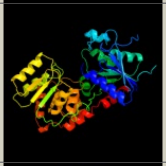
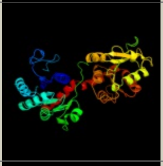
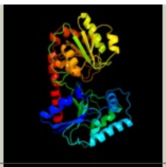
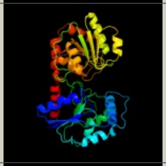
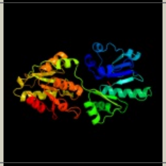
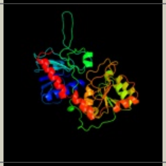
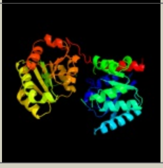
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P27127
Date	Thu Jan 5 11:43:14 GMT 2012
Unique Job ID	5c45fc5e4fc02c32

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c4vB_	Alignment		100.0	15	**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.
2	d2bisa1	Alignment		100.0	20	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
3	c2gejA_	Alignment		100.0	11	**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
4	c2jjmH_	Alignment		100.0	17	**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.
5	c2qzsA_	Alignment		100.0	15	**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)
6	d1rzua_	Alignment		100.0	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
7	c2r60A_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
8	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
9	c3okaA_	Alignment		100.0	16	**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)
10	d2iw1a1	Alignment		100.0	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
11	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.

12	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
13	c2x6rA_	Alignment		100.0	15	**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
14	c2x0dA_	Alignment		100.0	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
15	c2iv3B_	Alignment		100.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyltransferase; **PDBTitle:** crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
16	c1uquB_	Alignment		100.0	15	**PDB header:**synthase **Chain:** B: **PDB Molecule:**alpha, alpha-trehalose-phosphate synthase; **PDBTitle:** trehalose-6-phosphate from e. coli bound with udp-glucose.
17	c3o3cD_	Alignment		100.0	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glycogen synthase basal state udp complex
18	c3nb0A_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glucose-6-phosphate activated form of yeast glycogen synthase
19	d1uqta_	Alignment		100.0	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Trehalose-6-phosphate synthase, OtsA
20	c3ot5D_	Alignment		100.0	11	**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
21	c3dzcA_	Alignment	not modelled	100.0	10	**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.
22	c3rhzB_	Alignment	not modelled	100.0	13	**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
23	d1f6da_	Alignment	not modelled	100.0	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
24	c2q6vA_	Alignment	not modelled	99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucuronosyltransferase gumk; **PDBTitle:** crystal structure of gumk in complex with udp
25	d1v4va_	Alignment	not modelled	99.9	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
26	c2xcuC_	Alignment	not modelled	99.9	11	**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	d1o6ca_	Alignment	not modelled	99.9	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
28	d1f0ka_	Alignment	not modelled	99.9	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG

29	c3ia7A_	Alignment	not modelled	99.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
30	c3iaaB_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**calg2; **PDBTitle:** crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
31	c3othB_	Alignment	not modelled	99.8	12	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
32	c2p6pB_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
33	d2f9fa1	Alignment	not modelled	99.8	17	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
34	c2iyaB_	Alignment	not modelled	99.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
35	c2iyfA_	Alignment	not modelled	99.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
36	c2vsnB_	Alignment	not modelled	99.7	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
37	d2bfwa1	Alignment	not modelled	99.6	25	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
38	c3qhpB_	Alignment	not modelled	99.6	13	**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
39	d1iira_	Alignment	not modelled	99.6	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
40	c3d0qB_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
41	d1pn3a_	Alignment	not modelled	99.5	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
42	d1rrva_	Alignment	not modelled	99.5	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
43	c3pe3D_	Alignment	not modelled	99.5	11	**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
44	d2c1xa1	Alignment	not modelled	98.6	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
45	d2acva1	Alignment	not modelled	98.6	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
46	c3hbjA_	Alignment	not modelled	98.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**flavonoid 3-o-glucosyltransferase; **PDBTitle:** structure of ugt78g1 complexed with udp
47	c3hbmA_	Alignment	not modelled	98.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**udp-sugar hydrolase; **PDBTitle:** crystal structure of pseg from campylobacter jejuni
48	d2pq6a1	Alignment	not modelled	98.2	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
49	c3l7mC_	Alignment	not modelled	97.9	10	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**teichoic acid biosynthesis protein f; **PDBTitle:** structure of the wall teichoic acid polymerase tagf, h548a
50	d2vcha1	Alignment	not modelled	97.9	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
51	c2h1fB_	Alignment	not modelled	97.7	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipopolysaccharide heptosyltransferase-1; **PDBTitle:** e. coli heptosyltransferase waac with adp
52	c3q3hA_	Alignment	not modelled	97.5	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase; **PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
53	c3ddsB_	Alignment	not modelled	96.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycogen phosphorylase, liver form; **PDBTitle:** crystal structure of glycogen phosphorylase complexed with an2 anthranilimide based inhibitor gsk261
54	c2c4mA_	Alignment	not modelled	96.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen phosphorylase; **PDBTitle:** starch phosphorylase: structural studies explain oxyanion-2 dependent kinetic stability and regulatory control.

55	d1pswa_	Alignment	not modelled	96.5	10	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**ADP-heptose LPS heptosyltransferase II
56	d1ygpa_	Alignment	not modelled	96.0	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
57	d2gj4a1	Alignment	not modelled	96.0	14	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
58	c2o6lA_	Alignment	not modelled	95.6	11	**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
59	d2atia1	Alignment	not modelled	95.5	11	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
60	c2ixdB_	Alignment	not modelled	95.4	20	**PDB header:**hydrolase **Chain: B: PDB Molecule:**lmbe-related protein; **PDBTitle:** crystal structure of the putative deacetylase bc1534 from2 bacilus cereus
61	c3tovB_	Alignment	not modelled	95.4	8	**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
62	d1l5wa_	Alignment	not modelled	94.7	10	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Oligosaccharide phosphorylase
63	d1uana_	Alignment	not modelled	94.6	17	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
64	d1ydga_	Alignment	not modelled	93.4	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
65	d2d1pa1	Alignment	not modelled	92.2	10	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
66	d2hy5a1	Alignment	not modelled	91.3	12	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
67	d1s3ia2	Alignment	not modelled	89.6	15	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
68	c3m2pD_	Alignment	not modelled	89.4	19	**PDB header:**isomerase **Chain: D: PDB Molecule:**udp-n-acetylglucosamine 4-epimerase; **PDBTitle:** the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
69	d1udca_	Alignment	not modelled	89.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
70	c1y6gB_	Alignment	not modelled	89.3	13	**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
71	c3icpA_	Alignment	not modelled	89.3	10	**PDB header:**isomerase **Chain: A: PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of udp-galactose 4-epimerase
72	c1gshA_	Alignment	not modelled	89.2	2	**PDB header:**glutathione biosynthesis ligase **Chain: A: PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
73	d1vl0a_	Alignment	not modelled	89.2	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
74	d1jaya_	Alignment	not modelled	89.1	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
75	c2wooC_	Alignment	not modelled	88.8	18	**PDB header:**hydrolase **Chain: C: PDB Molecule:**atpase get3; **PDBTitle:** nucleotide-free form of s. pombe get3
76	c2x4gA_	Alignment	not modelled	88.3	14	**PDB header:**isomerase **Chain: A: PDB Molecule:**nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
77	d1gsaa1	Alignment	not modelled	88.2	2	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
78	c2pk3B_	Alignment	not modelled	88.2	13	**PDB header:**oxidoreductase **Chain: B: PDB Molecule:**gdp-6-deoxy-d-lyxo-4-hexulose reductase; **PDBTitle:** crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
79	c2pzlB_	Alignment	not modelled	88.1	18	**PDB header:**sugar binding protein **Chain: B: PDB Molecule:**putative nucleotide sugar epimerase/dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme2 wbmg in complex with nad and udp
80	c3ibgF_	Alignment	not modelled	88.1	15	**PDB header:**hydrolase **Chain: F: PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp

81	c3lcmB_	Alignment	not modelled	88.1	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
82	c2p5uC_	Alignment	not modelled	87.5	10	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
83	d2blla1	Alignment	not modelled	86.3	4	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
84	c2q1wC_	Alignment	not modelled	86.2	10	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
85	c2zkiH_	Alignment	not modelled	86.1	7	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
86	d2c5aa1	Alignment	not modelled	85.6	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
87	c2ggsB_	Alignment	not modelled	84.7	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**273aa long hypothetical dtdp-4-dehydrorhamnose **PDBTitle:** crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
88	c2ofpB_	Alignment	not modelled	84.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketopantoate reductase; **PDBTitle:** crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
89	d1txga2	Alignment	not modelled	84.6	6	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
90	d1n2sa_	Alignment	not modelled	84.5	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
91	c2iz6A_	Alignment	not modelled	84.4	14	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
92	d2f1ka2	Alignment	not modelled	83.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
93	c3kjgB_	Alignment	not modelled	82.9	20	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase complex, accessory **PDBTitle:** adp-bound state of cooc1
94	c3fmfA_	Alignment	not modelled	82.8	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
95	d1kewa_	Alignment	not modelled	82.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
96	d2hy5b1	Alignment	not modelled	82.0	10	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
97	c3sc6F_	Alignment	not modelled	81.8	18	**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
98	c1ks9A_	Alignment	not modelled	81.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** ketopantoate reductase from escherichia coli
99	c2hunB_	Alignment	not modelled	81.5	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**336aa long hypothetical dtdp-glucose 4,6-dehydratase; **PDBTitle:** crystal structure of hypothetical protein ph0414 from pyrococcus2 horikoshii ot3
100	d1ks9a2	Alignment	not modelled	81.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
101	c3oh8A_	Alignment	not modelled	80.3	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**nucleoside-diphosphate sugar epimerase (sula family); **PDBTitle:** crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
102	c1hyqA_	Alignment	not modelled	80.1	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division inhibitor (mind-1); **PDBTitle:** mind bacterial cell division regulator from a. fulgidus
103	d1hyqa_	Alignment	not modelled	80.1	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
104	c2f1kD_	Alignment	not modelled	79.6	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
						Fold: Flavodoxin-like

105	d1qrda_	Alignment	not modelled	78.9	0	**Superfamily:**Flavoproteins **Family:**Quinone reductase
106	d1rtta_	Alignment	not modelled	78.8	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
107	d1fjha_	Alignment	not modelled	78.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
108	d2bw0a2	Alignment	not modelled	78.3	15	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
109	d1mv8a2	Alignment	not modelled	77.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
110	c3g17H_	Alignment	not modelled	77.4	18	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**similar to 2-dehydropantoate 2-reductase; **PDBTitle:** structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
111	d2fzva1	Alignment	not modelled	77.4	6	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
112	c3l4bG_	Alignment	not modelled	75.9	9	**PDB header:**transport protein **Chain:** G: **PDB Molecule:**trka k+ channel protien tm1088b; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
113	d1bxka_	Alignment	not modelled	75.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
114	d2blna2	Alignment	not modelled	74.7	12	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
115	d1lssa_	Alignment	not modelled	74.4	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
116	c1txgA_	Alignment	not modelled	74.0	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
117	c3dojA_	Alignment	not modelled	74.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase-like protein; **PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
118	d1ycga1	Alignment	not modelled	73.8	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
119	d1oc2a_	Alignment	not modelled	73.4	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
120	d1pgja2	Alignment	not modelled	73.1	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain