



Structural integrity & functionality

- Size measured as hydrodynamic radius (R_h).
- Validate your protein stability
- Get insight into folding/unfolding and conformational changes.



Viscosity

- Every measurement you take provides viscosity data.
- Viscosity compensation



Aggregation

 Protein/particle aggregates are clearly detectable and quantifiable whilst still leaving the core signal useful for standard measurement.



PDB Correlator

- Use the absolute size as a firm reference point.
- Compatible with Protein Data Bank, Pymol or AlphaFold.



Labelling efficiency

- Option of measuring size of up to 3 species in solution.
- Can e.g. reveal the percentage of free vs. conjugated fluorophore in your sample when you choose to use Fida 1 for labelled assays.



Stickiness

- The shape of the core signal will reveal any stickiness of your binding partners or your binding complexes.
- The core signal is useful for standard measurement despite of the stickiness.



Heterogeneity (PDI)

 PDI Index allows for checking the heterogeneity of your sample.



Sample Loss

- Transparently exposed
- Troubleshoot efficiently

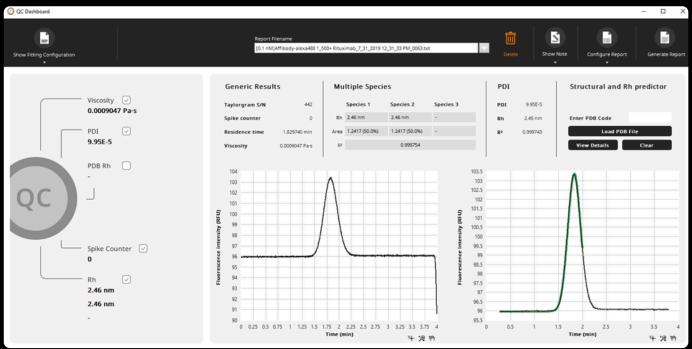




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