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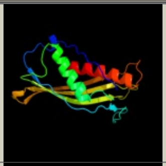
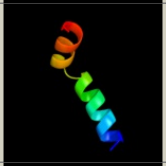
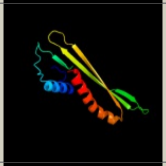
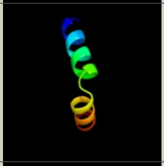
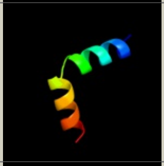
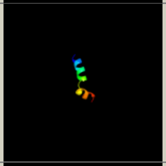
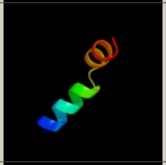
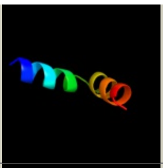
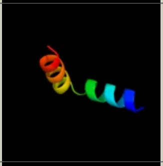
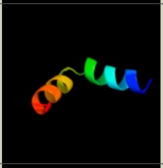
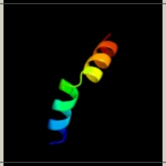
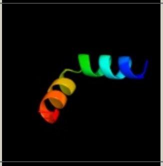
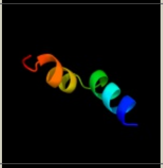
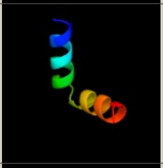
Description	P0ADA5
Date	Thu Jan 5 11:20:27 GMT 2012
Unique Job ID	45a9b2c9887e8fe0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2iqia1	Alignment		97.6	12	**Fold:**Anticodon-binding domain-like **Superfamily:**XCC0632-like **Family:**XCC0632-like
2	c2k7rA_	Alignment		85.6	20	**PDB header:**replication **Chain:** A: **PDB Molecule:**primosomal protein dnai; **PDBTitle:** n-terminal domain of the bacillus subtilis helicase-loading2 protein dnai
3	c2r76A_	Alignment		81.9	6	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**rare lipoprotein b; **PDBTitle:** crystal structure of the rare lipoprotein b (so_1173) from shewanella2 oneidensis, northeast structural genomics consortium target sor91a
4	c3qhpB_	Alignment		46.6	12	**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
5	d2iw1a1	Alignment		45.2	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
6	c2jxpA_	Alignment		41.9	9	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein b; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
7	c3iaaB_	Alignment		41.8	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calg2; **PDBTitle:** crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
8	c2iyfA_	Alignment		36.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
9	c3ia7A_	Alignment		36.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
10	d2bfwa1	Alignment		36.0	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
11	c2kw3C_	Alignment		35.7	12	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**regulatory factor x-associated protein; **PDBTitle:** heterotrimeric interaction between rfx5 and rfxap

12	c2r60A_	Alignment		35.3	0	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
13	c3okaA_	Alignment		34.4	12	**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)
14	c3c4vB_	Alignment		30.8	16	**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.
15	c2iyaB_	Alignment		29.8	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
16	c2jjmH_	Alignment		29.3	20	**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	c3dzcA_	Alignment		28.9	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.
18	c2xmpB_	Alignment		25.6	4	**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
19	c2gejA_	Alignment		25.2	8	**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
20	c2fu2A_	Alignment		24.5	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein spy2152; **PDBTitle:** crystal structure of protein spy2152 from streptococcus pyogenes
21	c2x6rA_	Alignment	not modelled	22.5	4	**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
22	c3bf2A_	Alignment	not modelled	20.5	9	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of the a1ksw9_neimf protein from2 neisseria meningitidis. northeast structural genomics3 consortium target mr36a
23	c3othB_	Alignment	not modelled	20.0	8	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
24	d1o6ca_	Alignment	not modelled	18.3	8	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
25	c3s29C_	Alignment	not modelled	18.1	20	**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.
26	c2p6pB_	Alignment	not modelled	17.0	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
27	d2ijra1	Alignment	not modelled	15.1	71	**Fold:**Api92-like **Superfamily:**Api92-like **Family:**Api92-like
28	c2qpqC_	Alignment	not modelled	15.0	26	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis

29	c2kw0A_	Alignment	not modelled	14.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
30	d1f6da_	Alignment	not modelled	14.3	4	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
31	d1v4va_	Alignment	not modelled	13.6	0	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
32	c2hl7A_	Alignment	not modelled	13.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
33	d2f9fa1	Alignment	not modelled	12.3	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
34	c3ot5D_	Alignment	not modelled	11.7	20	**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
35	c2dvzA_	Alignment	not modelled	11.5	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
36	c3iq2B_	Alignment	not modelled	10.9	17	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sorting nexin-7; **PDBTitle:** human sorting nexin 7, phox homology (px) domain
37	c2cskA_	Alignment	not modelled	10.1	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sorting nexin 12; **PDBTitle:** solution structure of px domain from human snx12
38	d1m6ex_	Alignment	not modelled	9.5	33	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Salicylic acid carboxyl methyltransferase (SAMT)
39	c2f5xC_	Alignment	not modelled	9.1	23	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bugd; **PDBTitle:** structure of periplasmic binding protein bugd
40	c3b5iB_	Alignment	not modelled	8.7	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosyl-l-methionine:salicylic acid carboxyl **PDBTitle:** crystal structure of indole-3-acetic acid methyltransferase
41	c3d0qB_	Alignment	not modelled	8.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
42	c3kjlG_	Alignment	not modelled	7.5	36	**PDB header:**transcription **Chain:** G: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
43	d1kmda_	Alignment	not modelled	7.4	7	**Fold:**PX domain **Superfamily:**PX domain **Family:**PX domain
44	d1pvea_	Alignment	not modelled	7.2	17	**Fold:**XPC-binding domain **Superfamily:**XPC-binding domain **Family:**XPC-binding domain
45	c3kikE_	Alignment	not modelled	7.0	36	**PDB header:**transcription **Chain:** E: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
46	c3kikF_	Alignment	not modelled	7.0	36	**PDB header:**transcription **Chain:** F: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
47	c3kikH_	Alignment	not modelled	6.9	36	**PDB header:**transcription **Chain:** H: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
48	c2eg5C_	Alignment	not modelled	6.7	56	**PDB header:**transferase **Chain:** C: **PDB Molecule:**xanthosine methyltransferase; **PDBTitle:** the structure of xanthosine methyltransferase
49	c1xteA_	Alignment	not modelled	6.7	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase sgk3; **PDBTitle:** crystal structure of cisk-px domain
50	d1xtea_	Alignment	not modelled	6.7	4	**Fold:**PX domain **Superfamily:**PX domain **Family:**PX domain
51	c3kikG_	Alignment	not modelled	6.7	36	**PDB header:**transcription **Chain:** G: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
52	c1x3wB_	Alignment	not modelled	6.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uv excision repair protein rad23; **PDBTitle:** structure of a peptide:n-glycanase-rad23 complex
53	c3fogA_	Alignment	not modelled	6.5	7	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sorting nexin-17; **PDBTitle:** crystal structure of the px domain of sorting nexin-172 (snx17)
54	d2f4mb1	Alignment	not modelled	6.3	17	**Fold:**XPC-binding domain **Superfamily:**XPC-binding domain **Family:**XPC-binding domain
55	c2i4kA_	Alignment	not modelled	6.3	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sorting nexin-1;

						PDBTitle: solution structure of the px domain of sorting nexin 1
56	c3onoA_	Alignment	not modelled	6.3	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
57	c3kjlF_	Alignment	not modelled	6.3	36	**PDB header:**transcription **Chain:** F: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
58	c3kjlH_	Alignment	not modelled	5.6	36	**PDB header:**transcription **Chain:** H: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
59	c3kjlE_	Alignment	not modelled	5.6	36	**PDB header:**transcription **Chain:** E: **PDB Molecule:**saga-associated factor 11; **PDBTitle:** sgf11:sus1 complex
60	d2fhea1	Alignment	not modelled	5.5	17	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
61	c3c5yD_	Alignment	not modelled	5.3	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution