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METYNHTYRH HNFSH KDLSD LTFTA CTFIR SDFRR ANLRD
TTFVN CKFIE QGDIE G CHFDV ADLRD ASFQQ CQLAM ANFSN
ANCYG IEFRA CDLKG ANFSR TNFAH QVSNR MYFCS AFISG
CNLSY ANMER VCLEK CELFE NRWIG TNLAG ASLKE SDLSR
GVFSE DVWGQ FS LQGAN LCHAE LDG LDPRKVDTSGIKIAAWQ
QELILEALGIVVYPD

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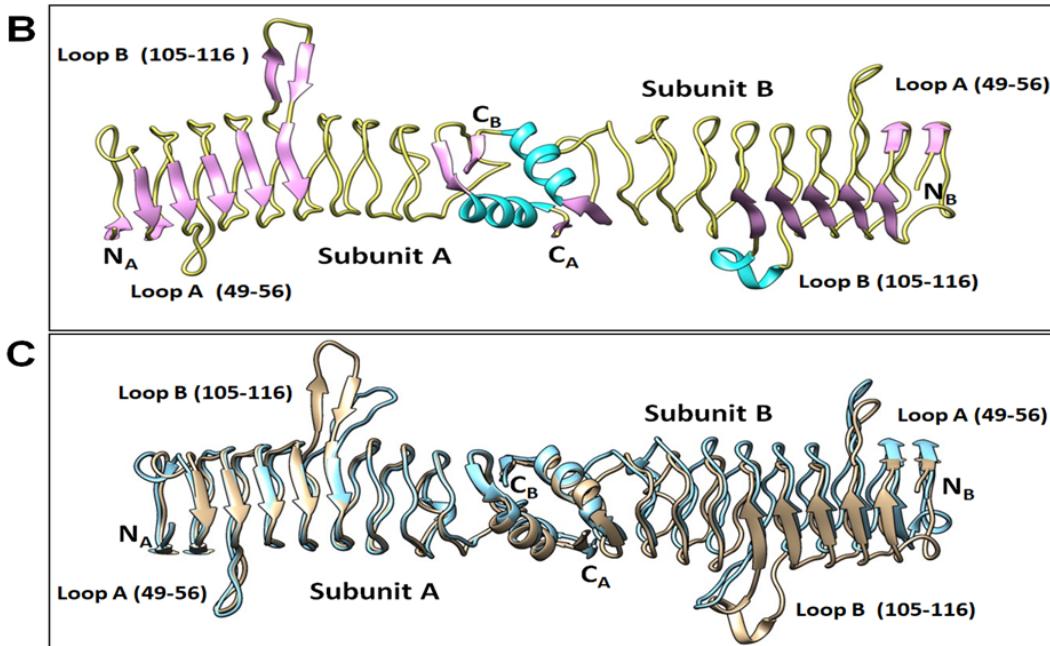


Figure S1. Sequence and homology modelling of QnrS.

- A. Amino acid sequence of ECU32 QnrS1 display the consensus sequence of S/T/A/V/C-D/N-L/F-S/T/R-G, pentapeptide repeating unit residues shown as bold face and the underlined residues indicate loop regions of A and B.
- B. Homology model of homodimer ECU32 QnrS1 using template of QnrB1 (PDB: 2xtx.1)
- C. Superimposition of modeled homodimer ECU32 QnrS1 (light orange color) with AhQnr (light blue color), the Qnr protein from *Aeromonas hydrophila* (PDB:3psz.1).