

Job offer ref. #12-20021

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG) is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology IME aiming to intensify biodiversity genomics in basic and applied research. We will establish a new and taxonomically broad genome collection to study genomic and functional diversity across the tree of life and make genomic resources accessible for societal-demand driven applied research.

The Hiller Lab at the LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG) in Frankfurt is looking for an ambitious

PostDoc (m/f/d) – Comparative Genomics

The mission of our group is to discover genomic determinants of phenotypic differences between species, which is important to understand how nature's fascinating phenotypic diversity evolved and how it is encoded in the genome. Work in the lab ranges from genome assembly and alignment to annotating genes, developing and applying comparative genomic methods to discover key differences in genes (such as loss, gain, selection) and regulatory elements, and using statistical approaches to associate genomic to phenotypic differences [1-8].

The postdoc will join our efforts to extend our methods repertoire to accurately detect additional types of genomic changes, to adopt them to other taxonomic groups, and to apply them on a large-scale to existing and numerous newly-sequenced genomes generated by us and our TBG collaborators.

Your profile:

- PhD degree in bioinformatics / computational biology, genomics or a related area
- a strong publication record
- excellent programming skills in a Linux environment as well as experience with shell scripting and Unix tools
- previous experience in large-scale comparative genomic data analysis is an advantage.

Salary and benefits are according to a public service position in Germany (TV-H E 13, 100%). The contract should start as soon as possible and will be initially for 2 years, but funding is available to extend it further. The Senckenberg Gesellschaft für Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference.

Please send your application before **October 25th, 2020** as a single pdf file via email to recruiting@senckenberg.de, mentioning the reference of this job offer (**ref. #12-20021**). The attached single pdf file should include the CV with publication list, contact information for at least two references, and a summary of your previous research experience (max 1 page).

For more information please contact
Prof. Dr. Michael Hiller (michael.hiller@senckenberg.de).



Recent publications

- [1] Jebb *et al.* Six reference-quality genomes reveal evolution of bat adaptations. *Nature*, 583, 578–584, 2020
- [2] Huelsmann *et al.* Genes lost during the transition from land to water in cetaceans highlight genomic changes associated with aquatic adaptations. *Science Adv*, 5(9), eaaw6671, 2019

- [3] Hecker *et al.* Convergent gene losses illuminate metabolic and physiological changes in herbivores and carnivores. PNAS, 116(8), 3036-3041, 2019
- [4] Roscito *et al.* Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. Nature Communications, 9:4737, 2018
- [5] Langer *et al.* REforge associates transcription factor binding site divergence in regulatory elements with phenotypic differences between species. MBE, 35(12), 3027–3040, 2018
- [6] Lee *et al.* Molecular parallelism in fast-twitch muscle proteins in echolocating mammals. Science Adv, 4(9), eaat9660, 2018
- [7] Sharma *et al.* A genomics approach reveals insights into the importance of gene losses for mammalian adaptations. Nature Communications, 9(1), 1215, 2018
- [8] Nowoshilow *et al.* The axolotl genome and the evolution of key tissue formation regulators. Nature, 554(7690), 50-55, 2018