Phyre2

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Description	RVBD1505c_(-)_1695287_1695952
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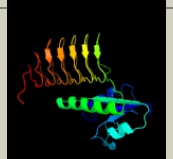
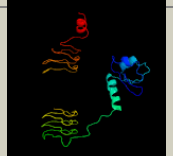
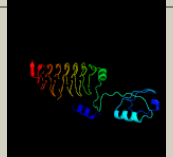
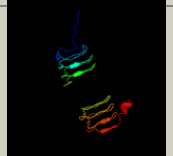
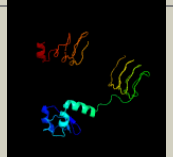
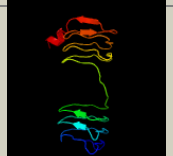
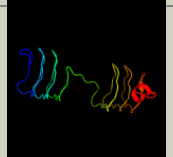
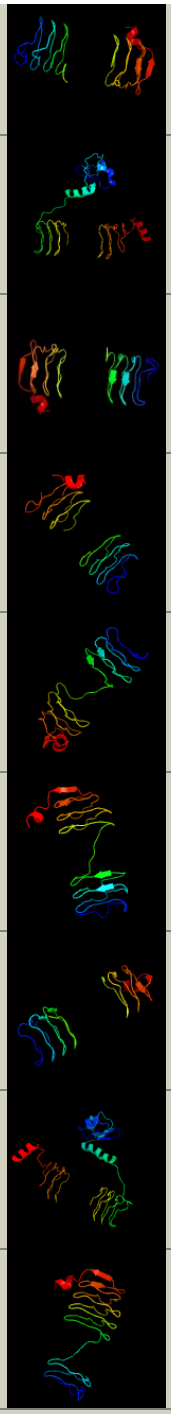
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4m98A_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pilin glycosylation protein; **PDBTitle:** acetyltransferase domain of pglb from neisseria gonorrhoeae fa1090
2	c4m9cC_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**bacterial transferase hexapeptide (three repeats) family **PDBTitle:** weei from acinetobacter baumannii aye
3	c4ea8A_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**perosamine n-acetyltransferase; **PDBTitle:** x-ray crystal structure of perb from caulobacter crescentus in complex2 with coenzyme a and gdp-n-acetylperosamine at 1 angstrom resolution
4	d3bswa1	Alignment		100.0	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**PglD-like
5	c2iu9C_	Alignment		100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine **PDBTitle:** chlamydia trachomatis lpxd with 100mm udpglcnac (complex ii)
6	c3cj8B_	Alignment		100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-carboxylate n-2 succinyltransferase from enterococcus faecalis v583
7	c4e6tA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** structure of lpxa from acinetobacter baumannii at 1.8a resolution2 (p212121 form)
8	c3eh0C_	Alignment		100.0	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n- **PDBTitle:** crystal structure of lpxd from escherichia coli
9	c4eqyC_	Alignment		100.0	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** crystal structure of acyl-[acyl-carrier-protein]--udp-n-2 acetylglucosamine o-acyltransferase from burkholderia thailandensis
10	c3i3aC_	Alignment		100.0	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n- **PDBTitle:** structural basis for the sugar nucleotide and acyl chain2 selectivity of leptospira interrogans lpxa
11	c4r36A_	Alignment		100.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyl-[acyl-carrier-protein]--udp-n- **PDBTitle:** crystal structure analysis of lpxa, a udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343

12	c3r0sA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** udp-n-acetylglucosamine acyltransferase from campylobacter jejuni
13	c3pmoA_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-3-o-[3-hydroxymyristoyl] glucosamine n-acyltransferase; **PDBTitle:** the structure of lpxd from pseudomonas aeruginosa at 1.3 a resolution
14	c5jxxC_	Alignment		100.0	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** crystal structure of udp-n-acetylglucosamine o-acyltransferase (lpxa)2 from moraxella catarrhalis rh4.
15	c5f42B_	Alignment		100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** activity and crystal structure of francisella novicida udp-n-2 acetylglucosamine acyltransferase
16	d2jf2a1	Alignment		100.0	25	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
17	d1j2za_	Alignment		100.0	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
18	c3t57A_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine o-acyltransferase domain-containing **PDBTitle:** activity and crystal structure of arabidopsis udp-n-acetylglucosamine2 acyltransferase
19	c4e75A_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-3-o-acylglucosamine n-acyltransferase; **PDBTitle:** structure of lpxd from acinetobacter baumannii at 2.85a resolution2 (p21 form)
20	c5dg3D_	Alignment		100.0	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine o- **PDBTitle:** structure of pseudomonas aeruginosa lpxa in complex with udp-3-o-(r-3-2 hydroxydecanoyl)-glcnac
21	c3fttA_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase sacol2570; **PDBTitle:** crystal structure of the galactoside o-acetyltransferase from2 staphylococcus aureus
22	c3srtB_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**maltose o-acetyltransferase; **PDBTitle:** the crystal structure of a maltose o-acetyltransferase from2 clostridium difficile 630
23	d1krra_	Alignment	not modelled	100.0	19	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
24	c4mzuG_	Alignment	not modelled	100.0	26	**PDB header:**isomerase, transferase **Chain:** G: **PDB Molecule:**wxcm-like protein; **PDBTitle:** crystal structure of fdtd, a bifunctional ketoisomerase/n-2 acetyltransferase from shewanella denitrificans
25	c3ectA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide-repeat containing-acetyltransferase; **PDBTitle:** crystal structure of the hexapeptide-repeat containing-2 acetyltransferase vca0836 from vibrio cholerae
26	c2ic7A_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**maltose transacetylase; **PDBTitle:** crystal structure of maltose transacetylase from geobacillus2 kaustophilus
27	c3r8yD_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** structure of the bacillus anthracis tetrahydropicolinate2 succinyltransferase
28	d1ocxa_	Alignment	not modelled	99.9	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like

29	c3fsbB_	Alignment	not modelled	99.9	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**qdtc; **PDBTitle:** crystal structure of qdtc, the dtdp-3-amino-3,6-dideoxy-d-2 glucose n-acetyl transferase from thermoanaerobacterium3 thermosaccharolyticum in complex with coa and dtdp-3-amino-4 quinovose
30	c3mqhD_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**lipopolysaccharides biosynthesis acetyltransferase; **PDBTitle:** crystal structure of the 3-n-acetyl transferase wlbb from bordetella2 petrii in complex with coa and udp-3-amino-2-acetamido-2,3-dideoxy3 glucuronic acid
31	c3vbnA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**galactoside o-acetyltransferase; **PDBTitle:** crystal structure of the d94a mutant of antd, an n-acyltransferase2 from bacillus cereus in complex with dtdp and coenzyme a
32	d1t3da_	Alignment	not modelled	99.9	16	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
33	c1t3dB_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
34	d1mr7a_	Alignment	not modelled	99.9	15	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
35	c4e8lC_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**virginiamycin a acetyltransferase; **PDBTitle:** crystal structure of streptogramin group a antibiotic2 acetyltransferase vata from staphylococcus aureus
36	c6mfkA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase from2 elizabethkingia anophelis
37	d1g97a1	Alignment	not modelled	99.9	25	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
38	d1ssqa_	Alignment	not modelled	99.9	13	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
39	c3jqyB_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystal strucutre of the polysia specific acetyltransferase neuo
40	c4n6bB_	Alignment	not modelled	99.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase apoenzyme; **PDBTitle:** soybean serine acetyltransferase complexed with coa
41	d1xata_	Alignment	not modelled	99.9	16	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
42	c3ixcA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexapeptide transferase family protein; **PDBTitle:** crystal structure of hexapeptide transferase family protein from2 anaplasma phagocytophilum
43	c3mc4A_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ww/rsp5/wwp domain:bacterial transferase hexapeptide **PDBTitle:** crystal structure of ww/rsp5/wwp domain: bacterial transferase2 hexapeptide repeat: serine o-acetyltransferase from brucella3 melitensis
44	c4n27D_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**bacterial transferase hexapeptide repeat; **PDBTitle:** x-ray structure of brucella abortus rica
45	c4aa7A_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e.coli glmu in complex with an antibacterial inhibitor
46	d2oi6a1	Alignment	not modelled	99.9	21	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
47	c3eg4A_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase from brucella melitensis3 biovar abortus 2308
48	c3d8vA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis2 in complex with uridine-diphosphate-n-acetylglucosamine
49	c5ux9D_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** the crystal structure of chloramphenicol acetyltransferase from vibrio2 fischeri es114
50	c3foqA_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of n-acetylglucosamine-1-phosphate2 uridyltransferase (glmu) from mycobacterium tuberculosis in3 a cubic space group.
51	c2wlgA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polysialic acid o-acetyltransferase; **PDBTitle:** crystallographic analysis of the polysialic acid o-2 acetyltransferase oatwy
52	d1v3wa_	Alignment	not modelled	99.9	17	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes

						Family:gamma-carbonic anhydrase-like
53	c3eevC_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**chloramphenicol acetyltransferase; **PDBTitle:** crystal structure of chloramphenicol acetyltransferase vca0300 from2 vibrio cholerae o1 biovar eltor
54	c3q1xA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of entamoeba histolytica serine acetyltransferase 12 in complex with l-serine
55	c3r3rA_	Alignment	not modelled	99.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ferripyochelin binding protein; **PDBTitle:** structure of the yrda ferripyochelin binding protein from salmonella2 enterica
56	d3tdta_	Alignment	not modelled	99.9	16	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Tetrahydrodipicolinate-N-succinlytransferase, THDP-succinlytransferase, DapD
57	c3c8vA_	Alignment	not modelled	99.9	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of putative acetyltransferase (yp_390128.1) from2 desulfovibrio desulfuricans g20 at 2.28 a resolution
58	c5afuU_	Alignment	not modelled	99.9	16	**PDB header:**motor protein **Chain:** U: **PDB Molecule:**dynactin; **PDBTitle:** cryo-em structure of dynein tail-dynactin-bicd2n complex
59	c6iveA_	Alignment	not modelled	99.9	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ferripyochelin-binding protein; **PDBTitle:** molecular structure of a thermostable and a zinc ion binding gamma-2 class carbonic anhydrase
60	c4mfgA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acyltransferase; **PDBTitle:** 2.0 angstrom resolution crystal structure of putative carbonic2 anhydrase from clostridium difficile.
61	c1hm8A_	Alignment	not modelled	99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine-1-phosphate uridyltransferase; **PDBTitle:** crystal structure of s.pneumoniae n-acetylglucosamine-1-phosphate2 uridyltransferase, glmu, bound to acetyl coenzyme a
62	c6cktA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal structure of 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n-2 succinyltransferase from legionella pneumophila philadelphia 1
63	d1xhda_	Alignment	not modelled	99.8	18	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
64	c3r1wA_	Alignment	not modelled	99.8	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of a carbonic anhydrase from a crude oil degrading2 psychrophilic library
65	c5afuV_	Alignment	not modelled	99.8	14	**PDB header:**motor protein **Chain:** V: **PDB Molecule:**dynactin; **PDBTitle:** cryo-em structure of dynein tail-dynactin-bicd2n complex
66	c3f1xA_	Alignment	not modelled	99.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** three dimensional structure of the serine acetyltransferase from2 bacteroides vulgatus, northeast structural genomics consortium target3 bvr62.
67	c2v0hA_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** characterization of substrate binding and catalysis of the2 potential antibacterial target n-acetylglucosamine-1-3 phosphate uridyltransferase (glmu)
68	c3kwcD_	Alignment	not modelled	99.8	20	**PDB header:**lyase, protein binding, photosynthesis **Chain:** D: **PDB Molecule:**carbon dioxide concentrating mechanism protein; **PDBTitle:** oxidized, active structure of the beta-carboxysomal gamma-carbonic2 anhydrase, ccmm
69	c2oi6A_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** e. coli glmu- complex with udp-glcnac, coa and glcn-1-po4
70	c3r5dA_	Alignment	not modelled	99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tetrahydrodipicolinate n-succinyletransferase; **PDBTitle:** pseudomonas aeruginosa dapd (pa3666) apoprotein
71	c5e3pA_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n- **PDBTitle:** crystal strcuture of dapd from corynebacterium glutamicum
72	c3tv0A_	Alignment	not modelled	99.8	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**dynactin subunit 6; **PDBTitle:** structure of dynactin p27 subunit
73	c1qreA_	Alignment	not modelled	99.8	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** a closer look at the active site of gamma-carbonic anhydrases: high2 resolution crystallographic studies of the carbonic anhydrase from3 methanosarcina thermophila
74	d1qrea_	Alignment	not modelled	99.8	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**gamma-carbonic anhydrase-like
75	c3fsyC_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**tetrahydrodipicolinate n-succinyltransferase; **PDBTitle:** structure of tetrahydrodipicolinate n-succinyltransferase2 (rv1201c;dapd) in complex with succinyl-coa from mycobacterium3 tuberculosis

76	c3kwdA_	Alignment	not modelled	99.7	19	**PDB header:**lyase, protein binding, photosynthesis **Chain:** A: **PDB Molecule:**carbon dioxide concentrating mechanism protein; **PDBTitle:** inactive truncation of the beta-carboxysomal gamma-carbonic anhydrase,2 ccmm, form 1
77	c2ggqA_	Alignment	not modelled	99.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**401aa long hypothetical glucose-1-phosphate **PDBTitle:** complex of hypothetical glucose-1-phosphate thymidylyltransferase from2 sulfolobus tokodaii
78	c5vmkB_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of a bifunctional glmu udp-n-acetylglucosamine2 diphosphorylase/glucosamine-1- phosphate n-acetyltransferase from3 acinetobacter baumannii
79	d2f9ca1	Alignment	not modelled	99.6	17	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**YdcK-like
80	c6i3mG_	Alignment	not modelled	99.6	20	**PDB header:**translation **Chain:** G: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** eif2b:eif2 complex, phosphorylated on eif2 alpha serine 52.
81	c5b04I_	Alignment	not modelled	99.6	13	**PDB header:**translation **Chain:** I: **PDB Molecule:**probable translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
82	c6jlwJ_	Alignment	not modelled	99.5	7	**PDB header:**translation **Chain:** J: **PDB Molecule:**translation initiation factor eif-2b subunit epsilon; **PDBTitle:** eif2 - eif2b complex
83	c6ezoJ_	Alignment	not modelled	99.5	13	**PDB header:**membrane protein **Chain:** J: **PDB Molecule:**human eukaryotic initiation factor eif2b epsilon subunits; **PDBTitle:** eukaryotic initiation factor eif2b in complex with isrib
84	c5b04F_	Alignment	not modelled	99.5	16	**PDB header:**translation **Chain:** F: **PDB Molecule:**probable translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
85	c3d98A_	Alignment	not modelled	99.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** crystal structure of glmu from mycobacterium tuberculosis, ligand-free2 form
86	c2rijA_	Alignment	not modelled	99.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 2,3,4,5-tetrahydropyridine-2-carboxylate n- **PDBTitle:** crystal structure of a putative 2,3,4,5-tetrahydropyridine-2-2 carboxylate n-succinyltransferase (cj1605c, dapd) from campylobacter3 jejuni at 1.90 a resolution
87	c6qg2F_	Alignment	not modelled	99.4	11	**PDB header:**translation **Chain:** F: **PDB Molecule:**translation initiation factor eif-2b subunit gamma; **PDBTitle:** structure of eif2b-eif2 (phosphorylated at ser51) complex (model a)
88	c2qkxA_	Alignment	not modelled	99.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional protein glmu; **PDBTitle:** n-acetyl glucosamine 1-phosphate uridyltransferase from mycobacterium2 tuberculosis complex with n-acetyl glucosamine 1-phosphate
89	d1fxja1	Alignment	not modelled	99.2	20	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
90	d1yp2a1	Alignment	not modelled	99.2	11	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
91	c6ezoF_	Alignment	not modelled	99.2	20	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**translation initiation factor eif-2b subunit gamma; **PDBTitle:** eukaryotic initiation factor eif2b in complex with isrib
92	c1yp3C_	Alignment	not modelled	99.2	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucose-1-phosphate adenylyltransferase small **PDBTitle:** crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
93	c5l6sF_	Alignment	not modelled	99.1	13	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of e. coli adp-glucose pyrophosphorylase (agpase) in2 complex with a positive allosteric regulator beta-fructose-1,6-3 diphosphate (fbp) - agpase*fbp
94	c1fwyA_	Alignment	not modelled	98.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of n-acetylglucosamine 1-phosphate2 uridyltransferase bound to udp-glcnac
95	c3brkX_	Alignment	not modelled	98.9	16	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glucose-1-phosphate adenylyltransferase; **PDBTitle:** crystal structure of adp-glucose pyrophosphorylase from agrobacterium2 tumefaciens
96	c3nklA_	Alignment	not modelled	98.7	14	**PDB header:**oxidoreductase/lyase **Chain:** A: **PDB Molecule:**udp-d-quinovosamine 4-dehydrogenase; **PDBTitle:** crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
97	c2dt5A_	Alignment	not modelled	98.2	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
98	d2py6a1	Alignment	not modelled	98.0	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases

						Family: FkbM-like
99	c2vt2A_	Alignment	not modelled	97.9	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** structure and functional properties of the bacillus subtilis2 transcriptional repressor rex
100	c3wg9D_	Alignment	not modelled	97.8	9	**PDB header:**transcription **Chain:** D: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of rsp, a rex-family repressor
101	d2dt5a2	Alignment	not modelled	97.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Transcriptional repressor Rex, C-terminal domain
102	c5zz5D_	Alignment	not modelled	97.4	14	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** redox-sensing transcriptional repressor rex
103	c3ketA_	Alignment	not modelled	97.2	12	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
104	c3gfgB_	Alignment	not modelled	95.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
105	d1kjqa2	Alignment	not modelled	94.8	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
106	d1ek6a_	Alignment	not modelled	94.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
107	c6norB_	Alignment	not modelled	94.5	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nad dependent dehydrogenase; **PDBTitle:** crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
108	c3euwB_	Alignment	not modelled	94.4	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
109	d1f06a1	Alignment	not modelled	94.4	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
110	c3dapB_	Alignment	not modelled	94.2	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
111	c2hjrK_	Alignment	not modelled	94.1	18	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of cryptosporidium parvum malate2 dehydrogenase
112	c3dhnA_	Alignment	not modelled	93.9	16	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn from2 bacteroides thetaiotaomicron. northeast structural genomics3 consortium target btr310.
113	c4wpgA_	Alignment	not modelled	93.8	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase; **PDBTitle:** group a streptococcus gaca is an essential dtdp-4-dehydrorhamnose2 reductase (rmld)
114	c3k96B_	Alignment	not modelled	93.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
115	c3e18A_	Alignment	not modelled	93.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
116	c3sc6F_	Alignment	not modelled	93.6	23	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase; **PDBTitle:** 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
117	c2ph5A_	Alignment	not modelled	93.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
118	c2gr2A_	Alignment	not modelled	93.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase, bpha4 (oxidized form)
119	c5gmoA_	Alignment	not modelled	93.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein induced by osmotic stress; **PDBTitle:** x-ray structure of carbonyl reductase sscr
120	c3m2tA_	Alignment	not modelled	93.1	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum