

**Table 5: Comparison of features associated with protein aggregation between high abundant proteins and the remaining detected proteins. The high abundant group is defined as described in Material and Methods.**

<i>Property</i>	<i>Low abundant proteins Mean (Median)</i>	<i>High abundant proteins Mean (Median)</i>	<i>P-value KS-, MW-test</i>
Protein length (in amino acids)	386 (327)	309 (252)	10 <sup>-6</sup> , 10 <sup>-7</sup>
Number of alternating hydrophobic-/hydrophilic stretches (> = 5aa)	11.7 (9.0)	9.5 (8.0)	0.03, 10 <sup>-4</sup>
pI distance from neutrality	1.52 (1.50)	1.69 (1.84)	0.003, 0.01
Hydrophobicity (Kyte-Doolite scale)	-0.20 (-0.21)	-0.25 (-0.24)	0.17, 0.08