Phyre^2

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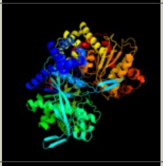
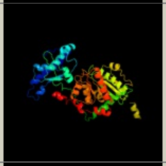
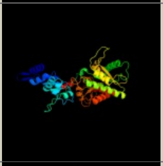
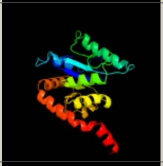
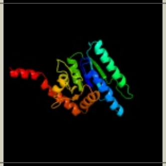
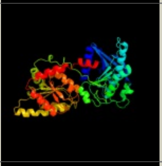
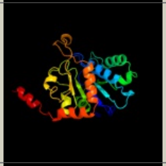
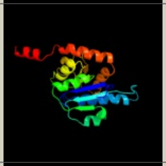
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ddsB_	Alignment		100.0	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogen phosphorylase, liver form; **PDBTitle:** crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
2	d2gj4a1	Alignment		100.0	50	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
3	d2atia1	Alignment		100.0	51	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
4	d1ygpa_	Alignment		100.0	47	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
5	c2c4mA_	Alignment		100.0	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen phosphorylase; **PDBTitle:** starch phosphorylase: structural studies explain oxyanion-2 dependent kinetic stability and regulatory control.
6	d1l5wa_	Alignment		100.0	46	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
7	c3nb0A_	Alignment		99.4	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glucose-6-phosphate activated form of yeast glycogen synthase
8	c3o3cD_	Alignment		99.3	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glycogen synthase basal state udp complex
9	d1rzua_	Alignment		98.7	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
10	c2x6rA_	Alignment		98.6	19	**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	c2xmpB_	Alignment		98.3	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

12	c2qzsA_	Alignment		98.3	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)
13	c2r60A_	Alignment		98.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
14	d1uqta_	Alignment		97.9	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Trehalose-6-phosphate synthase, OtsA
15	c1uquB_	Alignment		97.9	11	**PDB header:**synthase **Chain:** B: **PDB Molecule:**alpha, alpha-trehalose-phosphate synthase; **PDBTitle:** trehalose-6-phosphate from e. coli bound with udp-glucose.
16	d2bisa1	Alignment		97.8	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
17	c3oy2A_	Alignment		97.7	16	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**glycosyltransferase b736l; **PDBTitle:** crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
18	c3s29C_	Alignment		97.7	17	**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.
19	c3c4vB_	Alignment		97.5	18	**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.
20	c3okaA_	Alignment		97.0	18	**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)
21	d2bfwa1	Alignment	not modelled	96.8	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
22	c2gejA_	Alignment	not modelled	96.4	13	**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
23	c2jjmH_	Alignment	not modelled	96.4	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.
24	d2f9fa1	Alignment	not modelled	96.0	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
25	d2iw1a1	Alignment	not modelled	95.3	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
26	c2x0dA_	Alignment	not modelled	93.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
27	c2vsnB_	Alignment	not modelled	93.3	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
						PDB header:isomerase

28	c3ot5D_	Alignment	not modelled	93.2	12	**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
29	d1f6da_	Alignment	not modelled	90.5	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
30	c3pe3D_	Alignment	not modelled	90.2	18	**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
31	c3dzcA_	Alignment	not modelled	84.0	11	**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.
32	c3rhzB_	Alignment	not modelled	79.6	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
33	c2iv3B_	Alignment	not modelled	62.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyltransferase; **PDBTitle:** crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
34	c3qhpB_	Alignment	not modelled	61.2	15	**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
35	c1yz4A_	Alignment	not modelled	59.2	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase-like 15 isoform a; **PDBTitle:** crystal structure of dusp15
36	c2g6zB_	Alignment	not modelled	47.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 5; **PDBTitle:** crystal structure of human dusp5
37	d1w36c1	Alignment	not modelled	45.6	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
38	c2z8tX_	Alignment	not modelled	41.3	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**protein-glutaminase; **PDBTitle:** crystal structure of protein-glutaminase of c.proteolyticum2 strain 9670
39	d1m3ga_	Alignment	not modelled	38.4	16	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
40	c1wrmA_	Alignment	not modelled	37.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 22; **PDBTitle:** crystal structure of jsp-1
41	c2e0tA_	Alignment	not modelled	37.0	24	**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
42	d1x99a_	Alignment	not modelled	33.1	44	**Fold:**Cytolysin/lectin **Superfamily:**Cytolysin/lectin **Family:**Fungal fruit body lectin
43	d1y2ta_	Alignment	not modelled	32.6	44	**Fold:**Cytolysin/lectin **Superfamily:**Cytolysin/lectin **Family:**Fungal fruit body lectin
44	c2oudA_	Alignment	not modelled	31.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the catalytic domain of human mkp5
45	d1vhra_	Alignment	not modelled	30.4	19	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
46	c3rgqA_	Alignment	not modelled	29.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine phosphatase mitochondrial 1; **PDBTitle:** crystal structure of ptpmt1 in complex with pi(5)p
47	c2npiB_	Alignment	not modelled	27.9	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein clp1; **PDBTitle:** clp1-atp-pcf11 complex
48	c2ofeA_	Alignment	not modelled	27.8	44	**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
49	c2wgpA_	Alignment	not modelled	25.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 14; **PDBTitle:** crystal structure of human dual specificity phosphatase 14
50	c2hcmA_	Alignment	not modelled	25.7	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
51	d3etja2	Alignment	not modelled	24.7	38	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
52	c3se4B_	Alignment	not modelled	24.5	25	**PDB header:**immune system receptor **Chain:** B: **PDB Molecule:**interferon omega-1; **PDBTitle:** human ifnw-ifnar ternary complex
53	c2y96A_	Alignment	not modelled	22.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase dupd1; **PDBTitle:** structure of human dual-specificity phosphatase 27
						PDB header:oxygen storage/transport

54	c1yhuA_	Alignment	not modelled	22.6	16	**Chain:** A: **PDB Molecule:**hemoglobin a1 chain; **PDBTitle:** crystal structure of riftia pachyptila c1 hemoglobin reveals novel2 assembly of 24 subunits.
55	c2imgA_	Alignment	not modelled	22.5	11	**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
56	c3emuA_	Alignment	not modelled	22.0	18	**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
57	c2j17A_	Alignment	not modelled	21.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase yil113w; **PDBTitle:** ptyr bound form of sdp-1
58	c3prjB_	Alignment	not modelled	21.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
59	d1m1nb_	Alignment	not modelled	20.9	19	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
60	c2nt2C_	Alignment	not modelled	20.8	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein phosphatase slingshot homolog 2; **PDBTitle:** crystal structure of slingshot phosphatase 2
61	c3piwA_	Alignment	not modelled	19.5	24	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**type i interferon 2; **PDBTitle:** zebrafish interferon 2
62	d1u3da1	Alignment	not modelled	19.4	26	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
63	d1mv8a1	Alignment	not modelled	19.4	17	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
64	d1dlja1	Alignment	not modelled	19.1	28	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**UDP-glucose/GDP-mannose dehydrogenase dimerisation domain
65	c2gwoC_	Alignment	not modelled	19.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dual specificity protein phosphatase 13; **PDBTitle:** crystal structure of tmdp
66	c3bdkB_	Alignment	not modelled	18.8	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
67	d1v3aa_	Alignment	not modelled	18.8	27	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
68	c3pn1A_	Alignment	not modelled	18.5	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
69	d1v9pa3	Alignment	not modelled	18.0	13	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
70	c2a6aB_	Alignment	not modelled	17.7	16	**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
71	c2r0bA_	Alignment	not modelled	17.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine/tyrosine-interacting protein; **PDBTitle:** crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
72	d2f8la1	Alignment	not modelled	17.4	20	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**N-6 DNA Methylase-like
73	d1o58a_	Alignment	not modelled	17.1	16	**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
74	d1ta8a_	Alignment	not modelled	16.9	26	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
75	d3buxb2	Alignment	not modelled	16.6	20	**Fold:**N-cbl like **Superfamily:**N-terminal domain of cbl (N-cbl) **Family:**N-terminal domain of cbl (N-cbl)
76	d1b5la_	Alignment	not modelled	15.4	24	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
77	d1v4va_	Alignment	not modelled	15.2	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
78	d1r30a_	Alignment	not modelled	15.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Biotin synthase
						PDB header:transferase

79	c1r30A_	Alignment	not modelled	15.0	14	**Chain:** A: **PDB Molecule:**biotin synthase; **PDBTitle:** the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
80	c3bacA_	Alignment	not modelled	14.7	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** structural basis for the inhibition of bacterial nad+2 dependent dna ligase
81	c2y0dB_	Alignment	not modelled	14.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
82	c2k29A_	Alignment	not modelled	14.2	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
83	c1eysC_	Alignment	not modelled	13.8	18	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
84	d1eysc_	Alignment	not modelled	13.8	18	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Photosynthetic reaction centre (cytochrome subunit)
85	d1mkpa_	Alignment	not modelled	13.5	13	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
86	c3f4yF_	Alignment	not modelled	13.4	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
87	c2o3jC_	Alignment	not modelled	13.3	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of caenorhabditis elegans udp-glucose dehydrogenase
88	d1ohea2	Alignment	not modelled	12.9	13	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
89	c2esbA_	Alignment	not modelled	12.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 18; **PDBTitle:** crystal structure of human dusp18
90	c3rz2B_	Alignment	not modelled	12.6	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein tyrosine phosphatase type iva 1; **PDBTitle:** crystal of prl-1 complexed with peptide
91	d1au1a_	Alignment	not modelled	12.6	10	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
92	d1qkia1	Alignment	not modelled	12.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
93	d1rh2a_	Alignment	not modelled	12.6	29	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
94	c3r6mD_	Alignment	not modelled	12.5	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**yeaz, resuscitation promoting factor; **PDBTitle:** crystal structure of vibrio parahaemolyticus yeaz
95	c3cvyA_	Alignment	not modelled	12.3	23	**PDB header:**lyase/dna **Chain:** A: **PDB Molecule:**re11660p; **PDBTitle:** drosophila melanogaster (6-4) photolyase bound to repaired2 ds dna
96	d1di1a_	Alignment	not modelled	12.3	13	**Fold:**Terpenoid synthases **Superfamily:**Terpenoid synthases **Family:**Aristolochene/pentalenene synthase
97	c1fbvA_	Alignment	not modelled	12.2	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**signal transduction protein cbl; **PDBTitle:** structure of a cbl-ubch7 complex: ring domain function in2 ubiquitin-protein ligases
98	d1i9sa_	Alignment	not modelled	12.1	14	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
99	d1wu3i_	Alignment	not modelled	12.1	10	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)