

Supplementary Table S1. Parameters used for protein alignment. Alignment of protein sequences for chemical shift transfer and scoring was performed using the Biopython library within Python 3.7.0. To yield an alignment score independent of sequence length and within the range [0, 1], each score was normalized by that of the alignment of the respective target protein to itself.

Aligner object	Bio.Align.PairwiseAligner
Alignment type	Local
Gap-opening score	-10
Gap extension score	-0.5
Substitution matrix	BLOSUM45