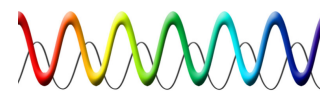**WWW.CSS.HHU.DE**

CSS
CENTER FOR STRUCTURAL STUDIES

Center for Structural Studies
Building 26.24, Floor 02, Rooms 062/064/024/082/084
Building 26.24, Floor 01, Room 101

Order form - SAXS measurements

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 (https://www.css.hhu.de/en/translate-to-english-kontakt-und-service).

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)

Name and/or acronym of the protein:

Source organism: Safety level: S1   S2

Expression organism: Safety level: S1   S2

        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):

Total no. of residues (incl. tag):

Store/stable at [°C]:

Exact size of the protein [kDa]:

Extinktion coefficient:

Oligomeric state, symmetry:

Protein concentration [mg/ml]:

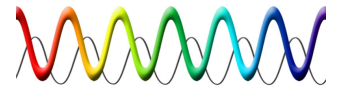Total volume of protein [µl]:

Composition of protein buffer:

SEC column:

Enclosed substrate(s) (name, concentration, K_d value):

Short sample description of the protein (function, catalyzed reaction, …):

Enclosed files/analyses/solutions (**obligatory**):

10 ml protein buffer (original)
protein sequence incl. tag (electronical file to be send
 via email)

Is the above mentioned project (protein) **funded by third party**? If so, please give the grant and the corresponding grant number (**obligatory**):

Additional files/analyses/info:

SDS-Page
gel filtration
structure or homology model
other