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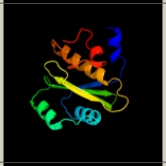
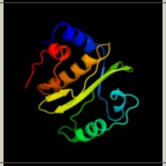
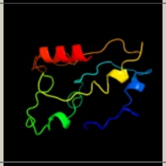
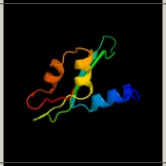
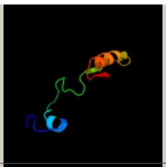
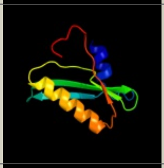
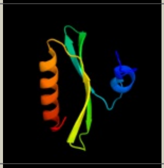
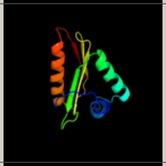
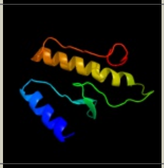
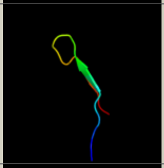
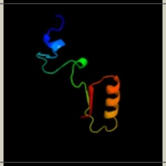
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cxaa1	Alignment		100.0	96	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**LFTR-like
2	c2cxaA_	Alignment		100.0	96	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucyl/phenylalanyl-trna-protein transferase; **PDBTitle:** crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
3	d1ne9a2	Alignment		97.1	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
4	c1p4nA_	Alignment		96.1	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**femx; **PDBTitle:** crystal structure of weissella viridescens femx:udp-murnac-2 pentapeptide complex
5	d1lrza3	Alignment		92.4	9	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
6	c1lrzA_	Alignment		51.0	12	**PDB header:**antibiotic inhibitor **Chain:** A: **PDB Molecule:**factor essential for expression of methicillin **PDBTitle:** x-ray crystal structure of staphylococcus aureus fema
7	c3thdD_	Alignment		49.4	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
8	c3iwgB_	Alignment		46.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** acetyltransferase from gnat family from colwellia psychrerythraea.
9	c2ozhA_	Alignment		45.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein xcc2953; **PDBTitle:** crystal structure of a putative acetyltransferase belonging to the2 gnat family (xcc2953) from xanthomonas campestris pv. campestris at3 1.40 a resolution
10	c3s6fA_	Alignment		41.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical acetyltransferase; **PDBTitle:** crystal structure of a hypotetical acetyltransferase (dr_1678) from2 deinococcus radiodurans at 1.19 a resolution
11	c2kxeA_	Alignment		33.5	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii small subunit; **PDBTitle:** n-terminal domain of the dp1 subunit of an archaeal d-family dna2 polymerase

12	c1qf6A_	Alignment		31.5	24	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
13	d1yvka1	Alignment		28.5	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
14	d1cm0a_	Alignment		22.0	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
15	d1y7ra1	Alignment		17.6	10	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
16	d1s7ka1	Alignment		17.3	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
17	d2hq2a1	Alignment		17.1	25	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
18	c2oixA_	Alignment		16.3	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xanthomonas outer protein d; **PDBTitle:** xanthomonas xopd c470a mutant
19	c1nyqA_	Alignment		16.3	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
20	d2beia1	Alignment		16.1	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
21	d1euva_	Alignment	not modelled	15.2	12	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
22	d2j0pa1	Alignment	not modelled	15.0	25	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
23	d1pn0a3	Alignment	not modelled	14.4	10	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**PHBH-like
24	c2q7bA_	Alignment	not modelled	13.3	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of acetyltransferase (np_689019.1) from2 streptococcus agalactiae 2603 at 2.00 a resolution
25	c3i7tA_	Alignment	not modelled	13.2	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of rv2704, a member of highly conserved2 yjgf/yer057c/uk114 family, from mycobacterium tuberculosis
26	c3d3aA_	Alignment	not modelled	12.7	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
27	c3l47A_	Alignment	not modelled	12.3	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**odorant binding protein (agap010409-pa); **PDBTitle:** crystal structure of the anopheles gambiae odorant-binding protein 22a
28	c3qr3B_	Alignment	not modelled	11.2	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase eg-ii; **PDBTitle:** crystal structure of cel5a (eg2) from hypocrea jecorina

						(trichoderma2 reesei)
29	c2zzjA_	Alignment	not modelled	10.7	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**glucuronan lyase a; **PDBTitle:** crystal structure of endo-beta-1,4-glucuronan lyase from2 fungus trichoderma reesei
30	c3eayA_	Alignment	not modelled	10.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sentrin-specific protease 7; **PDBTitle:** crystal structure of the human senp7 catalytic domain
31	d2iy1a1	Alignment	not modelled	10.7	12	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
32	d1wfxa_	Alignment	not modelled	10.5	15	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Tpt1/KptA
33	d1th0a_	Alignment	not modelled	10.2	24	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
34	d1jnda1	Alignment	not modelled	9.7	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
35	c1pbtA_	Alignment	not modelled	9.6	21	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
36	c1vp7D_	Alignment	not modelled	9.6	38	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**exodeoxyribonuclease vii small subunit; **PDBTitle:** crystal structure of exodeoxyribonuclease vii small subunit2 (np_881400.1) from bordetella pertussis at 2.40 a resolution
37	c2r8rB_	Alignment	not modelled	9.0	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
38	d1fnna1	Alignment	not modelled	8.9	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
39	d2fr1a1	Alignment	not modelled	8.5	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
40	d1dqua_	Alignment	not modelled	8.1	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
41	c3ga9S_	Alignment	not modelled	8.1	31	**PDB header:**hydrolase **Chain:** S: **PDB Molecule:**capsule biosynthesis protein capd; **PDBTitle:** crystal structure of bacillus anthracis transpeptidase enzyme capd,2 crystal form ii
42	c3nnqA_	Alignment	not modelled	8.0	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**n-terminal domain of moloney murine leukemia virus **PDBTitle:** crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
43	d1tdja2	Alignment	not modelled	8.0	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
44	d1z4ra1	Alignment	not modelled	8.0	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
45	c1ur8B_	Alignment	not modelled	7.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**chitinase b; **PDBTitle:** interactions of a family 18 chitinase with the designed2 inhibitor hm508, and its degradation product,3 chitobiono-delta-lactone
46	c3qokA_	Alignment	not modelled	7.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative chitinase ii; **PDBTitle:** crystal structure of putative chitinase ii from klebsiella pneumoniae
47	c3g3sA_	Alignment	not modelled	7.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of gcn5-related n-acetyltransferase-like protein2 (zp_00874857) (zp_00874857.1) from streptococcus suis 89/1591 at 1.803 a resolution
48	d1n71a_	Alignment	not modelled	7.3	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
49	d2g4da1	Alignment	not modelled	7.1	12	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
50	d1xpja_	Alignment	not modelled	7.1	28	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
51	d1q2ya_	Alignment	not modelled	7.0	12	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
52	c2qw5B_	Alignment	not modelled	7.0	8	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
53	d1vp7a_	Alignment	not modelled	6.8	41	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like

54	c2uwqA_	Alignment	not modelled	6.8	31	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**apoptosis-stimulating of p53 protein 2; **PDBTitle:** solution structure of aspp2 n-terminus
55	d1vhxa_	Alignment	not modelled	6.8	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
56	c1g5hA_	Alignment	not modelled	6.7	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mitochondrial dna polymerase accessory subunit; **PDBTitle:** crystal structure of the accessory subunit of murine mitochondrial2 polymerase gamma
57	d1u5la_	Alignment	not modelled	6.7	38	**Fold:**Prion-like **Superfamily:**Prion-like **Family:**Prion-like
58	d2atra1	Alignment	not modelled	6.6	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
59	d2bkra1	Alignment	not modelled	6.6	6	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
60	d1qf6a1	Alignment	not modelled	6.6	14	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
61	d1vp7b_	Alignment	not modelled	6.6	41	**Fold:**Spectrin repeat-like **Superfamily:**XseB-like **Family:**XseB-like
62	c3duzA_	Alignment	not modelled	6.5	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**major envelope glycoprotein; **PDBTitle:** crystal structure of the postfusion form of baculovirus2 fusion protein gp64
63	d1y9wa1	Alignment	not modelled	6.4	13	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
64	c2dskA_	Alignment	not modelled	6.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of catalytic domain of hyperthermophilic chitinase2 from pyrococcus furiosus
65	d1vpqa_	Alignment	not modelled	6.3	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**TM1631-like **Family:**TM1631-like
66	c1rk8C_	Alignment	not modelled	6.1	56	**PDB header:**translation **Chain:** C: **PDB Molecule:**within the bgcn gene intron protein; **PDBTitle:** structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
67	d1rk8c_	Alignment	not modelled	6.1	56	**Fold:**WW domain-like **Superfamily:**Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain **Family:**Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
68	c1yb2A_	Alignment	not modelled	6.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ta0852; **PDBTitle:** structure of a putative methyltransferase from thermoplasma2 acidophilum.
69	d1yb2a1	Alignment	not modelled	6.1	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
70	c2huzB_	Alignment	not modelled	6.1	11	**PDB header:**structural genomics, transferase **Chain:** B: **PDB Molecule:**glucosamine 6-phosphate n-acetyltransferase; **PDBTitle:** crystal structure of gnpnat1
71	c3dd7A_	Alignment	not modelled	6.0	24	**PDB header:**ribosome inhibitor **Chain:** A: **PDB Molecule:**death on curing protein; **PDBTitle:** structure of doch66y in complex with the c-terminal domain of phd
72	d2hd9a1	Alignment	not modelled	5.8	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
73	c3kruC_	Alignment	not modelled	5.8	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
74	d1jeyb1	Alignment	not modelled	5.7	18	**Fold:**SPOC domain-like **Superfamily:**SPOC domain-like **Family:**Ku80 subunit middle domain
75	c3grcD_	Alignment	not modelled	5.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
76	d1h4pa_	Alignment	not modelled	5.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
77	c2l6pA_	Alignment	not modelled	5.2	26	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**phac1, phac2 and phad genes; **PDBTitle:** nmr solution structure of the protein np_253742.1