

This figure displays a sequence alignment of various protein variants across 190 positions. The alignment is color-coded by position, where each color represents a different variant or group of variants. The sequences are highly conserved, with most positions showing identical amino acids across all variants. The alignment is presented in a grid format, with the first 100 positions at the top and the last 100 positions at the bottom. The variants listed on the left include 18400528.p, 15235845.p, 37750007.q, AK101327.q, 53810018.q, AK099003.q, 18424175.p, 15232680.p, 47490019.q, AK067065.q, AK102467.q, 49770027.q, 15220773.p, 83603491.q, 83500074.q, and lias_TGFB. The alignment shows that most positions are conserved, with variations primarily occurring in specific regions, such as positions 10-20, 100-110, and 180-190.

