

Feb 1st: Genomic sequencing

Koblan LW, et al. In vivo base editing rescues Hutchinson-Gilford progeria syndrome in mice. *Nature*. 2021 Jan 6. doi: 10.1038/s41586-020-03086-7.

Reviews: (Choose the best ideas from Review papers. you don't have to use everything, most important is to tell a story)

Note to speakers: Talk about next-gen sequencing (ie what is it and how it works), the history, and then how model organisms are facilitating disease diagnosis. You need to make a story to lead into the primary paper above.

- Next-generation sequencing: impact of exome sequencing in characterizing Mendelian disorders. Rabbani B, et al, *J Hum Genet*. 2012 Oct;57(10):621-32. doi: 10.1038/jhg.2012.91. Epub 2012 Jul 26. Review. PMID: 22832387
- Model Organisms Facilitate Rare Disease Diagnosis and Therapeutic Research. Wangler MF, Y et al., *Genetics*. 2017 Sep;207(1):9-27. doi: 10.1534/genetics.117.203067. Review.
- Progeria video: <https://www.youtube.com/watch?v=GO306dK8m8c>

Feb 8th: Phylogenomics

Worobey M, Pekar J, Larsen BB, Nelson MI, Hill V, Joy JB, Rambaut A, Suchard MA, Wertheim JO, Lemey P. The emergence of SARS-CoV-2 in Europe and North America. *Science*. 2020 Oct 30;370(6516):564-570. doi: 10.1126/science.abc8169. Epub 2020 Sep 10. PMID: 32912998; PMCID: PMC7810038.

Reviews:

- Geoghegan JL, Holmes EC. The phylogenomics of evolving virus virulence. *Nat Rev Genet*. 2018 Dec;19(12):756-769. doi: 10.1038/s41576-018-0055-5. PMID: 30305704; PMCID: PMC7096893.
- Phylogeny for the faint of heart: a tutorial. Baldauf SL. *Trends Genet*. 2003 Jun;19(6):345-51. PMID: 12801728
- **Nextstrain: <https://www.fredhutch.org/en/research/diseases/coronavirus/understanding-nextstrain.html>
- **Reuter's visualization of the virus mutations: <https://graphics.reuters.com/HEALTH-CORONAVIRUS/EVOLUTION/yxmpjqkdzvr/>
- Trevor Bedford's website and data visualizations: <https://bedford.io/>
- *Baum, D (2008): (some good images here for intro): <https://www.nature.com/scitable/topicpage/reading-a-phylogenetic-tree-the-meaning-of-41956>

Feb 15th: Domain and motif discovery

Pastuzyn ED, et al., The Neuronal Gene Arc Encodes a Repurposed Retrotransposon Gag Protein that Mediates Intercellular RNA Transfer. *Cell*. 2018 Jan 11;172(1-2):275-288.e18. doi: 10.1016/j.cell.2017.12.024.

Reviews:

- David Lee, Oliver Redfern & Christine Orengo, Predicting protein function from sequence and structure *Nature Reviews Molecular Cell Biology* 8, 995-1005 (December 2007) | doi:10.1038/nrm2281
- Overview of back to back papers in Cell: [http://www.cell.com/cell/fulltext/S0092-8674\(17\)31509-X](http://www.cell.com/cell/fulltext/S0092-8674(17)31509-X)
- Popular Press Article (A recommended read): <https://www.theatlantic.com/science/archive/2018/01/brain-cells-can-share-information-using-a-gene-that-came-from-viruses/550403/>

Feb 20th: read for lab

*Tools to find domains & motifs: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC150457/>

SMART database: <https://www.ncbi.nlm.nih.gov/pubmed/25300481>

Gene ontology: http://www.nature.com/ng/journal/v25/n1/full/ng0500_25.html

DNA motifs: <http://www.nature.com/nbt/journal/v24/n8/full/nbt0806-959.html>

Ontologies: Scientific Data Sharing Made Easy. Nicole Washington & Suzanna Lewis (2008) <https://www.nature.com/scitable/topicpage/ontologies-scientific-data-sharing-made-easy-77972/>

Feb 22nd: Genome-wide CRISPR screens

Daniloski Z, Jordan TX, Wessels HH, Hoagland DA, Kasela S, Legut M, Maniatis S, Mimitou EP, Lu L, Geller E, Danziger O, Rosenberg BR, Phatnani H, Smibert P, Lappalainen T, tenOever BR, Sanjana NE. Identification of Required Host Factors for SARS-CoV-2 Infection in Human Cells. *Cell*. 2021 Jan 7;184(1):92-105.e16. doi: 10.1016/j.cell.2020.10.030. Epub 2020 Oct 24.

Review:

- Xiong, X, et al., CRISPR/Cas9 for Human Genome Engineering and Disease Research. *Annu Rev Genomics Hum Genet*. 2016 Aug 31;17:131-54. doi: 10.1146/annurev-genom-083115-022258. Epub 2016 May 23.

Feb 29th: Single Cell Transcriptomics

Qian F, et al. Single-cell RNA-sequencing of zebrafish hair cells reveals novel genes potentially involved in hearing loss. *Cell Mol Life Sci.* 2022 Jun 26;79(7):385. doi: 10.1007/s00018-022-04410-2. PMID: 35753015

Review:

- Single-cell RNA sequencing technologies and bioinformatics pipelines. Hwang B, Lee JH, Bang D. *Exp Mol Med.* 2018 Aug 7;50(8):96. doi: 10.1038/s12276-018-0071-8. Review. PMID: 30089861

Mar 7th: Chemical Genomics

Asad Z, Sachidanandan C. Chemical screens in a zebrafish model of CHARGE syndrome identifies small molecules that ameliorate disease-like phenotypes in embryo. *Eur J Med Genet.* 2020 Feb;63(2):103661. doi: 10.1016/j.ejmg.2019.04.018. Epub 2019 May 1. PMID: 31051269

Review:

- Markossian, S, et al., Small-Molecule Screening for Genetic Diseases. *Annu Rev Genomics Hum Genet.* 2018 Aug 31;19:263-288. doi: 10.1146/annurev-genom-083117-021452. Epub 2018 May 23.

*Identifying Novel Cancer Therapies Using Chemical Genetics and Zebrafish. <https://www.ncbi.nlm.nih.gov/pubmed/27165351>

*Chemical genetic screening in the zebrafish embryo. https://link.springer.com/chapter/10.1007%2F978-3-319-30654-4_5

*Animal models of human disease: zebrafish swim into view. <https://www.nature.com/articles/nrg2091>

*Using zebrafish to model autism: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7686559/>

Mar 21st: Proteomics 1-Biological Networks (in vivo proteomics–BioID/TurboID/APEX)

Zhang Y, Shang L, Zhang J, Liu Y, Jin C, Zhao Y, Lei X, Wang W, Xiao X, Zhang X, Liu Y, Liu L, Zhuang MW, Mi Q, Tian C, Wang J, He F, Wang PH, Wang J. An antibody-based proximity labeling map reveals mechanisms of SARS-CoV-2 inhibition of antiviral immunity. *Cell Chem Biol.* 2022 Jan 20;29(1):5-18.e6. doi: 10.1016/j.chembiol.2021.10.008. Epub 2021 Oct 20. PMID: 34672954; PMCID: PMC8527578.

Reviews:

- Varnaité R, MacNeill SA. Meet the neighbors: Mapping local protein interactomes by proximity-dependent labeling with BioID. *Proteomics.* 2016 Oct;16(19):2503-2518. doi: 10.1002/pmic.201600123. Epub 2016 Jul 27. PMID: 27329485; PMCID: PMC5053326.
- The Proteome: Discovering the Structure and Function of Proteins: Jill Adams (2008). <https://www.nature.com/scitable/topicpage/the-proteome-discovering-the-structure-and-function-613/>

April 4th: Proteomics 2- SILAC

Choi S, Engelke R, Goswami N, Schmidt F. Proteomic profiling of metformin effects in 3T3-L1 adipocytes by SILAC-based quantification. *Proteomics.* 2022 Jun;22(11-12):e2100196. doi: 10.1002/pmic.202100196. Epub 2022 Mar 22. PMID: 35275438.

Reviews:

- Ong SE1, Mann M. A practical recipe for stable isotope labeling by amino acids in cell culture (SILAC). *Nat Protoc.* 2006;1(6):2650-60.
- Geiger T, Wisniewski JR, Cox J, Zanivan S, Kruger M, Ishihama Y, Mann M. Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. *Nat Protoc.* 2011 Feb;6(2):147-57. doi: 10.1038/nprot.2010.192. PMID: 21293456.

April 11th: Proteomics 3: Quantitative proteomics (iTRAQ or TMT labeling)

Chen M, Zhang F, Chen B, Lau C, Xu K, Tong T, Huo C, Han Q, Su T, Kwan HY. Omics approach to reveal the effects of obesity on the protein profiles of the exosomes derived from different adipose depots. *Cell Mol Life Sci.* 2022 Oct 28;79(11):570. doi: 10.1007/s00018-022-04597-4. PMID: 36306016.

Reviews:

- Giambruno R, Mihailovich M, Bonaldi T. Mass Spectrometry-Based Proteomics to Unveil the Non-coding RNA World. *Front Mol Biosci.* 2018, Nov 8;5:90. doi: 10.3389/fmolb.2018.00090. eCollection 2018.
- Jürgen Cox and Matthias Mann, Quantitative, high-resolution proteomics for data-driven systems biology. *Annu Rev Biochem.* 2011;80:273-99. doi: 10.1146/annurev-biochem-061308-093216.