

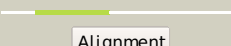
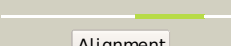
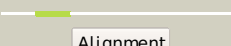
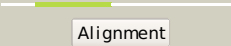
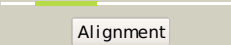
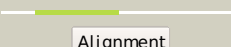
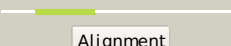
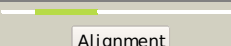
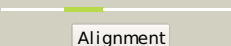
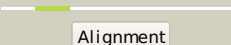
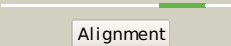
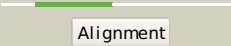
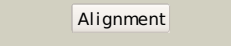
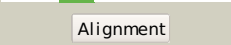
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pswa_	 Alignment		99.5	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II
2	c3tovB_	 Alignment		99.4	10	PDB 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
3	d1o6ca_	 Alignment		99.4	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
4	c3ot5D_	 Alignment		99.2	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
5	c2h1fB_	 Alignment		99.2	14	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
6	d1v4va_	 Alignment		99.1	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
7	c2x6rA_	 Alignment		99.1	13	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
8	c3c4vB_	 Alignment		99.1	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.
9	c2xmpB_	 Alignment		99.0	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
10	d1f6da_	 Alignment		98.9	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
11	c3oy2A_	 Alignment		98.9	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

12	c2xcuC_	Alignment		98.8	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, complex with cmp
13	c2jimH_	Alignment		98.6	12	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.
14	d2bisa1	Alignment		98.6	13	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
15	c2gejA_	Alignment		98.5	13	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
16	c3dzcA_	Alignment		98.3	11	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.
17	c3okaA_	Alignment		98.2	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)
18	c3l7mC_	Alignment		98.1	10	PDB header: structural protein Chain: C: PDB Molecule: teichoic acid biosynthesis protein f; PDBTitle: structure of the wall teichoic acid polymerase tagf, h548a
19	c2r60A_	Alignment		98.1	10	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix oronii
20	d1pn3a_	Alignment		98.0	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
21	c3rhzb_	Alignment	not modelled	97.9	10	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
22	d1iira_	Alignment	not modelled	97.2	18	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
23	d1rrva_	Alignment		96.8	16	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
24	d1uqta_	Alignment	not modelled	96.7	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Trehalose-6-phosphate synthase, OtsA
25	d1rzua_	Alignment	not modelled	96.6	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
26	c2iyaB_	Alignment	not modelled	96.3	10	PDB header: transferase Chain: B: PDB Molecule: oleandomycin glycosyltransferase; PDBTitle: the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
27	c2p6pB_	Alignment	not modelled	95.9	11	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
						PDB header: synthase Chain: B: PDB Molecule: alpha, alpha-trehalose-phosphate

28	c1uquB_	Alignment	not modelled	95.9	11	synthase; PDBTitle: trehalose-6-phosphate from e. coli bound with udp-glucose.
29	c3d0qB_	Alignment	not modelled	95.7	14	PDB header: transferase Chain: B: PDB Molecule: protein calg3; PDBTitle: crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
30	c3othB_	Alignment	not modelled	95.5	12	PDB header: transferase/antibiotic Chain: B: PDB Molecule: calg1; PDBTitle: crystal structure of calg1, calicheamicin glycosyltransferase, tdp2 and calicheamicin alpha3i bound form
31	d1t0ia_	Alignment	not modelled	95.4	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
32	c3pe3D_	Alignment	not modelled	95.3	14	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnac transferase and its complex with a peptide2 substrate
33	d2c1xa1	Alignment	not modelled	95.0	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
34	c2fzvC_	Alignment	not modelled	94.9	10	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative arsenical resistance protein; PDBTitle: crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
35	c2o6lA_	Alignment	not modelled	94.8	8	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
36	c2qzsA_	Alignment	not modelled	94.6	12	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)
37	c2vsnB_	Alignment	not modelled	94.2	14	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
38	c3hbjA_	Alignment	not modelled	94.0	8	PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
39	d2vcha1	Alignment	not modelled	93.8	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
40	d2fzva1	Alignment	not modelled	93.6	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
41	d2pq6a1	Alignment	not modelled	93.3	6	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
42	c3iaaB_	Alignment	not modelled	93.2	14	PDB header: transferase Chain: B: PDB Molecule: calg2; PDBTitle: crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
43	d1rtta_	Alignment	not modelled	93.1	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
44	d1ka9h_	Alignment	not modelled	93.1	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
45	c2x0dA_	Alignment	not modelled	93.0	9	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
46	c2q62A_	Alignment	not modelled	92.7	12	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
47	d2acva1	Alignment	not modelled	92.2	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
48	d1fyea_	Alignment	not modelled	91.8	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
49	c3q3hA_	Alignment	not modelled	91.2	14	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
50	d2a9va1	Alignment	not modelled	90.5	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
51	d2f9fa1	Alignment	not modelled	90.3	11	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
52	d1k9vf_	Alignment	not modelled	90.2	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
53	d2iw1a1	Alignment	not modelled	89.5	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
54	d1ydga_	Alignment	not modelled	89.4	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like

55	d1hyea1	Alignment	not modelled	89.4	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
56	c3ic5A_	Alignment	not modelled	89.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroiyi.
57	c2vrcD_	Alignment	not modelled	88.5	14	PDB header: oxidoreductase Chain: D: PDB Molecule: triphenylmethane reductase; PDBTitle: crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
58	c3pu6A_	Alignment	not modelled	85.9	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of an uncharacterized protein from wolinnella2 succinogenes
59	c3lcmB_	Alignment	not modelled	85.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of smu.1420 from streptococcus mutans ua159
60	c3hbmA_	Alignment	not modelled	85.7	11	PDB header: hydrolase Chain: A: PDB Molecule: udp-sugar hydrolase; PDBTitle: crystal structure of pseg from campylobacter jejuni
61	c3p0rA_	Alignment	not modelled	85.1	8	PDB header: oxidoreductase Chain: A: PDB Molecule: azoreductase; PDBTitle: crystal structure of azoreductase from bacillus anthracis str. sterne
62	c3eywA_	Alignment	not modelled	84.5	15	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
63	c3m2pD_	Alignment	not modelled	83.9	11	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
64	c3k1yE_	Alignment	not modelled	83.6	11	PDB header: oxidoreductase Chain: E: PDB Molecule: oxi doreductase; PDBTitle: x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorombic crystal form, northeast structural3 genomics consortium target cdr100d
65	d1cfza_	Alignment	not modelled	83.4	21	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD
66	c2e85B_	Alignment	not modelled	83.2	14	PDB header: hydrolase Chain: B: PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
67	c2issF_	Alignment	not modelled	82.8	29	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
68	c2pk3B_	Alignment	not modelled	82.4	26	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
69	c3icpA_	Alignment	not modelled	82.1	26	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
70	d1f0ka_	Alignment	not modelled	81.8	10	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
71	d1up7a1	Alignment	not modelled	81.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
72	c2pzlB_	Alignment	not modelled	80.9	21	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
73	c2zkiH_	Alignment	not modelled	80.4	12	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)
74	d2cmda1	Alignment	not modelled	80.1	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
75	c3s29C_	Alignment	not modelled	79.8	11	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.
76	c2zklA_	Alignment	not modelled	79.4	20	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
77	d1t5ba_	Alignment	not modelled	79.3	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
78	d1s6ya1	Alignment	not modelled	79.2	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
79	c2p5uC_	Alignment	not modelled	78.5	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
80	c1a5zA	Alignment	not modelled	78.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: lactate dehydrogenase from thermotoga maritima (tml dh)
81	d1udca	Alignment	not modelled	78.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	d2z98a1	Alignment	not modelled	78.2	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
83	d2bli1a1	Alignment	not modelled	77.5	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
84	c2hunB	Alignment	not modelled	77.2	27	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
85	c2x4gA	Alignment	not modelled	77.0	18	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
86	d1obba1	Alignment	not modelled	77.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
87	c2ggsB	Alignment	not modelled	75.2	20	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	d1qyia	Alignment	not modelled	72.6	14	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
89	c3l4eA	Alignment	not modelled	72.5	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
90	d1txga2	Alignment	not modelled	71.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
91	d1vl0a	Alignment	not modelled	71.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
92	c3l4bG	Alignment	not modelled	70.9	15	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
93	d1b8pa1	Alignment	not modelled	70.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
94	d7mdha1	Alignment	not modelled	70.3	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
95	d1a5za1	Alignment	not modelled	70.3	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
96	c7mdhA	Alignment	not modelled	70.1	8	PDB header: chloroplastic malate dehydrogenase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: structural basis for light acitvation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
97	d2c5aa1	Alignment	not modelled	70.1	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
98	c3fniA	Alignment	not modelled	69.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (al13895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
99	c3c7cB	Alignment	not modelled	68.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: octopine dehydrogenase; PDBTitle: a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
100	c5mdhB	Alignment	not modelled	68.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of ternary complex of porcine cytoplasmic malate2 dehydrogenase alpha-ketomalonate and tnad at 2.4 angstroms resolution
101	c2v9cA	Alignment	not modelled	67.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fmm-dependent nadh-azoreductase 1; PDBTitle: x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
102	c2z2vA	Alignment	not modelled	66.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
103	c2jzcA	Alignment	not modelled	66.3	14	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine transferase subunit PDBTitle: nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1

104	c3l7nA_	 Alignment	not modelled	66.1	28	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
105	c1gv1D_	 Alignment	not modelled	66.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: malate dehydrogenase; PDBTitle: structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
106	c2vzhA_	 Alignment	not modelled	64.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-dependent fmn reductase; PDBTitle: structures of nadh:fmn oxidoreductase (emob)-fmn complex
107	c2pr7A_	 Alignment	not modelled	64.4	9	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
108	c2q1wC_	 Alignment	not modelled	63.6	20	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+
109	c2ywjA_	 Alignment	not modelled	63.2	23	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
110	d1y7ta1	 Alignment	not modelled	62.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
111	c3fwwA_	 Alignment	not modelled	62.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nad(p)h-dependent fmn reductase; PDBTitle: crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
112	c1obbB_	 Alignment	not modelled	62.0	16	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
113	c1b8vA_	 Alignment	not modelled	60.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: malate dehydrogenase from aquaspirillum arcticum
114	c3edoA_	 Alignment	not modelled	60.4	11	PDB header: flavoprotein Chain: A: PDB Molecule: putative trp repressor binding protein; PDBTitle: crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
115	d1n2sa_	 Alignment	not modelled	60.1	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
116	c3qhpB_	 Alignment	not modelled	59.9	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
117	d1o1ya_	 Alignment	not modelled	59.7	28	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
118	d1e5da1	 Alignment	not modelled	59.4	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
119	c3cwcB_	 Alignment	not modelled	59.0	20	PDB header: transferase Chain: B: PDB Molecule: putative glycerate kinase 2; PDBTitle: crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
120	d1kewa_	 Alignment	not modelled	58.8	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases