

This figure displays a sequence alignment of various TGF β receptor (TGFbR) isoforms. The alignment is presented in four horizontal panels, each corresponding to a different region of the protein sequence. The regions are defined by numerical tick marks at the top of each panel: 10-20, 20-30, 30-40, 40-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-110, 110-120, 120-130, 130-140, 140-150, 150-160, 160-170, 170-180, and 180-190.

The sequences are color-coded by residue type: A (green), C (blue), D (red), E (purple), F (orange), G (yellow), H (pink), I (light green), K (dark blue), L (light blue), M (teal), N (light purple), P (light pink), Q (light teal), R (dark red), S (light red), T (light pink), V (light green), W (light orange), and Y (light pink). The alignment shows high conservation of certain amino acid residues across all isoforms, particularly in the signal peptide and transmembrane domains.

Key features visible in the alignment include:

- Signal Peptide:** The first 20-30 positions are highly conserved, showing a typical cleavage site around position 20.
- Transmembrane Domains:** The alignment shows two distinct transmembrane domains, indicated by vertical bars and bolded segments of the sequence.
- Conservation:** Many amino acid positions are highly conserved across all isoforms, such as the hydrophobic core of the transmembrane domains and the conserved cysteine residues involved in disulfide bonding.
- Variable Domains:** There are several regions of higher sequence variation, particularly in the extracellular and intracellular domains.

The isoforms listed on the left side of the alignment include:

- 83506214.q
- AK066000.q
- AK103589.q
- AK067392.q
- 20521280.q
- 15225456.p
- 15235780.p
- lir3_IRK
- 2phk_PhK
- lias_TGFbR