Jevtic, Allram et al., Supplementary Table 2

Methods	Description	References: Digital Object Identifier (DOI):
Fluorescence microscopy	Tracking *in vitro* reconstituted condensates (droplets) over time and testing their formation, dissolution kinetics, mechanistic properties in various physico-chemical conditions. *In vivo* condensates can be analyzed using single-molecule assays to determine the stoichiometry of condensate constituents.	https://doi.org/10.1016/j.tibs.2020.05.011
Biochemical assays	Identification of protein and RNA constituents within biomolecular condensates by using combined proteomic profiling and DNA/RNA-seq. Crosslinking assays can be used to identify protein-protein and protein-RNA interactions.	https://doi.org/10.1016/j.jprot.2012.04.030
Optogenetic approaches	Analyzing the biophysical properties of biomolecular condensates by fusing the photolyase homology region (PHR) domain of the *Arabidopsis thaliana* cryptochrome 2 (CRY2) to various IDR domains, enabling inducible and reversible condensation in living cells.	https://doi.org/10.1002/wsbm.1415
NMR spectroscopy	Acquiring atomic-resolution view on intra/interprotein interactions over various timescales providing the information on domain/loop motions of *in vitro* reconstituted condensates.	Https://doi.org/10.1042/EBC20220056
Microfluidics	Generating and high-throughput screening of thousands of well-defined microcompartments within a short time. Condensate composition can be manipulated by introducing additional molecules.	https://doi.org/10.1016/j.bbamcr.2020.118823
Cryo-electron tomography	Visualizing the condensate netowrk in 3D with nanometer resolution through repeating, aligning, and averaging acquired structures.	https://doi.org/10.1016/j.devcel.2020.09.003