Phyre2

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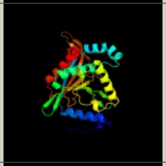
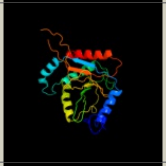
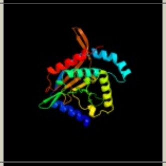
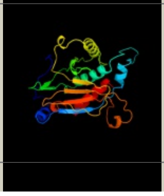
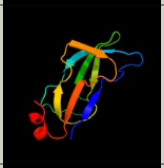
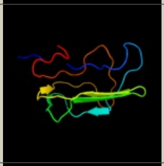
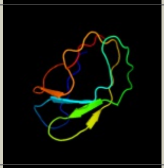
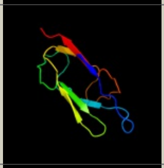
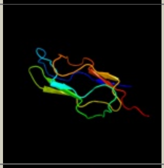
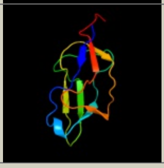
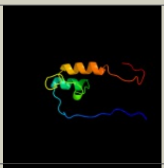
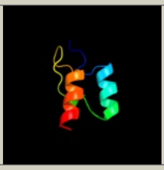
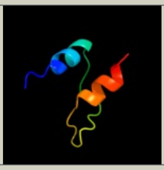
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1b5sa_	Alignment		100.0	36	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
2	d1dpba_	Alignment		100.0	30	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
3	c2ii4C_	Alignment		100.0	30	**PDB header:**transferase **Chain:** C: **PDB Molecule:**lipoamide acyltransferase component of branched-chain **PDBTitle:** crystal structure of a cubic core of the dihydrolipoamide2 acyltransferase (e2b) component in the branched-chain alpha-ketoacid3 dehydrogenase complex (bckdc), coenzyme a-bound form
4	c3l60A_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**branched-chain alpha-keto acid dehydrogenase; **PDBTitle:** crystal structure of branched-chain alpha-keto acid2 dehydrogenase subunit e2 from mycobacterium tuberculosis
5	d1scza_	Alignment		100.0	100	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
6	c3b8kA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase; **PDBTitle:** structure of the truncated human dihydrolipoyl2 acetyltransferase (e2)
7	c3maeA_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-oxoisovalerate dehydrogenase e2 component, **PDBTitle:** crystal structure of probable dihydrolipamide2 acetyltransferase from listeria monocytogenes 4b f2365
8	c3rqcB_	Alignment		100.0	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable lipoamide acyltransferase; **PDBTitle:** crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
9	d1q23a_	Alignment		100.0	8	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
10	d3claa_	Alignment		100.0	10	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**CAT-like
11	c2i9dC_	Alignment		100.0	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** chloramphenicol acetyltransferase

12	c2dneA_	Alignment		99.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
13	c2dncA_	Alignment		99.9	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
14	d1y8ob1	Alignment		99.9	28	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
15	c2q8iB_	Alignment		99.9	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
16	d1k8ma_	Alignment		99.8	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
17	c2l5tA_	Alignment		99.8	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
18	d1ghja_	Alignment		99.8	60	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
19	d1gjxa_	Alignment		99.8	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
20	d1qjoa_	Alignment		99.8	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
21	d1laba_	Alignment	not modelled	99.8	35	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
22	d1pmra_	Alignment	not modelled	99.8	100	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
23	d1iyua_	Alignment	not modelled	99.8	28	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
24	c2xt6B_	Alignment	not modelled	99.7	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
25	d2pnrc1	Alignment	not modelled	99.7	36	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
26	c2ejmA_	Alignment	not modelled	99.7	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
27	c2dn8A_	Alignment	not modelled	99.7	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
28	c2kccA_	Alignment	not modelled	99.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
29	c2b8gA_	Alignment	not modelled	99.6	23	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein;

29	c2b8gA_	Alignment	not modelled	99.6	23	**PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
30	d1dcza_	Alignment	not modelled	99.5	30	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
31	c2ejgD_	Alignment	not modelled	99.5	30	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
32	d1o78a_	Alignment	not modelled	99.4	30	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
33	c3n6rK_	Alignment	not modelled	99.4	15	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
34	d1bdoa_	Alignment	not modelled	99.4	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
35	c2cooA_	Alignment		99.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
36	d1bala_	Alignment		99.1	100	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
37	c1zwvA_	Alignment	not modelled	99.1	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
38	c1w4kA_	Alignment	not modelled	99.1	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase e2; **PDBTitle:** peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
39	c1w3dA_	Alignment	not modelled	99.1	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
40	d1w4ha1	Alignment		99.1	100	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
41	c3dv0I_	Alignment	not modelled	99.1	32	**PDB header:**oxidoreductase/transferase **Chain:** I: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
42	c2eq9C_	Alignment	not modelled	99.0	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
43	d1w85i_	Alignment	not modelled	99.0	32	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
44	d2cyua1	Alignment		99.0	100	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
45	c2eq7C_	Alignment	not modelled	98.9	41	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
46	c2eq8C_	Alignment	not modelled	98.9	42	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
47	c2qf7A_	Alignment	not modelled	98.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
						PDB header:membrane protein, transport protein

48	c2k33A_	Alignment	not modelled	98.1	25	**Chain:** A: **PDB Molecule:**acra; **PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation
49	c3h9iB_	Alignment	not modelled	97.5	23	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cation efflux system protein cusb; **PDBTitle:** crystal structure of the membrane fusion protein cusb from escherichia2 coli
50	d1onla_	Alignment	not modelled	97.4	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
51	c2edgA_	Alignment	not modelled	97.3	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** solution structure of the gcv_h domain from mouse glycine
52	d1hpca_	Alignment	not modelled	97.3	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
53	c3iftA_	Alignment	not modelled	97.3	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
54	c3mxuA_	Alignment	not modelled	97.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from bartonella2 henselae
55	c2f5zK_	Alignment	not modelled	97.1	46	**PDB header:**oxidoreductase/protein binding **Chain:** K: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** crystal structure of human dihydrolipoamide dehydrogenase2 (e3) complexed to the e3-binding domain of human e3-3 binding protein
56	c1zy8M_	Alignment	not modelled	97.1	42	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**pyruvate dehydrogenase protein x component, **PDBTitle:** the crystal structure of dihydrolipoamide dehydrogenase and2 dihydrolipoamide dehydrogenase-binding protein (didomain)3 subcomplex of human pyruvate dehydrogenase complex.
57	c2ka7A_	Alignment	not modelled	96.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** nmr solution structure of tm0212 at 40 c
58	c3a8jF_	Alignment	not modelled	96.9	19	**PDB header:**transferase/transport protein **Chain:** F: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of et-ehred complex
59	c2qj8B_	Alignment	not modelled	96.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
60	c3fmcC_	Alignment	not modelled	96.5	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase; **PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
61	c3na6A_	Alignment	not modelled	96.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase; **PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
62	c2aukA_	Alignment	not modelled	96.3	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
63	c1t5eB_	Alignment	not modelled	95.9	29	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
64	c3fppB_	Alignment	not modelled	95.8	23	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
65	d1vf7a_	Alignment	not modelled	95.7	29	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
66	c3cdxB_	Alignment	not modelled	95.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
67	c3lnnB_	Alignment	not modelled	95.2	15	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux **PDBTitle:** crystal structure of zneb from cupriavidus metallidurans
68	c2f1mA_	Alignment	not modelled	95.1	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
69	d2gpra_	Alignment	not modelled	94.1	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
70	d1brwa3	Alignment	not modelled	93.1	38	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
71	c2jkuA_	Alignment	not modelled	93.1	38	**PDB header:**ligase **Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain, **PDBTitle:** crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase

72	c2aujD_	Alignment	not modelled	92.8	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
73	c3d4rE_	Alignment	not modelled	91.6	17	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**domain of unknown function from the pfam-b_34464 family; **PDBTitle:** crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
74	d1glaf_	Alignment	not modelled	91.5	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
75	d1gpra_	Alignment	not modelled	90.4	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
76	d2f3ga_	Alignment	not modelled	90.2	12	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
77	d2tpta3	Alignment	not modelled	90.0	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
78	c3h5qA_	Alignment	not modelled	90.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
79	d1o4ua2	Alignment	not modelled	90.0	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
80	d1uoua3	Alignment	not modelled	89.8	17	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
81	c2dsjA_	Alignment	not modelled	89.6	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
82	c1brwB_	Alignment	not modelled	89.4	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
83	c2j0fC_	Alignment	not modelled	88.8	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
84	d1qapa2	Alignment	not modelled	88.2	33	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
85	c1otpA_	Alignment	not modelled	86.8	25	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
86	d1qpoa2	Alignment	not modelled	86.8	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
87	c3gnnA_	Alignment	not modelled	86.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
88	c3pajA_	Alignment	not modelled	85.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
89	c1o4uA_	Alignment	not modelled	84.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
90	c2jbmA_	Alignment	not modelled	83.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
91	c1qpoA_	Alignment	not modelled	83.2	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
92	c1qapA_	Alignment	not modelled	82.7	33	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
93	c3tqvA_	Alignment	not modelled	82.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
94	c3l0gD_	Alignment	not modelled	82.4	38	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide

						pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
95	c2b7pA_	Alignment	not modelled	81.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
96	c1x1oC_	Alignment	not modelled	81.1	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
97	c2zbaD_	Alignment	not modelled	79.4	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trichothecene 3-o-acetyltransferase; **PDBTitle:** crystal sructure of f. sporotrichioides tri101 complexed with coenzyme2 a and t-2
98	c2jgpA_	Alignment	not modelled	78.6	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrocidine synthetase 3; **PDBTitle:** structure of the tycc5-6 pcp-c bidomain of the tyrocidine2 synthetase tycc
99	c2gu1A_	Alignment	not modelled	77.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
100	d1e2wa2	Alignment	not modelled	72.6	31	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
101	c2e1uA_	Alignment	not modelled	72.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl transferase; **PDBTitle:** crystal structure of dendranthema morifolium dmat
102	c2vsqA_	Alignment	not modelled	70.9	11	**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
103	d1ci3m2	Alignment	not modelled	68.8	22	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
104	c2hsiB_	Alignment	not modelled	65.4	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23; **PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
105	c2bghA_	Alignment	not modelled	60.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vinorine synthase; **PDBTitle:** crystal structure of vinorine synthase
106	d1qwya_	Alignment	not modelled	59.6	6	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
107	c2xr7A_	Alignment	not modelled	58.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malonyltransferase; **PDBTitle:** crystal structure of nicotiana tabacum malonyltransferase (ntmat1)2 complexed with malonyl-coa
108	c3c2vA_	Alignment	not modelled	55.6	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of the quinolinate phosphoribosyl2 transferase (bna6) from saccharomyces cerevisiae complexed3 with prpp and the inhibitor phthalate
109	c2b44A_	Alignment	not modelled	54.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
110	c1e2vB_	Alignment	not modelled	52.8	31	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
111	c1tu2B_	Alignment	not modelled	47.5	25	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**apocytochrome f; **PDBTitle:** the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
112	c1q90A_	Alignment	not modelled	46.9	31	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
113	c2xhaB_	Alignment	not modelled	46.8	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
114	d1hcza2	Alignment	not modelled	43.9	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
115	c3fotA_	Alignment	not modelled	43.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**15-o-acetyltransferase; **PDBTitle:** structural and functional characterization of tri3 trichothecene 15-o-2 acetyltransferase from fusarium sporotrichioides
116	c2e75C_	Alignment	not modelled	42.5	31	**PDB header:**photosynthesis **Chain:** C: **PDB Molecule:**apocytochrome f; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
117	c2xhgA_	Alignment	not modelled	42.2	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tyrocidine synthetase a; **PDBTitle:** crystal structure of the epimerization domain from the initiation2 module of tyrocidine biosynthesis
118	d1tu2b2	Alignment	not modelled	40.8	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain

119	c3it5B_	Alignment	not modelled	40.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
120	c3nyyA_	Alignment	not modelled	38.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycyl-glycine endopeptidase lytm; **PDBTitle:** crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution