

Gene	Product	EC no.	Ncar locus	Ntbl locus	Identity	Length	Narc locus	Identity	Best BLAST hit in SwissProt (tbls)	Best BLAST hit in TrEMBL (tbls)	Functional Domains			Class	Description	GO terms	notes	TM domains	
											Description	Family	E-value						
N-glycosylation																			
	Oleosaccharyl transferase STT3, required for N-linked etc. 2.4.99.18 Isoelectrical protein		Ncar_c06000 Ncar_c09400	NVE_021270 NVE_021090	69.43 50.66	921 601	Narc1 Narc1_1203	74.0008 34.40	Narc1 : Homo sapiens. P46977.27.93 % Sulfobolus islandicus : C1M1P72.21.25%	Canarchaeum tombosum. A8RY10.46.28 % Sulfobolus islandicus : C1M1P72.21.25%	transferase, STT3 subunit UniCharcterized member	PF02516 COG1287	3.50E-43 117	3	This family consists of the oleosaccharyl transferase STT3 subunit and Molecular Function: oleosaccharyl transferase activity not in mammals			13	
Oleosaccharin																			
	uncharacterised oleosaccharin transferase, related to UDP-glucose 2.4.1.227		Ncar_c12850	NVE_040420	69.23	396			Methanocaldococcus jannaschii, OS8052.24.40% Methanocaldococcus jannaschii, OS8052.24.33%	uncultured marine microorganism, B3756, 34.53%	Glycosyl transferase, fat	IPR037235	1.2E-11	COG1815	Glycosyl transferases, related to UDP-glucosyltransferase Molecular Function: transferase activity, transferring hexosyl groups (GO:0016175), Biological Process: lipid glycosylation (GO:0030250)				
	putative UDP-glucosaminyltransferase Six-hairpin glycosylase-like protein		Ncar_c00310 Ncar_c12930	NVE_021060 NVE_010510	71.72 77.33	343 703	Narc1_1180001		Methanocaldococcus jannaschii, OS8052.24.33% Candidatus Nitrososphaera koronensis, F9CY99.31.63%	Glycosyl transferase, fat Six-hairpin glycosylase	IPR037235 IPR008928	1.0E-11 1,40E-38		similar to E.coli N-acetylglucosaminyl transferase (26.67%), involved in biosynthesis and degradation of murin sacculus and peptidoglycan in all thubates					
Cell wall biosynthesis																			
	Surface associated S-layer protein Surface associated S-layer protein		Ncar_c00760 Ncar_c00770	NVE_020970 NVE_018090	46.58 33.84	340 1202								30.6% to Ncar_1546 23.9% identity to Ncar_1201 (S-layer protein 1/1631 and 23.54% to Ncar_1547 (tbls))					
dpm	dolichol-phosphate mannosyltransferase	2.4.1.83	Ncar_c18120	NVE_004280	69.21	392			Ditychellium discolorum, Q5ALP3, 34.14 % un cultured marine ctenarchaeote, B3756, 60.36 %	GPA-like protein Glycosyl transferase, family 2	PF04138 PF00535	1,20E-19 2,00E-35		Glycosyltransferases involved in cell wall biogenesis (COG0463) Biological Process: polysaccharide biosynthetic process (GO:0000271), Biological Process: transport (GO:0006810), Cellular Component: integral to membrane (GO:0016021)					
	putative glycosyl transferase Family 2 outstate alcohol transferase Family 2 outstate alcohol transferase Family 2	2.4.1.212 Hv	Ncar_c19470	NVE_023920 NVE_023980 NVE_013470 31.12 to above	53.08 45.8 45.8	457 458			Streptococcus pyogenes, POC090, 28.98% Hyaluronan synthase	Streptococcus viridans, B51089.30.8%	Glycosyl transferase, family 2	IPR001173	5.30E-35	also COG5: COG0463, COG1215 Glycosyltransferases involved in cell wall biosynthesis	This domain is found in a di 5 This domain is found in a diverse family of glycosyl transferases that transfer the sugar from UDP-glucose, UDP-N-acetylglucosamine, GDP-mannose or CDP-abequose, to a range of substrates including cellulose, dolichol phosphate and teichoic acids.				
	putative glycosyl transferase, Family 2		Ncar_c05800	NVE_008700	39.25	277	Narc1_70013				Glycosyl transferase, family 2	PF00535	1,20E-20	COG0463	Glycosyltransferases involved in cell wall biosynthesis	only in Ncar, not in 1.14			
	putative glycosyl transferase, Family 2		nope	NVE_016690	296						Glycosyl transferase, family 2	PF00535	5E-10	COG0463	Glycosyltransferases involved in cell wall biosynthesis	This domain is found in a diverse family of glycosyl transferases that transfer the sugar from UDP-glucose, UDP-N-acetylglucosamine, GDP-mannose or CDP-abequose, to a range of substrates including cellulose, dolichol phosphate and teichoic acids.			
	putative glycosyl transferase, Family 2		Ncar_c12310	NVE_011320	64.49	419			GDA7.1, <i>Caulobacter crescentus</i> , 50.0% sartal	PF0265, <i>Methylobacterium methanica</i> , 47% sartal	Glycosyl transferase, family 2	IPR00535							
	putative UDP-3-O-acetylglucosamine N-acyltransferase Acetyltransferase, GNAT Family7?? Isoelectrical protein	2.3.1.129	nope nope nope	NVE_016700 NVE_016720 NVE_016760	176 236														
	putative exported polysaccharide deacetylase family protein		Ncar_c10480	NVE_023910	30.61	257			Cellulomonas feni, P54865, 21.57 % Clostridium clariflavum, GBM088, 30.97 % Streptomyces hemastetensis, D9W100, 32.71 %	Polysaccharide deacetylase	PF03522	6.4E-11	3	COG0726: Predicted xylanase/chitin deacetylase. Adjacent to a UDP-glucose/mannose dehydrogenase					
	putative exported polysaccharide deacetylase family protein outstate exported polysaccharide deacetylase family protein outstate oohsaccharide deacetylase putative polysaccharide deacetylase domain containing outstate oohsaccharide deacetylase outstate oohsaccharide deacetylase outstate oohsaccharide deacetylase (exported or cell surface associate)		Ncar_c10480 nope nope nope nope nope	NVE_023910 NVE_023910 NVE_016680 NVE_017890 60.2 to NVE NVE_001730 48.34 to NVE NVE_004670 46.67 NVE_015388 33.9 to NVE_016680	246 431 341 318 386						Polysaccharide deacetylase	IPR02509, IPR011330	8.3E-10						
uggp	Undecaprenyl-diphosphatase	3.6.1.27	NVE_005360		276	Narc1_1201		Carboxylothermus hydrogeniformans, C11902.40.81 % SO-9, C18ACT1.40.82 % N-acetylmuramoyl-L-alanine amidase sls1	Candidatus Kuenenia stuttgartensis, C11902.40.81 % N-acetylmuramoyl-L-alanine amidase sls1	Bacitracin resistance enzyme Bactr type, C-terminal Peptidoglycan-binding Nin domain hydrolase activity,	PF02673 PF00754 PF04176 PF00725	0.10E-47 3.0E-18 2.9E-11 0.000027		Antibiotic resistance: Cell membrane: Cell shape: Cell wall biosynthesis/alteration: Hydrolyase: Membrane: Peptidoglycan synthesis: Transmembrane: Transmembrane helix					
	exported protein of unknown function / Protein containing BMR/Arg-box repeats		NVE_010850								Sialidases (neuraminidases)	IPR011040	4.3E-15		Cell wall hits in Swell Prot				
	putative glutamate racemase protein of unknown function Six-hairpin glycosylase Family protein	5.1.1.3	Ncar_c19500 Ncar_c11850	NVE_018800 NVE_023720 NVE_024570	87.22% 77.1	271			Thermoanaerobacter tengcongensis, Q8RA00, 33% Candidatus Kuenenia stuttgartensis, G1PVT4.44.7% Glutamate racemase Peptidoglycan-binding 8 Six-hairpin glycosylases	IPR040301 (TIGR00067) PF05471 SF48208	2.10E-39 3.00E-18 2.5E-15	3	Glutamate racemase (EC:5.1.1.3) provides the (R)-glutamic acid requ Molecular Function: glutamate racemase activity (GO:0008861), Biological Process: peptidoglycan biosynthetic process (GO:0009252)						