Stanford

Jarod Evert Rutledge

Postdoctoral Scholar, Genetics

Bio

BIO

Jarod Rutledge is currently a joint postdoctoral fellow at EMBL Heidelberg and Stanford University. His research is focused on the application of deep learning tools to cellular imaging and omics data to enable new experimental paradigms in functional genomics and translational medicine. Jarod received his Ph.D. from Stanford University School of Medicine, where he worked with Professor Tony Wyss-Coray and Professor Stephen Montgomery. He researched ways to combine proteomics, genetics, and machine learning to discover new quantitative biomarkers of aging, Alzheimer's disease, and Parkinson's disease to enable precision preventative medicine. Jarod has also made previous contributions to the fields of medicinal chemistry and synthetic biology, where he worked to develop new therapies for neglected tropical diseases and inflammatory bowel diseases.

LINKS

- Google Scholar Profile: https://scholar.google.com/citations?user=3UAm85sAAAAJ&hl=en

Publications

PUBLICATIONS

- **Post-translational modifications linked to preclinical Alzheimer's disease-related pathological and cognitive changes.** *Alzheimer's & dementia : the journal of the Alzheimer's Association*
  Abiose, O., Rutledge, J., Moran-Losada, P., Belloy, M. E., Wilson, E. N., He, Z., Trelle, A. N., Channappa, D., Romero, A., Park, J., Yutsis, M. V., Sha, S. J., Andreasson, et al
  2023

- **Organ aging signatures in the plasma proteome track health and disease.** *Nature*
  Oh, H. S., Rutledge, J., Nachun, D., Pálovics, R., Abiose, O., Moran-Losada, P., Channappa, D., Urey, D. Y., Kim, K., Sung, Y. J., Wang, L., Timsina, J., Western, et al
  2023; 624 (7990): 164-172

- **Proteomics of brain, CSF, and plasma identifies molecular signatures for distinguishing sporadic and genetic Alzheimer's disease.** *Science translational medicine*
  Sung, Y. J., Yang, C., Norton, J., Johnson, M., Fagan, A., Bateman, R. J., Perrin, R. J., Morris, J. C., Farlow, M. R., Chhatwal, J. P., Schofield, P. R., Chui, H., Wang, et al
  2023; 15 (703): eabq5923

- **Proteogenomic analysis of human cerebrospinal fluid identifies neurologically relevant regulation and informs causal proteins for Alzheimer's disease.** *Research square*
  Cruchaga, C., Western, D., Timsina, J., Wang, L., Wang, C., Yang, C., Ali, M., Beric, A., Gorijala, P., Kohlfeld, P., Budde, J., Levey, A., Morris, et al
  2023

- **Cerebrospinal fluid immune dysregulation during healthy brain aging and cognitive impairment.** *Cell*
  Piehl, N., van Olst, L., Ramakrishnan, A., Teregulova, V., Simonton, B., Zhang, Z., Tapp, E., Channappa, D., Oh, H., Losada, P. M., Rutledge, J., Trelle, A. N., Mormino, et al
  2022

- **Measuring biological age using omics data.** *Nature reviews. Genetics*
  Rutledge, J., Oh, H., Wyss-Coray, T.

2022

- **Publisher Correction: Limited proteolysis-mass spectrometry reveals aging-associated changes in cerebrospinal fluid protein abundances and structures.** *Nature aging*
  Shuken, S. R., Rutledge, J., Iram, T., Losada, P. M., Wilson, E. N., Andreasson, K. I., Leib, R. D., Wyss-Coray, T.
  2022; 2 (5): 455

- **Limited proteolysis-mass spectrometry reveals aging-associated changes in cerebrospinal fluid protein abundances and structures (vol 2, pg 379, 2022)** *NATURE AGING*
  Shuken, S. R., Rutledge, J., Iram, T., Losada, P., Wilson, E. N., Andreasson, K. I., Leib, R. D., Wyss-Coray, T.
  2022; 2 (5): 455

- **Limited proteolysis–mass spectrometry reveals aging-associated changes in cerebrospinal fluid protein abundances and structures** *Nature Aging*
  Shuken, S. R., Rutledge, J., Iram, T., Moran Losada, P., Wilson, E. N., Andreasson, K. I., Leib, R. D., Wyss-Coray, T.
  2022

- **Genome-wide analysis of common and rare variants via multiple knockoffs at biobank scale, with an application to Alzheimer disease genetics.** *American journal of human genetics*
  He, Z., Le Guen, Y., Liu, L., Lee, J., Ma, S., Yang, A. C., Liu, X., Rutledge, J., Losada, P. M., Song, B., Belloy, M. E., Butler, R. R., Longo, et al
  2021