

**Table S3:** Updated annotation of *epa* locus genes of *Enterococcus faecalis* V583

Protein	Size (AA)	Annotated prediction (UniProt); Predicted domains(s) <sup>a</sup>	Functionally characterized homologs <sup>a</sup>	Predicted function	Blast prot against ref prot exclusionEnterococcaceae
EF2198 (EpaA)	378	Glycosyl transferase, group 4 family protein; 11 TMH, PF00953	<b>UDP-GlcNAc:undecaprenyl phosphate N-acetylglucosaminyl 1-P transferase TagO</b> (358AA) of <i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168: 40% (145/361) amino acid identity and (64%) (233/361) amino acid similari (Soldo et al, 2002)	Transfers GlcNAc-P onto undecaprenyl-phosphate	Undecaprenyl/decaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase [ <i>Carnobacterium divergens</i> ] Sequence ID: WP_051915676.1 (366 AA) 222/365(61%) 287/365(78%) 2/365(0%)
EF2197 (EpaB)	262	Glycosyl transferase, group 2 family protein; PF10111	<b>α 1-3 rhamnosyl transferase WsaD</b> (289 AA) of <i>Geobacillus stearothermophilus</i> NRS 2004/3a: 27% (66/244) amino acid identity and 48% (119/244) amino acid similarity (Steiner et al, 2008).	Transfers the first rhamnose to the lipid linked und-PP-Glc intermediate	Glycosyltransferase family 2 protein [ <i>Carnobacterium divergens</i> ] Sequence ID: WP_135022433.1 (260 AA) 153/260(59%) 194/260(74%) 0/260(0%)
EF2196 (EpaC)	275	Glycosyl transferase, group 2 family protein; PF00535	<b>Predicted rhamnosyltransferaseLGG_00279</b> (273 AA, RfbF) of <i>Lactobacillus rhamnosus</i> GG 35% (88/254) amino acid identity and 51% (132/254) amino acid similarity (Sanchez-Rodriguez et al, 2014).	Transfers rhamnose	Glycosyltransferase [ <i>Bacillus thermoamylovorans</i> ] Sequence ID: WP_041848106.1 (282 AA) 115/281(41%) 167/281(59%) 9/281(3%)
EF2195 (EpaD)	237	Glycosyl transferase, group 2 family protein; PF00535	<b>α 1-3 rhamnosyltransferaseCps2F</b> (305 AA) of <i>Streptococcus pneumoniae</i> D39: 35% (75/215) amino acid identity and 53% (116/215) amino acid similarity (James et al, 2013).	Catalyzes the formation ofα 1,3-Rha linkages	Glycosyltransferase family 2 protein [ <i>Bacillus niacini</i> ] Sequence ID: WP_034674026.1 (238 AA) 111/221(50%) 152/221(68%) 0/221(0%)
EF2194 (EpaE, RfbA)	288	Glucose-1-phosphate thymidyllyltransferase; PF12804		Converts Glc-1-phosphate into dTDP-Glc	Glucose-1-phosphate thymidyllyltransferase RfbA [ <i>Carnobacterium divergens</i> ] Sequence ID: WP_074401346.1 (290 AA) 254/286(89%) 271/286(94%) 0/286(0%)
EF2193 (EpaF, RfbC)	190	dTDP-4-dehydroharmnose 3,5-epimerase; PF00908		Converts dTDP-4-keto-6-deoxy-D-Glc into dTDP-4-keto-L-Rha	dTDP-4-dehydroharmnose 3,5-epimerase [ <i>Lactobacillus mali</i> ] Sequence ID: WP_056990349.1 (193 AA) 153/190(81%) 172/190(90%) 0/190(0%)
EF2192 (EpaG, RfbB)	342	dTDP-glucose 4,6-dehydratase; PF16363		Oxidizes and dehydrates dTDP-Glc into dTDP-4-keto-6-deoxy-D-Glc	dTDP-glucose 4,6-dehydratase [ <i>Carnobacterium alterfunditum</i> ] Sequence ID: WP_034545369.1 (342 AA) 294/342(86%) 317/342(92%) 0/342(0%)
EF2191 (EpaH, RmdI)	299	dTDP-4-dehydroharmnose reductase; PF04321		Reduces dTDP-4-keto-L-Rha into dTDP-6-Rha	dTDP-4-dehydroharmnose reductase [ <i>Carnobacterium maltaromaticum</i> ] Sequence ID: WP_010051523.1 (280 AA) 182/279(65%) 233/279(83%) 1/279(0%)
EF2190 (EpaI)	241	Glycosyl transferase, group 2 family protein; PF00535	<b>UDP-GlcNAc:Und-P GlcNAc transferaseGaci</b> or M5005_Spy0610 (239 AA) of <i>Streptococcus pyogenes</i> 46% (113/247) amino acid identity and 59% (148/247) amino acid similarity (Rush et al 2017)	Transfers GlcNAc from UDP-GlcNAc to Und-P to yield GlcNAc-P-Und.	Glycosyltransferase family 2 protein [ <i>Streptococcus suis</i> ] Sequence ID: WP_024413034.1 (238 AA) 157/241(66%) 193/241(80%) 3/241(1%)
EF2189 (EpaJ)	121	Uncharacterized protein; 3 TMH, DUF2304 (PF10066)		Aids EF2190	DUF2304 domain-containing protein [ <i>Streptococcus suis</i> ] Sequence ID: WP_044760012.1 (118 AA) 50/117(43%) 79/117(67%) 1/117(0%)
EF2188 interrupted by an IS256	234	Racemase domain protein; 7 TMH, PF01757		Not assigned because of the IS insertion	Acyltransferase family protein [ <i>Lactobacillus plantarum</i> ] Sequence ID: WP_080373076.1 (353 AA) 63/175(36%) 96/175(54%) 9/175(5%)
EF2184 (EpaK)	113	Uncharacterized protein; 4 TMH		Aids for transfer of Glc on the polyrrhamnose	EamA family transporter [ <i>Eubacterium limosum</i> ] Sequence ID: WP_058693542.1 (117 AA) 48/113(42%) 79/113(69%) 0/113(0%)
EF2183 (EpaL)	264	Transport permease protein; 6 TMH, PF01061		Transports the polyrrhamnose to the external face of the cytoplasmic membrane	ABC transporter permease [ <i>Eubacterium limosum</i> ] Sequence ID: WP_058693533.1 (268 AA) 164/268(61%) 216/268(80%) 4/268(1%)
EF2182 (EpaM)	405	ABC transporter, ATP-binding protein; PF14524, PF00005		Catalyses transport of polyrrhamnose	ABC transporter ATP-binding protein [ <i>Eubacterium</i> sp. AM05-23] Sequence ID: WP_118518606.1 (401 AA) 289/399(72%) 345/399(86%) 0/399(0%)
EF2181 (EpaN)	1047	Glycosyl transferase, group 2 family protein; IPR029063, PF00535	<b>α 1-2, α 1-3 bifunctional rhamnosyl transferase WsaE</b> (1127 AA) of <i>Geobacillus stearothermophilus</i> NRS 2004/3a: 40% (198/500) of amino acid identity and 57% (288/500) of amino acid similarity (Steiner et al, 2008).	Catalyzes the formation ofα 1,2-Rha linkages	Glycosyltransferase [ <i>Eubacterium callanderi</i> ] Sequence ID: WP_073383644.1 (1092 AA) 453/1092(41%) 654/1092(59%) 55/1092(5%)
EF2180 (EpaO)	713	Glycosyl transferase, group 2 family protein; 2 PF00535 domains	<b>α 1-2, α 1-3 bifunctional rhamnosyl transferase WsaE</b> (1127 AA) of <i>Geobacillus stearothermophilus</i> 35% (134/388) amino acid identity and 62% (370/592) of amino acid similarity (Steiner et al, 2008).	Catalyzes the formation ofα 1,2-Rha linkages	Glycosyltransferase family 2 protein [ <i>Listeria monocytogenes</i> ] Sequence ID: WP_075491555.1 (712 AA) 408/713(57%) 514/713(72%) 6/713(0%)
EF2179 EpaP)	656	Uncharacterized protein; 13 TMH		Participates to transfer Glc or GlcNAc on polyrrhamnose	Hypothetical protein [ <i>Lactobacillus plantarum</i> ] Sequence ID: WP_063485480.1 (648 AA) 262/644(41%) 399/644(61%) 10/644(1%)
EF2178 (EpaQ)	433	Membrane protein, putative; 12 TMH		Participates to transfer Glc or GlcNAc on polyrrhamnose	Hypothetical protein <i>Paenibacillus</i> sp. ASL46] Sequence ID: WP_138494814.1 (401 AA) 83/297(28%) 140/297(47%) 26/297(8%)
EF2177 (EpaR)	465	Bacterial sugar transferase; 5 TMH, PF02397	<b>Undecaprenyl-phosphate glucose phosphotransferase WsaR</b> (471AA) of <i>Geobacillus stearothermophilus</i> 35% (134/388) amino acid identity and 54% (211/388) amino acid similarity (Steiner et al, 2007).	Transfers Glc from UDP-Glc to Und-P-P to yield Glc-P-P-Und	Sugar transferase [ <i>Lactobacillus manihotivorans</i> ] Sequence ID: WP_056964297.1 (466 AA) 270/447(60%) 360/447(80%) 0/447(0%)
EF2176 (EpaS)	252	Glycosyl transferase, group 2 family protein; PF00535	<b>UDP-Glc:alpha-D-GlcNAc-diphosphoundecaprenol beta-1,3-glucosyltransferase WfgD</b> of <i>Escherichia coli</i> BSL3F2 41% (104/253) amino acid identity and 56% (142/253) amino acid similarity (Brockhausen et al, 2008).	Transfers GalNAc on a TA chain	Glycosyltransferase family 2 protein [ <i>Brucacter ebronensis</i> ] Sequence ID: WP_129086999.1 (248 AA) 113/247(46%) 166/247(67%) 1/247(0%); glycosyltransferase family 2 protein [ <i>Carnobacterium divergens</i> ] Sequence ID: WP_135020075.1 (249 AA) 116/242(48%) 161/242(66%) 4/242(1%)
EF2175 (EpaT)	282	LicD-related protein; PF04991		Adds Rbo-P on a TA chain	2-C-methyl-D-erythritol 4-phosphate cytidyllyltransferase [ <i>Parvimonas micra</i> ] Sequence ID: WP_118058863.1 (281 AA) 161/274(59%) 197/274(71%) 0/274(0%)
EF2174 (EpaU)	893	Uncharacterized protein; Signal peptide, Glycoside hydrolase family 25 (PF01183)		Participates to peptidoglycan remodelling	Hypothetical protein [Weissella bombi] Sequence ID: WP_092461148.1 (678AA) 116/318(36%) 171/318(53%) 16/318(5%) on the first 363 amino acid residues of EF2174; Hypothetical protein [ <i>Brochothrix thermosphacta</i> ] WP_119946283.1 (724 AA) 212/536(40%) 306/536(57%) 20/536(3%) on the last -500 amino acids of EF2174
EF2172 (EpaV, ispD)	234	2-C-methyl-D-erythritol 4-phosphate cytidyllyltransferase; PF01128	<b>Ribitol-5-phosphate cytidyllyltransferase Tatl</b> (235 AA) of <i>Streptococcus pneumoniae</i> : 30% (74/241) amino acid similarity and 47% (115/241) amino acid similarity (Baur et al 2009).	Transfers the cytidyllyl group of CTP to D-ribitol 5-phosphate to yield CDP-ribitol	2-C-methyl-D-erythritol 4-phosphate cytidyllyltransferase [ <i>Lactobacillus porciniae</i> ] Sequence ID: WP_125709417.1 (234AA) 173/234(74%) 205/234(87%) 0/234(0%)
EF2171 (EpaW)	352	Epimerase/dehydratase, putative; PF01370		Converts an unknown substrate to UDP-Rha	NAD-dependent epimerase/dehydratase family protein [ <i>Lactobacillus paracasei</i> ] Sequence ID: WP_016366206.1 (353 AA) 203/352(58%) 264/352(75%) 1/352(0%)
EF2170 (EpaX)	324	Glycosyl transferase, group 2 family protein; PF00535	<b>UDP-Glc:GalNAcα-diphosphatellipid β1,3-Glc-transferaseWbdN</b> (260 AA) of <i>Escherichia coli</i> O157: 30% (60/202) amino acid identity and 53% (108/202) amino acid similarity (Gao et al, 2012).	Transfers GalNAc on a TA chain	Glycosyltransferase [ <i>Lactobacillus camelliae</i> ] Sequence ID: WP_056989625.1 (319 AA) 196/318(62%) 248/318(77%) 2/318(0%)
EF2169 (EpaY)	467	Membrane protein, putative; 11 TMH, O-Antigen ligase (PF04932)		Polymerizes the decoration building blocks	O-antigen ligase family protein [ <i>Lactobacillus paracasei</i> ] Sequence ID: WP_123156247.1 (463 AA) 124/462(27%) 232/462(50%) 46/462(9%)
EF2168 (EpaZ)	274	LicD1 protein, putative; PF04991		Adds Rbo-P on a TA chain	LicD family protein [ <i>Lactobacillus camelliae</i> ] Sequence ID: WP_054665109.1 (274 AA) 143/274(52%) 185/274(67%) 3/274(1%)
EF2167	323	Glycosyl transferase, group 2 family protein; PF00535	<b>Predicted rhamnosyltransferaseGBS1484</b> (315 AA) of <i>Streptococcus agalactiae</i> NEM316: 31% (75/244) amino acid identity and 53% (130/244) amino acid similarity (Sutcliffe et al, 2008).	Transfers Rha on a TA chain	Glycosyltransferase [ <i>Lactobacillus cacaonum</i> ] Sequence ID: WP_057829283.1 (308 AA) 108/292(37%) 158/292(54%) 22/292(7%)
EF2166	473	Membrane protein, putative; 12 TMH		Transports the decoration chain to the external face of the cytoplasmic membrane	Hypothetical protein [ <i>Virgibacillus halodentificans</i> ] Sequence ID: WP_077358726.1 (472 AA) 214/474(45%) 317/474(66%) 3/474(0%)
EF2165	324	NAD-dependent epimerase/dehydratase family protein; PF01370	<b>UDP-N-acetylglucosamine 4-epimerase WbpP</b> (341 AA) of <i>Pseudomonas aeruginosa</i> 36% (116/321) amino acid identity and 55% (178/321) amino acid similarity (Ishiyama et al, 2004).	Converts UDP-GlcNAc to UDP-GalNAc	NAD-dependent epimerase/dehydratase family protein [ <i>Streptococcus lactis</i> ] Sequence ID: WP_032946528.1 (309 AA) 199/312(64%) 246/312(78%) 6/312(1%)
EF2164	603	Membrane protein, putative; 11 TMH, PF11808		Links the TA chains to form the decoration building block	Hypothetical protein [ <i>Kineothrix alysoides</i> ] Sequence ID: WP_031392404.1 (455 AA) 144/457(32%) 245/457(53%) 29/457(6%); Hypothetical protein [ <i>Lactobacillus composti</i> ] Sequence ID: WP_035452870.1 (460 AA) 135/441(31%) 232/441(52%) 22/441(4%); hypothetical protein [ <i>Lactobacillus selangorensis</i> ] Sequence ID: WP_057771220.1 (454 AA) 128/437(29%) 219/437(50%) 16/437(3%); hypothetical protein [ <i>Lactobacillus sakei</i> ] Sequence ID: WP_076648356.1 (425 AA) 126/423(30%) 211/423(49%) 12/423(2%)

<sup>a</sup>: TMH for trans membrane helices(s)

<sup>b</sup>: with the exception of the functionality of EF2167 homolog, which is predicte

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