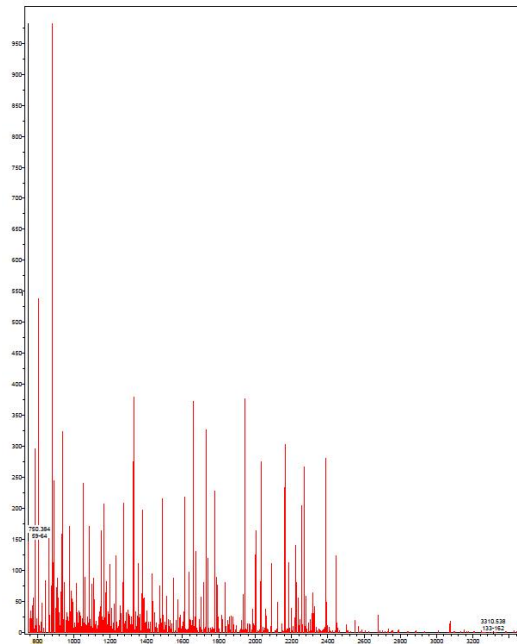


A

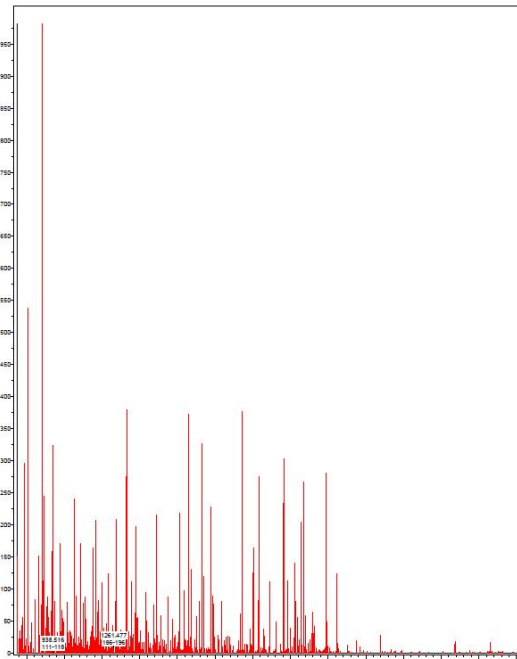
Outer membrane protein IIIA OS=Rhizobium leguminosarum bv. viciae GN=ropA PE=1 SV=1 OM3A_RHILV MH+ (mono): 1.008 MH+ (avg): 1.008 Tolerance (Da): 5.500 Number of Peaks: 909



MNIRMVLLASAAFAASTPVLAADAIVAAEPEPVEYVRVCDAYGTGYFYIPGTETCLK**IEGYIR**FQVNVGDNPGGDNDSDWDAVTAVRFSSRKSDTE YGPLTGVIVMQFNADNASDQDAILDSAYLDVAGFR**AGLFYSWWDDGLSGETDDIGSVVTLHNSIR**YQYESGTFYAGLSVDELEDGVYQGTFTPGVI PGTTDFTADDGPNNVGVAFGIGGTAGAFSYQVTGGWDVDNEDGAIRAMGTVEIGPGTFGLAGVYSSGPNYSYSSAEWAVAAEYAIKATDKLKITPGR WHGHVPEDFDGLGDAWKVGLTVDYQIVENFYAKASVQYLPQDGEDSTSGYFACSVRSNHLVDAPGLRIGSTTISF

B

22 kDa outer membrane protein OS=Rhizobium leguminosarum bv. viciae GN=ropB PE=3 SV=1 ROPB_RHILV MH+ (mono): 1.008 MH+ (avg): 1.008 Tolerance (Da): 5.500 Number of Peaks: 909



MRVLIAGLMASVFAIAGVSAQAADRVDQVPEAPVAQEAPVKPAGSWEGFYLGGAGTYNMGDFGSDRHTYGFGGQVFTGYNWQQGQIVYGVESD LGYSGDDVSSGGVENK**YGNWSVR**GRVGYDMNPFLLYGTAGLAIGDVKSDDTSDESKTNFGYTVGAGVEAFVTNNITRLEYRYTDYQSK**DYDL****SGSF**RGYDENSVKLGICVKF

Figure S1. Mass spectrometry identification data of the RopA (OmpIIIA) (A) and RopB (B) proteins. Amino acid sequences of the RopA (A) and RopB (B) proteins are shown. Peptides identified by mass spectrometry are indicated in yellow.