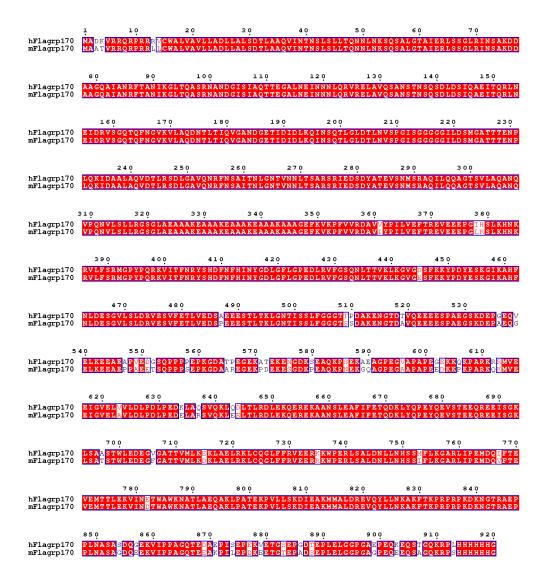
## **Supplementary Figure S2**



**Supplementary Figure S2. Sequence alignment of human and mouse versions of Flagrp170.** Multiple sequence alignment of hFlagrp170 and mFlagrp170 amino acid sequence was performed using CLUSTAL/W method. Data are displayed by ENDscript server. The conserved residues are shown in red frame. Conservative substitutions are shown as red text. The overall similarity between hFlagrp170 and mFlagrp170 protein is 93.5%.