

5 Conclusion & outlook

5.1 Conclusion

5.2 Outlook

5.2.1 Small RNA

5.2.2 Effect of host human products on natural transformation

5.2.3 Analyzing hotspots along the genome (homologous recombination)

References

- Abascal, Federico, Rafael Zardoya, and David Posada. 2005. "ProtTest: Selection of Best-Fit Models of Protein Evolution." *Bioinformatics*. <https://doi.org/10.1093/bioinformatics/bti263>.
- Altenhoff, Adrian M., Manuel Gil, Gaston H. Gonnet, and Christophe Dessimoz. 2013. "Inferring Hierarchical Orthologous Groups from Orthologous Gene Pairs." *PLoS ONE*. <https://doi.org/10.1371/journal.pone.0053786>.
- Altschul, S F, W Gish, W Miller, E W Myers, and D J Lipman. 1990. "Basic Local Alignment Search Tool." *Journal of Molecular Biology*. [https://doi.org/10.1016/S0022-2836\(05\)80360-2](https://doi.org/10.1016/S0022-2836(05)80360-2).
- Buchfink, Benjamin, Chao Xie, and Daniel Huson. 2015. "Fast and Sensitive Protein Alignment Using {DIAMOND}." *Nat Methods*. <https://doi.org/10.1038/nmeth.3176>.
- Felsenstein, J. 1985. "Confidence Limits on Phylogenies: An Approach Using the Bootstrap." *Evolution*. <https://doi.org/10.2307/2408678>.
- Goldman, Jon P. Anderson, Allen G., Nick. 2000. "Likelihood-Based Tests of Topologies in Phylogenetics." *Systematic Biology*. <https://doi.org/10.1080/106351500750049752>.
- Huson, Daniel H., Alexander F. Auch, Ji Qi, and Stephan C. Schuster. 2007. "MEGAN Analysis of Metagenomic Data." *Genome Research*. <https://doi.org/10.1101/gr.5969107>.
- Huson, Daniel H., and David Bryant. 2006. "Application of Phylogenetic Networks in Evolutionary Studies." *Molecular Biology and Evolution*. <https://doi.org/10.1093/molbev/msj030>.
- Katoh, Kazutaka, Kazuharu Misawa, Kei-ichi Kuma, and Takashi Miyata. 2002. "MAFFT: A Novel Method for Rapid Multiple Sequence Alignment Based on Fast Fourier Transform." *Nucleic Acids Research*. <https://doi.org/10.1093/nar/gkf436>.
- Larkin, M. A., G. Blackshields, N. P. Brown, R. Chenna, P. A. Mcgettigan, H.