

2025 version: Links to preprints (let's use March 1st as an approximate posting cutoff for consideration) that would be fun to review for our class:

- <https://www.biorxiv.org/content/10.1101/2025.03.22.644747v1> - Scalable and cost-efficient custom gene library assembly from oligopools
- <https://www.biorxiv.org/content/10.1101/2025.03.28.645293v1?rss=1> - Generative Landscapes and Dynamics to Design Multidomain Artificial Transmembrane Transporters
- <https://www.biorxiv.org/content/10.1101/2025.03.30.646233v1?rss=1> - Biophysical fitness landscape design traps viral evolution
- <https://www.biorxiv.org/content/10.1101/2025.03.27.644168v1?rss=1> - Counting particles could give wrong probabilities in Cryo-Electron Microscopy
- <https://www.biorxiv.org/content/10.1101/2025.03.19.642801v1?rss=1> - Learning millisecond protein dynamics from what is missing in NMR spectra
- <https://www.biorxiv.org/content/10.1101/2025.04.09.647630v1.full.pdf> - Energetic and structural control of polyspecificity in a multidrug transporter
- <https://www.biorxiv.org/content/10.1101/2025.04.08.647882v1> - Proteome wide thermal shift assays - cool studies of folding
- <https://www.biorxiv.org/content/10.1101/2025.04.11.648485v1?rss=1> - RNA-protein interaction scanning with base editors
- <https://www.biorxiv.org/content/10.1101/2025.04.08.647855v1> - nascent chain structural biology of folding
- <https://www.biorxiv.org/content/10.1101/2025.04.12.648556v1.full.pdf+html> - fitness landscapes and determinants of ruggedness
- <https://www.biorxiv.org/content/10.1101/2025.04.14.648755v1> - single molecule studies of how kinetics of an enzyme evolves
- <https://www.biorxiv.org/content/10.1101/2025.04.07.647236v1.full.pdf+html> - comprehensive study of dynamics of a folding protein by F19 nmr
- <https://www.biorxiv.org/content/10.1101/2025.04.08.647864v1> - statistical approaches for studying epistasis
- <https://www.biorxiv.org/content/10.1101/2025.04.02.646878v1> - predicting mutational effects across distinct proteins
- <https://www.biorxiv.org/content/10.1101/2025.04.02.646877v1.full> - Conserved energetic changes drive function in an ancient protein fold
- <https://www.biorxiv.org/content/10.1101/2025.04.16.649219v1> - AF2 χ : Predicting protein side-chain rotamer distributions with AlphaFold2
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2024 Version! Don't use these

<https://www.biorxiv.org/content/10.1101/2024.03.07.583947v1>

<https://www.biorxiv.org/content/10.1101/2024.03.11.584210v1.full> - JF asked to review by a journal, will review with Priyanka in advance of class

<https://www.biorxiv.org/content/10.1101/2024.02.28.582624v1>

<https://www.biorxiv.org/content/10.1101/2023.05.09.540044v3>

<https://www.biorxiv.org/content/10.1101/2024.03.05.583551v1>

<https://www.biorxiv.org/content/10.1101/2024.01.10.574250v1>

<https://www.biorxiv.org/content/10.1101/2024.04.08.588516v1> single measurements of ribosome translation - in contrast conventionally riboseq is a bulk measurement

<https://www.biorxiv.org/content/10.1101/2024.02.28.582624v2> (the analysis is big data, but not technically high throughput. could also invite Margaux to help with presentation)

<https://www.biorxiv.org/content/10.1101/2024.03.03.583197v1?rss=1> - involves high throughput chemical probe discovery

<https://www.biorxiv.org/content/10.1101/2024.03.13.583470v1?rss=1> - 234 xray datasets, is that high throughput?

<https://www.biorxiv.org/content/10.1101/2024.03.08.584161v1?rss=1> - big evolutionary analysis of kinases

<https://www.biorxiv.org/content/10.1101/2024.03.13.584147v1?rss=1> - low throughput - but could be a good contrast to something WCM selects?

<https://www.biorxiv.org/content/10.1101/2024.03.15.585128v1> Protein language model trained on Rosetta allows protein engineering and exploration of biophysical properties

<https://www.biorxiv.org/content/10.1101/2024.03.21.585615v2> ML-guided directed evolution of nucleases

<https://www.biorxiv.org/content/10.1101/2024.04.18.590141v1?rss=1> - using ProteinMPNN to stabilize iron containing enzymes for directed evolution

<https://www.biorxiv.org/content/10.1101/2024.04.17.589973v1?rss=1> - protein design of miniprotein agonists for manipulating immune signalling

<https://www.biorxiv.org/content/10.1101/2024.04.12.589296v1?rss=1> - small orfs - predictions and biophysics

<https://www.biorxiv.org/content/10.1101/2024.04.10.588871v1?rss=1> - allostery in estrogen receptor

<https://www.biorxiv.org/content/10.1101/2024.04.10.588894v1?rss=1> - circular permutant ribosomes

<https://www.biorxiv.org/content/10.1101/2024.03.28.587262v1?rss=1> - new Ai tools for docking

<https://www.biorxiv.org/content/10.1101/2024.03.25.585721v1?rss=1> - deep learning for molecular glues

<https://www.biorxiv.org/content/10.1101/2024.03.08.584161v1?rss=1> - kinase biophysics of activation

<https://www.biorxiv.org/content/10.1101/2023.12.13.571465v1> - TCELL base editing

<https://www.biorxiv.org/content/10.1101/2024.04.25.591103v1> - perfect paper for this class!

<https://www.biorxiv.org/content/biorxiv/early/2024/04/20/2024.04.19.590094.full.pdf> - label seq