



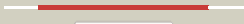








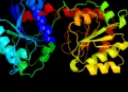
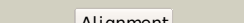

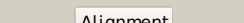

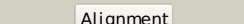

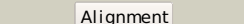









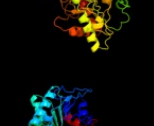



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1v4va_	 Alignment		100.0	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
2	d1o6ca_	 Alignment		100.0	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
3	c3ot5D_	 Alignment		100.0	13	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
4	d1f6da_	 Alignment		100.0	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
5	c3c4vB_	 Alignment		100.0	14	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.
6	c3dzcA_	 Alignment		100.0	15	PDB header: isomerase Chain: A: PDB Molecule: udp-n-acetylglucosamine 2-epimerase; PDBTitle: 2.35 angstrom resolution structure of webc (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
7	c2jlmH_	 Alignment		100.0	14	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.
8	c3s29C_	 Alignment		100.0	16	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.
9	c2qzsA_	 Alignment		100.0	13	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)
10	c2r60A_	 Alignment		100.0	14	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix oreni i
11	c2gejA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannosyltransferase (pima); PDBTitle: crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man

12	c3okaA	Alignment		100.0	11	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)
13	d2bisa1	Alignment		100.0	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
14	c2x6rA	Alignment		100.0	12	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
15	d1rzua	Alignment		100.0	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
16	d1f0ka	Alignment		99.9	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
17	c2xmpB	Alignment		99.9	13	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
18	d2iw1a1	Alignment		99.9	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
19	c3oy2A	Alignment		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
20	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.
21	c2xcuC	Alignment	not modelled	99.9	13	PDB header: transferase Chain: C: PDB Molecule: 3-deoxy-d-manno-2-octulosonic acid transferase; PDBTitle: membrane-embedded monofunctional glycosyltransferase waaa of aquifex2 aeolicus, comlex with cmp
22	c3ia7A	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: calg4; PDBTitle: crystal structure of calg4, the calicheamicin glycosyltransferase
23	c2iyaB	Alignment	not modelled	99.9	11	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
24	d1uqta	Alignment	not modelled	99.9	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
25	c3iaaB	Alignment	not modelled	99.9	13	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
26	c2iyfA	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
27	c3nb0A	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase
28	c3o3cD	Alignment	not modelled	99.9	12	PDB header: transferase Chain: D: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glycogen synthase basal state udp complex
						PDB header: transferase/antibiotic

29	c30thB_	Alignment	not modelled	99.9	11	Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
30	c2x0dA_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
31	c2p6pB_	Alignment	not modelled	99.9	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
32	c2q6vA_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: glucuronosyltransferase gumk; PDBTitle: crystal structure of gumk in complex with udp
33	c3d0qB_	Alignment	not modelled	99.8	10	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
34	d1pn3a_	Alignment	not modelled	99.8	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
35	d1rrva_	Alignment	not modelled	99.8	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
36	d1iira_	Alignment	not modelled	99.8	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
37	c2iv3B_	Alignment	not modelled	99.8	14	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
38	c3hbjA_	Alignment	not modelled	99.8	9	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
39	c3rhzB_	Alignment	not modelled	99.7	11	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
40	c2vsnB_	Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
41	d2acva1	Alignment	not modelled	99.7	8	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
42	d2c1xa1	Alignment	not modelled	99.7	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
43	d2pq6a1	Alignment	not modelled	99.6	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
44	c3qhpB_	Alignment	not modelled	99.5	14	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
45	d2vcha1	Alignment	not modelled	99.5	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
46	c3pe3D_	Alignment	not modelled	99.4	13	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
47	c3hbmA_	Alignment	not modelled	99.4	11	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
48	d2bfwa1	Alignment	not modelled	99.4	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
49	d2f9fa1	Alignment	not modelled	99.3	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
50	c3tovB_	Alignment	not modelled	99.0	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
51	c2h1fB_	Alignment	not modelled	98.7	7	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
52	c3q3hA_	Alignment	not modelled	98.7	10	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	d1pswa_	Alignment	not modelled	98.7	14	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
54	c2o6lA_	Alignment	not modelled	98.4	9	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

55	c3l7mC	 Alignment	not modelled	98.4	13	PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a
56	c2jzcA	 Alignment	not modelled	96.9	17	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine transferase subunit PDBTitle: nmr solution structure of alg13: the sugar donor subunit of 2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
57	c2pzlB	 Alignment	not modelled	95.4	22	PDB header: sugar binding protein Chain: B: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme2 wbmj in complex with nad and udp
58	c3oh8A	 Alignment	not modelled	95.2	22	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
59	d2c5aa1	 Alignment	not modelled	94.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
60	c2hunB	 Alignment	not modelled	94.7	26	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
61	c1zh8B	 Alignment	not modelled	94.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
62	c2nvwB	 Alignment	not modelled	94.3	9	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of transcriptional regulator gal80p from2 kluyveromyces lactis
63	c3l77A	 Alignment	not modelled	94.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain alcohol dehydrogenase; PDBTitle: x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
64	d1ydgA	 Alignment	not modelled	93.9	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
65	c3zquA	 Alignment	not modelled	93.8	24	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
66	c3e5nA	 Alignment	not modelled	93.7	18	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
67	d1fjha	 Alignment	not modelled	93.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
68	c3q2kB	 Alignment	not modelled	92.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glnaca
69	d1zh8a1	 Alignment	not modelled	92.4	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
70	d1mkza	 Alignment	not modelled	92.4	23	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
71	c3lwbA	 Alignment	not modelled	92.2	21	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
72	c3tqrA	 Alignment	not modelled	92.1	13	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
73	d1e7wa	 Alignment	not modelled	92.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
74	d3c96a1	 Alignment	not modelled	91.5	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
75	c3enkB	 Alignment	not modelled	91.5	29	PDB header: isomerase Chain: B: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
76	c3allA	 Alignment	not modelled	91.2	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
77	c2qhxB	 Alignment	not modelled	91.2	17	PDB header: oxidoreductase Chain: B: PDB Molecule: pteridine reductase 1; PDBTitle: structure of pteridine reductase from leishmania major2 complexed with a ligand
78	c3tgtB	 Alignment	not modelled	91.1	13	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella

						burneti
79	c3i4fD_	Alignment	not modelled	90.9	22	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-oxoacyl-[acyl-carrier protein] reductase; PDBTitle: structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
80	c3icpA_	Alignment	not modelled	90.9	30	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
81	c2p5uC_	Alignment	not modelled	90.9	20	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
82	c3m2pD_	Alignment	not modelled	90.6	29	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
83	c2pvpB_	Alignment	not modelled	90.6	23	PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
84	d1wmaa1	Alignment	not modelled	90.6	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
85	c1qzuB_	Alignment	not modelled	90.5	12	PDB header: lyase Chain: B: PDB Molecule: hypothetical protein mds018; PDBTitle: crystal structure of human phosphopantothoenylcysteine decarboxylase
86	d2ag5a1	Alignment	not modelled	90.4	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
87	c3se7A_	Alignment	not modelled	90.2	16	PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana
88	d1u7za_	Alignment	not modelled	90.1	26	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
89	c1fmtA_	Alignment	not modelled	90.1	20	PDB header: formyltransferase Chain: A: PDB Molecule: methionyl-trna fmet formyltransferase; PDBTitle: methionyl-trnafmet formyltransferase from escherichia coli
90	c3tfoD_	Alignment	not modelled	90.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: putative 3-oxoacyl-(acyl-carrier-protein) reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-(acyl-carrier-protein)2 reductase from sinorhizobium meliloti
91	c3p19A_	Alignment	not modelled	89.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative blue fluorescent protein; PDBTitle: improved nadph-dependent blue fluorescent protein
92	c3ceaA_	Alignment	not modelled	89.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
93	d1jaya_	Alignment	not modelled	89.7	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
94	d1kewa_	Alignment	not modelled	89.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
95	c2jahB_	Alignment	not modelled	89.6	26	PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
96	c2x4gA_	Alignment	not modelled	89.6	19	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
97	c1zx9A_	Alignment	not modelled	89.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera
98	c3i1jB_	Alignment	not modelled	89.5	26	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain PDBTitle: structure of a putative short chain dehydrogenase from2 pseudomonas syringae
99	d1fmta2	Alignment	not modelled	89.4	17	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
100	d1udca_	Alignment	not modelled	89.4	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
101	c3l6dB_	Alignment	not modelled	89.3	7	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
102	c3rkuC_	Alignment	not modelled	89.2	17	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase ymr226c; PDBTitle: substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+
103	d1b74a1	Alignment	not modelled	89.1	13	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
						PDB header: oxidoreductase

104	c3edmD_	Alignment	not modelled	89.0	15	Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from agrobacterium2 tumefaciens
105	c3h7aC_	Alignment	not modelled	88.9	13	PDB header: oxidoreductase Chain: C: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a betaketoacyl-[acp] reductase from2 rhodospseudomonas palustris
106	d1o5ia_	Alignment	not modelled	88.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
107	c3nywD_	Alignment	not modelled	88.8	15	PDB header: oxidoreductase Chain: D: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a betaketoacyl-[acp] reductase (fabg) from2 bacteroides thetaiotaomicron
108	c1ofgF_	Alignment	not modelled	88.8	16	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
109	c1h6dL_	Alignment	not modelled	88.8	16	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
110	d2f1ka2	Alignment	not modelled	88.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
111	c2ekqB_	Alignment	not modelled	88.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-deoxy-d-gluconate 3-dehydrogenase; PDBTitle: structure of tt0495 protein from thermus thermophilus
112	c2ehdB_	Alignment	not modelled	88.4	23	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short-chain dehydrogenase/reductase family; PDBTitle: crystal structure analysis of oxidoreductase
113	c2vouA_	Alignment	not modelled	88.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
114	c2pk3B_	Alignment	not modelled	88.3	16	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
115	d2iida1	Alignment	not modelled	88.2	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
116	c2p68A_	Alignment	not modelled	88.2	28	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] reductase; PDBTitle: crystal structure of aq_1716 from aquifex aeolicus vf5
117	c3v2hB_	Alignment	not modelled	88.1	25	PDB header: oxidoreductase Chain: B: PDB Molecule: d-beta-hydroxybutyrate dehydrogenase; PDBTitle: the crystal structure of d-beta-hydroxybutyrate dehydrogenase from2 sinorhizobium meliloti
118	c2pd6D_	Alignment	not modelled	88.1	23	PDB header: oxidoreductase Chain: D: PDB Molecule: estradiol 17-beta-dehydrogenase 8; PDBTitle: structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
119	d2a4ka1	Alignment	not modelled	88.1	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
120	d1gega_	Alignment	not modelled	88.1	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases