

Figure S1. Heat map of the average amino acids identity (%) of proteins homologous to Re78 (REMIM1_PF00478) and Re79 (REMIM1_PF00479) of *Rhizobium etli* Mim1. The alignments were performed using ClustalW, version 1.2.4. of UniprotKB webserver.

(a)

<i>R. etli</i> Mim1 Re78 (AGS26143.1)	MIVSAATERL	NDILVELPKY	KSQWEANVSS	PYVRAYDLAI	DNFQKTTKAC	50
<i>Neorhizobium</i> (CDN51818.1)	MIVASANQRL	GDILVKLPKY	KSQWELNVAS	PYVRAYDAV	LSYNNEMKAC	50
<i>Sinorhizobium</i> (APG87637.1)	MIVSSATDRL	TDILVELPKY	KSQWQSNVAN	PYVRAYDLAV	ENFQRTLKAC	50
<i>R. phaseoli</i> (ANMO8143.1)	--MSAATERL	NDILVELPKY	KSQWEANVSS	PYVRAYDLAI	DNFQKTTKAC	48
<i>Agrobacterium</i> (WP_027675286.1)	--MSLATDRL	NNILIELPKY	KSQWQLNVAS	PYVRAYDLAI	DNYNKKMQEQ	48
<i>R. ruizarguesonis</i> (NKQ86457.1)	--MSAATDRL	NDILIELPKY	KSQWETNVAN	PYVRAYDLAI	DNYQKTTKAC	48
<i>R. oryzae</i> (WP_075641707)	--MSSAKDRL	TSIMDELDDK	KSQWEVSVVS	PYVRSYDFAY	NNYQNTLKAC	48
<i>Rhizobium</i> (WP_062451316)	--MSLAKERL	NNILIELPKY	ESQWESNIVL	PYSRAYDLAI	YLNKNVTKEQ	48
<i>Sphingomonas</i> (WP_156477649)	-----MADRL	QTYRNQVSDA	VDAAQANVCN	PYIIAYNTAY	KSADVFFKKQ	45
<i>Azospirillum</i> (WP_089286101)	-----MSDEI	RNYLDELEAK	AIRWRIFCR-	DYASAYHLAH	DQYKATWAAQ	44
<i>R. etli</i> Mim1 Re78 (AGS26143.1)	EARDRLAEL	FVFSASILTQ	SIMMAAFATT	SVRVLAGRAA	LSVICNNNLN	100
<i>Neorhizobium</i> (CDN51818.1)	GERDRATAEM	FVLAASILTQ	SVMMAAFATT	SVRVLAGRAI	VRVICNNNLN	100
<i>Sinorhizobium</i> (APG87637.1)	EARDKMTAEL	FVFAASVLSG	SVLMAAFATA	SLRVLAGRAA	LRVVCNNNLN	100
<i>R. phaseoli</i> (ANMO8143.1)	EARDRLAEL	FVFSASILTQ	SIMMAAFATT	SVRVLAGRAA	LSVICNNNLN	98
<i>Agrobacterium</i> (WP_027675286.1)	AARDKMAEL	FVMSASILTQ	SVMMAVFATT	SLRTLAGRAA	LRVICNNNLN	98
<i>R. ruizarguesonis</i> (NKQ86457.1)	EARDRLAEL	FVFSASVLTG	SIMMAAFATT	SVRVLAGRTA	LRVICNNNLN	98
<i>R. oryzae</i> (WP_075641707)	VARDKMGAE	LVTAGVLSG	SVLMAAFASS	SLRVLAGRAL	LRTICNNNLN	98
<i>Rhizobium</i> (WP_062451316)	EARDKLKAE	FVMSASILTQ	SVMMAAFATT	SLRVLAGRAA	LHVICNNNLN	98
<i>Sphingomonas</i> (WP_156477649)	DDSDKARAE	FVTAAAILPG	SILMATAATS	SLRVIANRTA	VRLLAGRSTS	95
<i>Azospirillum</i> (WP_089286101)	EKSDKEKAE	IVLALSVAAS	TVLMAAFATN	SLRVLAGRAA	LNVICNNNLN	94
<i>R. etli</i> Mim1 Re78 (AGS26143.1)	RTFNVMHAAA	SNKVVMFALG	GVLDEAKKLA	NKQVTSAAEK	LTSSAPVASA	150
<i>Neorhizobium</i> (CDN51818.1)	RTFNLMAAAN	NNKAFMFALG	GVLDEAKKVA	NKQVTKLVEG	LTSTGTQISA	150
<i>Sinorhizobium</i> (APG87637.1)	RTFDLMHAAA	SNKVMFALG	GILDEAKKFA	GKQITSAAEK	LTSSAPIASS	150
<i>R. phaseoli</i> (ANMO8143.1)	RTFNVMHAAA	SNKVVMFALG	GVLDEAKKLA	NKQVTSAAEK	LTSSAPVAAA	148
<i>Agrobacterium</i> (WP_027675286.1)	RTFNAFHAVS	ESKVMFALG	GVLDEVKKLA	GKHVTAAVEG	LTSSDAIASA	148
<i>R. ruizarguesonis</i> (NKQ86457.1)	RTFDLMHAAA	TSKPMFALG	GVLDEAKKLA	NKQVTSAAEK	LTSSAPIASA	148
<i>R. oryzae</i> (WP_075641707)	RTFDVAVHVT	NNKAMFALG	SVLDKAKGIA	GQHITAAVEN	FTVRTSGGQS	148
<i>Rhizobium</i> (WP_062451316)	RTFEAMRAAS	ANKALMFALG	SVLDEAKKLA	GKQVTSAVEG	LVSSASIASA	148
<i>Sphingomonas</i> (WP_156477649)	RALGVYNABA	SNATATFAIG	KALDIVKDET	GKAIKDSVVK	TMSNTRDLLA	145
<i>Azospirillum</i> (WP_089286101)	RTFNALHLVS	NNKAMFALG	AVMDAADAKA	KKYIEEKAGT	LTRSAPTPAV	144
<i>R. etli</i> Mim1 Re78 (AGS26143.1)	PTALNFKTRI	DDFIINHVC	VHEFIRGVQQ	DNTISEAGKS	RLADLVGQTP	200
<i>Neorhizobium</i> (CDN51818.1)	PTSVNYESRL	MDFIRVSHIC	THSFIEGVKE	DNSISETHKA	QVADMAARIP	200
<i>Sinorhizobium</i> (APG87637.1)	PTAINFLTRI	EDFINVNHC	VHEFIAGVRD	DRAISETDKL	KVADLVGKTP	200
<i>R. phaseoli</i> (ANMO8143.1)	PTALNFKTRI	DDFIINHVC	VHDFVRGVQH	DNTISEAGKS	RLADLVQATP	198
<i>Agrobacterium</i> (WP_027675286.1)	PTALNFLTLM	EDFINVNHC	VHNFVQGVVD	DASISDANKT	HIAELVGKTP	198
<i>R. ruizarguesonis</i> (NKQ86457.1)	PTALNFMTRI	ADFIDTNHC	VHDFVRGVQQ	DNSISEANKS	RLADLVGKTP	198
<i>R. oryzae</i> (WP_075641707)	QTSVNFTRL	QDFVNVSFIA	VHEFVTGVVN	DNSIKESDKL	KLADMVEATP	198
<i>Rhizobium</i> (WP_062451316)	PTGLNFESRM	KTFVNDNHC	VHSFVQGVVD	DGSLKDDDKM	HIAELATKMP	198
<i>Sphingomonas</i> (WP_156477649)	TDPLNRDKQL	NSWLNHKLK	AYDAADAIER	SRMSERDKQ	RAYDLLRAAP	195
<i>Azospirillum</i> (WP_089286101)	TNPAVLQNDL	INYVESNQLY	AMEVAFAIRD	DKSLSEADRA	ILVGSGLKRA	194
<i>R. etli</i> Mim1 Re78 (AGS26143.1)	FCNPPESSRV	DENRLSQKME	LLFYMSAVLD	SDKLVITYAPS	TGGTVGGVGR	250
<i>Neorhizobium</i> (CDN51818.1)	FCNPPESSSI	DEPKLANKME	LLFYMSVLD	SDRLVITYAPA	TGGSFGGMGQ	250
<i>Sinorhizobium</i> (APG87637.1)	FCNPPEAGRRV	DENRLSQKME	LLFYMSAVMD	SDRLVTFVFP	TGGSVPGTAR	250
<i>R. phaseoli</i> (ANMO8143.1)	FCNPPESSRV	DENRLSQKME	LLFYMSAVLD	SDKLVITYAPS	TGGTVGGIGR	248
<i>Agrobacterium</i> (WP_027675286.1)	FCNPPEARRV	DENRLSQKME	LLFYMDAVLE	SDKLVKFASV	TSSTTMLL-Q	247
<i>R. ruizarguesonis</i> (NKQ86457.1)	FCNPPESSRV	DENRLSRKME	LLFYMSAVLD	SDKLVITYVPA	TGGTVGGMGR	248
<i>R. oryzae</i> (WP_075641707)	FWLPPRANRV	DENKLAQKME	LLFYMTSVLD	SDTLVRHAPS	IGNGIGGGIG	248
<i>Rhizobium</i> (WP_062451316)	FCNPPESSRI	DENRLSQKME	LLFYMDAVLE	SDKLVITYAPA	SGERAMG--R	246
<i>Sphingomonas</i> (WP_156477649)	IANKPENG-KI	DPARLSPKIE	LGIFYMLWLD	SDELVTQAP	AGPYGGGG--	242
<i>Azospirillum</i> (WP_089286101)	LFKPEVN-EI	KRERLTDHIE	LSLHMSAMLD	SDFLVDIPMH	EMSTAGGLGS	243
<i>R. etli</i> Mim1 Re78 (AGS26143.1)	DIEYSKKAIP	QLPSAT-DYP	KSISPRLTGR	PFQPYDPGQR	IEYDNIGSVV	299
<i>Neorhizobium</i> (CDN51818.1)	DVEYSRKIS	QMPSTNGHY	KAASPKFVGR	PFVPPYDPGQR	IEYENIGSGI	300
<i>Sinorhizobium</i> (APG87637.1)	ELVLARKKIP	QMPSSA-DYP	RETAPRLTGK	LLQPFEPGTR	IEYSNIGSAV	299
<i>R. phaseoli</i> (ANMO8143.1)	DIEYKKAIP	QLPSAT-DYP	KSISPRLTGR	PFQPYDPGQR	IEYDNIGSVV	297
<i>Agrobacterium</i> (WP_027675286.1)	DVEFSRTPIA	QLPSST-DYP	REIGPQSGGI	PITSKNIGQR	VKYENLGSQI	296
<i>R. ruizarguesonis</i> (NKQ86457.1)	DIEYSKNAIP	QLPSAT-DYP	KATSPRFIGR	PLQPFEPGQR	VEYDNIGSVV	297
<i>R. oryzae</i> (WP_075641707)	EGIRSKERIN	QMPSTNGHY	KAASPKFVGR	PFVPPYDPGQR	IEYENIGSGI	295
<i>Rhizobium</i> (WP_062451316)	DVEYSGKPS	QMPSSA-NYP	KAIAPKFTGR	PFSPYDPGQR	VEYNNIGSAV	295
<i>Sphingomonas</i> (WP_156477649)	--RYSSKPID	ALPSAA-DYP	R-----GN	TDPKRGPIQW	VGVTRPGGDV	282
<i>Azospirillum</i> (WP_089286101)	VFGAKERIP	QLPSAS-DYP	RGTPFR---T	SLGVVHAQVS	VRVERPGPIV	289
<i>R. etli</i> Mim1 Re78 (AGS26143.1)	RERINTLSRL	TGNSSEFYPEQ	NS-VEKLFID	PTSGAQMVKA	EQIINRISAD	348
<i>Neorhizobium</i> (CDN51818.1)	RDRINKLSIS	TGNGPFYPNQ	SF-VERKLFID	PTGHAQMVKA	EQIINKLYND	349
<i>Sinorhizobium</i> (APG87637.1)	RERIDTSLRQ	YGGSPFYPQ	NF-AEKILID	PTGRAQMIRA	EQIINRLSAD	348
<i>R. phaseoli</i> (ANMO8143.1)	RERINTLSRL	TGNSSEFYPEQ	NS-LEKLFID	PTSGAQMAKA	EQIINRLSAD	346
<i>Agrobacterium</i> (WP_027675286.1)	RQRIDTSLKL	TGNSSEFYPEQ	SA-VER-FFD	PTGNAQLLKA	EQIINRLSIE	344
<i>R. ruizarguesonis</i> (NKQ86457.1)	RDRINTLSRL	TGNSSEFYPEQ	NF-AEKLLID	PTGSQLAKA	EQIINRLSTE	346
<i>R. oryzae</i> (WP_075641707)	RARIDTSLRA	YGGSPFYPQ	SIGMRIAGND	PTGREQMVKA	EHIISRLSAQ	345
<i>Rhizobium</i> (WP_062451316)	RERIDMLSRM	TGNSSEFYPEQ	NF-AERLLID	PTGNAQMVKA	EQIINRLSAS	344
<i>Sphingomonas</i> (WP_156477649)	EDQIDKVRHQ	VRGSAFYAPG	GW-FGKSDVN	QARLKEVAEA	ERVLAWLSDK	331
<i>Azospirillum</i> (WP_089286101)	QTKIDELNGR	IFNEKEFSAS	SWQGGQNGPM	P----ALVRA	ETTLNRLAEA	335
<i>R. etli</i> Mim1 Re78 (AGS26143.1)	ARPKQLTDVR	MI	360			
<i>Neorhizobium</i> (CDN51818.1)	ARPKQLTDVR	MI	361			
<i>Sinorhizobium</i> (APG87637.1)	ARPKQLVDVR	MI	360			
<i>R. phaseoli</i> (ANMO8143.1)	ARPKQLTDVR	MI	358			
<i>Agrobacterium</i> (WP_027675286.1)	ARPKELTDVK	VI	356			
<i>R. ruizarguesonis</i> (NKQ86457.1)	ARPKQLTDVR	MI	358			
<i>R. oryzae</i> (WP_075641707)	TRPKQLSDVF	MM	357			
<i>Rhizobium</i> (WP_062451316)	ARPKDITDVR	MM	356			
<i>Sphingomonas</i> (WP_156477649)	TQPLAPLGLR	T-	342			
<i>Azospirillum</i> (WP_089286101)	SRPLQLDAAR	V-	346			

(b)	R. etli Mim1 Re79 (AGS26144.1)	--MLLTGLIK	QGFLGRMRWP	LAAVTIVGVM	AASAAAMVGA	SGSTDQSLIQ	IEAVSSRLSA	58
	Neorhizobium (CDN51817.1)	-MKLISFFSP	SVRTGPILRQ	SRNVAVAFAM	AVWAPAFAAA	SDEIDETLLQ	IERVGPRLSA	59
	Sinorhizobium (APG87638.1)	-----	-----	-----	-----	MIAGT	SNPIDQSLVQ	25
	R. phaseoli (ANM08142.1)	--MLLTDFLK	RGLMGRMRWS	LVAAFTGAM	VASAAAMVGA	SGSTDQSLLE	IEAVSSRLSA	58
	Agrobacterium (WP_027675287.1)	MLFNDFTSHV	KKICLLKLCA	FACLVVCILL	TASHVSADQA	NNTIDSVVIR	AERLDQRLAD	60
	R. ruizarguesonis (NKQ86458.1)	-----	---MGRMRWP	LIAAALVCM	AASAGMVGA	SDTTDQSLIQ	IEQVASRLSG	47
	R. oryzae (WP_175577311.1)	-----	--MIRGLKHS	IRGGLCLGGM	GMLSPVAACA	DPSIDASLVQ	IEQVGERVAN	48
	Rhizobium (WP_062451254.1)	MMLLVDTVAV	LNRVRKVTFI	IAAPVLAIML	TGCDAGAESS	KSSVDASLLR	AERVDERLAL	60
	Azospirillum (WP_143270660.1)	-----M	RQELSLLLKW	SGLLLVLTAL	LLAGCSRSGE	AEKSDETMMQ	MEQVASYLQS	51
	Aureimonas (WP_183201854.1)	-----	-----MRWT	TAALALVGVL	AAILPGRAMA	DPAGDERYLR	LEDAERYVAG	44
	R. etli Mim1 Re79 (AGS26144.1)	TPAAVETVAK	AAADRSVPTS	-DAQPLLETA	ARSSFADAGM	LAEISKAVAE	AGSDA-VDPR	116
	Neorhizobium (CDN51817.1)	MPSEVENVVK	AATDRGNDEA	SKAGPILEPV	VRASFDPKGM	VAEISHSLAE	VEGGK-IDPA	118
	Sinorhizobium (APG87638.1)	APSAVKTVSK	ALAENGNAEV	PAAEALLETA	VHSSFDESEM	GAAILKNIGE	VDGGS-IDPE	84
	R. phaseoli (ANM08142.1)	TPGAVGSVAK	AAADRSVPAS	-DAQPLLETA	ARSSFADAGM	FAEISKAVAE	AGSDA-VDPR	116
	Agrobacterium (WP_027675287.1)	INAMVENSVA	IEAAGTKLDV	AKTKPLMLKA	ISQKFDLLQM	KRTIVAAIEA	PDNDY-QNFK	119
	R. ruizarguesonis (NKQ86458.1)	TPAAVENVAK	AAADRGISAT	SDAQPLLETA	ARSSFQVDSM	FAEISKAVGE	AGDDA-VDPK	106
	R. oryzae (WP_175577311.1)	AGLLADNVLK	YISDQEGLHD	KQADSMIESA	TRDAFNAQAF	VTEIQNSMQN	VGNSS-IDAQ	107
	Rhizobium (WP_062451254.1)	PQALIRNAAS	ARRDDKNADI	AKTEPLLISS	SEKAFDAGEM	RKKILVIEA	TPGGY-ADVA	119
	Azospirillum (WP_143270660.1)	MPGLVDIVGG	DVRKEFGAGV	DADLPLLRQS	VVKAFDPADL	LARVRRELKA	VDAGGGAIEP	111
	Aureimonas (WP_183201854.1)	MAEFARMQGP	LIEVSDRREL	PALAERGATL	AAQTEAVAGA	RDAMLERLRK	TPGEV---PV	101
	R. etli Mim1 Re79 (AGS26144.1)	AFAKAAAAWH	EGQAKVARMY	QAQDQVAAKE	IETRLADPKD	GPQIKALADL	MAGPDLAVES	176
	Neorhizobium (CDN51817.1)	TLAKAAAAFE	DGRKKIAEMY	RSQDQAIKQ	IEARIAGADD	GPRIKQLADL	MASPELAAET	178
	Sinorhizobium (APG87638.1)	AFARAAAAFE	EGRGKIARIY	EAQDQTAAKE	IEARLADPET	GARLRQLTDL	MAAPELAVES	144
	R. phaseoli (ANM08142.1)	AFAKAAAAWH	EGQAKVARMY	QAQDQVAAKE	IETRLADPKD	GPQIKALADL	MAGPDLAVES	176
	Agrobacterium (WP_027675287.1)	ALDKAVSALI	VSYAQIDKIY	TDKDEVAGKS	IQARLGNPKT	RETVDNVALN	MASPKLAADA	179
	R. ruizarguesonis (NKQ86458.1)	AFAKVAAALE	AGQAKIARMY	EAQDQTAAKD	IEMLANPDN	GPRIQSALADL	MAGPDLAVDT	166
	R. oryzae (WP_175577311.1)	RLAKIADDLN	ASRKKIETLA	QSKGDAALQT	MDAEIVKKAD	SPRVEQLAQL	MASPDLALET	167
	Rhizobium (WP_062451254.1)	AFDTATAALA	DGYRAVDMKY	ADKDEDGFKK	IETRLASPEA	KSTIEEVASL	MASPDLALET	179
	Azospirillum (WP_143270660.1)	AFLAAANDFI	RTQSAVEAES	RVDPGKVIQS	ATDAYEVRAD	KGRIDALAGA	MAAADIQVEG	171
	Aureimonas (WP_183201854.1)	AFDAIVARMR	AVEAEFASRS	LEALQAGEAD	AVAHYEAREPD	RASIDAVDGA	MAAPDLARET	161
	R. etli Mim1 Re79 (AGS26144.1)	AVTWQTMYYL	LEALSSADAE	KLASVSQDKL	QSEMNGVIAS	LRAR---SEN	EKPLPKDMAR	233
	Neorhizobium (CDN51817.1)	ALTAQVMYVS	LEAFSDPNSA	ELASASSEKR	KSELGGVIAS	LRDR---TEN	EKPPVRDIAR	235
	Sinorhizobium (APG87638.1)	AFTSQLMYAA	MEAFSDPSAA	ELASSS----	---ETPHVIAS	LRSR---NEN	EKPIAKDAAR	195
	R. phaseoli (ANM08142.1)	AVTWQTMYYL	LEALSSADAE	KLASVSQDKL	QSEMNGVIAS	LRAR---SEN	EKPLPKDMAR	233
	Agrobacterium (WP_027675287.1)	ASFQQAQVGA	LKISSDPGIY	ELNEEDQKKF	LADLPNFLAN	LRER---EVN	QSAYSRVITE	236
	R. ruizarguesonis (NKQ86458.1)	AFTAQLMYLC	LEALSNSDVE	TLASASKDKL	QSEMQGVISS	LRSK---SEN	EKPPVPKDIAR	223
	R. oryzae (WP_175577311.1)	AVTAQAMYYA	VHAFNSDPS	QFAALSQEQR	QDMPTQILSY	LQKQ---TEN	EKPPSKDANR	224
	Rhizobium (WP_062451254.1)	AVTQQAISAV	LTMETGSPAL	DPSSEEHKQL	KATLPSLLPE	FRNR---PDQ	GGAYSKEKAS	236
	Azospirillum (WP_143270660.1)	TLLGLRLQGA	AALRHLEKPV	LWQGLDDQGR	DRYADQFTRR	TRAEG--DAN	HSPPRYEIAR	229
	Aureimonas (WP_183201854.1)	AVTGLRVKWI	YETLLTGNDM	EMRAMTPALV	ETGIREVLDR	TRAPDDPEYG	APPLRKLVR	221
	R. etli Mim1 Re79 (AGS26144.1)	ADEKARLTFV	LATMPPEPDL	VLTDFYESSG	GKAKRDALVE	SYRRVSDQAN	KQMLGQYFQA	293
	Neorhizobium (CDN51817.1)	MEKARLTFV	LALPKDDLS	VLSDFYQSAE	GKAKRQALVE	TYRQVSDQAN	TRMLEKYFSA	295
	Sinorhizobium (APG87638.1)	LEEQQQLSFI	LATLSDEPDL	VLLDFYRSSG	GKTKRQALVD	SYVKVSDQAN	TKMLQAYFSA	255
	R. phaseoli (ANM08142.1)	ADEKARLTFV	LATMPPEPDL	VLTDFYESSG	GKAKRDALVE	SYRRVSDQAN	KQMLGQYFQA	293
	Agrobacterium (WP_027675287.1)	EYARNELSYA	LATLSDDQLD	TKMFYSSPT	GIAKTEALKK	TYKDILSENT	SIALDQYFRL	296
	R. ruizarguesonis (NKQ86458.1)	ANEKRLTFV	LATLSPEPDL	VLTDFYESSG	GKAKRDALIA	SYRQASDQAN	TEMLGQYFQA	283
	R. oryzae (WP_175577311.1)	ANEKRLGLA	LATLSDDQIL	YLTNLYQSPE	GKAKRAALD	RYKRLSTDAN	QKMLQDYFTQ	284
	Rhizobium (WP_062451254.1)	AFETAGLTFA	LATLTDKDL	ALKSFYAGSY	GKSKRQELLG	AYQQVWDAAD	TTMLTTYIEE	296
	Azospirillum (WP_143270660.1)	FLAIQRLTII	LLRLPEPSLK	ALDFYNSDL	GKAKRKALVA	AVAAQSDADT	QMMVEYLRQ	289
	Aureimonas (WP_183201854.1)	EQARMVKRMV	LSHLPEADVA	ALAAFYASDV	GKAKRRALVE	AFGARNDDEG	ARFRQLLER	281
	R. etli Mim1 Re79 (AGS26144.1)	LAEYFKTHPR	PQQQQ	308				
	Neorhizobium (CDN51817.1)	LAGEYFKTHPR	PQQQ-	309				
	Sinorhizobium (APG87638.1)	LANYLKTHPR	PQQQ-	269				
	R. phaseoli (ANM08142.1)	LAEYFKTHPR	PQQQQ	308				
	Agrobacterium (WP_027675287.1)	IFAEQVKN--	----	304				
	R. ruizarguesonis (NKQ86458.1)	LADYLKTHPR	PQQQQ	298				
	R. oryzae (WP_175577311.1)	LADNLTKRKS	NN--	296				
	Rhizobium (WP_062451254.1)	LAKQHPAAVK	AQ--	308				
	Azospirillum (WP_143270660.1)	LR-----	----	291				
	Aureimonas (WP_183201854.1)	ERSRTP----	----	287				

Figure S2. Complete alignment of Re78 and Re79 with homologous proteins. (a) Re78 (ReMim1 AGS26143.1) alignment showed 39 identical amino acids (red). (b) Re79 (ReMim1 AGS26144.1) alignment presented 11 identical amino acid (red). The amino acid position of residues is indicated on the right side of the sequences. The NCBI ID is shown on the left of each sequence.

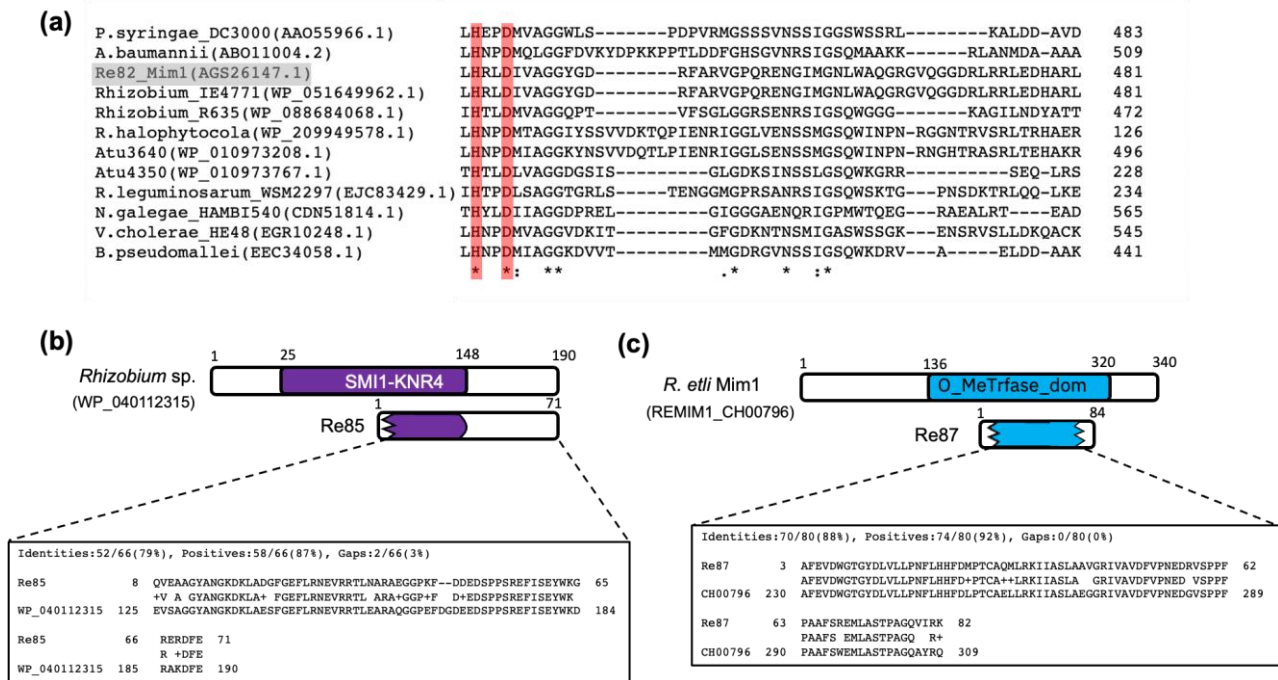


Figure S3. Relevant characteristics of the Re82, Re85 and Re87 proteins encoded in the T6SS cluster of ReMim1. (a) Partial sequence alignment of Re82 and members of a superfamily of T6SS-dependent DNase effectors. The HxxD catalytic motif is highlighted in red. Asterisks and dots indicate conserved amino acid and conservative changes, respectively. The amino acid position of residues shown is indicated on the right of the sequences. The NCBI ID are shown on the left of each sequence (b) Alignment of protein Re85 with a representative of a BLAST search, *Rhizobium* sp. (WP_040112315). SMI1-KNR4 domain is highlighter in purple. (c) Alignment of protein Re87 with a representative of a BLAST search, *Rhizobium etli* Mim1 (REMIM1_CH00796). O-methyltransferase domain is highlighted in blue. Organism names and protein accession numbers are on the left and the amino acid position in the alignments is indicated on each side of the sequences.

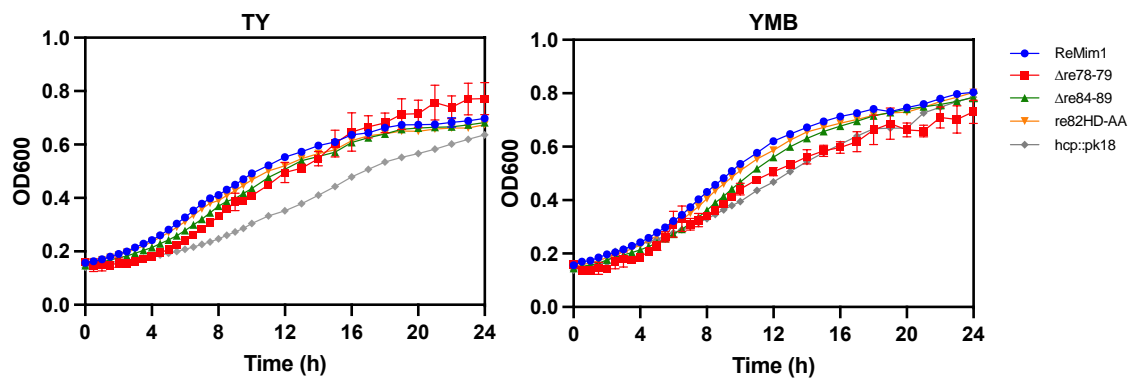


Figure S4. Growth curves of *Rhizobium etli* Mim1 strain and T6SS-derivative mutants in TY and YMB media at 28 °C.

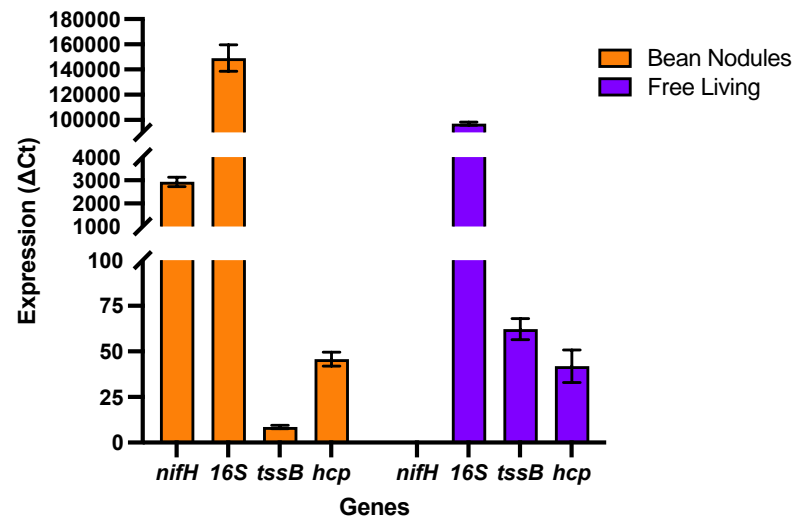


Figure S5. RT-qPCR analysis of T6SS genes *tssB*, *hcp* and *16S rRNA* gene (constitutive) and *nifH* gene (expressed in symbiotic condition). RNA from *tssB*, *hcp* and *16S rRNA* were analysed in free-living cells (TY medium) and RNA from *tssB*, *hcp* and *nifH* were analysed from bean nodules induced by *Rhizobium etli* Mim1, 28 dpi. Data were normalized using expression of *rpoD* gene. Bars values are average of two biological assays with three replicates.

Table S1. Bacterial strains and plasmids, related to Experimental Procedures.

Strain or Plasmid	Relevance Characteristics	Reference or Source
<i>Escherichia coli</i>		
DH5α	Host for DNA cloning	Gibco-BRL
BL21(DE3)	Host for protein expression	New England Biolabs
S17.1	Host for conjugation	[72]
HB101	Host for conjugation, triparental mating	[73]
<i>Rhizobium</i>		
<i>Rhizobium etil</i> Mim1 (ReMim1)	Wild-type strain able to induce nodules in <i>Phaseolus vulgaris</i> plants	[74]
hcp::pk18	ReMim1 <i>hcp</i> mutant, Km ^r	[21]
Δre78-79	ReMim1 <i>re78</i> and <i>re79</i> deletion mutant	This work
re82HD-AA	ReMim1 derivative by site-directed mutagenesis in amino acids H431 and D434 has been substituted for Alanines	This work
Δre84-89	ReMim1 derivative with <i>re84</i> to <i>re89</i> genes deleted	This work
Plasmids		
pCR2.1-TOPO	Vector for optimize cloning PCR products, Amp ^r , Km ^r	Invitrogen
TOPO.Re79StrepTag	pCR2.1-TOPO derivative containing <i>re79</i> gene	This work
pCR2.1-P6	pCR2.1-TOPO derivative containing P6 region (1242-bp) of T6SS from ReMim1	This work
pSCA	Vector for optimize cloning PCR products, Amp ^r , Km ^r	Agilent Technologies
pSCA-re82	pSCA derivative containing <i>re82</i> gene	This work
pSCA-HD→A	pSCA derivative containing <i>re82</i> H ₄₃₁ A	This work
pSCA-AD→A	pSCA derivative containing <i>re82</i> H ₄₃₁ A-D ₄₃₄ A	This work
pK18 <i>mobsacB</i> (pK18)	Suicide vector; <i>sacB</i> gene for double crossover event selection, Km ^r	[75]
pK18 <i>mobsacB</i> .Δre78-79	pK18 derivative to generate a <i>re78-79</i> deletion	This work
pK18 <i>mobsacB</i> .Δre84-89	pK18 derivative to generate a <i>re84-89</i> deletion	This work
pK18 <i>mobsacB</i> .re82HDAA	pK18 derivative to generate <i>re82</i> H ₄₃₁ A-D ₄₃₄ A	This work
pET22b(+)	T7 promoter vector with N-terminal signal peptide (PelB), Amp ^r	Novagen
pET22b.Re78SP	pET22b derivative expressing Re78 with a N-terminal PelB sequence	This work
pET22b.Re78	pET22b derivative expressing Re78	This work
pBAD33	Plasmid for cloning, L-arabinose inducible, araBAD promoter, Cm ^r	[76]
pBAD33.Re79	pBAD33 expressing immunity protein Re79, Cm ^r	This work
pLMB509	Broad-host range expression vector with a taurine inducible promoter, Gm ^r	[77]
pLMB509-Re79StrepTag	pLMB509 derivative expressing Re79 with a C-terminal Strep-tag	This work
pMP220	Cloning vector with a promoter-less <i>lacZ</i> gene, Tc ^r	[78]
pMP220-PTssA	pMP220 cloned P6 of ReMim1 and <i>tssA</i> region, Tc ^r	This work
pMP220-PHcp	pMP220 cloned P6 of Remim1 and <i>tssH</i> region, Tc ^r	This work
pHC60	Green Fluorescent Protein (GFP) gene under a constitutive promoter, Tc ^r	[79]
pCMB13	Contains the <i>Discosoma</i> Red fluorescent protein (DsRed) gene under a constitutive promoter, Sp ^r	[80]

Antibiotic Abbreviations: Amp (ampicillin), Km (kanamycin), Sp (spectinomycin), Tc (tetracycline), Gm (gentamicin), Cm (chloramphenicol).

Table S2. Primers used in this study, related to experimental procedures.

Primer	Sequence (5'-3')	Use
P78.F	CCGGCCATATGATCGTGTGCGCTGCAACTGA	Cloning of <i>re78</i> in pET22b without PelB
P78.R	CCGGGCTCGAGTTAATGGTGATGGTGATGGTGAATCATCCTGACATC	
P78sp.F	CCGGGGGATCCGTCGGCTGCAACTGAGCGGCA	Cloning of <i>re78</i> with PelB (N-terminal)
P78sp.R	CCGGGCTCGAGTTAATGGTGATGGTGATGGTGAATCATCCTGACATC	
P79.F	CCGGCCATATGCTGTTGACCGGTCTTATCAAG	Cloning of <i>re79</i> in pBAD33
P79.R	CCGGCAGCGCTTTAATGGTGATGGTGATGGTGCTGCTGCTGTTGCGGCCGGGG	
P79.NdeI	CCGGGCATATGCTGTTGACCGGTCTTATC	Cloning of <i>re79</i> in PCR2.1 TOPO and pLMB509
P79.NdeIStrep	CCCGGCATATGTTACTTTTCGAACTGCGGGTGGCTCCAGCTAGCCTGCTGCTGTTGCG G	
P78.1	CCTACCAAGGTCAGCGATT	Deletion of <i>re78</i> to <i>re79</i>
P78.2	CACCAAACGTGGCTTGCCGTACTTGGGGAGTTCTACCAGA	
P79.3	GGCAAGCCACGTTTGGTGCGCTGGCGGAGTATTCAA	
P79.4	CGACCGAGGTCTTGTCATC	
P84.1	GCGAAAACGGGATTATGGGC	Deletion of <i>re84</i> to <i>re89</i>
P84.2	ACCCGCTTCATAGCGATCATCGGTCCAACG	
P89.1	TGATCGCTATGAAGCGGGTCGATTAGGAGG	
P89.1	GCTGGCGCGCAATACAATTA	
P82.F	GATTGGCAGGCTAGGCAGAT	Site-directed mutagenesis in which amino acids H ₄₃₁ and D ₄₃₄ have been substituted for Alanines
P82.R	TGAAGACGGGATTGTAGGCG	
PH.A.F	CTGGCCGCACTGGCACGCCTTGATATT	
PH.A.R	AATATCAAGGCGTGCCAGTGCGGCCAG	
PD.A.F	TGGCACGCCTTGCTATTGTGGCGGG	
PD.A.R	CCCGCCACAATAGCAAGGCGTGCCA	
pMP220 F	AGCTCCTGAAAATCTCGTCG	Confirmation of P6 orientation in pMP220
pMP220 R	TAAAAAACCCCACTCCGGCAA	
P6.1	GTCGAGCATTGCCCGGT	Amplification of ReMim1 P6 promoter region
P6.2	CCGACATCCGTGCGACA	
78.RT.F	GAGCGTTTGAACGATATTCT	qPCR of T6SS genes
78.RT.R	CTGACATAGGGACTGGAAAC	
79.RT.F	TGACGGAATTCTATGAGAGC	
79.RT.R	GGGATGGGTCTTGAAATACT	
81.RT.F	TTCTGCCAGAGAACCCAAAC	
81.RT.R	CCATAGGCCTTACTCCAGCA	
82.RT.F	GACGTAGATGATGTCGAGGA	
82.RT.R	ACTGGTTCTTCTCTCGGTCT	
83.RT.F	AGTGCTCTCGGACCTCTGAA	
83.RT.R	CTCGACCCCTATACGGACAA	
84.RT.F	CTATTTCCGAGACAGGAATG	
84.RT.R	GACTTCAACTGCGAATGAAT	
85.RT.F	GTTCTGCGCAACGAAGT	
85.RT.R	GTTCCCGACCCCTCCAGTAT	
86.RT.F	GGCAGTGGGTCTGGACATAG	
86.RT.R	GATACGACTGCGGAGCACAC	
87.RT.F	CTGCCTTCGAGGTAGATTGG	
87.RT.R	CGATGATCTTTCGGAGCATT	
88.RT.F	ACCGCACGCTATCAGCTC	
88.RT.R	GTCGAGAACCGGCTTCAG	
89.RT.F	GCTGCCGGATCATAGTCAAA	
89.RT.R	GGCAGCAAGGTTTGAAAAGT	

hcp.RT.F	TTTCGGAAGTGATCCTCACC
hcp.RT.R	ATATAGGTGTCGCCGGGATT
nifH.RT.F	GGTCTTCATGATGCCGAAGT
nifH.RT.R	CTAGCCGAGAAGATCCATGC
tssB.RT.F	AAGCTCCGTTCGTCCTTCT
tssB.RT.R	ATCCGACACAGCCTCTCAAG
16S.RT.F	ACGTGCTACAATGGTGGTGA
16S.RT.R	CAGAGTGCAATCCGAACTGA
rpoD.RT.F	GATGAAGTCGATCGGCAATCTG
rpoD.RT.R	GCTTCGACCATTTCCTTCTTG

Table S3. Proteomic analysis of Re78/79 from secretomes of *Rhizobium etli* Mim1 and hcp::pk18 mutant.

Protein	Accession	MW (kDa)	SignalP ^a	Score ^b		Peptides ^c		PSM ^d	
				ReMim1	hcp::pk18	ReMim1	hcp::pk18	ReMim1	hcp::pk18
Re78	S5S7Y0	39.5	No	160.97	11.68	18	2	54	4
Re79	S5SXD8	32.8	Yes	42.25	35.21	6	6	14	13

^aSignalpeptide identified by SignalP 5.0; ^bMeasure of the goodness of fit of experimental peptide fragments to theoretical spectra; ^cTotal number of distinct peptide sequences identified; ^dRelative Peptide-Spectrum-Match.