(초청강연)

Crystal structure of the BAFF-BAFF-R complex and its implications for receptor activation

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B-cell activating factor (BAFF) is a key regulator of B-lymphocyte development. Its biological role is mediated by the specific receptors BCMA, TACI, and BAFF-R. We have determined the crystal structure of BAFF-R extracellular domain bound to BAFF at a resolution of 3.3 ?. The cysteine-rich domain(CRD) of the BAFF-R extracellular domain adopts a b-hairpin structure and binds to the virus-like BAFF cage in a 1:1 molar ratio. The conserved DxL motif of BAFF-R is located on the tip of the b-turn, and plays an indispensable role in the binding of BAFF. The crystal structure shows that a unique dimeric contact occurs between the BAFF-R monomers in the virus-like cage complex. Both of the CRDs of TACI contain the DxL motifs and simultaneously interact with the BAFF dimer in the virus-like cage.