Phyre^2

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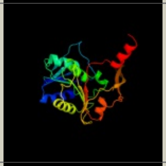
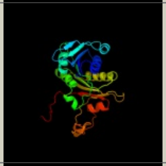
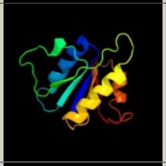
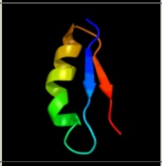
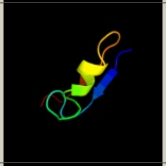
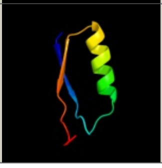
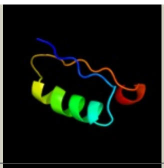
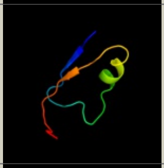
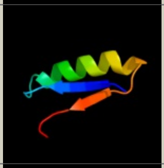
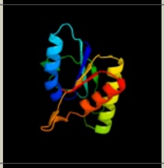
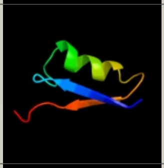
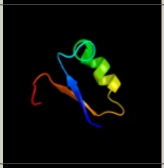
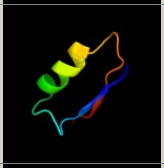
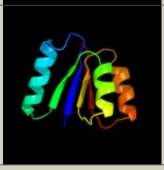
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v4oB_	Alignment		100.0	92	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**multifunctional protein sur e; **PDBTitle:** crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
2	c2phjA_	Alignment		100.0	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of sure protein from aquifex aeolicus
3	d1j9ja_	Alignment		100.0	39	**Fold:**SurE-like **Superfamily:**SurE-like **Family:**SurE-like
4	d1l5xa_	Alignment		100.0	33	**Fold:**SurE-like **Superfamily:**SurE-like **Family:**SurE-like
5	c2e6gI_	Alignment		100.0	38	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of the stationary phase survival protein sure from2 thermus thermophilus hb8 in complex with phosphate
6	c1yxoB_	Alignment		91.6	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
7	c3hbjA_	Alignment		89.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**flavonoid 3-o-glucosyltransferase; **PDBTitle:** structure of ugt78g1 complexed with udp
8	c2p6pB_	Alignment		87.3	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
9	c2gejA_	Alignment		86.5	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol mannosyltransferase (pima); **PDBTitle:** crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
10	c2qzsA_	Alignment		85.1	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen synthase; **PDBTitle:** crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
11	d2bisa1	Alignment		81.5	29	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1

12	d1rrva_	Alignment		81.1	31	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
13	c3c4vB_	Alignment		80.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted glycosyltransferases; **PDBTitle:** structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
14	c3ej6D_	Alignment		79.9	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase-3; **PDBTitle:** neurospora crassa catalase-3 crystal structure
15	c3ot5D_	Alignment		78.9	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
16	d1rzua_	Alignment		77.3	22	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
17	d1ka9h_	Alignment		74.0	29	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
18	d1pn3a_	Alignment		72.4	39	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
19	d1o6ca_	Alignment		72.3	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
20	c2hqoA_	Alignment		71.4	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
21	c3l3bA_	Alignment	not modelled	69.7	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**es1 family protein; **PDBTitle:** crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
22	c2iv3B_	Alignment	not modelled	69.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyltransferase; **PDBTitle:** crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
23	d1iira_	Alignment	not modelled	67.3	39	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
24	c3r0jA_	Alignment	not modelled	66.5	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**possible two component system response transcriptional **PDBTitle:** structure of phop from mycobacterium tuberculosis
25	c2jjmH_	Alignment	not modelled	63.3	15	**PDB header:**transferase **Chain:** H: **PDB Molecule:**glycosyl transferase, group 1 family protein; **PDBTitle:** crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
26	c1vkzA_	Alignment	not modelled	62.4	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
27	d1kgsa2	Alignment	not modelled	62.1	22	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
28	d1ny5a1	Alignment	not modelled	61.2	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

29	d1s3la_	Alignment	not modelled	57.5	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
30	c1s3mA_	Alignment	not modelled	57.5	16	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
31	c3uk7B_	Alignment	not modelled	55.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing **PDBTitle:** crystal structure of arabidopsis thaliana dj-1d
32	c1sy7B_	Alignment	not modelled	50.4	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase 1; **PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
33	c2iufA_	Alignment	not modelled	49.6	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase; **PDBTitle:** the structures of penicillium vitale catalase: resting2 state, oxidised state (compound i) and complex with3 aminotriazole
34	d1dz3a_	Alignment	not modelled	49.1	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
35	d1p80a1	Alignment	not modelled	46.0	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
36	d1a2oa1	Alignment	not modelled	45.5	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
37	d1f6da_	Alignment	not modelled	44.7	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
38	c3h1gA_	Alignment	not modelled	44.2	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis protein chey homolog; **PDBTitle:** crystal structure of chey mutant t84a of helicobacter pylori
39	c2iyaB_	Alignment	not modelled	43.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
40	c2r60A_	Alignment	not modelled	43.4	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
41	c3c97A_	Alignment	not modelled	42.4	20	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**signal transduction histidine kinase; **PDBTitle:** crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
42	c3oy2A_	Alignment	not modelled	41.9	13	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**glycosyltransferase b736l; **PDBTitle:** crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
43	d1wd5a_	Alignment	not modelled	41.5	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
44	c1p81A_	Alignment	not modelled	37.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of the d181e variant of catalase hpii2 from e. coli
45	c3d0qB_	Alignment	not modelled	35.7	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
46	d1ptma_	Alignment	not modelled	35.5	11	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
47	c3lp8A_	Alignment	not modelled	35.5	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
48	c3othB_	Alignment	not modelled	34.5	25	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
49	c2qv0A_	Alignment	not modelled	34.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
50	d2acva1	Alignment	not modelled	33.7	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
51	d1vhqa_	Alignment	not modelled	32.7	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
52	c3f6cB_	Alignment	not modelled	32.4	9	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**positive transcription regulator evga; **PDBTitle:** crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
53	d1qo0d_	Alignment	not modelled	30.8	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Positive regulator of the amidase operon AmiR
54	c2fe9A_	Alignment	not modelled	29.3	27	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein vts1; **PDBTitle:** solution structure of the vts1 sam domain in the presence2 of rna

55	c3ia7A_	Alignment	not modelled	29.2	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
56	d1y0ya2	Alignment	not modelled	28.9	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
57	d2r25b1	Alignment	not modelled	28.3	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
58	d1vi1a_	Alignment	not modelled	27.0	22	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
59	d2a9va1	Alignment	not modelled	26.6	28	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
60	d1sy7a1	Alignment	not modelled	26.5	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
61	d2blla1	Alignment	not modelled	26.1	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
62	c3n7tA_	Alignment	not modelled	25.1	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**macrophage binding protein; **PDBTitle:** crystal structure of a macrophage binding protein from coccidioides2 immitis
63	c1kgsA_	Alignment	not modelled	24.9	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna binding response regulator d; **PDBTitle:** crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
64	c1ulzA_	Alignment	not modelled	23.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
65	d1wl8a1	Alignment	not modelled	23.5	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
66	c2eseA_	Alignment	not modelled	23.1	21	**PDB header:**protein/rna complex **Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** structure of the sam domain of vts1p in complex with rna
67	d1dbwa_	Alignment	not modelled	23.0	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
68	c3icpA_	Alignment	not modelled	22.9	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of udp-galactose 4-epimerase
69	c3ihsB_	Alignment	not modelled	21.8	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
70	c2b6gA_	Alignment	not modelled	21.7	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** rna recognition by the vts1 sam domain
71	c3gt7A_	Alignment	not modelled	21.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
72	c2xdqA_	Alignment	not modelled	20.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
73	c2gpwC_	Alignment	not modelled	20.0	17	**PDB header:**ligase **Chain:** C: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
74	c1ny5A_	Alignment	not modelled	19.9	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
75	d1ecfa1	Alignment	not modelled	19.6	27	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
76	c2h1fB_	Alignment	not modelled	19.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
77	c2iyfA_	Alignment	not modelled	19.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
78	d1w25a1	Alignment	not modelled	19.2	32	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
79	c2dzdB_	Alignment	not modelled	19.1	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
80	c3m2pD_	Alignment	not modelled	19.1	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 4-epimerase; **PDBTitle:** the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
						Fold:7-stranded beta/alpha barrel

81	d2c1ia1	Alignment	not modelled	19.0	16	**Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
82	c3hfwA_	Alignment	not modelled	18.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein adp-ribosylarginine hydrolase; **PDBTitle:** crystal structure of human adp-ribosylhydrolase 1 (harh1)
83	d1o94c_	Alignment	not modelled	18.5	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
84	c3hdgE_	Alignment	not modelled	18.3	20	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
85	c3le1B_	Alignment	not modelled	18.1	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, hpr-related proteins; **PDBTitle:** crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis
86	c2p5uC_	Alignment	not modelled	17.9	28	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
87	d1vkza2	Alignment	not modelled	17.9	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
88	c3ouzA_	Alignment	not modelled	17.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
89	c3nooB_	Alignment	not modelled	16.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
90	c3iaaB_	Alignment	not modelled	16.9	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calg2; **PDBTitle:** crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
91	d1dcfa_	Alignment	not modelled	16.6	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
92	d1n2sa_	Alignment	not modelled	16.4	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	c1ecjB_	Alignment	not modelled	16.3	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
94	c3eodA_	Alignment	not modelled	16.2	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
95	c3eulB_	Alignment	not modelled	16.1	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**possible nitrate/nitrite response transcriptional **PDBTitle:** structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
96	d1f0ka_	Alignment	not modelled	16.0	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
97	c1gsoA_	Alignment	not modelled	15.6	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (glycinamide ribonucleotide synthetase); **PDBTitle:** glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
98	c3d8tB_	Alignment	not modelled	15.5	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** thermus thermophilus uroporphyrinogen iii synthase
99	c3l4bG_	Alignment	not modelled	15.4	21	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**trka k+ channel protien tm1088b; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima