



KEYNOTE SPEAKER



PROF.

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<https://scholar.google.ch/citations?user=qKbjZK4AAAAJ&hl=de&oi=sra>

Publication Highlights

[1] Paloots R, **Baudis M**. cancerclines. org—a novel resource for genomic variants in cancer cell lines. Database. 2024 Jan 1;2024:baae030.

[2] Danis D, **Baudis M**, *et al*. Phenopacket-tools: Building and validating GA4GH Phenopackets. PloS one. 2023 May 17;18(5):e0285433.

[3] Ladewig MS, Jacobsen JO, Wagner AH, Danis D, El Kassaby B, Gargano M, Groza T, **Baudis M**, Steinhaus R, Seelow D, Bechrakis NE. GA4GH phenopackets: A practical introduction. Advanced Genetics. 2023 Mar;4(1):2200016.

[4] Jacobsen JO, **Baudis M**, Baynam GS, Beckmann JS, Beltran S, Buske OJ, Callahan TJ, Chute CG, Courtot M, Danis D, Elemento O. The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature biotechnology. 2022 Jun;40(6):817-20.

[5] Rambla J, **Baudis M**, Ariosa R, Beck T, Fromont LA, Navarro A, Paloots R, Rueda M, Saunders G, Singh B, Spalding JD. Beacon v2 and Beacon networks: a “lingua franca” for federated data discovery in biomedical genomics, and beyond. Human mutation. 2022 Jun;43(6):791-9.

[6] Huang Q, Carrio-Cordo P, Gao B, Paloots R, **Baudis M**. The Progenetix oncogenomic resource in 2021. Database. 2021 Jan 1;2021:baab043.

[7] Wagner AH, Babb L, Alterovitz G, **Baudis M**, Brush M, Cameron DL, Cline M, Griffith M, Griffith OL, Hunt SE, Kreda D. The GA4GH variation representation specification: a computational framework for variation representation and federated identification. Cell genomics. 2021 Nov 10;1(2).