

Table S1. Amyloid prediction of sequential variants in the 39 to 46 positions of the Sup35-27 PFD. PSI⁺ and PSI⁻ correspond to 8 residues stretches able to support or not prion conversion when substituting the original sequence in the Sup35-27 variant, respectively. As described by as Toombs and co-workers (Mol Cell Biol. 2010 30(1):319-32). Sequences predicted to be amyloidogenic by WALTZ using the default parameters are shown in bold.

PSI ⁺	PSI ⁻
VNIFPYYN	CKSVCNFD TDPWVPHF
VTSGSYNT	ADSASNAS AQDSHPDI
AHTTNMIV	ICWHTEPY NPEVNPAN
LLVHSNAI	NNPQYLFK THHSHTLP
HSNVSVIH	GANSAITN DERPWCPE
TRIWNFSG	SVNPALYR TAYVRHID
GSLSLQYF	CFLRSYMG YLPFMDTP
MLSSNFIH	NISPFSKD GPTMNNRD
SSGPLNFI	KMTTNTKH PPIVKPRT
QFVARVFR	THRHNKHR VDDRHMFS
LKSVITWN	KGSPSTPT EAPSKSAQ
SVHVNSTS	GISTRSQE RPERRSNP
ASNIVMNC	QVASQNGR VSLSKNRL
YNCSVNML	LRDPDTCS CIKHINSI
FSIYMPYK	RKATDLFP PVPSSSQP
WGARQFNI	DRYK GKPH SHLWRRNR
VTTDILAM	DPNAALVF DSHTGTTPR
RRDYLTRF	HIHPLFIH STVPPPHH
STVICGVI	TLARRDPP VNCARGTA
IHFWRAP	PNASGIHY SSNKFMHT
TWAPIMVY	NGPAYPLA GFTKALPG
MFQHGIGV	ALSSRQWS SGVSTAVR
YHSVEFRI	IDKNLMSH LNRITLRN
TTVNHFFN	IVPRNVNC VALIPKTA
IFDIANHS	HNLANHSH MTQNPPIF
LQPCYCSR	LSARPLGH LGNPTFHY
CLSPAECR	