Figure S1. Alignment of cloned SIAT catalytic domains

Edited sequences were aligned in MEGA-X and formatted for printing in GeneDoc. The L, S, III and VS motifs common to all SIATs are shown. Sequence differences from accession nos. are highlighted. Cys-184 (in full-length human ST6 Gal I) is shown with a blue arrow (paired Cys are shown in same colour). Sequence zST6 is foreshortened for alignment purposes – see Table 1 and Table S3 for full details.