

Supplemental Table 8

Nicastrin, 72kDa, 1 transmembrane domain		
Sequence	Peptide presence in all identifications	Predicted to be proteotypic
NQVEDLLATLEK	77%	Y
APDVTTLP	62%	Y
LLYGFLIK	43%	Y
ADVLFIAPR	36%	Y
GKFPVQLENVDSFVELGQVALR	32%	N
Presenilin 1, 53kDa, 9 transmembrane domains		
Sequence	Peptide presence in all identifications	Predicted to be proteotypic
MLVETAQER	63%	Y
AAVQELSSSILAGEDPEER	47%	Y
DGQLIYTPFTEDTETVGQR	40%	N
QVVEQDEEEDTELK	37%	N
YNAESTER	27%	Y
LGLGDFIFYSVLVGK	22%	Y
APH-1A ,29kDa, 7 transmembrane domains		
Sequence	Peptide presence in all identifications	Predicted to be proteotypic
ADEGLASLSEDGR	100%	Y
Pen-2 ,12kDa, 2 transmembrane domains		
Sequence	Peptide presence in all identifications	Predicted to be proteotypic
EAFLVPAYTEQSQIK	93%	Y
VSNEEKLNLGR	22%	N

Comparison of empirically observed peptide presence with those made by prediction for human γ -secretase, a protein complex consisting of a number of (multi-pass) transmembrane domain proteins. Peptides that are experimentally identified most frequently are also generally predicted to be proteotypic.