**Table S2** *Xenorhabdus* Antimicrobial Peptide-Rich Fractions Separated from EMA CFCM. Two of which (EMA\_PF2 and EMA30 were selected for Liquid Bioassays in *Agrobacterium* Bioassays

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Name Of Preparation | | Origin | WAY OF PURIFICATION | Agar Diffusion Bioassay on | | | |
| SAR  JE | EC  HGB2226 | XN  HGB 1975 | CA  JE |
| EMAPF | | AmberlitR XAD1180; Methanol elution | +++ | +++ | +++ | +++ |
| EMAPF1 | | EMAPF | Ultrafiltration;  MW > 10,000 D fraction | +++ | +++ | +++ | +++ |
| EMAPF2 | | Ultraliltration;  MW < 10,000 D fraction; | +++ | +++ | +++ | +++ |
| EMA(30) | AF103\* | CFCM | RPCC; Eluted with  30 % AN / 0.1% TFA | +++ | +++ | +++ | +++ |
| HPLC Fraction 40 | | AF103\* | HPLC | +++ | +++ | +++ | +++ |
| HPLC Fraction 43 | | HPLC | +++ | +++ | +++ | +++ |
| HPLC Fraction 44 | | HPLC | +++ | +++ | +++ | +++ |

**Footnotes to Table S2**: +++ = very strong antimicrobial activity; Abbreviations: EMA= *Xenorhabdus budapestensis* HGB033; CFCM = Cell-Free Culture Medium; PF = Peptide Rich Fraction; \* = Name of HPLC Sample; RPCC = Reverse Phase Column Chromatography; Test organisms; CA =*Candida albicans*; SA = .*Staphylococcus aureus*; EC = *Escherichia coli* HGB2226; XN = a *Xenorhabdus nematophila* lab isolate which is extreme sensitive to *Xenorhabdus* antibiotics. **HGB1795** is a transposon-induced insertion mutant of the XNC1\_2022 gene (Gene ID: 9430524; Gene Page Link: NCBI UniProtKB; Locus Tag: XNC1\_2022 see gene page for GenePage for the XNC1\_2022 gene EcoGene-RefSeq) from *X. nematophila* (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6), provided by Prof. Helge Bode via Prof. Heidi Goodrich-Blair. We used this mutant since previously Bicornutin A was believed as the active EMA antibiotic molecule (Böszörményi et al., 2009) and the XNC1\_2022 gene of *X. nematophila* was believed to be a homologue of *X. budapestensis* *Nrp*S (nrpS) gene, (GenBank: Accession Number is JX424818.1; gene synonym="bicA) which is responsible for the biosynthesis of Bicornutin A (Fuchs et al., 2012). It turned out that it is not the case. However, some role in the scenario related to antibiotics activity and self-resistance cannot be ruled out, since Bicornutin A and fabclavine coexist in our peptide-preparations.