

Statistics for proteome:

To verify whether the used fixation method influences the detection of proteins we applied the chi-squared test, which allows us to look at the relationship between two nominal variables and determine whether they are independent of each other in the population. For each donor we determined a percentage of proteins identified only in HOPE, only in SF and then the intersection between both fixation methods (Table 1). The established null hypothesis was that the detection of proteins for each donor and the fixation method are independent at 0.05 significance level.

Table 1. Percentage of proteins identified in HOPE, SF and in both fixation methods

	<b>Donor 1</b>	<b>Donor 2</b>	<b>Donor 3</b>	<b>Donor 4</b>
<b>HOPE</b>	14.05660	11.90695	15.46001	14.37459
<b>SF</b>	28.36478	26.72176	27.47392	20.03929
<b>HOPE <math>\cap</math> SF</b>	57.57862	61.37129	57.06608	65.58612

The resulting P-value of the chi-squared test was calculated to be 0.8161.

Statistics for phosphoproteome:

To verify whether the used fixation method influences the detection of phosphopeptides for each donor we applied the same chi-squared test. For each donor we determined a percentage of phosphopeptides identified only in HOPE, only in SF and then the intersection between both fixation methods (Table 2). The established null hypothesis was that the detection of phosphopeptides for each donor and the fixation method are independent at 0.05 significance level.

Table 2. Percentage of phosphopeptides identified in HOPE, SF and in both fixation methods

	<b>Donor 1</b>	<b>Donor 2</b>	<b>Donor 3</b>	<b>Donor 4</b>
<b>HOPE</b>	21.91834	25.38541	23.60999	29.43793
<b>SF</b>	44.06780	42.30901	38.23529	27.41609
<b>HOPE <math>\cap</math> SF</b>	34.01387	32.30558	38.15471	43.14598

The resulting P-value of the chi-squared test was calculated to be 0.9408.