitle:** crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
34	d1q74a_	Alignment	not modelled	74.5	20	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
35	c2ebdB_	Alignment	not modelled	73.0	19	**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
36	d1y0ba1	Alignment	not modelled	72.3	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
37	d1l1qa_	Alignment	not modelled	71.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
38	d1ozha1	Alignment	not modelled	70.9	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
39	c3krtC_	Alignment	not modelled	70.9	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**crotonyl coa reductase; **PDBTitle:** crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
40	c1u9yD_	Alignment	not modelled	70.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
41	d1mjha_	Alignment	not modelled	70.1	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
42	d1tv5a1	Alignment	not modelled	68.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
43	c1tv5A_	Alignment	not modelled	68.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydroorotate dehydrogenase homolog, mitochondrial; **PDBTitle:** plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
44	d1znna1	Alignment	not modelled	66.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
45	c1znnF_	Alignment	not modelled	66.5	19	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
46	c2c4kD_	Alignment	not modelled	66.1	12	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
47	c3efhB_	Alignment	not modelled	65.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
48	d1o57a2	Alignment	not modelled	65.5	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
49	d1f6da_	Alignment	not modelled	65.5	10	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
50	c1kh2D_	Alignment	not modelled	65.1	21	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
51	d1m1nb_	Alignment	not modelled	64.9	14	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
52	c2dy0A_	Alignment	not modelled	64.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
						PDB header:lyase **Chain:** B: **PDB Molecule:**cobalamin (vitamin b12) biosynthesis

53	c3lyhB_	Alignment	not modelled	64.4	11	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
54	c3il5D_	Alignment	not modelled	64.0	19	**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
55	d2ji7a1	Alignment	not modelled	64.0	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
56	d1m1na_	Alignment	not modelled	64.0	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
57	d1qh8a_	Alignment	not modelled	62.7	12	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
58	d1iowa1	Alignment	not modelled	62.7	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
59	c3s29C_	Alignment	not modelled	62.2	24	**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.
60	c1o57A_	Alignment	not modelled	61.4	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
61	d2iyva1	Alignment	not modelled	60.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
62	d1hg3a_	Alignment	not modelled	60.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
63	c1q7tA_	Alignment	not modelled	58.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein rv1170; **PDBTitle:** rv1170 (mshb) from mycobacterium tuberculosis
64	c2dumD_	Alignment	not modelled	58.8	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein ph0823; **PDBTitle:** crystal structure of hypothetical protein, ph0823
65	c2vu2D_	Alignment	not modelled	58.4	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** biosynthetic thiolase from z. ramigera. complex with s-2 pantetheine-11-pivalate.
66	c2xdqB_	Alignment	not modelled	57.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
67	c3op1A_	Alignment	not modelled	57.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
68	c3ab8B_	Alignment	not modelled	56.6	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein ttha0350; **PDBTitle:** crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
69	c3olqA_	Alignment	not modelled	56.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein e; **PDBTitle:** the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
70	d1ovma1	Alignment	not modelled	55.0	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
71	d1rkba_	Alignment	not modelled	54.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
72	c1w96B_	Alignment	not modelled	54.4	12	**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
73	d1zpda1	Alignment	not modelled	53.7	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
74	d1kaga_	Alignment	not modelled	53.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
75	d1jlja_	Alignment	not modelled	52.5	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
76	c2x3eA_	Alignment	not modelled	51.6	18	**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
77	c3jzdA_	Alignment	not modelled	50.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of putative alcohol dehedrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution

78	c1ub7A_	Alignment	not modelled	50.6	12	**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.
79	d2gm3a1	Alignment	not modelled	50.5	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
80	d1vdma1	Alignment	not modelled	50.4	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
81	d1g2qa_	Alignment	not modelled	49.3	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
82	d1di6a_	Alignment	not modelled	47.3	7	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
83	c2qnxA_	Alignment	not modelled	46.9	16	**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 [(decyloxycarbonyl)dithio]-undecanoic acid
84	c1zuiA_	Alignment	not modelled	46.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**shikimate kinase; **PDBTitle:** structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
85	d2vgna3	Alignment	not modelled	46.8	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
86	d1a9xa4	Alignment	not modelled	46.8	11	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
87	d1hnja1	Alignment	not modelled	46.6	14	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
88	c2v4wB_	Alignment	not modelled	46.1	7	**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)
89	c3il3A_	Alignment	not modelled	45.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] synthase 3; **PDBTitle:** structure of haemophilus influenzae fabh
90	c2iikA_	Alignment	not modelled	45.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-ketoacyl-coa thiolase, peroxisomal; **PDBTitle:** crystal structure of human peroxisomal acetyl-coa acyl transferase 12 (acaa1)
91	c3qvjB_	Alignment	not modelled	45.7	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae
92	c3gwaA_	Alignment	not modelled	45.7	15	**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
93	c3dfiA_	Alignment	not modelled	45.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pseudoaglycone deacetylase dbv21; **PDBTitle:** the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
94	d2djia1	Alignment	not modelled	45.4	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
95	d1sfla_	Alignment	not modelled	45.2	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
96	c3ss6B_	Alignment	not modelled	44.9	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa acetyltransferase; **PDBTitle:** crystal structure of the bacillus anthracis acetyl-coa2 acetyltransferase
97	d1viaa_	Alignment	not modelled	42.7	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
98	d1qh8b_	Alignment	not modelled	42.7	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
99	c3cgxA_	Alignment	not modelled	42.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative nucleotide-diphospho-sugar transferase; **PDBTitle:** crystal structure of putative nucleotide-diphospho-sugar transferase2 (yp_389115.1) from desulfovibrio desulfuricans g20 at 1.90 a3 resolution
100	d1e6ca_	Alignment	not modelled	42.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
101	c3fdiA_	Alignment	not modelled	41.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein from eubacterium2 ventriosum atcc 27560.
102	c2nv2U_	Alignment	not modelled	41.8	23	**PDB header:**lyase/transferase **Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
						PDB header:transferase

103	c2ibyD_	Alignment	not modelled	40.9	13	**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
104	c3vh3A_	Alignment	not modelled	40.3	20	**PDB header:**metal binding protein/protein transport **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of atg7ctd-atg8 complex
105	d1zq1a2	Alignment	not modelled	39.9	26	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
106	d1a9xa3	Alignment	not modelled	39.7	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
107	c3aerB_	Alignment	not modelled	39.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
108	d1q6za1	Alignment	not modelled	39.0	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
109	d1ybha1	Alignment	not modelled	38.9	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
110	c3hdtB_	Alignment	not modelled	38.7	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase from clostridium symbiosum atcc2 14940
111	c2h92C_	Alignment	not modelled	38.5	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**cytidylate kinase; **PDBTitle:** crystal structure of staphylococcus aureus cytidine2 monophosphate kinase in complex with cytidine-5'-3 monophosphate
112	c3pdiB_	Alignment	not modelled	37.7	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
113	c1mzjB_	Alignment	not modelled	37.2	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**beta-ketoacylsynthase iii; **PDBTitle:** crystal structure of the priming beta-ketosynthase from the2 r1128 polyketide biosynthetic pathway
114	c2pt5D_	Alignment	not modelled	37.2	37	**PDB header:**transferase **Chain:** D: **PDB Molecule:**shikimate kinase; **PDBTitle:** crystal structure of shikimate kinase (aq_2177) from aquifex aeolicus2 vf5
115	d2ihta1	Alignment	not modelled	37.1	24	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
116	d1s3ga1	Alignment	not modelled	36.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
117	c1olsB_	Alignment	not modelled	36.2	8	**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
118	d1qb7a_	Alignment	not modelled	36.1	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
119	c2zbtB_	Alignment	not modelled	35.8	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
120	d2cdna1	Alignment	not modelled	35.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases