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ProteoPlex
advanced protein science

understand
macromolecular
proteins

- a Max-Planck spinoff company -

How good is my protein sample?

Does it crystallize *because* or *despite* its quality?

What about macromolecules?

Can I test it easily?

Do I get improvement recommendations?

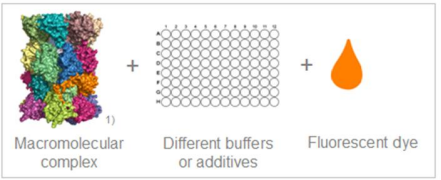
ProteoPlex MacroDSF...

your validation & optimization tool

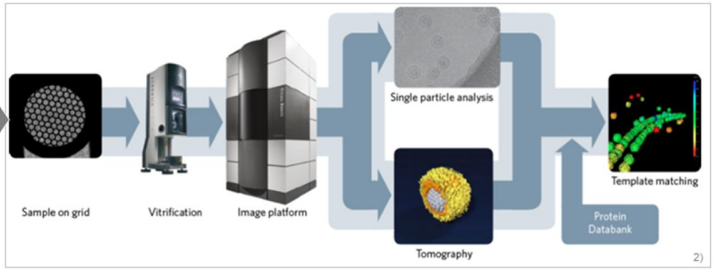
to produce ultra-high-quality samples

for X-ray crystallography & cryo-EM

MacroDSF in cryo-EM



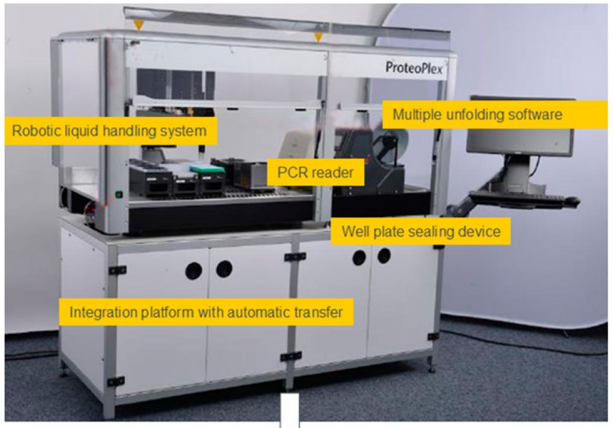
MacroDSF initial sample optimization



Ultra-high sample quality throughout your entire process

1) Löwe et al., Science, 1995; Groll et al., Nature, 1997 2) www.fei.com

MacroDSF machine & patented algorithm



Better protein yield - better crystallization - more stable proteins - more active proteins

Structure determination with higher resolution

Differential scanning fluorimetry (DSF) is a widely used sample optimization technique.

MacroDSF uses an advanced, proprietary analytical method to extend DSF functionality into macromolecular complexes.

MacroDSF can automatically determine the best buffers and additives to achieve maximum stability of your protein sample.

MacroDSF data can guide you to
- better protein yield
- better crystallization
- more stable proteins
- more active proteins

This allows structure determination with significantly higher resolution.

Want to dig deeper?

Chari et al. (2015).
ProteoPlex: Stability optimization of macromolecular complexes by sparse-matrix screening of chemical space. Nature Methods 12, 859-865

Application example - SelA

- Recording of unfolding transitions of selenocysteine synthase (SelA) in different buffer conditions
- SelA is a homodecameric complex with 600kDa and 12 subunits
- Buffers and resulting unfolding transitions were recorded and analyzed with the ProteoPlex biophysical unfolding model
- TEM micrographs of SelA with different buffers were recorded
- Buffer conditions that yielded unfolding transitions close to two-state unfolding showed a monodisperse field of single particles (in contrast to full or partial aggregation at distinct polyphasic unfolding transitions)