Table S1. List of the 23 and 35 *Myxococcus xanthus* genes identified by two transposon mutagenesis experiments (Yo = [16]; Yu = [17]). For each gene, the locus_tag in the genome of *M. xanthus*, the accession number of the corresponding protein in the ref_seq database and the original functional annotation are provided. For each protein, we indicated the presence of functional conserved domains, of signal peptide and of transmembrane domains. $ signs design false positive genes that have been removed from the current version of the *M. xanthus* genome. Asterisks correspond to the 28 genes fitting our criteria as putative components of the gliding machinery. Among them we showed that nine (in red) co-localize in three small genomic regions.

	Locus_tag/ Ref_seq	**Gene**	**Lengh (aa)**	**Former annotation**	**Domain function (pfam)**	**Signal peptide**	**Transmembrane domain**	
Yo	($)	agmB	-	ATP-dependent RNA helicase NP643917, *Xanthomonas axonopodis*	-	-	-	
Yo	MXAN_0635/ YP_628903	agmE	319	Soj/Par CAB16134, *Bacillus subtilis*	CobQ/CobB/MinD/ParA nucleotide binding domain	no	no	
Yo	MXAN_1673/ YP_629925	agmN	513	Hypothetical protein BAB99656, *Corynebacterium glutamicum*	-	no	no	
Yo	MXAN_2538/ YP_630757	agmO	170	Proto-oncogene tyrosine-protein kinase c-ABL CAA34438, *Homo sapiens*	-	yes	no	*
Yo	MXAN_2542/ YP_630761	agmP	427	Multidrug resistance membrane protein, *Chlorobium tepidum*	Major Facilitator Superfamily	no	10	*
Yo	MXAN_2923/ YP_631134	agmQ	698	Leucine aminopeptidase-rekated protein AAF96710, *Vibrio cholerae*	Bacterial pre-peptidase C-terminal domain	no	no	
Yo	MXAN_3352/ YP_631549	agmF	346	Pseudouridylate synthase AAM24749, *Thermoanaerobacter tengcongensis*	RNA pseudouridylate synthase	no	no	
Yo	MXAN_3502/ YP_631696	agmI	304	Hypothetical protein ZP00079645, *Geobacter metallireducens*	Sporulation related domain	no	1	*
Yo	MXAN_3537/ YP_631730	agmL	432	Isocitrate dehydrogenase BAB06878, *Bacillus halodurans*	socitrate/isopropylmalate dehydrogenase	no	no	
Yo	MXAN_3842/ YP_632024	agmD	347	tRNA synthetase CAB74224, *Campylobacter jejuni*	tRNA synthetases class I (W and Y)	no	no	
Yo	MXAN_3886/ YP_632066	agmA	599	N-acetylmuramoyl L-alanine amidase CAB73523, *Campylobacter jejuni*	N-acetylmuramoyl-L-alanine amidase	yes	no	*
Yo	MXAN_4638/ YP_632804	agmH	279	Lysophospholipase ANN50803, *Leptospira interrogens*	Putative lysophospholipase	no	no	
Yo	MXAN_4798/ YP_632959	agmC	1731	Putative haemagglutinin/haemolysin-related protein CAD18331, *Ralstonia solanacearum*	Protein of unknown function (DUF3607)	no	1	*
Yo	MXAN_4865/ AAO66319 ($)	agmV	1151	No significant similarity	-	no	no	
Yo	MXAN_4869/ YP_633027	aglT	478	Predicted N-acetylglucosaminyl tranferase (AGR99) AAH42083, *Homo sapiens*	Tetratricopeptide repeat	yes	no	*
Yo	MXAN_4870/ YP_633028	agmU	1218	TPR-domain containing protein AAM05026, *Methanosarcina acetivorans*	Tetratricopeptide repeat	yes	no	*
Yo	MXAN_5715/ YP_633853	agmZ	399	No significant similarity	Response regulator receiver domain Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase	no	no	
Yo	MXAN_5744/ YP_633881	agmW	458	Carboxy-terminal protease BAC45699, *Bradyrhizobium japonicum*	PDZ domain (Also known as DHR or GLGF) Peptidase family S41	yes	no	*
Yo	MXAN_5753/ YP_633890	aglX	236	TolQ bioploymer transport protein I64064, *Haemophilus influenza*	MotA/TolQ/ExbB proton channel family	no	3	*
Yo	MXAN_5754/ YP_633891	aglV	153	ExbD/TolR AAM71873, *Chlorobium tepidum*	Biopolymer transport protein ExbD/TolR	no	1	*
Yo	MXAN_5756/ YP_633893	aglW	431	TolB AAM71875, *C. tepidum*	TolB amino-terminal domain WD40-like Beta Propeller Repeat	yes	no	*
Yo	MXAN_5818/ YP_633955	agmR	371	Putative ion transporting ATPase CAB45559, *Streptomyces coelicolor*	Anion-transporting ATPase	no	no	
Yo	MXAN_5820/ YP_633957	agmM	360	Putative metalloprotease C69831, *Bacillus subtilis*	Peptidase family M48	no	5	*
Yo	MXAN_6259/ YP_634388	agmJ	636	ABC transporter BAB59028, *Penicillium digitatum*	Protein of unknown function (DUF2629)	no	no	
Yo	MXAN_6519/ YP_634642	agmG	712	Site-specific recombinase CAD14714, *Ralstonia solanacearum*	Site-specific recombinase	no	7	*
Yo	MXAN_6608/ YP_634726	agmS	263	Enoyl-CoA hydratase AE011275, *Leptospira interrogans*	Enoyl-CoA hydratase/isomerase family	no	no	
Yo	MXAN_6860/ YP_634977	aglS	194	ExbD/TolR ACC45288, *Neisseria gonorrhoea*	Biopolymer transport protein ExbD/TolR	no	1	*
Yo	MXAN_6862/ YP_634979	aglR	245	MotA/TolQ/ExbB proton channel AAM72811, *Chlorobium tepidum*	MotA/TolQ/ExbB proton channel family protein	no	3	*
Yo/Yu	MXAN_6607/ YP_634725	agmT	339	Predicted periplasmic solute-binding protein (*Trichodesmium erythraeum*)	YceG-like family	yes	no	*
Yo/Yu	MXAN_1925/ YP_630169	mglA	195	SAR1-like small GTPase / GTPase Sar1p, CAA35978, *Saccharomyces cerevisiae*	ADP-ribosylation factor family	no	no	
Yo/Yu	MXAN_1926/ YP_630170	mglB	159	Guanine nucleotide exchange factor for MglA / Ca2+ binding calreticulin AF340232, *Taenia solium*; roadblock-LC7 domain	Roadblock/LC7 domain	no	no	
Yo/Yu	MXAN_3008/ YP_631217	aglU	547	WD-repeat lipoprotein, acylaminoacyl-peptidase / b-transducin-like protein HET-E2C AAL37299, Podospora anserina; TolB *M.acetivorans*	WD40-like Beta Propeller Repeat	yes	no	*
Yo/Yu	MXAN_3060/ YP_631268	cglB	416	Outer membrane lipoprotein / No significant similarity	-	yes	no	*
Yo/Yu	MXAN_4862/ YP_633021	agmX	674	Outer membrane lipoprotein / Putative DnaJ-domain containing protein AC018929, *Oryza sativa*	-	no	1	*
Yo/Yu	MXAN_4863/ YP_633022	agmK	3822	TPR repeat protein / TPR protein AAF31047, *Leishmania major*	Tetratricopeptide repeat	no	no	*

	Locus_tag/ Ref_seq	**Gene**	**Lengh (aa)**	**Former annotation**	**Domain function (pfam)**	**Signal peptide**	**Transmembrane domain**	
Yu	MXAN_2050/ YP_630279	pglH	927	TPR repeat, CheY-like receiver domain, and a winged-helix DNA-binding domain	Response regulator receiver domain	no	no	
Yu	MXAN_2541/ YP_630760	agnA	673	Unknown	Tetratricopeptide repeat	yes	no	*
Yu	MXAN_2919/ YP_631130	pglJ	441	Integral membrane protein similar to *S. coelicolor* gi:1098142 with local similarity to Wzy_C polymerase	O-Antigen ligase	no	8	*
Yu	MXAN_2921/ YP_631132	pglB	381	Glycosyltranferase similar to YP_000604 of *Leptospira interrogans*	Glycosyl transferases group 1	no	no	
Yu	MXAN_4148/ YP_632323	pglK	302	Predicted transmembrane transcriptional regulator	-	no	1	*
Yu	MXAN_4616/ YP_632784	pglF	750	Glycosyltranferase 1 domain and glycosyltranferase 2 domain	Starch synthase catalytic domain Glycosyl transferases group 1 Glycosyl transferase family 2	no	no	
Yu	MXAN_4710/ YP_632872	pglN	328	ADP-heptose synthase, bifunctional sugar kinase/adenylyltranferase RfaE_like	pfkB family carbohydrate kinase	no	no	
Yu	MXAN_4867/ YP_633025	pglI	640	Hypothetical abductin-like protein	FHA domain Gram-negative bacterial tonB protein	no	1	*
Yu	MXAN_5319/ YP_633470	pglC	841	TPR repeat	Tetratricopeptide repeat	no	no	*
Yu	MXAN_5382/ NC_008095	aspT	77pb	tRNA-Asp	tRNA-Asp			
Yu	MXAN_5585/ YP_633724	pglE	727	Glycosyltransferase of PMT family	Dolichyl-phosphate-mannose-protein mannosyltransferase	yes	17	*
Yu	MXAN_6403/ YP_634527	agnB	408	ABC-type transporter permease protein (*Vibrio fischeri*)	Predicted permease	yes	3	*
Yu	MXAN_6501/ YP_634624	pglD	354	GDP-mannose synthesis	Nucleotidyl transferase Mannose-6-phosphate isomerase	no	no	
Yu	MXAN_7160/ YP_635273	pglM	409	Alanine racemase	Alanine racemase, N-terminal domain Alanine racemase, C-terminal domain	no	no	
Yu	MXAN_7252/ YP_635365	pglA	222	Exopolysaccharide synthesis, ExoD	Exopolysaccharide synthesis, ExoD	no	3	*
Yu	MXAN_7296/ YP_635409	agnC	139	Unknown	Protein of unknown function (DUF3478)	no	1	*