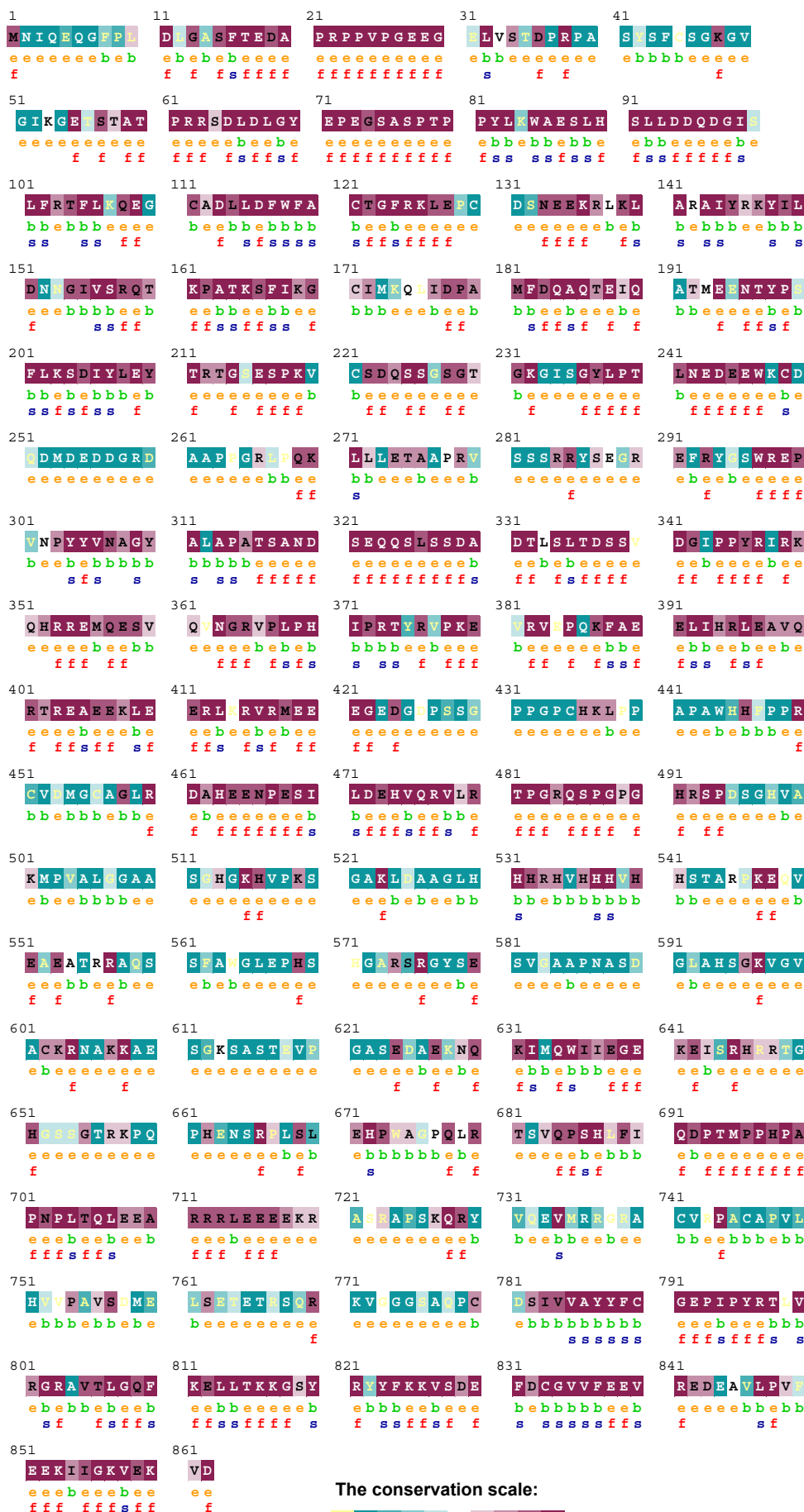
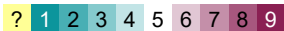


ConSurf Results of human AXIN1



The conservation scale:



Variable Average Conserved

- e - An exposed residue according to the neural-network algorithm.
- b - A buried residue according to the neural-network algorithm.
- f - A predicted functional residue (highly conserved and exposed).
- s - A predicted structural residue (highly conserved and buried).
- X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

Supplementary Fig.3 Analysis of evolutionarily conserved AXIN1 residues using the ConSurf tool. Analysis is based on the human 862 amino acid isoform of AXIN1 (Uniprot O15169-1).