



Instrumentation



- Orbitrap Fusion Lumos (ThermoFisher)
- UltiMate 3000 RSLC (ThermoFisher)

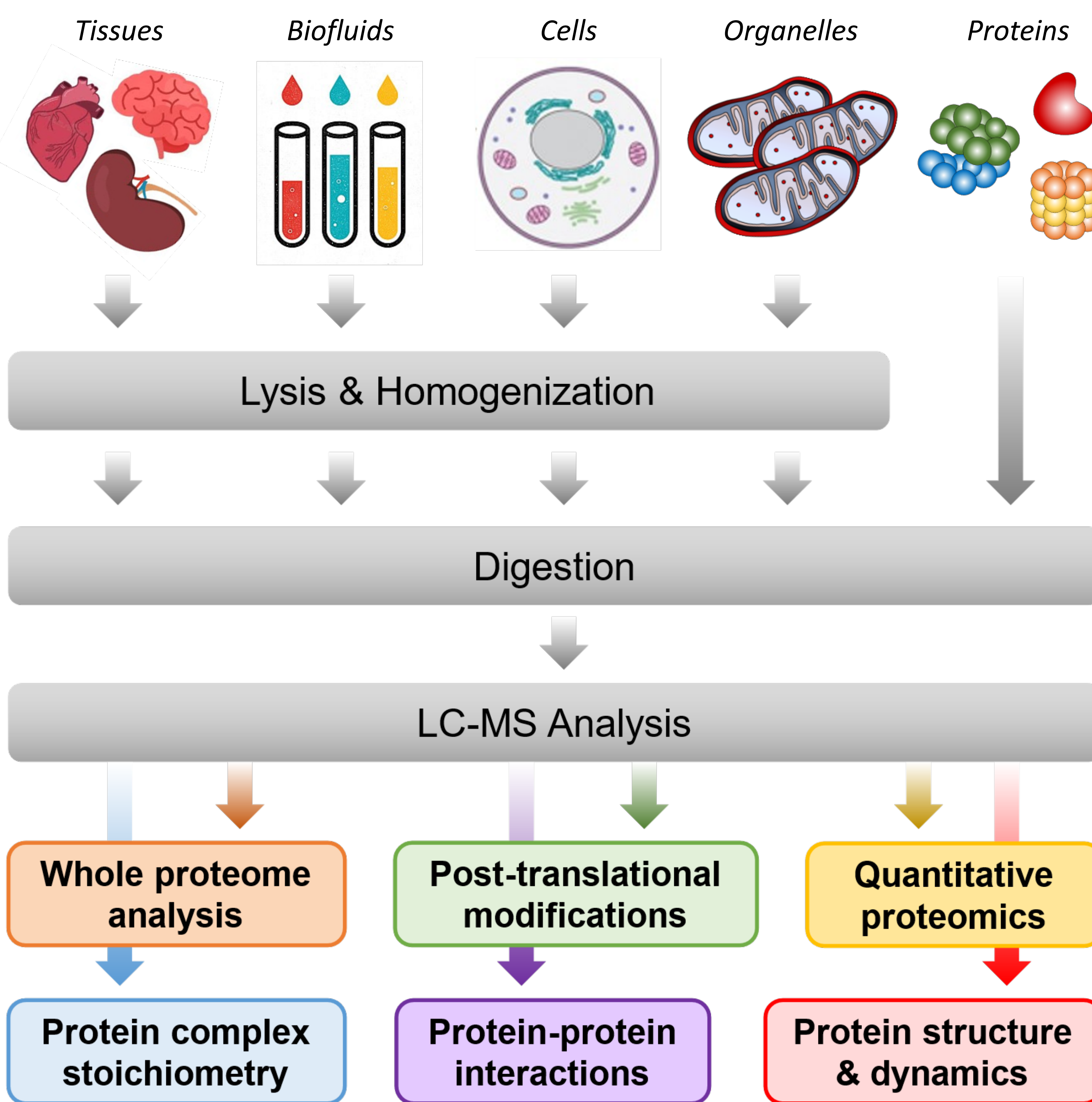


- Orbitrap LTQ-XL (ThermoFisher)
- Easy-nLC 1000 (ThermoFisher)



- Agilent 1200 Infinity II HPLCs
- Thermo Scientific Savant SPD131DDA SpeedVac

General proteomics workflow



HMSF Services

- Qualitative and quantitative profiling of whole proteomes
- Multiplexed, targeted, and label-free quantitative proteomics
- Characterization and quantification of post-translational modifications (PTMs)
- Protein interaction and structural analysis using cross-linking (XL-MS)

HMSF Leadership

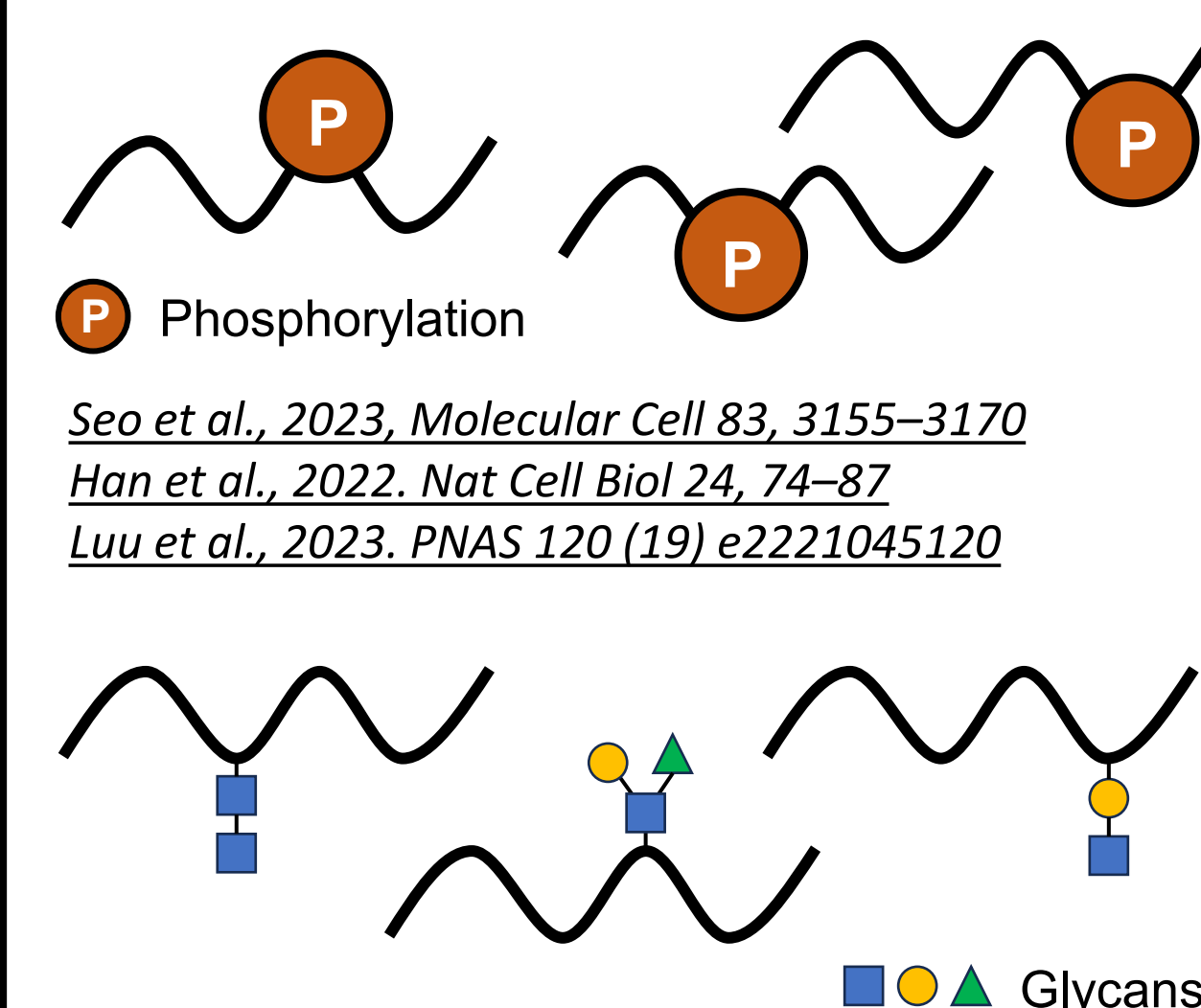


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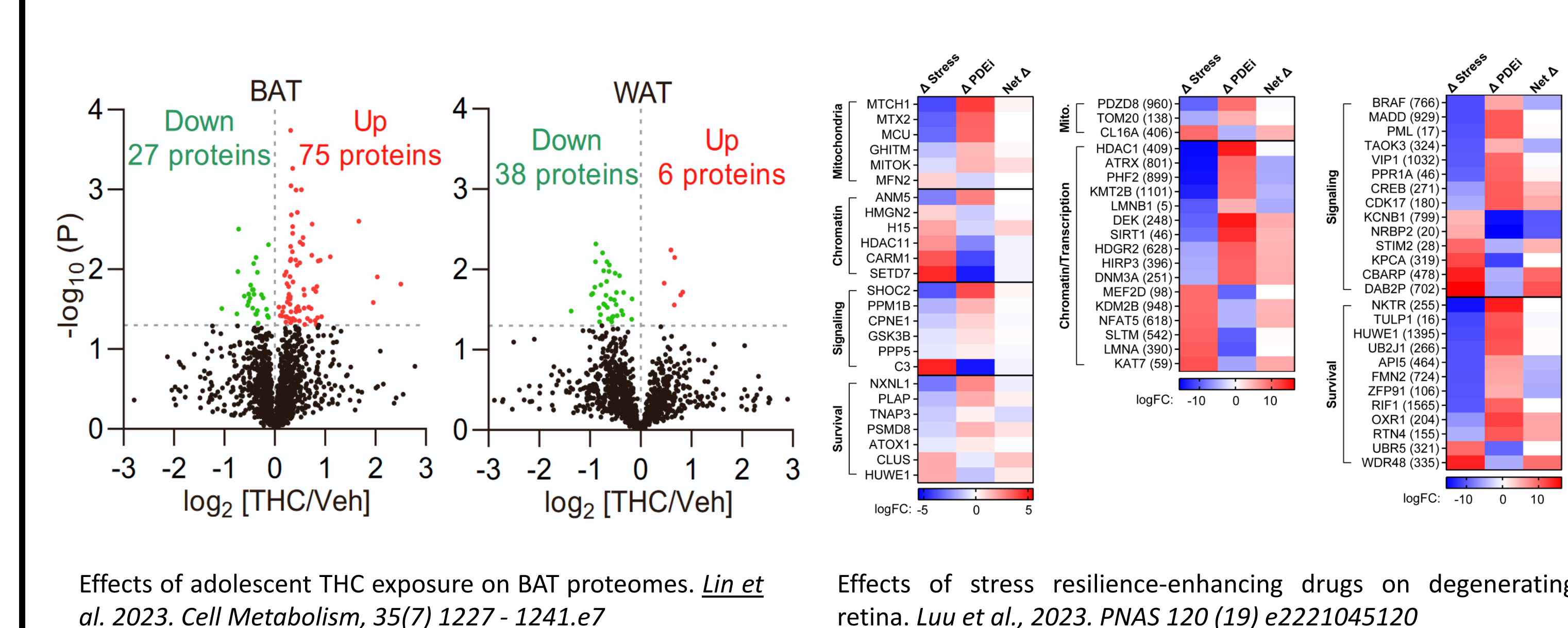


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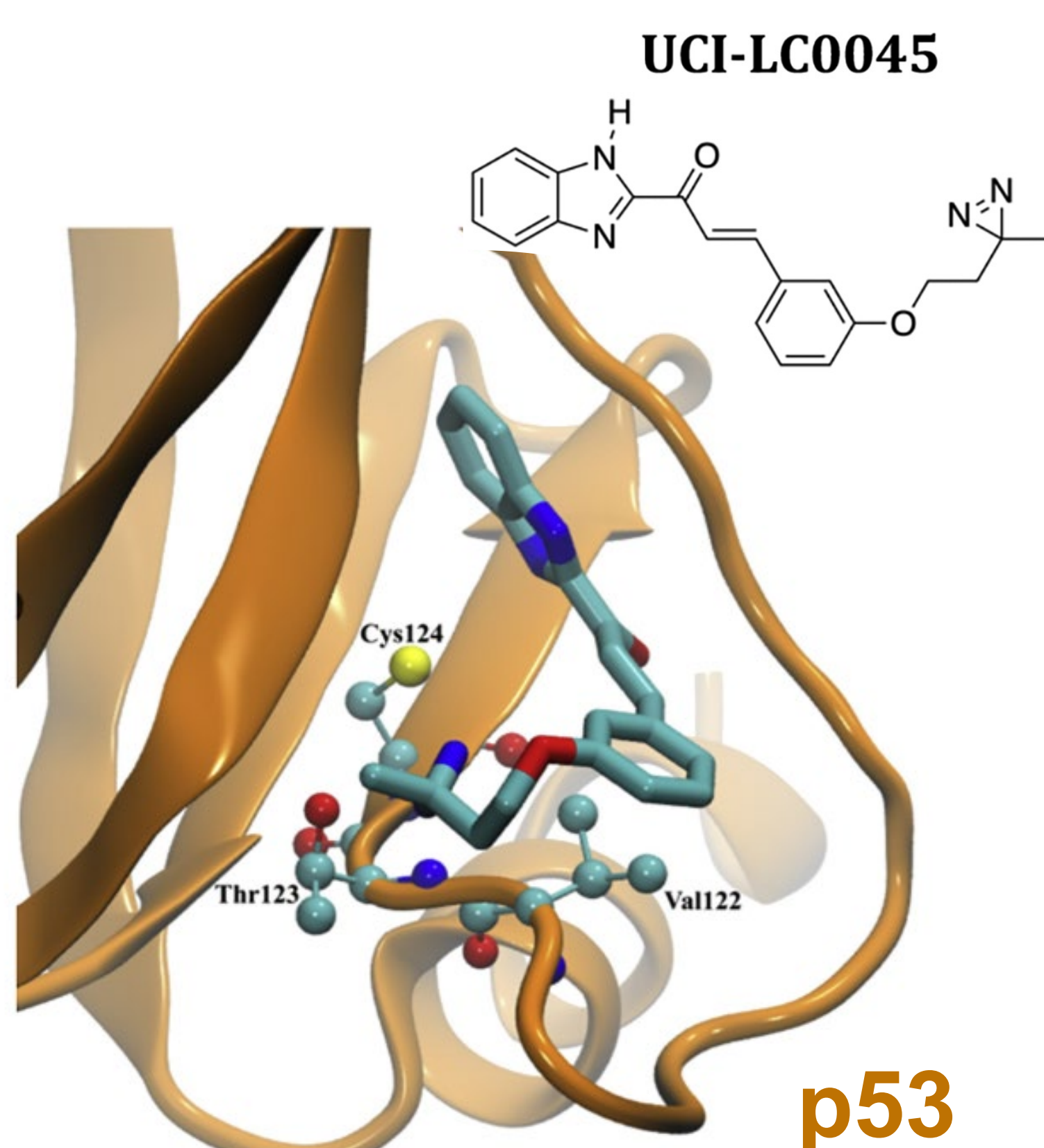
Post-translational modifications



Quantitative proteome-wide proteomics

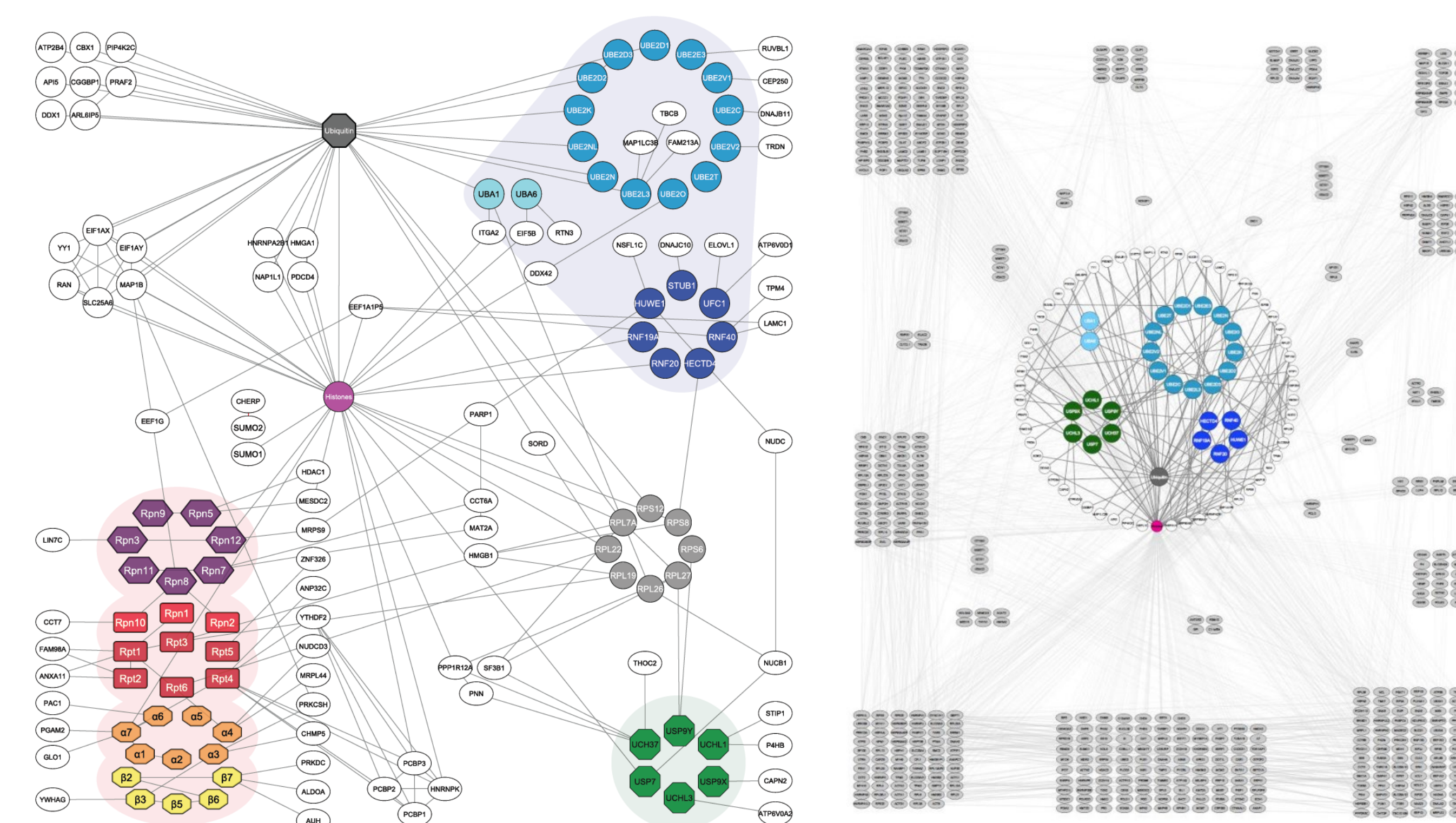


Localizing drug interactions



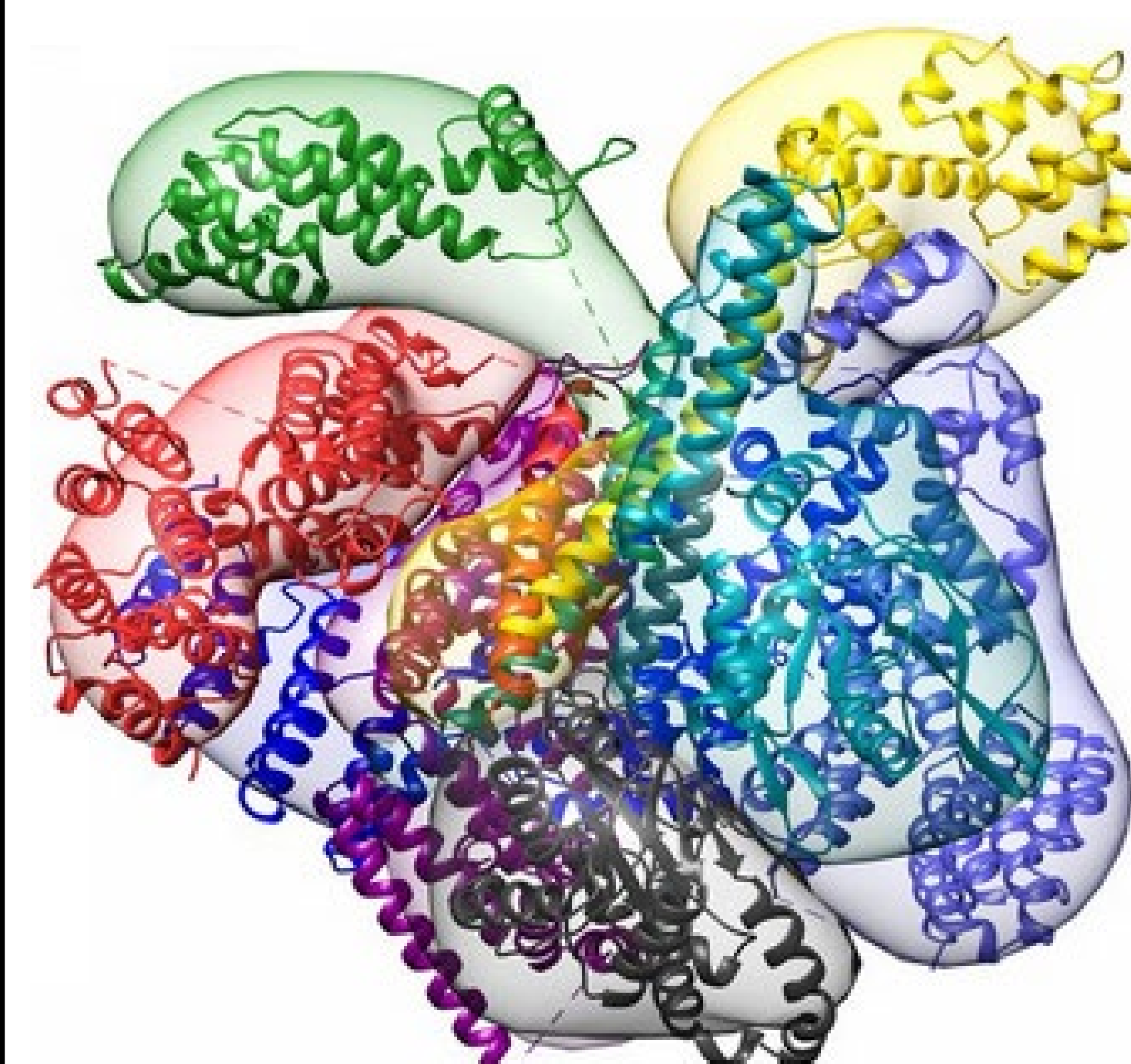
Durairaj, et al., 2022, Cell Chem Biol. 2022 29(9):1381-1395.e13

Protein-protein interactions



Wheat, et al., 2021, PNAS 118(32):e2023360118

Protein structure / Integrative modeling



XL-MS directed integrative model of the CSN (COP9 signalosome) complex *Gutierrez, et al., 2020, PNAS 117 (8) 4088-4098*

Protein dynamics / Conformational changes

