Phyre2

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Description	P0AC75
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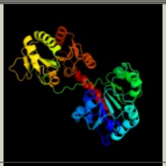
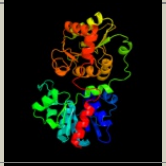
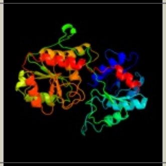
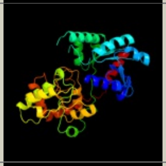
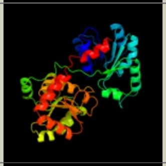
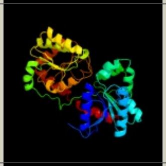
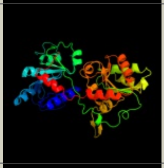
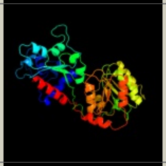
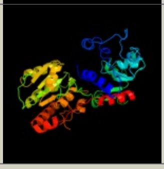
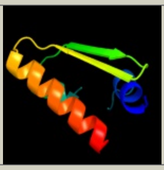
Unique Job ID	ea568add9037e470

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xcuC_	Alignment		100.0	28	**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
2	c3ot5D_	Alignment		100.0	15	**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
3	c2r60A_	Alignment		100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
4	c3s29C_	Alignment		100.0	18	**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.
5	d1v4va_	Alignment		100.0	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
6	d1f6da_	Alignment		100.0	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
7	c3c4vB_	Alignment		100.0	17	**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.
8	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)
9	c2xmpB_	Alignment		100.0	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
10	c2jjmH_	Alignment		100.0	15	**PDB header:**transferase **Chain:** H: **PDB Molecule:**glycosyl transferase, group 1 family protein; **PDBTitle:** crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
11	d1o6ca_	Alignment		100.0	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase

12	c2x6rA_	Alignment		100.0	17	**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
13	c3dzcA_	Alignment		100.0	15	**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.
14	c2gejA_	Alignment		100.0	16	**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
15	d2iw1a1	Alignment		99.9	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
16	c1uquB_	Alignment		99.9	14	**PDB header:**synthase **Chain:** B: **PDB Molecule:**alpha, alpha-trehalose-phosphate synthase; **PDBTitle:** trehalose-6-phosphate from e. coli bound with udp-glucose.
17	d1uqta_	Alignment		99.9	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Trehalose-6-phosphate synthase, OtsA
18	d2bisa1	Alignment		99.9	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
19	d1rzua_	Alignment		99.9	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
20	c2qzsA_	Alignment		99.9	17	**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)
21	c3oy2A_	Alignment	not modelled	99.9	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
22	c2x0dA_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
23	c3rhzB_	Alignment	not modelled	99.9	14	**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
24	c2vsnB_	Alignment	not modelled	99.9	13	**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
25	c3nb0A_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glucose-6-phosphate activated form of yeast glycogen synthase
26	c2q6vA_	Alignment	not modelled	99.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucuronosyltransferase gumk; **PDBTitle:** crystal structure of gumk in complex with udp
27	c3iaaB_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calg2; **PDBTitle:** crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
28	c3o3cD_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glycogen synthase basal state udp complex

29	d1f0ka_	Alignment	not modelled	99.8	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
30	c3ia7A_	Alignment	not modelled	99.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
31	c2iyfA_	Alignment	not modelled	99.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
32	c3othB_	Alignment	not modelled	99.8	18	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
33	c2iv3B_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyltransferase; **PDBTitle:** crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
34	c2iyaB_	Alignment	not modelled	99.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
35	c3pe3D_	Alignment	not modelled	99.7	14	**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
36	d2f9fa1	Alignment	not modelled	99.6	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
37	c3qhpB_	Alignment	not modelled	99.5	19	**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
38	c2p6pB_	Alignment	not modelled	99.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
39	c3d0qB_	Alignment	not modelled	99.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
40	c3hbjA_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**flavonoid 3-o-glucosyltransferase; **PDBTitle:** structure of ugt78g1 complexed with udp
41	d1rrva_	Alignment	not modelled	99.5	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
42	d1iira_	Alignment	not modelled	99.5	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
43	d2bfwa1	Alignment	not modelled	99.5	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
44	d1pn3a_	Alignment	not modelled	99.4	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
45	d2acva1	Alignment	not modelled	99.4	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
46	c3l7mC_	Alignment	not modelled	99.3	12	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**teichoic acid biosynthesis protein f; **PDBTitle:** structure of the wall teichoic acid polymerase tagf, h548a
47	d2c1xa1	Alignment	not modelled	99.3	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
48	d2vcha1	Alignment	not modelled	99.3	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
49	c3hbmA_	Alignment	not modelled	99.3	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
50	d2pq6a1	Alignment	not modelled	99.3	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
51	c3q3hA_	Alignment	not modelled	99.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase; **PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
52	d1pswa_	Alignment	not modelled	98.9	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**ADP-heptose LPS heptosyltransferase II
53	c2o6lA_	Alignment	not modelled	98.6	16	**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
54	c3tovB_	Alignment	not modelled	98.4	13	**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

55	c2h1fB_	Alignment	not modelled	97.9	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
56	c2jzcA_	Alignment	not modelled	97.5	13	**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
57	c2iz6A_	Alignment	not modelled	96.3	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
58	d1qapa1	Alignment	not modelled	86.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
59	c3l0gD_	Alignment	not modelled	85.9	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
60	d1m1na_	Alignment	not modelled	85.8	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
61	c1qapA_	Alignment	not modelled	84.9	14	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
62	c2vp8A_	Alignment	not modelled	77.1	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
63	d1qh8a_	Alignment	not modelled	76.9	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
64	d1qyia_	Alignment	not modelled	76.5	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein MW1667 (SA1546)
65	d2h1qa1	Alignment	not modelled	75.2	14	**Fold:**PLP-dependent transferase-like **Superfamily:**Dhaf3308-like **Family:**Dhaf3308-like
66	c1rcuB_	Alignment	not modelled	74.2	14	**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
67	d1rcua_	Alignment	not modelled	74.2	14	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
68	d2ez9a1	Alignment	not modelled	73.1	7	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
69	c2q4oA_	Alignment	not modelled	73.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at2g37210/t2n18.3; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
70	d2q4oa1	Alignment	not modelled	73.0	13	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
71	d1w25a1	Alignment	not modelled	71.9	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
72	c3pajA_	Alignment	not modelled	71.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
73	d1a9xa3	Alignment	not modelled	70.7	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
74	d2ja9a2	Alignment		70.2	12	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
75	d1ozha1	Alignment	not modelled	69.0	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
76	d1pq4a_	Alignment	not modelled	67.3	18	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
77	d1a9xa4	Alignment	not modelled	67.3	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
78	d1ybha1	Alignment	not modelled	65.5	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain

79	d1t9ba1	Alignment	not modelled	65.2	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
80	d2nn6g3	Alignment	not modelled	65.1	18	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
81	c2dwcB_	Alignment	not modelled	64.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**433aa long hypothetical phosphoribosylglycinamide formyl **PDBTitle:** crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
82	c3grcD_	Alignment	not modelled	63.5	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**sensor protein, kinase; **PDBTitle:** crystal structure of a sensor protein from polaromonas sp.2 js666
83	d2djia1	Alignment	not modelled	62.0	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
84	c2ogwB_	Alignment	not modelled	61.2	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**high-affinity zinc uptake system protein znua **PDBTitle:** structure of abc type zinc transporter from e. coli
85	c2zkqb_	Alignment	not modelled	60.1	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
86	c2o1eB_	Alignment	not modelled	59.7	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ycdh; **PDBTitle:** crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
87	c2rdmB_	Alignment	not modelled	59.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
88	d1kjqa2	Alignment	not modelled	58.1	11	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
89	c1x1oC_	Alignment	not modelled	57.6	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
90	c2pz0B_	Alignment	not modelled	56.6	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
91	c2fzvC_	Alignment	not modelled	55.4	12	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
92	c3a0rB_	Alignment	not modelled	55.2	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
93	d1ajza_	Alignment	not modelled	53.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
94	c3cx3A_	Alignment	not modelled	53.1	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**lipoprotein; **PDBTitle:** crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
95	c1m6vE_	Alignment	not modelled	51.4	15	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
96	d2uubb1	Alignment	not modelled	50.8	11	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
97	d1o8ca2	Alignment	not modelled	50.5	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
98	d2ihta1	Alignment	not modelled	50.0	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
99	c3bchA_	Alignment	not modelled	49.2	10	**PDB header:**cell adhesion, ribosomal protein **Chain:** A: **PDB Molecule:**40s ribosomal protein sa; **PDBTitle:** crystal structure of the human laminin receptor precursor
100	d1q6za1	Alignment	not modelled	49.0	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
101	d1oi7a2	Alignment	not modelled	47.3	12	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
102	d1mvoa_	Alignment	not modelled	47.1	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
103	d1qpoa1	Alignment	not modelled	46.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like

						Family: NadC C-terminal domain-like
104	c3bbnB_	Alignment	not modelled	46.7	14	**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.
105	d2gy9b1	Alignment	not modelled	45.8	13	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
106	c2ja9A_	Alignment	not modelled	45.3	12	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp40; **PDBTitle:** structure of the n-terminal deletion of yeast exosome2 component rrp40
107	c1toaA_	Alignment	not modelled	45.0	13	**PDB header:**binding protein **Chain:** A: **PDB Molecule:**protein (periplasmic binding protein troa); **PDBTitle:** periplasmic zinc binding protein troa from treponema pallidum
108	d1toaa_	Alignment	not modelled	45.0	13	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
109	d2nzwa1	Alignment	not modelled	44.8	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**FucT-like
110	c1s1hB_	Alignment	not modelled	44.5	18	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
111	c1o4uA_	Alignment	not modelled	44.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
112	d2ayxa1	Alignment	not modelled	43.2	11	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
113	d1o94c_	Alignment	not modelled	42.2	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
114	c1af7A_	Alignment	not modelled	42.0	19	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**chemotaxis receptor methyltransferase cher; **PDBTitle:** cher from salmonella typhimurium
115	d1t5oa_	Alignment	not modelled	42.0	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
116	c3nhzA_	Alignment	not modelled	41.5	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
117	d1zesa1	Alignment	not modelled	40.6	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
118	c2xznB_	Alignment	not modelled	40.2	13	**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
119	c1qpoA_	Alignment	not modelled	40.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
120	c2ps3A_	Alignment	not modelled	39.5	14	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli