

Supplementary Table 2. Peptides identified in JlpA variants following trypsin digest and MALDI or ESI-MS/MS.

Mass	Sequence Position	MS-MS Sequence
845.47	282-288	ENLQTLK
877.52	156-162	IRSFINK*
885.48	53-59	IEFSDFK
1024.60	255-262	YIILNNFK
1091.54	114-121	EYYNDLFK
1209.60	208-217	EDLLNYLDSK
1364.74	29-39	KYENQLNQTVK*
1373.65	269-281	TEGVFSSYIATAK
1417.78	196-207	LNFNTNLNINLK
1426.75	125-136	SIQSNLVFEDFK
1478.74	179-190	QENNYLDNLDIK
1613.70	80-92	DNNDEYQELFQAK
1620.78	289-302	AQSQNEEQALIFDK
1660.87	141-155	VVSDINASLFQQDPK
1705.90	303-317	ALAILNNITQNDDYK
1712.78	60-75	<u>C</u> NADGDFIA <u>C</u> LSPNFK (expected mass 1714.76]
1723.94	98-113	SNEIYKGEANASISIK*
1790.86	163-178	LSSDSYTLSDNSINK
1865.97	326-342	NIPVSDYSTQGIDSIEK
2057.02	76-92	TLTKDNNDEYQELFQAK*
2402.36	303-323	ALAILNNITQNDDYKLNLDLK*
2608.38	196-217	LNFNTNLNINLKEDLLNYLDSK*
2724.34	231-254	QAINELLNIANYEQASDFSNTIQK
3250.53	163-190	LSSDSYTLSDNSINKQENNYLDNLDIK*

* Indicates missed cleavage. Underlined residues were found linked by disulfide bond.