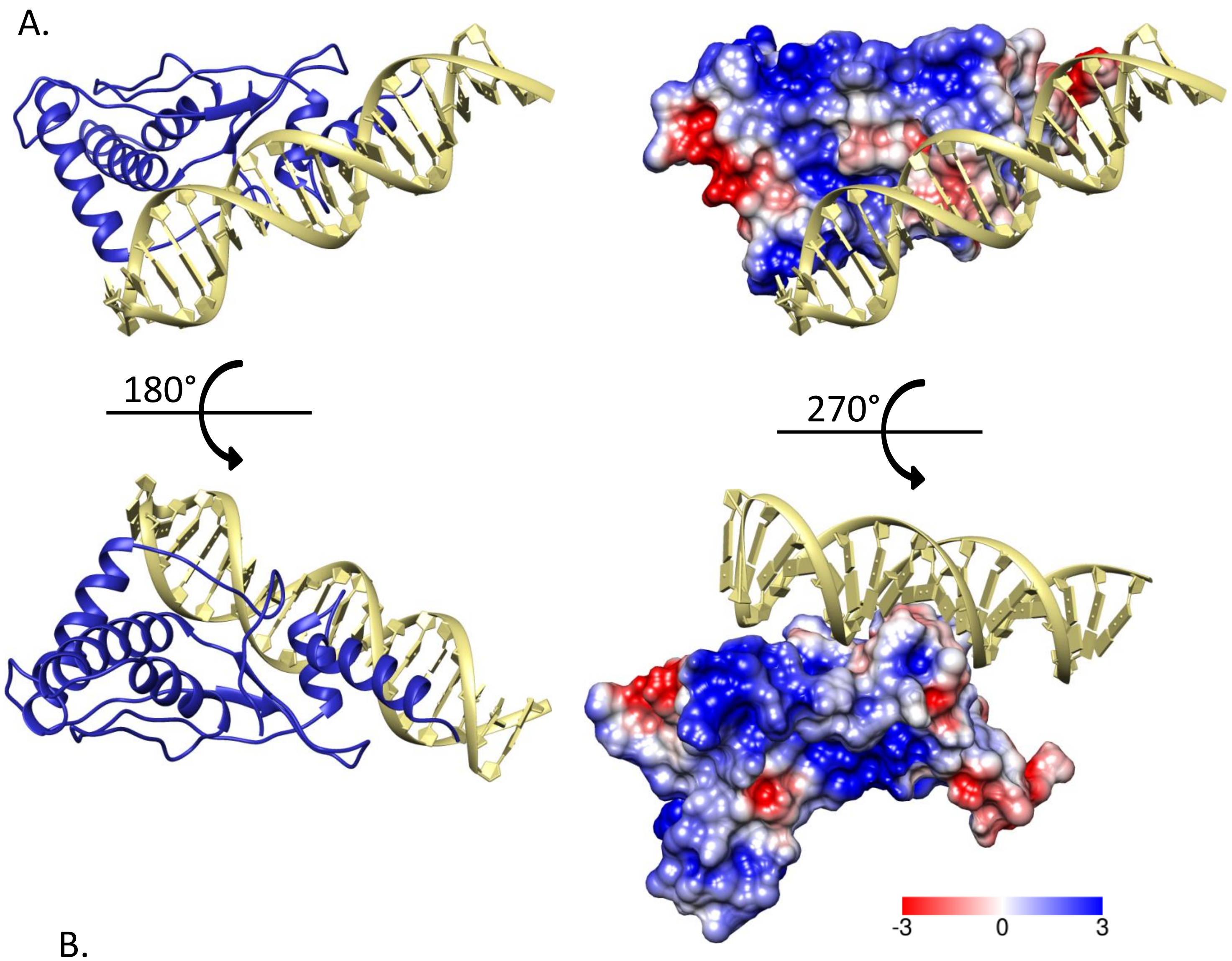


B.

>gi|21327769|gb|AAM11681.2|AF493796_1 GmrS [Escherichia coli]

MKSETLTIQQIFQNQRQYRVPFY**QRAY**VWT**Q**RN**Q**WSALLEDIFEKAQSRLSGTKPTPHFLGAVVLEPQLK

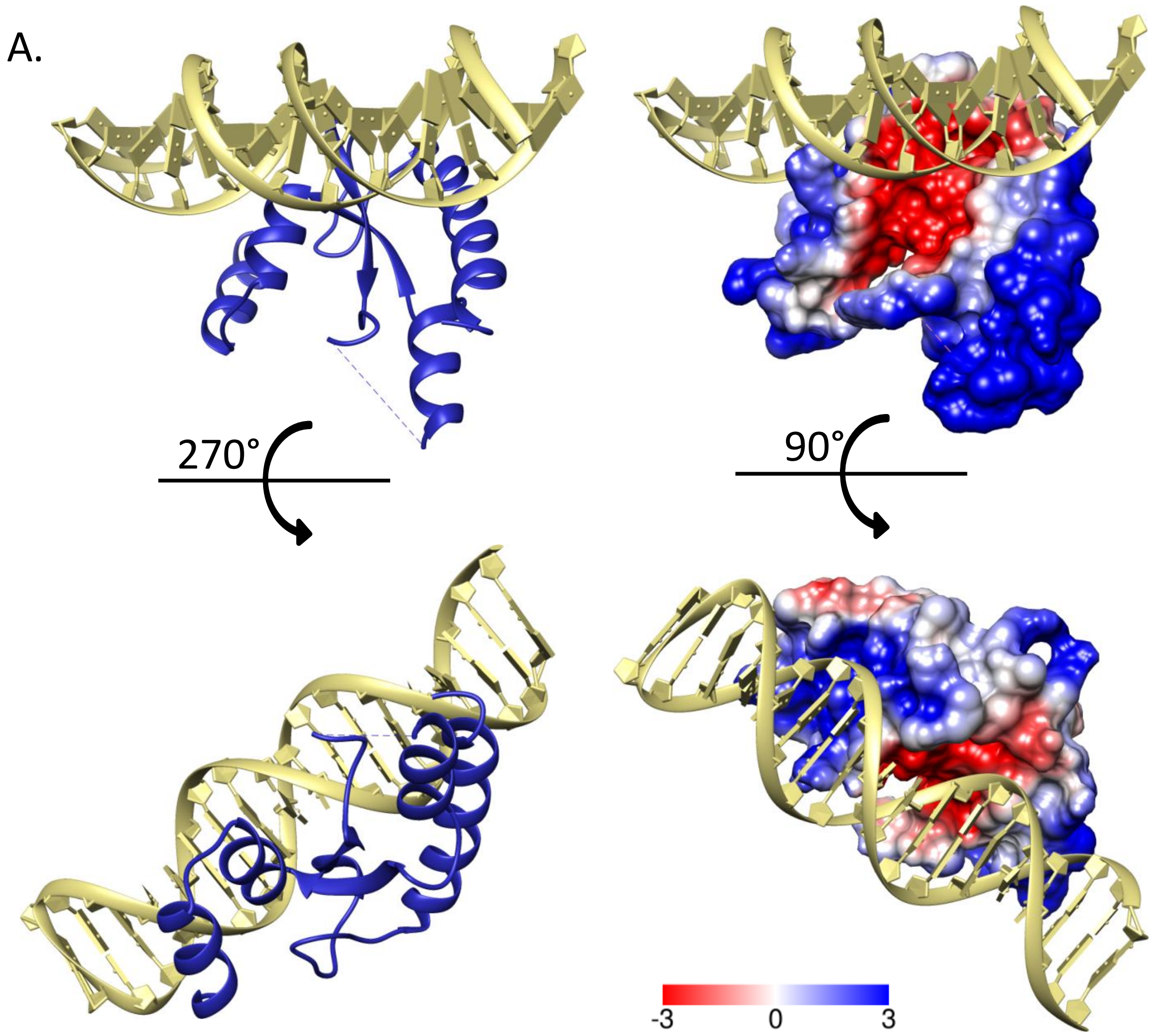
NSLLGVDTIHI**I**DGQQRLTTLQYILASLASIRLSLRATGLSELEGLVLTCLKNTNEATMRNKKVECFKLW

PTFRD**Q**T**H**F**IQSLNV**D**N**IDDLRNVFSDSFTQHGTLRKHFNHPPSLEALWFFTEAFIKWIKIENHSPQENA

VALIEAVLTDLKLVSIFLEAEDDAQIIFETLNGRGAELHATDLIRNYIFMCAEHENINAIELYENEWKIF

EDKYWSEKQRRGRINKPRMEWLVHATLQSERQQ

Supplementary Figure 1. **A.** The model of the GmrS domain in complex with DNA in the ribbon representation (left) and in the surface representation (right). The surface is colored according to the distribution of electrostatic potential, from red (negatively charged) to blue (positively charged. The structure of the complex was predicted using the NPdock server [1] with restraints on DNA-binding amino acid residues derived from sequence conservation and results from the RBscore server [2]. The distribution of electrostatic potential was calculated using the PDB2PQR server [3] and the APBS software package [4]. **B.** GmrS domain sequence with DNA-binding residues in bold and underlined. The DNA-binding residues were identified in the model using UCSF Chimera [5] and default contact criteria.



B.

>gi|21327771|gb|AAM11682.2|AF493797_1 GmrD [Escherichia coli]

MYNDLVSYVVRRSVCGLTPKNYNNVFMNVLRHLSKTEISSVELRNILNSLNGEASRWPGDSEFLNACINA
PLYPGRLDAPKM**R**SM**L**TELERELCRQVKTEKPDVPNL**SNLDI**DHLMPQSWYSCWPLENGHMVTNSDATVM
NQIVLSGTDLTPEQLLVRKRQQAIATLGNLTLL**NLS**VN**R**SV**Q**NAVFLKKRDALIV**H**TNLRLNIPLILKDK
WDESEIQERGKKLGEIALKVWPKYD

Supplementary Figure 2. **A.** The model of the GmrD domain in complex with DNA in the ribbon representation (left) and in the surface representation (right). The surface is colored according to the distribution of electrostatic potential, from red (negatively charged) to blue (positively charged. The structure of the complex was predicted using the NPdock server [1]. The distribution of electrostatic potential was calculated using the PDB2PQR server [3] and the APBS software package [4]. **B.** GmrD domain sequence with DNA-binding residues in bold and underlined. The DNA-binding residues were identified in the model using UCSF Chimera [5] and default contact criteria.

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