

**Corrections to “A novel computational approach for global alignment for multiple biological networks”**

**Ben Yahia, Sadok;** Djeddi, Warith Eddine; Nguifo, Engelbert Mephu IEEE/ACM transactions on computational biology and bioinformatics 2019 / p. 700 <https://doi.org/10.1109/TCBB.2019.2895762>

**Pathway and network analysis of more than 2500 whole cancer genomes**

Reyna, Matthew A.; Haan, David; Paczkowska, Marta; Verbeke, Lieven P. C.; Vazquez, Miguel; Kahraman, Abdullah; Pulido-Tamayo, Sergio; Barenboim, Jonathan; Wadi, Lina; Dhingra, Priyanka; **Uusküla-Reimand, Liis** Nature Communications 2020 / art. 729  
<https://doi.org/10.1038/s41467-020-14367-0> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

**Substitution of the Methionine Axial Ligand of the T1 copper for the fungal-like Phenylalanine Ligand (M298F) causes local structural perturbations that lead to thermal instability and reduced catalytic efficiency of the small Laccase from Streptomyces coelicolor A3(2)**

**Zovo, Kairit; Pupart, Hegne;** Van Wieren, Arie; Gillilan, Richard E.; **Lukk, Tiit** ACS omega 2022 / p. 6184-6194  
<https://doi.org/10.1021/acsomega.1c06668> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)