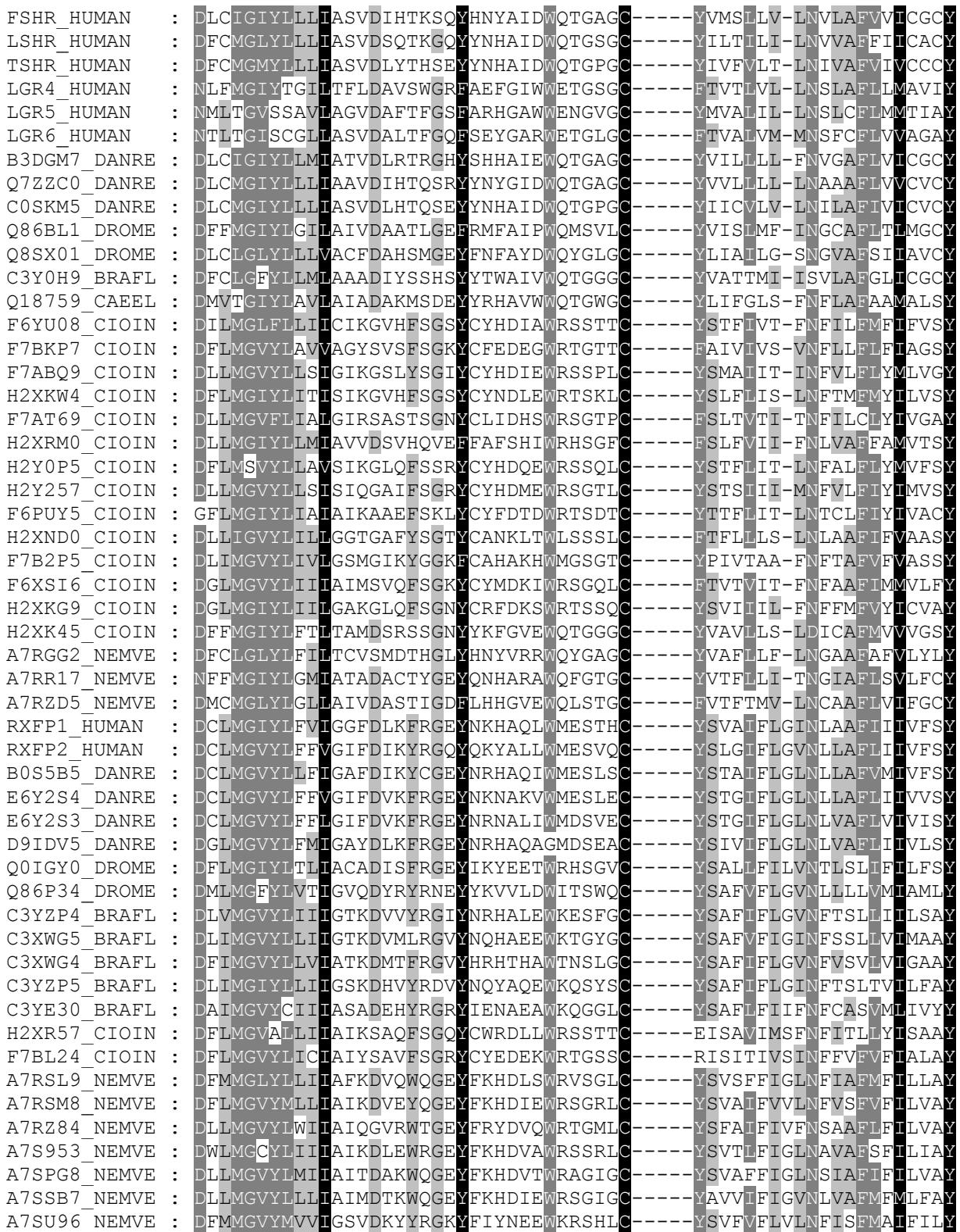


## S2 Align. Sequence alignment of the LGR receptors.



Sequence alignment of residues 2.50 to 3.25 and residues 5.38 to 5.58 of the 52 LGR receptors from *H. sapiens*, *D. rerio*, *C. intestinalis*, *B. Floridae*, *D. melanogaster*, *C. elegans* and *N. vectensis*. Fully conserved positions are shaded in black, partially conserved or type-conserved positions are shaded in dark grey (80% conservation) or light grey (60% conservation). The sequence names correspond to the Uniprot identifiers (entry names).