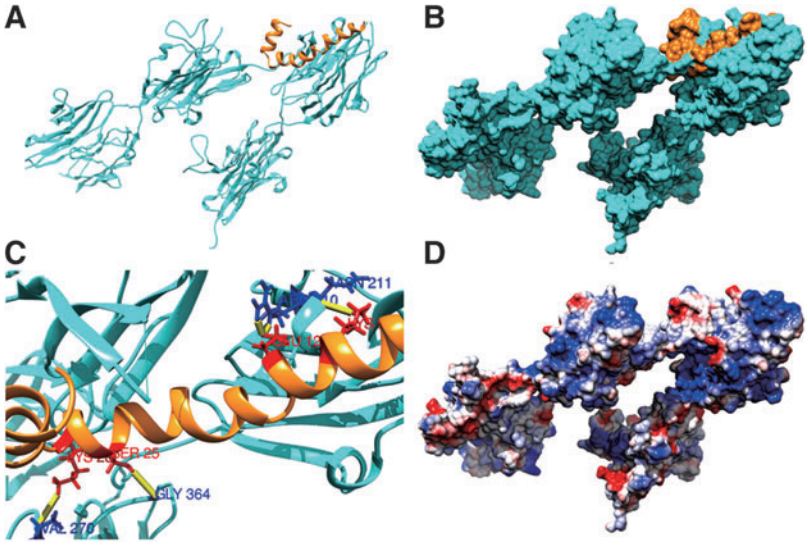
Supplementary Data



SUPPLEMENTARY FIG. S1. Molecular modeling of the interaction residues in the ARS-Interacting multi-functional protein 1 (AIMP1) peptide-fibroblast growth factor receptor 2 (FGFR2) complex. The AIMP1 peptide binding site in FGFR2 is shown with the ribbon presentation method **(A)** and surface model method **(B)**: *orange,* AIMP1 peptide; *cyan,* FGFR2. **(C)** There are five hydrogen bonds between AIMP1 peptide and FGFR2 at four residues (9Lys-$H^{\zeta 2}\cdots$O-211Arg.IV, 12Glu-$O^{\varepsilon 2}\cdots H^{\varepsilon}$-210Arg.IV, 12Glu-$O^{\varepsilon 2}\cdots H^{\eta 21}$-210Arg.IV, 25Ser-$H^{\gamma}\cdots$O-364Arg.cIII, and 28Lys-$H^{\zeta 1}\cdots$O-270Val.III). FGFR2 was a tetramer, and its subunits are designated as I-IV. The residues of AIMP1 peptide and FGFR2 are shown as *red* and *blue*, respectively. All hydrogen bonds between AIMP1 peptide and FGFR2 are displayed as *yellow lines*. **(D)** The electrostatic surface potential of the AIMP1 peptide-FGFR2 complex is colored *blue* (positively charged region) and *red* (negatively charged region) with an energy scale of $-5 \sim 5$ in units of kcal/(mole*e). The energy-based score of the complex was -160.93 from the FireDock results. The unit of the score is arbitrary, but the score is similar to the value expressed as kcal/mol that appears in other published data [1].

Reference

1. Benyamini H and A Friedler. (2011). The ASPP interaction network: electrostatic differentiation between pro- and anti-apoptotic proteins. J Mol Recognit 24:266–274.