**Functional exploration of co-expression networks identifies a nexus for modulating protein and citric acid titres in *Aspergillus niger* submerged culture**

**Timothy C. Cairns1,2, Claudia Feurstein1,2,3, Xiaomei Zheng1,2,4, Li Hui Zhang1,2,5, Ping Zheng1,2,4, Jibin Sun1,2,4, and Vera Meyer1,2,3,4**

1 Tianjin Institute of Industrial Biotechnology, Chinese Academy of Sciences, Tianjin, 300308, People’s Republic of China

2 Key Laboratory of Systems Microbial Biotechnology, Chinese Academy of Sciences, Tianjin 300308, People’s Republic of China

3Technische Universität Berlin, Institute of Biotechnology, Chair of Applied and Molecular Microbiology,

Straße des 17. Juni 135, 10623 Berlin, Germany

4 University of Chinese Academy of Sciences, Beijing, 100049 China

5 College of Biotechnology, Tianjin University of Science & Technology, Tianjin, 300457 China

Timothy C. Cairns: t.cairns@tu-berlin.de

Claudia Feurstein: c.feurstein@tu-berlin.de

Li Hui Zhang: zhanglh@tib.cas.cn

Xiaomei Zheng: zheng\_xm@tib.cas.cn

Jibin Sun: sun\_jb@tib.cas.cn

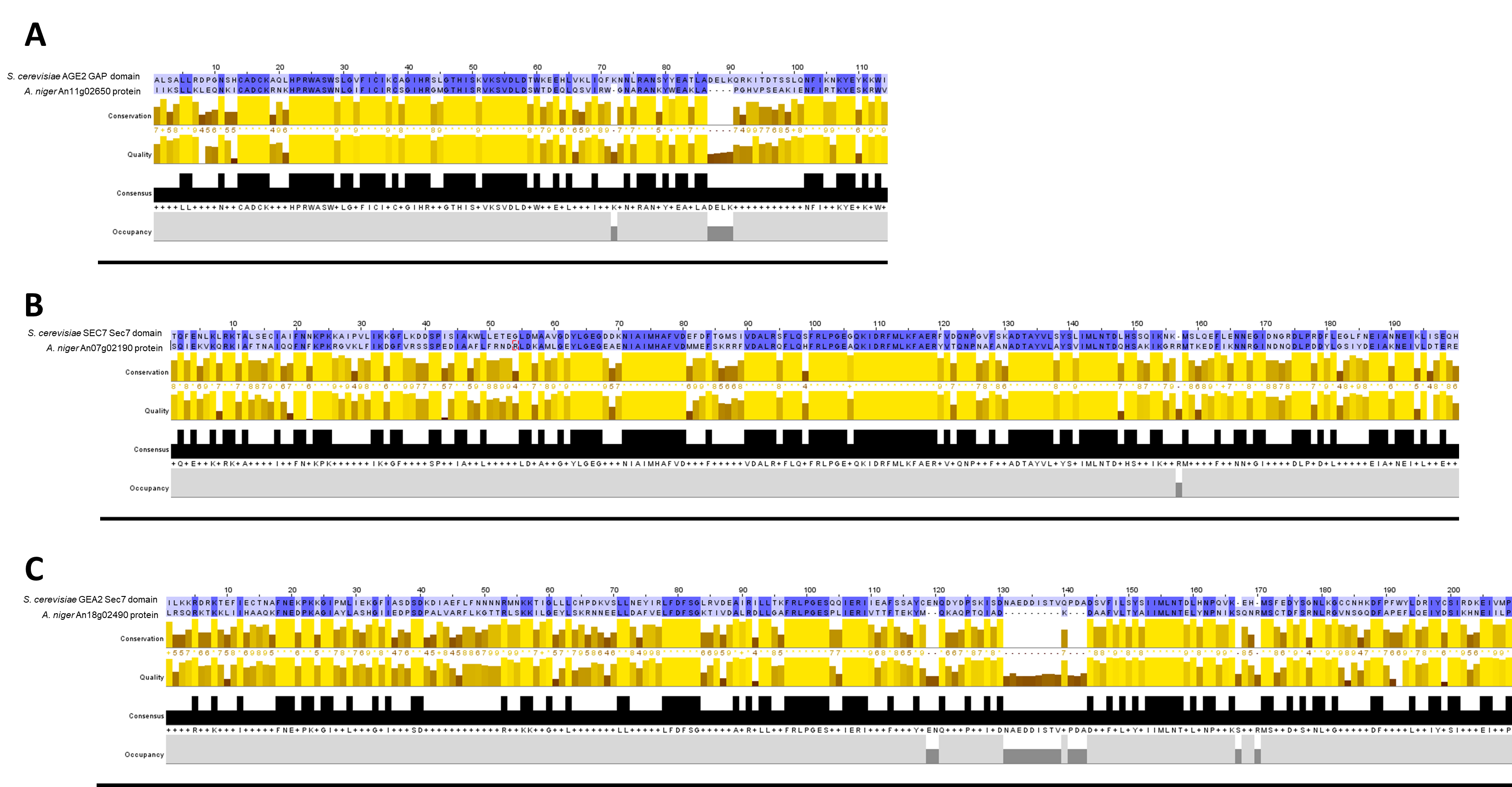
Ping Zheng: zheng\_p@tib.cas.cn

Vera Meyer: [vera.meyer@tu-berlin.de](mailto:vera.meyer@tu-berlin.de), ORCID 0000-0002-2298-2258

Contact details for corresponding authors:

Vera Meyer, Tel.: +49 30 314 72750, Fax: +49 30 314 72922, E-mail: [vera.meyer@tu-berlin.de](mailto:vera.meyer@tu-berlin.de)

Sun, Tel.: +86-8486 1949, Fax: +86-8486 1943, E-mail: [sun\_jb@tib.cas.cn](mailto:sun_jb@tib.cas.cn)



**Supplementary File 3: Conservation between yeast GEF and GAP domains with predicted *A. niger* Age1, Sec7, and Gea2 proteins.** *S. cerevisiae* domains were retrieved from the Saccharomyces genome database, whereas *A. niger* ORF sequences were downloaded from the Ensembl database. Pairwise alignments were performed with JalView Version 2 using default parameters. Total sequence conservation for *A. niger* Age1 (A), Sec7 (B), and Gea2 (C) and respective yeast domains was 51.8%, 55.5%, and 38.2%, respectively