

This figure displays a multiple sequence alignment of TGFBR genes from various species. The alignment is organized into several sections based on position:

- Top Section (Amino acids 1-150):** Positions 1-150. Contains entries for 25149878.w, 25149875.w, 31242421.i, 24644248.f, 7305215.m, KSR1.h, 34872860.m, KSR2.h, 17568897.w, and lias\_TGFB.R. The alignment shows highly conserved regions, particularly at the N-terminus.
- Middle Section (Amino acids 210-390):** Positions 210-390. Contains entries for 25149878.w, 25149875.w, 31242421.i, 24644248.f, 7305215.m, KSR1.h, 34872860.m, KSR2.h, 17568897.w, and lias\_TGFB.R. This section includes a notable insertion in the KSR1.h entry between positions 250-260.
- Bottom Section (Amino acids 410-590):** Positions 410-590. Contains entries for 25149878.w, 25149875.w, 31242421.i, 24644248.f, 7305215.m, KSR1.h, 34872860.m, KSR2.h, 17568897.w, and lias\_TGFB.R. The alignment highlights a large insertion in the 34872860.m entry between positions 450-500.
- Rightmost Section (Amino acids 610-990):** Positions 610-990. Contains entries for 25149878.w, 25149875.w, 31242421.i, 24644248.f, 7305215.m, KSR1.h, 34872860.m, KSR2.h, 17568897.w, and lias\_TGFB.R. This section shows significant divergence between the 34872860.m and KSR1.h entries.
- Final Section (Amino acids 1010-1140):** Positions 1010-1140. Contains entries for 25149878.w, 25149875.w, 31242421.i, 24644248.f, 7305215.m, KSR1.h, 34872860.m, KSR2.h, 17568897.w, and lias\_TGFB.R. The alignment ends here.

The color scale used for conservation is as follows:

- Green: Most conserved residues.
- Yellow: Moderately conserved residues.
- Blue: Less conserved residues.
- Red: Least conserved residues.