S1 Table: Gene nomenclature and annotation analyses

Gene Name	**Former Name [Ref]**	**Locus Tag**	**Protein Length (aa)**	**TMS†**	**Fold Recognition Hit (PDB)***	**Name of PDB Homologue**	**Probability (%)**	**E-value**
wzxX	–	*mxan_7416*	490	14	5T77_A	MOP-family lipid II flippase MurJ	100	1.3E-31
wzyX	*sgnF* [1]	*mxan_7442*	508	12	6BAR_A	Peptidoglycan glycosyltransferase RodA	98.66	3.3E-6
wzcX	*epsV* [1,2]	*mxan_7421*	507	2	4WL1_X	Polysaccharide co-polymerase WzzE	99.9	1.3E-24
wzeX	–	*mxan_7447*	186	–	3CIO_D	Tyrosine-protein kinase Etk, C-terminal Wzc domain	99.41	9.1E-14
wzaX	*epsY* [1]	*mxan_7417*	219	–	2J58_B	Outer-membrane lipoprotein Wza	100.0	1.3E-32
wzxS	*exoM* [3]	*mxan_3260*	506	14	5T77_A	MOP-family lipid II flippase MurJ	100	2.9E-33
wzyS	*exoJ* [3]	*mxan_3026*	426	12	6BAR_A	Peptidoglycan glycosyltransferase RodA	98.75	6.2E-7
wzcS	*exoC* [4]	*mxan_3227*	465	2	4WL1_X	Polysaccharide co-polymerase WzzE	99.93	7.0E-27
wzeS	*btkA* [5] *exoD* [6]	*mxan_3228*	231	–	3LA6_D	Nucleotide-binding domain of Tyr-protein kinase Wzc	99.9	9.3E-24
wzaS	*fdgA* [7] *exoA* [4,6]	*mxan_3225*	190	–	2J58_B	Outer-membrane lipoprotein Wza	100.0	4.4E-32
wzxB	– [4]	*mxan_1035*	506	14	5T77_A	MOP-family lipid II flippase MurJ	100	1.8E-33
wzyB	–	*mxan_1028*	486	12	6BAR_A	Peptidoglycan glycosyltransferase RodA	98.89	2.7E-7
wzcB	*btkB* [8]	*mxan_1025*	710	2	i) aa 2 – 391: 4WL1_X ii) aa 432 – 697: 3CIO_D	i) Polysaccharide co-polymerase WzzE ii) Tyrosine-protein kinase Etk	i) 99.88 ii) 99.92	i) 6.2E-24 ii) 6.7E-26
wzaB	– [9]	*mxan_1915*	204	–	2J58_B	Outer-membrane lipoprotein Wza	99.95	1.1E-29

†Consensus of OCTOPUS and TMHMM analyses. *Output from HHpred

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