

S5 Table . Sequence comparison of the B region of Bap between different staphylococcal species.

	Protein identity (%)	Protein similarity (%)	Theoretical pI ^a	EF-hand motifs ^b		
				aa	sequence	similarity
<i>S. aureus</i>	100	–	4.61	729-741 752-764	DYDKDGLLDRYEr DTDGDGKnDGDEV	89 % 91 %
<i>S. epidermidis</i>	97	99	4.56	729-741 752-764	DYDKDGLLDRYEr DTDGDGKnDGDEV	91 % 98 %
<i>S. simulans</i>	95	98	4.65	729-741 752-764	DYDKDGLLDRYEr DTDGDGKnDGDEI	91 % 89 %
<i>S. xylosus</i>	80	91	4.52	725-737 748-760	DYDKDGLLDRYEr DTDGDGKnDGDEV	91 % 89 %
<i>S. simiae</i>	68	80	4.43	612-624 651-663 743-755 766-778	DKDlIpFIESVEL DANGNGTITASDL DYDQDGLLDSEYEr DTDGDGKnDGDEV	80 % Identity 91 % 89 %
<i>S. saprophyticus</i>	58	74	4.74	557-569 580-592	DLDKDGLtDNFEF DTDGDGKnDGDEV	89 % 89 %

^aTheoretical pI corresponds to the estimated isoelectric point calculated using Compute pI/Mw tool of ExPaSy server.

^bEF- hand motifs corresponds to the predicted EF-hand-like calcium binding domains calculated using PROSCAN (PROSITE database). Residues that do not conform the EF- hand loop consensus sequence are in lowercase letters.