Calculation of de-amidation [%]

Modified Sequence	N	N2D	Q	Q2E	ratio N2D	ratio Q2E	Intensity	deam N[%]	deam Q[%]
NAAQAANAAQK	2	0	2	0	0/2	0/2	400	65.0	25.0
N(de)AAQAANAAQK	1	1	2	0	1/2	0/2	600	65.0	25.0
N(de)AAQAAN(de)AAQ(de)K	0	2	1	1	2/2	1/2	1000	65.0	25.0

Deamidation per peptide
→ average per protein
→ average per RawFile

*(ratio_0*abu_0 + ratio_1*abu_1 +
ratio_2*abu_2) / sum([abu_0, abu_1, abu_2])
short*