***Sequence of the fusion protein CitA-Xa-BSLA***

MGSSHHHHHHSSGLVPRGSHMDITEERLHYQVGQRALIQAMQISAMPELVEAVQKRDLARIKALIDPMRSFSDATYITVGDASGQRLYHVNPDEIGKSMEGGDSDEALINAKSYVSVRKGSLGSSLRGKSPIQDATGKVIGIVSVGYTIEQLENYEKLLEDSLTEITALSIEGREAEHNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKVANVVTLGGANRLTTGKALPGTDPNQKILYTSIYSSADMIVMNYLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN

Color code:

**blue** 🡪**His-Tag**

**yellow** 🡪citrate binding sensor domain **CitA** (*Klebsiella pneumoniae*) (PDB: 2J80)

**green** 🡪linker helix from blue light sensor **YtvA** (*Bacillus subtilis*) (PDB: 2PR5)

**purple** 🡪**Xa** protease site

**cyan** 🡪Lipase **BsLA** (*Bacillus subtilis*) (PDB: 1I6W)

Amino acids present in the respective pdb coordinates are shown **in bold underlined** with a bigger font.

Amino acids not represented in the coordinate file but present in the construct are color coded and shown in smaller letters

**Available pdb coordinates:**

2J80 (citrate sensor-domain with bound citrate)

2PR5 (YtvA-LOV in dark state (including linker helix))

1I6W (Lipase)

**Quaternary Structure:**

According to Sedimentation Velocity Analytical Ultracentrifugation fusion protein is a monomer with spherical shape.