Phyre2

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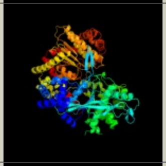
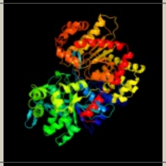
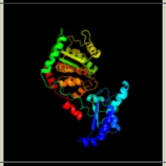
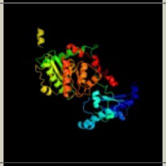
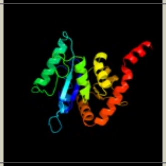
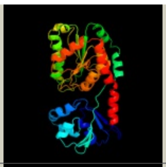
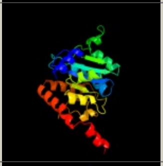
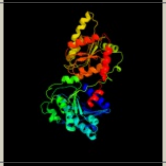
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l5wa_	Alignment		100.0	100	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
2	c3ddsB_	Alignment		100.0	44	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogen phosphorylase, liver form; **PDBTitle:** crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
3	d2atia1	Alignment		100.0	44	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
4	d2gj4a1	Alignment		100.0	44	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
5	c2c4mA_	Alignment		100.0	45	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen phosphorylase; **PDBTitle:** starch phosphorylase: structural studies explain oxyanion-2 dependent kinetic stability and regulatory control.
6	d1ygpa_	Alignment		100.0	43	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
7	c3o3cD_	Alignment		99.5	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glycogen synthase basal state udp complex
8	c3nb0A_	Alignment		99.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glucose-6-phosphate activated form of yeast glycogen synthase
9	d1rzua_	Alignment		98.8	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
10	c2x6rA_	Alignment		98.8	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**trehalose-synthase tret; **PDBTitle:** crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
11	c1uquB_	Alignment		98.7	13	**PDB header:**synthase **Chain:** B: **PDB Molecule:**alpha, alpha-trehalose-phosphate synthase; **PDBTitle:** trehalose-6-phosphate from e. coli bound with udp-glucose.

12	d1uqta_	Alignment		98.6	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Trehalose-6-phosphate synthase, OtsA
13	c2xmpB_	Alignment		98.6	17	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**trehalose-synthase tret; **PDBTitle:** crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
14	c2qzsA_	Alignment		98.4	18	**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)
15	d2bisa1	Alignment		98.1	19	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
16	c2r60A_	Alignment		98.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
17	c3s29C_	Alignment		97.9	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sucrose synthase 1; **PDBTitle:** the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
18	c3c4vB_	Alignment		97.8	23	**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.
19	c3oy2A_	Alignment		97.7	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
20	d2f9fa1	Alignment		96.8	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
21	d2bfwa1	Alignment	not modelled	96.8	19	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
22	c3okaA_	Alignment	not modelled	96.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol **PDBTitle:** crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
23	c2gejA_	Alignment	not modelled	96.6	17	**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
24	c2jjmH_	Alignment	not modelled	96.6	19	**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.
25	d2iw1a1	Alignment	not modelled	96.1	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
26	c2x0dA_	Alignment	not modelled	95.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
27	c3ot5D_	Alignment	not modelled	91.7	13	**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
						PDB header:transferase

28	c2vsnB_	Alignment	not modelled	89.7	20	**Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
29	d1f6da_	Alignment	not modelled	86.5	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
30	c3rhzB_	Alignment	not modelled	86.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleotide sugar synthetase-like protein; **PDBTitle:** structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions
31	c3pe3D_	Alignment	not modelled	78.7	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
32	c3dzcA_	Alignment	not modelled	70.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
33	c3r6mD_	Alignment	not modelled	57.3	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**yeaz, resuscitation promoting factor; **PDBTitle:** crystal structure of vibrio parahaemolyticus yeaz
34	c1okjB_	Alignment	not modelled	54.5	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protease yeaz; **PDBTitle:** crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
35	d1w36c1	Alignment	not modelled	51.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
36	c3qhpB_	Alignment	not modelled	46.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**type 1 capsular polysaccharide biosynthesis protein j **PDBTitle:** crystal structure of the catalytic domain of cholesterol-alpha-2 glucosyltransferase from helicobacter pylori
37	d1x99a_	Alignment	not modelled	33.5	33	**Fold:**Cytolysin/lectin **Superfamily:**Cytolysin/lectin **Family:**Fungal fruit body lectin
38	d1y2ta_	Alignment	not modelled	32.8	33	**Fold:**Cytolysin/lectin **Superfamily:**Cytolysin/lectin **Family:**Fungal fruit body lectin
39	d1v4va_	Alignment	not modelled	32.1	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
40	c1yz4A_	Alignment	not modelled	31.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase-like 15 isoform a; **PDBTitle:** crystal structure of dusp15
41	c2z8tX_	Alignment	not modelled	31.3	13	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**protein-glutaminase; **PDBTitle:** crystal structure of protein-glutaminase of c.proteolyticum2 strain 9670
42	c2ofeA_	Alignment	not modelled	27.5	33	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sclerotium rolfsii lectin; **PDBTitle:** the crystal structure of sclerotium rolfsii lectin in complex with n-2 acetyl-d-glucosamine
43	d1kx5b_	Alignment	not modelled	26.9	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
44	c2iv3B_	Alignment	not modelled	26.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyltransferase; **PDBTitle:** crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
45	c3g8qA_	Alignment	not modelled	25.0	42	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**predicted rna-binding protein, contains thump **PDBTitle:** a cytidine deaminase edits c-to-u in transfer rnas in2 archaea
46	c2g6zB_	Alignment	not modelled	23.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 5; **PDBTitle:** crystal structure of human dusp5
47	d2f8la1	Alignment	not modelled	21.5	30	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
48	c1zhcA_	Alignment	not modelled	20.9	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hp1242; **PDBTitle:** solution structure of hp1242 from helicobacter pylori
49	c2npiB_	Alignment	not modelled	20.9	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein clp1; **PDBTitle:** clp1-atp-pcf11 complex
50	c2oudA_	Alignment	not modelled	20.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the catalytic domain of human mkp5
51	d1id3b_	Alignment	not modelled	20.1	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
52	c3pn1A_	Alignment	not modelled	18.6	19	**PDB header:**ligase/ligase inhibitor **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
53	c1keeH_	Alignment	not modelled	17.0	17	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain;

						PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
54	c3se4B_	Alignment	not modelled	16.8	29	**PDB header:**immune system receptor **Chain:** B: **PDB Molecule:**interferon omega-1; **PDBTitle:** human ifnw-ifnar ternary complex
55	c1r30A_	Alignment	not modelled	16.3	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
56	d1r30a_	Alignment	not modelled	16.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase
57	d1bh9b_	Alignment	not modelled	16.1	18	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
58	d1yb3a1	Alignment	not modelled	16.0	21	**Fold:**YktB/PF0168-like **Superfamily:**YktB/PF0168-like **Family:**PF0168-like
59	c2a6aB_	Alignment	not modelled	15.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical protein tm0874; **PDBTitle:** crystal structure of glycoprotein endopeptidase (tm0874) from2 thermotoga maritima at 2.50 a resolution
60	c1wrmA_	Alignment	not modelled	15.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 22; **PDBTitle:** crystal structure of jsp-1
61	c3emuA_	Alignment	not modelled	14.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine rich repeat and phosphatase domain **PDBTitle:** crystal structure of a leucine rich repeat and phosphatase2 domain containing protein from entamoeba histolytica
62	d1m3ga_	Alignment	not modelled	14.8	14	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
63	c3rgqA_	Alignment	not modelled	14.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine phosphatase mitochondrial 1; **PDBTitle:** crystal structure of ptpmt1 in complex with pi(5)p
64	c2hcmA_	Alignment	not modelled	14.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural genomics3 consortium
65	c2e0tA_	Alignment	not modelled	14.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 26; **PDBTitle:** crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
66	d1o58a_	Alignment	not modelled	14.2	18	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
67	d2enda_	Alignment	not modelled	13.9	18	**Fold:**T4 endonuclease V **Superfamily:**T4 endonuclease V **Family:**T4 endonuclease V
68	d2huec1	Alignment	not modelled	13.9	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
69	c1yhuA_	Alignment	not modelled	13.3	17	**PDB header:**oxygen storage/transport **Chain:** A: **PDB Molecule:**hemoglobin a1 chain; **PDBTitle:** crystal structure of riftia pachyptila c1 hemoglobin reveals novel2 assembly of 24 subunits.
70	c3piwA_	Alignment	not modelled	12.1	24	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**type i interferon 2; **PDBTitle:** zebrafish interferon 2
71	d2csua3	Alignment	not modelled	12.1	35	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
72	c1eysC_	Alignment	not modelled	11.2	22	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
73	d1eysc_	Alignment	not modelled	11.2	22	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
74	c3bacA_	Alignment	not modelled	11.1	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** structural basis for the inhibition of bacterial nad+2 dependent dna ligase
75	d3cjrb1	Alignment	not modelled	11.0	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein L11, C-terminal domain **Family:**Ribosomal protein L11, C-terminal domain
76	d1v9pa3	Alignment	not modelled	10.6	16	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
77	d3etja2	Alignment	not modelled	10.5	38	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
78	c2bpsA_	Alignment	not modelled	10.3	22	**PDB header:**ubiquitin **Chain:** A: **PDB Molecule:**yukd protein; **PDBTitle:** ubiquitin-like protein yukd of bacillus subtilis

79	d1ta8a_	Alignment	not modelled	10.1	26	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
80	d1vhra_	Alignment	not modelled	10.1	19	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
81	c3f4yF_	Alignment	not modelled	10.0	64	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**mutant peptide derived from hiv gp41 chr domain; **PDBTitle:** hiv gp41 six-helix bundle containing a mutant chr alpha-2 peptide sequence
82	d1b5la_	Alignment	not modelled	9.5	29	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
83	c1hfeT_	Alignment	not modelled	9.5	31	**PDB header:**hydrogenase **Chain:** T: **PDB Molecule:**protein (fe-only hydrogenase (e.c.1.18.99.1) **PDBTitle:** 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
84	d1hfes_	Alignment	not modelled	9.5	31	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Fe-only hydrogenase smaller subunit **Family:**Fe-only hydrogenase smaller subunit
85	d1hbna2	Alignment	not modelled	9.3	30	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
86	d1qcsa1	Alignment	not modelled	9.0	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
87	d1u3da1	Alignment	not modelled	8.9	21	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
88	d1o82a_	Alignment	not modelled	8.6	70	**Fold:**Saposin-like **Superfamily:**Bacteriocin AS-48 **Family:**Bacteriocin AS-48
89	c2imgA_	Alignment	not modelled	8.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 23; **PDBTitle:** crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
90	c3bdkB_	Alignment	not modelled	8.6	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
91	d1di1a_	Alignment	not modelled	8.5	13	**Fold:**Terpenoid synthases **Superfamily:**Terpenoid synthases **Family:**Aristolochene/pentalenene synthase
92	d1pq4a_	Alignment	not modelled	8.5	18	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
93	d2ipqx1	Alignment	not modelled	8.4	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**STY4665 C-terminal domain-like
94	c1yl7F_	Alignment	not modelled	8.4	23	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c)
95	d2b0ja2	Alignment	not modelled	8.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
96	d3eeqa1	Alignment	not modelled	8.2	2	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
97	c2owoA_	Alignment	not modelled	8.2	19	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
98	c2ktlA_	Alignment	not modelled	8.2	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of c-terminal domain from mttyrrs of a. nidulans
99	c2diiA_	Alignment	not modelled	8.1	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit