Phyre2

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Description	P37751
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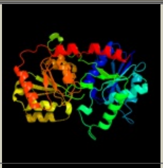
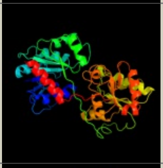
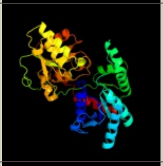
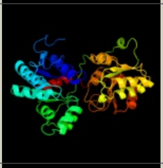
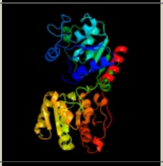
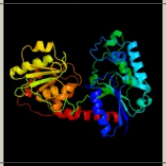
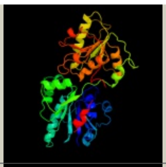
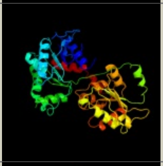
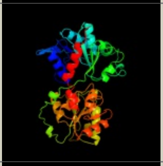
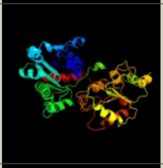
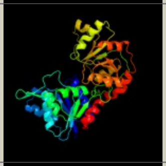
Unique Job ID	81e181f9adc0593c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3s29C_	Alignment		100.0	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.
2	c3oy2A_	Alignment		100.0	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
3	c2r60A_	Alignment		100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
4	c3c4vB_	Alignment		100.0	13	**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.
5	c3okaA_	Alignment		100.0	13	**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)
6	c2jjmH_	Alignment		100.0	13	**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.
7	d2bisa1	Alignment		100.0	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
8	c2qzsA_	Alignment		100.0	14	**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)
9	c2xmpB_	Alignment		100.0	14	**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
10	c2x6rA_	Alignment		100.0	14	**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	c2gejA_	Alignment		100.0	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

12	c2x0dA_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
13	c1uquB_	Alignment		100.0	12	**PDB header:**synthase **Chain:** B: **PDB Molecule:**alpha, alpha-trehalose-phosphate synthase; **PDBTitle:** trehalose-6-phosphate from e. coli bound with udp-glucose.
14	d1rzua_	Alignment		100.0	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
15	d2iw1a1	Alignment		100.0	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
16	d1uqta_	Alignment		100.0	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Trehalose-6-phosphate synthase, OtsA
17	c3o3cD_	Alignment		100.0	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glycogen synthase basal state udp complex
18	c3nb0A_	Alignment		100.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glucose-6-phosphate activated form of yeast glycogen synthase
19	c3rhzB_	Alignment		100.0	9	**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
20	c3dzcA_	Alignment		100.0	12	**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.
21	c3ot5D_	Alignment	not modelled	100.0	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
22	d1f6da_	Alignment	not modelled	100.0	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
23	d1v4va_	Alignment	not modelled	100.0	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
24	c2iv3B_	Alignment	not modelled	100.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyltransferase; **PDBTitle:** crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
25	c2q6vA_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucuronosyltransferase gumk; **PDBTitle:** crystal structure of gumk in complex with udp
26	c2xcuC_	Alignment	not modelled	100.0	13	**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
27	d2f9fa1	Alignment	not modelled	99.9	20	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
28	d1o6ca_	Alignment	not modelled	99.9	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
						PDB header:transferase

29	c3qhpB_	Alignment	not modelled	99.9	15	**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
30	d1f0ka_	Alignment	not modelled	99.8	9	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
31	c2vsnB_	Alignment	not modelled	99.8	11	**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
32	d2bfwa1	Alignment	not modelled	99.8	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
33	c3ia7A_	Alignment	not modelled	99.8	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
34	c3othB_	Alignment	not modelled	99.8	8	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
35	c3iaaB_	Alignment	not modelled	99.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calg2; **PDBTitle:** crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
36	c3pe3D_	Alignment	not modelled	99.7	7	**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
37	c2iyaB_	Alignment	not modelled	99.7	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
38	c2iyfA_	Alignment	not modelled	99.7	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
39	c2p6pB_	Alignment	not modelled	99.6	6	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
40	d1iira_	Alignment	not modelled	99.6	9	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
41	d1pn3a_	Alignment	not modelled	99.5	8	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
42	c3d0qB_	Alignment	not modelled	99.4	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
43	d1rrva_	Alignment	not modelled	99.3	10	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
44	c3hbmA_	Alignment	not modelled	98.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
45	c3l7mC_	Alignment	not modelled	98.4	9	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**teichoic acid biosynthesis protein f; **PDBTitle:** structure of the wall teichoic acid polymerase tagf, h548a
46	d2c1xa1	Alignment	not modelled	98.0	7	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
47	d2acva1	Alignment	not modelled	97.8	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
48	d1ygpa_	Alignment	not modelled	97.7	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
49	d2gj4a1	Alignment	not modelled	97.7	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
50	c2c4mA_	Alignment	not modelled	97.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen phosphorylase; **PDBTitle:** starch phosphorylase: structural studies explain oxyanion-2 dependent kinetic stability and regulatory control.
51	c3ddsB_	Alignment	not modelled	97.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogen phosphorylase, liver form; **PDBTitle:** crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
52	d1l5wa_	Alignment	not modelled	97.5	19	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
53	c3tovB_	Alignment	not modelled	97.5	11	**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
54	d2pq6a1	Alignment	not modelled	97.5	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
						PDB header:transferase **Chain:** A: **PDB Molecule:**udp-glucuronosyltransferase 2b7;

55	c2o6lA_	Alignment	not modelled	97.5	11	**PDBTitle:** crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
56	d2atia1	Alignment	not modelled	97.3	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
57	d2vcha1	Alignment	not modelled	97.2	7	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
58	c3hbjA_	Alignment	not modelled	97.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**flavonoid 3-o-glucosyltransferase; **PDBTitle:** structure of ugt78g1 complexed with udp
59	c3q3hA_	Alignment	not modelled	97.1	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
60	c2h1fB_	Alignment	not modelled	96.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
61	d1pswa_	Alignment	not modelled	96.3	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**ADP-heptose LPS heptosyltransferase II
62	c2jzcA_	Alignment	not modelled	94.6	8	**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
63	c2iz6A_	Alignment	not modelled	85.8	9	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
64	d1d4aa_	Alignment	not modelled	79.9	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
65	c2yy7B_	Alignment	not modelled	71.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-threonine dehydrogenase; **PDBTitle:** crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaris kuc-1
66	c1drwA_	Alignment	not modelled	55.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
67	d2qwxa1	Alignment	not modelled	53.8	11	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
68	d1vi6a_	Alignment	not modelled	52.3	20	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
69	c2qsjB_	Alignment	not modelled	50.2	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-binding response regulator, luxr family; **PDBTitle:** crystal structure of a luxr family dna-binding response2 regulator from silicibacter pomeroyi
70	c3rysA_	Alignment	not modelled	49.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase 1; **PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
71	c3bbnB_	Alignment	not modelled	45.1	16	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**ribosomal protein s2; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
72	c2zkqb_	Alignment	not modelled	41.8	10	**PDB header:**ribosomal protein/rna **Chain:** B: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
73	d2gy9b1	Alignment	not modelled	40.5	17	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
74	d1r8ka_	Alignment	not modelled	40.4	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
75	c2xznB_	Alignment	not modelled	40.4	12	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**rps0e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
76	c3bchA_	Alignment	not modelled	39.2	16	**PDB header:**cell adhesion, ribosomal protein **Chain:** A: **PDB Molecule:**40s ribosomal protein sa; **PDBTitle:** crystal structure of the human laminin receptor precursor
77	c3b2nA_	Alignment	not modelled	36.1	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**uncharacterized protein q99uf4; **PDBTitle:** crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
78	c3ktoA_	Alignment	not modelled	33.0	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
79	d1vfla1	Alignment	not modelled	32.8	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
80	d1e6ca_	Alignment	not modelled	32.7	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate

80	d1e0ca_	Alignment	not modelled	32.7	27	hydrolases **Family:**Shikimate kinase (AroK)
81	d1oi7a2	Alignment	not modelled	32.5	12	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
82	c3izbA_	Alignment	not modelled	31.6	18	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein rps0 (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
83	d1ny5a1	Alignment	not modelled	29.4	6	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
84	c3sc6F_	Alignment	not modelled	29.2	17	**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
85	c2h29A_	Alignment	not modelled	28.6	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
86	c3pg8B_	Alignment	not modelled	27.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
87	c3cm0A_	Alignment	not modelled	27.4	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of adenylate kinase from thermus2 thermophilus hb8
88	d1ys7a2	Alignment	not modelled	27.4	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
89	d1rcua_	Alignment	not modelled	26.0	12	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
90	c1rcuB_	Alignment	not modelled	26.0	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein vt76; **PDBTitle:** x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
91	c2qx7A_	Alignment	not modelled	26.0	5	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
92	d2uubb1	Alignment	not modelled	23.9	10	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
93	d1a4ma_	Alignment	not modelled	23.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
94	d1diha1	Alignment	not modelled	23.1	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
95	d1k66a_	Alignment	not modelled	22.6	16	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	c1y6gB_	Alignment	not modelled	22.5	12	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna alpha-glucosyltransferase; **PDBTitle:** alpha-glucosyltransferase in complex with udp and a 13_mer2 dna containing a hmu base at 2.8 a resolution
97	c3luaA_	Alignment	not modelled	22.3	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
98	d1a04a2	Alignment	not modelled	22.0	10	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
99	c3crnA_	Alignment	not modelled	21.8	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver domain protein, chey-like; **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
100	c3hzhA_	Alignment	not modelled	21.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis response regulator (chey-3); **PDBTitle:** crystal structure of the chex-chey-bef3-mg+2 complex from2 borrelia burgdorferi
101	c2j48A_	Alignment	not modelled	20.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
102	c3cu5B_	Alignment	not modelled	20.6	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**two component transcriptional regulator, arac family; **PDBTitle:** crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
103	c3h5iA_	Alignment	not modelled	20.5	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator/sensory box protein/ggdef **PDBTitle:** crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3 carboxydothermus hydrogenoformans
104	c1yxoB_	Alignment	not modelled	20.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 1;

PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593