Phyre2

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Description	P27242
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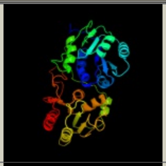
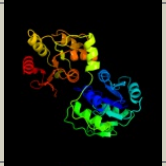
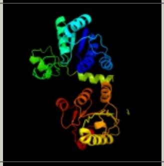
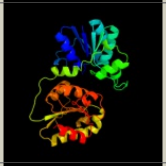
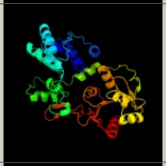
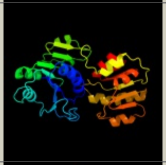
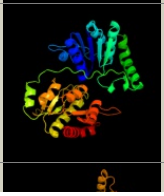
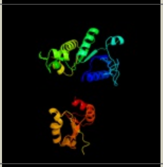
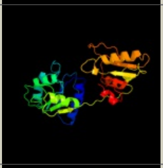
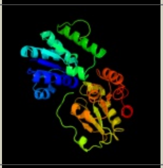
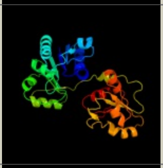
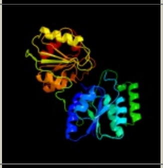
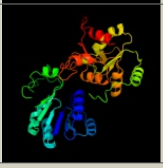
Unique Job ID	2fb8049e1689b393

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3tovB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 9; **PDBTitle:** the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
2	d1pswa_	Alignment		100.0	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**ADP-heptose LPS heptosyltransferase II
3	c2h1fB_	Alignment		100.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
4	d1v4va_	Alignment		99.2	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
5	c3ot5D_	Alignment		99.1	12	**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
6	d1o6ca_	Alignment		98.8	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
7	d1f6da_	Alignment		98.8	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
8	c3dzcA_	Alignment		98.4	13	**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.
9	c3hbmA_	Alignment		97.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
10	d1f0ka_	Alignment		97.9	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
11	d1pn3a_	Alignment		97.7	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
						

12	c2xcuC_	Alignment		97.3	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**3-deoxy-d-manno-2-octulosonic acid transferase; **PDBTitle:** membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, comlex with cmp
13	c2vsnB_	Alignment		97.1	9	**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
14	c2r60A_	Alignment		97.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
15	c3oy2A_	Alignment		96.8	11	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**glycosyltransferase b736l; **PDBTitle:** crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
16	c2jjmH_	Alignment		96.8	11	**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.
17	c3othB_	Alignment		96.7	12	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
18	c2gejA_	Alignment		96.6	10	**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
19	c3iaaB_	Alignment		96.3	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calg2; **PDBTitle:** crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
20	c3okaA_	Alignment		96.1	11	**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	c3d0qB_	Alignment	not modelled	95.4	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
22	c3c4vB_	Alignment	not modelled	95.3	12	**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.
23	d1rrva_	Alignment	not modelled	95.0	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
24	c2x6rA_	Alignment	not modelled	94.2	16	**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
25	c2p6pB_	Alignment	not modelled	93.5	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
26	c2o6lA_	Alignment	not modelled	93.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucuronosyltransferase 2b7; **PDBTitle:** crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
27	c2q6vA_	Alignment	not modelled	93.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucuronosyltransferase gumk; **PDBTitle:** crystal structure of gumk in complex with udp
28	c2iyaB_	Alignment	not modelled	93.1	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering

29	d1iira_	Alignment	not modelled	91.5	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
30	c3ia7A_	Alignment	not modelled	91.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
31	c3qhpB_	Alignment	not modelled	90.2	8	**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
32	d2ptza1	Alignment	not modelled	89.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
33	c2iyfA_	Alignment	not modelled	88.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
34	c2khzB_	Alignment	not modelled	88.2	15	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**c-myc-responsive protein rcl; **PDBTitle:** solution structure of rcl
35	d1w6ta1	Alignment	not modelled	87.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
36	c3ehdA_	Alignment	not modelled	87.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of conserved protein from enterococcus faecalis v583
37	d2acva1	Alignment	not modelled	86.6	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
38	d1iyxa1	Alignment	not modelled	85.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
39	d2akza1	Alignment	not modelled	81.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
40	d2f62a1	Alignment	not modelled	79.3	32	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
41	d2c1xa1	Alignment	not modelled	78.9	8	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
42	d1s2da_	Alignment	not modelled	78.1	16	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
43	c2xmpB_	Alignment	not modelled	77.9	18	**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
44	c3l7mC_	Alignment	not modelled	76.7	13	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**teichoic acid biosynthesis protein f; **PDBTitle:** structure of the wall teichoic acid polymerase tagf, h548a
45	d1f8ya_	Alignment	not modelled	76.2	22	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
46	c2x0dA_	Alignment	not modelled	72.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
47	c2ptwA_	Alignment	not modelled	70.6	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of the t. brucei enolase complexed with2 sulphate, identification of a metal binding site iv
48	c3zquA_	Alignment	not modelled	69.9	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
49	d2g8la1	Alignment	not modelled	68.8	10	**Fold:**AF1104-like **Superfamily:**AF1104-like **Family:**AF1104-like
50	d1a9xa3	Alignment	not modelled	67.7	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
51	c3pe3D_	Alignment	not modelled	67.5	10	**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
52	c3cwcB_	Alignment	not modelled	65.5	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
53	c3otrC_	Alignment	not modelled	65.4	7	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase; **PDBTitle:** 2.75 angstrom crystal structure of enolase 1 from toxoplasma gondii
54	d1pdza1	Alignment	not modelled	64.8	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
55	d2fyma1	Alignment	not modelled	62.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase

56	c3qjgD_	Alignment	not modelled	59.7	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**epidermin biosynthesis protein epid; **PDBTitle:** epidermin biosynthesis protein epid from staphylococcus aureus
57	c2jzcA_	Alignment	not modelled	58.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine transferase subunit **PDBTitle:** nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
58	c3pdiB_	Alignment	not modelled	57.4	9	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nitrogenase mofe cofactor biosynthesis protein nifn; **PDBTitle:** precursor bound nifen
59	d1mvla_	Alignment	not modelled	57.3	9	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
60	c1mvlA_	Alignment	not modelled	57.3	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ppc decarboxylase athal3a; **PDBTitle:** ppc decarboxylase mutant c175s
61	d2pq6a1	Alignment	not modelled	57.3	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
62	d2al1a1	Alignment	not modelled	56.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
63	c3qtpB_	Alignment	not modelled	53.5	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enolase 1; **PDBTitle:** crystal structure analysis of entamoeba histolytica enolase
64	c3uj2C_	Alignment	not modelled	51.8	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** crystal structure of an enolase from anaerostipes caccae (efi target2 efi-502054) with bound mg and sulfate
65	d1xfia_	Alignment	not modelled	51.1	33	**Fold:**AF1104-like **Superfamily:**AF1104-like **Family:**AF1104-like
66	c3afoB_	Alignment	not modelled	50.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nadh kinase pos5; **PDBTitle:** crystal structure of yeast nadh kinase complexed with nadh
67	c2ejbA_	Alignment	not modelled	48.1	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
68	c2pa6A_	Alignment	not modelled	47.5	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of mj0232 from methanococcus jannaschii
69	c3thdD_	Alignment	not modelled	47.2	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
70	d1vbga2	Alignment	not modelled	46.0	8	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
71	d1kbla2	Alignment	not modelled	45.9	7	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
72	d1ybha1	Alignment	not modelled	45.8	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
73	c2fymA_	Alignment	not modelled	44.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of e. coli enolase complexed with the2 minimal binding segment of rnase e.
74	d1p3y1_	Alignment	not modelled	41.0	16	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
75	c3tqpA_	Alignment	not modelled	39.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** structure of an enolase (eno) from coxiella burnetii
76	c3q3hA_	Alignment	not modelled	39.8	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase; **PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
77	c3d3aA_	Alignment	not modelled	38.9	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of a beta-galactosidase from bacteroides2 thetaiotaomicron
78	c3qn3B_	Alignment	not modelled	38.8	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enolase; **PDBTitle:** phosphopyruvate hydratase from campylobacter jejuni.
79	d1g5qa_	Alignment	not modelled	36.6	16	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
						PDB header:isomerase

80	c3qvjB_	Alignment	not modelled	34.3	17	**Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae
81	c3ogrA_	Alignment	not modelled	33.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** complex structure of beta-galactosidase from trichoderma reesei with2 galactose
82	c3aerB_	Alignment	not modelled	32.5	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**light-independent protochlorophyllide reductase subunit b; **PDBTitle:** structure of the light-independent protochlorophyllide reductase2 catalyzing a key reduction for greening in the dark
83	d1a9xa4	Alignment	not modelled	32.3	10	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
84	c3mcuF_	Alignment	not modelled	31.2	7	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dipicolinate synthase, b chain; **PDBTitle:** crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
85	d1to6a_	Alignment	not modelled	30.3	19	**Fold:**Glycerate kinase I **Superfamily:**Glycerate kinase I **Family:**Glycerate kinase I
86	c1qgeD_	Alignment	not modelled	29.6	7	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
87	c3k94A_	Alignment	not modelled	29.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin pyrophosphokinase; **PDBTitle:** crystal structure of thiamin pyrophosphokinase from geobacillus2 thermodenitrificans, northeast structural genomics consortium target3 gtr2
88	d2ffja1	Alignment	not modelled	29.3	14	**Fold:**AF1104-like **Superfamily:**AF1104-like **Family:**AF1104-like
89	d2f9fa1	Alignment	not modelled	27.5	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
90	d1m5wa_	Alignment	not modelled	26.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
91	d2jfga1	Alignment	not modelled	26.7	12	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
92	c3lqkA_	Alignment	not modelled	26.0	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
93	c1iyxA_	Alignment	not modelled	25.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of enolase from enterococcus hirae
94	c1l8pC_	Alignment	not modelled	23.9	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**enolase 1; **PDBTitle:** mg-phosphonoacetohydroxamate complex of s39a yeast enolase 1
95	c3cq9C_	Alignment	not modelled	23.2	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uncharacterized protein lp_1622; **PDBTitle:** crystal structure of the lp_1622 protein from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr114
96	d2bisa1	Alignment	not modelled	21.4	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
97	c3bzjA_	Alignment	not modelled	20.7	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uv endonuclease; **PDBTitle:** uvde k229l
98	c2hwwC_	Alignment	not modelled	19.3	17	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**telomerase-binding protein est1a; **PDBTitle:** structure of pin domain of human smg6
99	c3lm8D_	Alignment	not modelled	19.1	31	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine pyrophosphokinase; **PDBTitle:** crystal structure of thiamine pyrophosphokinase from2 bacillus subtilis, northeast structural genomics consortium3 target sr677