

The figure displays a sequence alignment of various TGF $\beta$  receptor isoforms (15221802.p, 15226361.p, AK066295.q, 15218941.p, 15229508.p, 83525516.q, 1ir3\_IRK, 2phk\_PhK, lias\_TGFbR) across multiple species. The alignment is color-coded by amino acid type: Aromatic (F, Y, W), Polar Uncharged (C, G, S, T, D, E), Polar Charged (R, K, H, D, E), and Non-polar (A, C, G, I, L, V, M, P, T). The x-axis represents the amino acid position from 1 to 990. The y-axis lists the protein names. The alignment shows high conservation of the extracellular domain (residues 1-400), particularly the Ig-like domains, and significant divergence in the intracellular kinase domain (residues 400-990).

15221802.p  
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