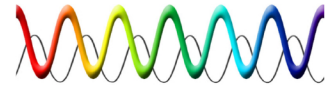


CENTER FOR STRUCTURAL STUDIES

BUILDING 26.02, FLOOR 01, ROOMS 62A/62B/66/68/70
BUILDING 26.43, FLOOR U1, ROOM 38



Order form - **PROTEIN CRYSTALLIZATION**

Name of user _____

Address (institute, working group) _____

Phone-no., email _____

I (budget responsible person) recognized the „terms of use“ and „charges and fees“ and agree on these (<http://www.css.hhu.de/en/contact-and-service/users-and-fee-regulations.html>).

All users of the CSS must acknowledge the DFG in their publications:

"The Center for Structural Studies is funded by the Deutsche Forschungsgemeinschaft (DFG Grant number 417919780)."
For X-ray diffraction data please mention also „INST 208/740-1 FUGG“ (X-ray diffractometer), for SAXS data „INST 208/761-1 FUGG“ (SAXS machine).

Date _____ signature (budget responsible person) _____

Screening apoprotein Screening with substrate(s)
enclosed substrate(s) (name, concentration, K_M value) _____

If already known, how many screens shall we set up (96 conditions per screen)? _____

Name and/or acronym of the protein _____

soluble protein membrane protein

Date of purification _____

Is there a tag fused to the protein? no
 yes (which tag, N- or C-terminal?) _____
 signal peptide? _____
 modifications? (e. g. phosphorylation, selenomethionine): _____

Store/stable at [°C] _____

Size of the protein [kDa], oligomeric state _____

Protein concentration [mg/ml] _____

Total volume of protein [μ l] _____

Composition of protein buffer _____

Are certain chemical agents needed for activity and/or stability (e. g. metal ions, cofactors etc.)? If yes, please specify:

Does the protein contain tryptophane(s)? If yes, how many? _____

Enclosed images/analyses:

(**!** = obligatory)

- SDS-Page
 gel filtration
 protein buffer **!**
 protein sequence incl. tag (word-file) **!**
 activity assay
