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### **PUBLICATIONS**

#### **Journal Articles**

- Jr., C. W. Carter et al. (2022). "Multidimensional phylogenetic metrics identify Class I aminoacyl-tRNA synthetase evolutionary mosaicity and inter-modular coupling". In: *International Journal of Molecular Sciences* 23 (1520). URL: https://doi.org/%2010.3390/ijms23031520.
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- Bouckaert, R. et al. (2019). "BEAST 2.5: An Advanced Software Platform for Bayesian Evolutionary Analysis". In: PLoS Computational Biology 15 (4). URL: https://www.doi.org/10.1371/journal.pcbi.1006650.
- Popinga, A., J. W. Demastes, et al. (2019). "Host-parasite associations of the *Cratogeomys fumosus* species group and their chewing lice, *Geomydoecus*". In: *Therya* 10 (2). URL: https://www.doi.org/10.12933/therya-19-739%20ISSN%202007-3364.
- Wasef, S. et al. (2019). "Mitogenomic diversity in sacred ibis mummies sheds light on early Egyptian practices". In: *PLoS One* 14 (11). URL: https://www.doi.org/10.1371/journal.pone.0223964.
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- Vaughan, T. et al. (2014). "Efficient Bayesian phylogenetic inference under the structured coalescent". In: Bioinformatics 30 (16), pp. 2272– 2279. URL: https://www.doi.org/10.1093/bioinformatics/ btu201.

## Conference Proceedings

- Popinga, A., Ant Poole, et al. (2019). "Resolving protein families using structural phylogenetics". In: AMMA Molecular Modelling Conference. Bintan, Indonesia.
- Popinga, A., R. Bouckaert, and P. Wills (2018a). "A new model of amino acid substitution using iteratively added exchangeability rates to improve phylogenetic inference of aminoacyl-tRNA synthetases".
  In: Te Ao Marama (Centre for Fundamental Inquiry) Meeting. The Royal New Zealand Yacht Squadron, Auckland.
- - (2018b). "Aminoacyl-tRNA synthetases: Protein structures and the dawn of the genetic code". In: Quantitative and Computational Chemistry Student Conference. Kioloa, Australia.
- Popinga, A. and P. Wills (2016). "The search for simple systems: Minimal genetic information and autocatalytic sets". In: New Zealand Astrobiology Workshop. Kaikoura, New Zealand.
- Popinga, A., C. W. Carter Jr., et al. (2015). "Complex phylogeny of aminoacyl-tRNA synthetases". In: *European Society for Evolutionary Biology Congress*. Lausanne, Switzerland.
- Popinga, A., T. Vaughan, D. Welch, et al. (2015). "Stochastic population dynamics in Bayesian epidemic parameter inference with the coalescent Susceptible-Infected-Removed (SIR) model". In: Annual Meeting of the Society for Molecular Biology and Evolution. Vienna, Austria.