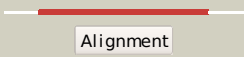

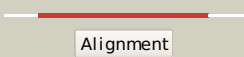

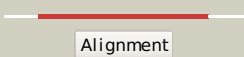

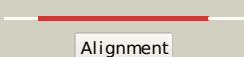

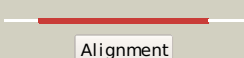

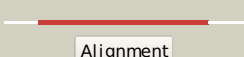

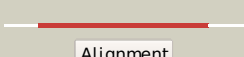

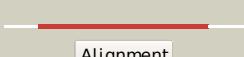

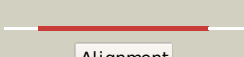

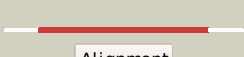





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2r60A_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyl transferase, group 1; <b>PDBTitle:</b> structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
2	<a href="#">c3c4vB_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> predicted glycosyltransferases; <b>PDBTitle:</b> 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.
3	<a href="#">c3s29C_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sucrose synthase 1; <b>PDBTitle:</b> the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
4	<a href="#">c2qzsA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen synthase; <b>PDBTitle:</b> crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
5	<a href="#">d2bisa1</a>	 Alignment		100.0	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
6	<a href="#">d1rzua_</a>	 Alignment		100.0	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
7	<a href="#">c2jlmH_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> glycosyl transferase, group 1 family protein; <b>PDBTitle:</b> crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
8	<a href="#">c3oy2A_</a>	 Alignment		100.0	11	<b>PDB header:</b> viral protein,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycosyltransferase b736l; <b>PDBTitle:</b> crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
9	<a href="#">c3okaA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol <b>PDBTitle:</b> crystal structure of corynebacterium glutamicum pimbl' in complex with2 gdp-man (triclinic crystal form)
10	<a href="#">c2xmpB_</a>	 Alignment		100.0	14	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret mutant e326a2 from p.horishiki in complex with udp
11	<a href="#">c2gejA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphatidylinositol mannosyltransferase (pima); <b>PDBTitle:</b> crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man

12	<a href="#">c2x6rA_</a>	Alignment		100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> trehalose-synthase tret; <b>PDBTitle:</b> crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
13	<a href="#">d2iw1a1</a>	Alignment		100.0	10	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
14	<a href="#">c1uquB_</a>	Alignment		100.0	15	<b>PDB header:</b> synthase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha, alpha-trehalose-phosphate synthase; <b>PDBTitle:</b> trehalose-6-phosphate from e. coli bound with udp-glucose.
15	<a href="#">d1uqta_</a>	Alignment		100.0	14	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Trehalose-6-phosphate synthase, OtsA
16	<a href="#">c3nb0A_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen [starch] synthase isoform 2; <b>PDBTitle:</b> glucose-6-phosphate activated form of yeast glycogen synthase
17	<a href="#">c2iv3B_</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyltransferase; <b>PDBTitle:</b> crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
18	<a href="#">c3o3cD_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycogen [starch] synthase isoform 2; <b>PDBTitle:</b> glycogen synthase basal state udp complex
19	<a href="#">c2x0dA_</a>	Alignment		100.0	9	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> wsaf; <b>PDBTitle:</b> apo structure of wsaf
20	<a href="#">c2q6vA_</a>	Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucuronosyltransferase gumk; <b>PDBTitle:</b> crystal structure of gumk in complex with udp
21	<a href="#">c3rhzb_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nucleotide sugar synthetase-like protein; <b>PDBTitle:</b> structure and functional analysis of a new subfamily of2 glycosyltransferases required for glycosylation of serine-rich3 streptococcal adhesions
22	<a href="#">c3ot5D_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
23	<a href="#">d1f6da_</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
24	<a href="#">d1v4va_</a>	Alignment	not modelled	99.9	10	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
25	<a href="#">c3dzcA_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
26	<a href="#">d1o6ca_</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDP-N-acetylglucosamine 2-epimerase
27	<a href="#">c3iaaB_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calg2; <b>PDBTitle:</b> crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
28	<a href="#">c2xcuC_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-2-octulosonic acid transferase; <b>PDBTitle:</b> membrane-embedded monofunctional

					glycosyltransferase waaa of aquifex2 aeolicus, comlex with cmp
29	<a href="#">d1f0ka_</a>	Alignment	not modelled	99.9	13 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
30	<a href="#">c3ia7A_</a>	Alignment	not modelled	99.9	10 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
31	<a href="#">c2p6pB_</a>	Alignment	not modelled	99.9	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycosyl transferase; <b>PDBTitle:</b> x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
32	<a href="#">c2iyfA_</a>	Alignment	not modelled	99.9	11 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
33	<a href="#">c2iyaB_</a>	Alignment	not modelled	99.9	13 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> oleandomycin glycosyltransferase; <b>PDBTitle:</b> the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
34	<a href="#">c3othB_</a>	Alignment	not modelled	99.9	11 <b>PDB header:</b> transferase/antibiotic <b>Chain:</b> B: <b>PDB Molecule:</b> calg1; <b>PDBTitle:</b> crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
35	<a href="#">c2vsnb_</a>	Alignment	not modelled	99.8	12 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> xcogt; <b>PDBTitle:</b> structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
36	<a href="#">d2f9fa1</a>	Alignment	not modelled	99.7	17 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
37	<a href="#">c3d0qB_</a>	Alignment	not modelled	99.7	11 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein calg3; <b>PDBTitle:</b> crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
38	<a href="#">d1iira_</a>	Alignment	not modelled	99.7	9 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
39	<a href="#">d1rrva_</a>	Alignment	not modelled	99.7	10 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
40	<a href="#">d2bfwa1</a>	Alignment	not modelled	99.7	14 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Glycosyl transferases group 1
41	<a href="#">d1pn3a_</a>	Alignment	not modelled	99.7	7 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
42	<a href="#">c3qhpB_</a>	Alignment	not modelled	99.6	13 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> type 1 capsular polysaccharide biosynthesis protein j <b>PDBTitle:</b> crystal structure of the catalytic domain of cholesterol-alpha-2 glucosyltransferase from helicobacter pylori
43	<a href="#">c3pe3D_</a>	Alignment	not modelled	99.6	9 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n- <b>PDBTitle:</b> structure of human o-glcna2 transferase and its complex with a peptide2 substrate
44	<a href="#">d2acva1</a>	Alignment	not modelled	99.3	9 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
45	<a href="#">c3hbjA_</a>	Alignment	not modelled	99.2	9 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> flavonoid 3-o-glucosyltransferase; <b>PDBTitle:</b> structure of ugt78g1 complexed with udp
46	<a href="#">d2c1xa1</a>	Alignment	not modelled	99.1	10 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
47	<a href="#">d2pq6a1</a>	Alignment	not modelled	99.1	7 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
48	<a href="#">d2vcha1</a>	Alignment	not modelled	99.0	11 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
49	<a href="#">c3hbmA_</a>	Alignment	not modelled	98.4	12 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-sugar hydrolase; <b>PDBTitle:</b> crystal structure of pseg from campylobacter jejuni
50	<a href="#">c3q3hA_</a>	Alignment	not modelled	98.1	7 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hmw1c-like glycosyltransferase; <b>PDBTitle:</b> crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
51	<a href="#">c2o6lA_</a>	Alignment	not modelled	97.7	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucuronosyltransferase 2b7; <b>PDBTitle:</b> crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
52	<a href="#">d1ygpa_</a>	Alignment	not modelled	96.8	19 <b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Oligosaccharide phosphorylase
53	<a href="#">c3l7mC_</a>	Alignment	not modelled	96.7	12 <b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> teichoic acid biosynthesis protein f; <b>PDBTitle:</b> structure of the wall teichoic acid polymerase tagf, h548a
54	<a href="#">c2c4mA_</a>	Alignment	not modelled	96.6	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycogen phosphorylase; <b>PDBTitle:</b> starch phosphorylase: structural studies explain

					oxyanion-2 dependent kinetic stability and regulatory control. <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycogen phosphorylase, liver form; <b>PDBTitle:</b> crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
55	<a href="#">c3ddsB_</a>	Alignment	not modelled	96.4	13
56	<a href="#">d2atia1</a>	Alignment	not modelled	95.8	13
57	<a href="#">d2gj4a1</a>	Alignment	not modelled	95.7	14
58	<a href="#">c2h1fB_</a>	Alignment	not modelled	95.3	15
59	<a href="#">d1l5wa_</a>	Alignment	not modelled	95.2	17
60	<a href="#">c1y6gB_</a>	Alignment	not modelled	94.9	12
61	<a href="#">c3ibgF_</a>	Alignment	not modelled	94.5	9
62	<a href="#">d1ydg_</a>	Alignment	not modelled	94.1	7
63	<a href="#">c2pzlB_</a>	Alignment	not modelled	93.8	27
64	<a href="#">c3icpA_</a>	Alignment	not modelled	93.5	26
65	<a href="#">c2pk3B_</a>	Alignment	not modelled	93.3	18
66	<a href="#">c3lcmB_</a>	Alignment	not modelled	93.0	16
67	<a href="#">d1udca_</a>	Alignment	not modelled	92.9	21
68	<a href="#">d2hy5a1</a>	Alignment	not modelled	92.9	17
69	<a href="#">c3m2pD_</a>	Alignment	not modelled	92.9	11
70	<a href="#">c2p5uC_</a>	Alignment	not modelled	92.4	28
71	<a href="#">c2q1wC_</a>	Alignment	not modelled	92.3	12
72	<a href="#">d2d1pa1</a>	Alignment	not modelled	92.2	19
73	<a href="#">c2wooc_</a>	Alignment	not modelled	92.1	8
74	<a href="#">c2ixdB_</a>	Alignment	not modelled	91.7	12
75	<a href="#">d2c5aa1</a>	Alignment	not modelled	91.6	12
76	<a href="#">c2x4gA_</a>	Alignment	not modelled	91.6	8
77	<a href="#">c2zkiH_</a>	Alignment	not modelled	91.1	19
78	<a href="#">d1hyqa_</a>	Alignment	not modelled	90.2	12
79	<a href="#">c1hyqA_</a>	Alignment	not modelled	90.2	12

80	<a href="#">d2bla1a</a>	Alignment	not modelled	90.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
81	<a href="#">c3sc6F</a>	Alignment	not modelled	90.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> ddtp-4-dehydrorhamnose reductase; <b>PDBTitle:</b> 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
82	<a href="#">c2ggsB</a>	Alignment	not modelled	89.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 273aa long hypothetical dtdp-4-dehydrorhamnose <b>PDBTitle:</b> crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
83	<a href="#">d1jaya</a>	Alignment	not modelled	89.7	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
84	<a href="#">c3oh8A</a>	Alignment	not modelled	89.3	11	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nucleoside-diphosphate sugar epimerase (sula family); <b>PDBTitle:</b> crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
85	<a href="#">c2ofpB</a>	Alignment	not modelled	89.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketopantoate reductase; <b>PDBTitle:</b> crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
86	<a href="#">d1kewa</a>	Alignment	not modelled	89.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
87	<a href="#">d1fjha</a>	Alignment	not modelled	89.0	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
88	<a href="#">d1uana</a>	Alignment	not modelled	88.5	10	<b>Fold:</b> LmbE-like <b>Superfamily:</b> LmbE-like <b>Family:</b> LmbE-like
89	<a href="#">c3l4bG</a>	Alignment	not modelled	88.4	16	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> trka k+ channel protien tm1088b; <b>PDBTitle:</b> crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
90	<a href="#">d2hy5b1</a>	Alignment	not modelled	88.3	12	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
91	<a href="#">d1s3ia2</a>	Alignment	not modelled	88.2	10	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
92	<a href="#">d1vl0a</a>	Alignment	not modelled	87.9	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
93	<a href="#">d1j9ja</a>	Alignment	not modelled	87.8	24	<b>Fold:</b> SurE-like <b>Superfamily:</b> SurE-like <b>Family:</b> SurE-like
94	<a href="#">c3fmfA</a>	Alignment	not modelled	87.5	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
95	<a href="#">c2hunB</a>	Alignment	not modelled	87.5	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 336aa long hypothetical dtdp-glucose 4,6-dehydratase; <b>PDBTitle:</b> crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
96	<a href="#">d2afhe1</a>	Alignment	not modelled	86.9	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
97	<a href="#">c3io3A</a>	Alignment	not modelled	86.9	10	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> deha2d07832p; <b>PDBTitle:</b> get3 with adp from d. hansenii in closed form
98	<a href="#">d1hdoa</a>	Alignment	not modelled	86.6	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
99	<a href="#">c2jzcA</a>	Alignment	not modelled	86.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine transferase subunit <b>PDBTitle:</b> nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
100	<a href="#">d2fzva1</a>	Alignment	not modelled	86.2	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
101	<a href="#">c3zq6D</a>	Alignment	not modelled	86.2	8	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative arsenical pump-driving atpase; <b>PDBTitle:</b> adp-alf4 complex of m. therm. trc40
102	<a href="#">d1rtta</a>	Alignment	not modelled	86.1	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
103	<a href="#">d1ks9a2</a>	Alignment	not modelled	86.0	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
104	<a href="#">c1ks9A</a>	Alignment	not modelled	85.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase;



						<b>PDBTitle:</b> ketopantoate reductase from escherichia coli
105	<a href="#">c3kjgB_</a>	Alignment	not modelled	85.5	20	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase complex, accessory <b>PDBTitle:</b> adp-bound state of cooc1
106	<a href="#">c1gshA_</a>	Alignment	not modelled	85.3	10	<b>PDB header:</b> glutathione biosynthesis ligase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione biosynthetic ligase; <b>PDBTitle:</b> structure of escherichia coli glutathione synthetase at ph 7.5
107	<a href="#">d1n2sa_</a>	Alignment	not modelled	85.2	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
108	<a href="#">c3ug7D_</a>	Alignment	not modelled	85.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> arsenical pump-driving atpase; <b>PDBTitle:</b> crystal structure of get3 from methanocaldococcus jannaschii
109	<a href="#">d1a9xa4</a>	Alignment	not modelled	84.9	16	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
110	<a href="#">d2f1ka2</a>	Alignment	not modelled	84.9	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
111	<a href="#">c2v4oB_</a>	Alignment	not modelled	84.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> multifunctional protein sur e; <b>PDBTitle:</b> crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
112	<a href="#">d1bxka_</a>	Alignment	not modelled	84.4	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
113	<a href="#">c3e8xA_</a>	Alignment	not modelled	84.2	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> putative nad-dependent epimerase/dehydratase from bacillus halodurans.
114	<a href="#">d2d1pb1</a>	Alignment	not modelled	83.6	17	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
115	<a href="#">c1vkzA_</a>	Alignment	not modelled	83.5	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
116	<a href="#">d1gsaa1</a>	Alignment	not modelled	83.3	10	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> Prokaryotic glutathione synthetase, N-terminal domain
117	<a href="#">c3g17H_</a>	Alignment	not modelled	83.2	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> similar to 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
118	<a href="#">d2blna2</a>	Alignment	not modelled	83.0	11	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
119	<a href="#">c3l77A_</a>	Alignment	not modelled	83.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> short-chain alcohol dehydrogenase; <b>PDBTitle:</b> x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
120	<a href="#">c3q0iA_</a>	Alignment	not modelled	82.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> methionyl-trna formyltransferase; <b>PDBTitle:</b> methionyl-trna formyltransferase from vibrio cholerae