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17. FNR regulation and gut dysbiosis in enteroaggregative E. coli (EAEC)
   Vanessa Abuhav and Uri Gophna

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24. Gene2Vec – NLP approach for predicting microbial gene function
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25. Long reads capture simultaneous enhancer-promoter methylation status for cell-type deconvolution
   Sapir Margalit, Yotam Abramson, Hila Sharim, Zohar Manber, Surajit Bhattacharya, Yi-Wen Chen, Eric Vilain, Hayk Barseghyan, Ran Elkon, Roded Sharan and Yuval Ebenstein

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   Dan Coster, Ilan Krause, Liron Sheena, Shani Shenhar-Tsarfaty, Shlomo Berliner, Ben Boursi and Ron Shamir
27. A LASSO-based approach to sample sites for phylogenetic tree search
   **Noa Ecker**, Dana Azouri, Ben Bettisworth, Alexandros Stamatakis, Yishay Mansour, Itay Mayrose and Tal Pupko

28. Detecting and understanding meaningful cancerous mutations based on computational models of mRNA splicing
   **Nicolas Lynn** and Tamir Tuller

29. Shared transcriptional profiles of atypical B cells suggest common drivers of expansion and function in malaria, HIV, and autoimmunity
   **Prasida Holla**, Brian Dizon, Abhijit A. Ambegaonkar, Noga Rogel, **Ella Goldschmidt**, Arun K. Boddapati, Haewon Sohn, Dan Sturdevant, James W. Austin, Lela Kardava, Li Yuesheng, Poching Liu, Susan Moir, Susan K. Pierce and Asaf Madi

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   **Zohar Zafrir**, Alon Diament*, Modi Roopin*, Shimshi Atar* and Tamir Tuller

34. A Machine learning model for predicting deterioration of COVID-19 inpatients
   **Omer Noy**, Dan Coster, Maya Metzger, Itai Attar, Shani Shenhar-Tsafiraty, Shlomo Berliner, Galia Rahav, Ori Rogowski and Ron Shamir

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   **Rotem Galron**, Mai Bonomo, Ido Rippin, Liyam Chitayat Levi, Yarin Udi, Ilya Breslavskiy, Rawan Ibrahim, Noy Meydani, Roni Gattegno, Ronnie Griness, Shir Michael, Moran Kama, Gali Altman, Yoav Navott, Matan Arbel, Adi Yannai and Tamir Tuller

38. Towards understanding protein degradation in bacteria: A combined proteomic-machine-learning approach
   **Natan Nagar** and Tal Pupko

39. Personalized phylogeny-guided detection of cancer driver genes
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40. m6A is required for resolving progenitor identity during planarian stem cell differentiation
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