

Publications / Publikationen Prof. Alexander Dilthey (DPhil)

47. Walker, A., Houwaart, T., Finzer, P., Ehlkes, L., Tyshaiyeva, A., Damagnez, M., Strelow, D., Duplessis, A., Nicolai, J., Wienemann, T., Tamayo, T., Kohns Vasconcelos, M., Hulse, L., Hoffmann, K., Lubke, N., Hauka, S., Andree, M., Daumer, M.P., Thielen, A., Kolbe-Busch, S., Gobels, K., Zotz, R., Pfeffer, K., Timm, J., **Dilthey, A.T.** & German, C.-O.I. Characterization of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection Clusters Based on Integrated Genomic Surveillance, Outbreak Analysis and Contact Tracing in an Urban Setting. *Clin Infect Dis* 74, 1039-1046 (2022).
46. Ebler, J., Ebert, P., Clarke, W.E., Rausch, T., Audano, P.A., Houwaart, T., Mao, Y., Korbelt, J.O., Eichler, E.E., Zody, M.C., **Dilthey, A.T.** & Marschall, T. Pangenome-based genome inference allows efficient and accurate genotyping across a wide spectrum of variant classes. *Nat Genet* 54, 518-525 (2022).
45. Curry, K.D., Wang, Q., Nute, M.G., Tyshaiyeva, A., Reeves, E., Soriano, S., Wu, Q., Graeber, E., Finzer, P., Mendling, W., Savidge, T., Villapol, S., **Dilthey, A.** & Treangen, T.J. Emu: species-level microbial community profiling of full-length 16S rRNA Oxford Nanopore sequencing data. *Nat Methods* 19, 845-853 (2022).
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42. Nodari, C.S., Fuchs, S.A., Xanthopoulou, K., Cayo, R., Seifert, H., Gales, A.C., **Dilthey, A.** & Higgins, P.G. pmrCAB Recombination Events among Colistin-Susceptible and -Resistant *Acinetobacter baumannii* Clinical Isolates Belonging to International Clone 7. *mSphere* 6, e0074621 (2021).
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40. Fritz, A., Bremges, A., Deng, Z.L., Lesker, T.R., Gotting, J., Ganzenmuller, T., Sczyrba, A., **Dilthey, A.**, Klawonn, F. & McHardy, A.C. Haploflow: Strain-resolved de novo assembly of viral genomes. *bioRxiv* (2021).
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37. Walker, A., Houwaart, T., Wienemann, T., Vasconcelos, M.K., Strelow, D., Senff, T., Hulse, L., Adams, O., Andree, M., Hauka, S., Feldt, T., Jensen, B.E., Keitel, V., Kindgen-Milles, D., Timm, J., Pfeffer, K. & **Dilthey, A.T.** Genetic structure of SARS-CoV-2 reflects clonal superspreading and multiple independent introduction events, North-Rhine Westphalia, Germany, February and March 2020. *Euro Surveill* 25(2020).

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