

Supplementary information to:

**EXPRESSION AND PURIFICATION OF UNTAGGED GLNK
PROTEINS FROM ACTINOBACTERIA**

Edileusa C.M. Gerhardt¹, Vivian R. Moure¹, Andrey W. Souza¹, Fabio O. Pedrosa¹,
Emanuel M. Souza¹, Lautaro Diacovich², Hugo Gramajo², Luciano F. Huergo^{1,3*}

¹ Departamento de Bioquímica e Biologia Molecular, UFPR, Curitiba, Brazil

² Instituto de Biología Molecular y Celular de Rosario (IBR-CONICET), Facultad de Ciencias Bioquímicas y Farmacéuticas, Universidad Nacional de Rosario, Rosario, Argentina

³ Setor Litoral, UFPR, Matinhos, Brazil

* Corresponding author: Prof Luciano F. Huergo – Universidade Federal do Paraná, Setor Litoral, Rua Jaguariaíva, 512, Caiobá - Matinhos - Paraná – Brazil, CEP: 83260-000, Phone +55 41 96765856, +55 41 35118321, +55 41 35118393;
E-mail: Luciano.huergo@gmail.com

<http://dx.doi.org/10.17179/excli2017-394>

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>).

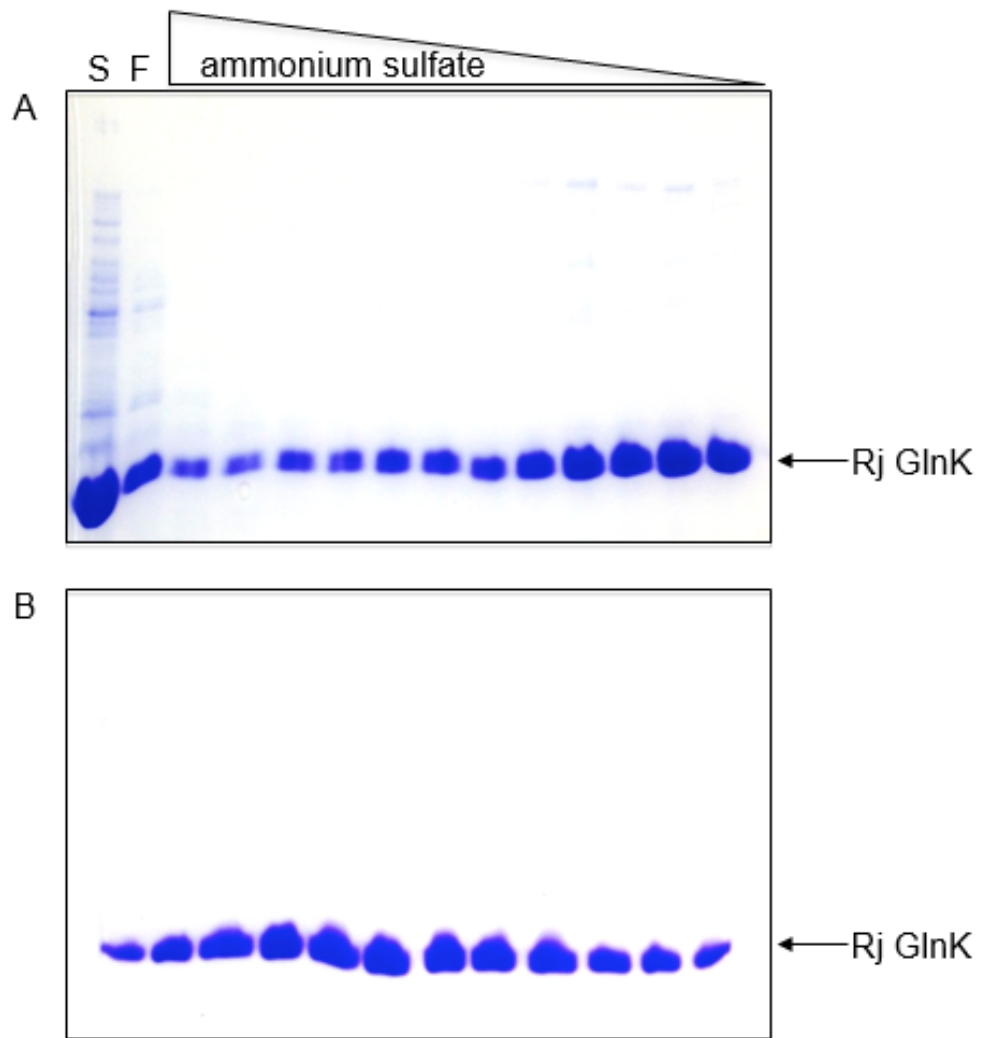


Figure S1: Purification profile of RjGlnK. Tricine-SDS-PAGE analysis of (A) Fractions eluted from Phenyl sepharose column by decreasing the ammonium sulfate concentration. (B) Fractions eluted from gel filtration Sephacryl S200. S – Soluble fraction; F – Flow through.

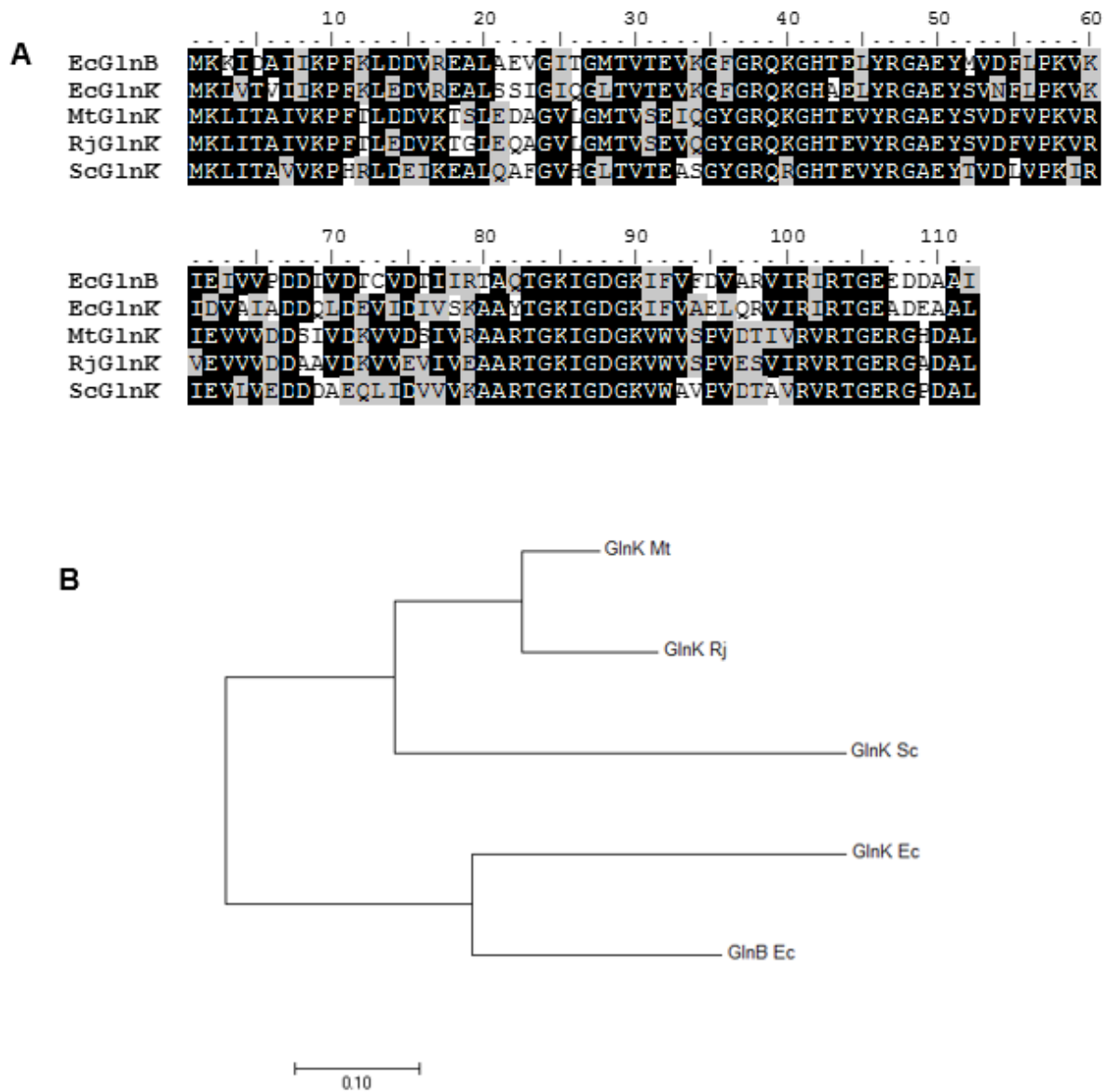


Figure S2: (A) Clustal W alignment of PII proteins from *E. coli*, *M. tuberculosis*, *R. jostii* and *S. coelicolor*. Identical amino acids are shown in black and similar in grey. (B) Molecular Phylogenetic analysis by the Maximum Likelihood method using MEGA7. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.