Supplementary Table: Intrinsic aggregation propensities of the amino acid sequences of the two polypeptide chains corresponding to utrophin and dystrophin N-ABDs, as predicted by various computational programs.

Computational Program	Dys N-ABD	Utr N-ABD
TANGO	2100	2268
AGGRESCAN	-5.1	-7.8
Net-CSSP	-7.9	-8.0
PASTA	-18.1	-16.3
Betascan	-377	-279
FoldAmyloid	5209	5474
Waltz	4447	4686