

Supplementary Figure 3

			20			40		
	CbiA	M - - - KKYLLF	I LLL - NL	INC	NLFNKNKNLD	HNLQPNKINN	36	
	HcpA	M - - - - RLYLS	MALLLSI	IIGC	ELLSKNAN - -	- - LQPKTLET	32	
	BhCRASP-1	MQLTKKYLP	A I LLLL	SLASC	DLFYKNRNSN	ANL - - - - -	33	
	BpcA	MK - - - KKCLLT	I LLL -	SLVNC	GLLSKNKNSE	TSL - - - - -	30	
	BtcA	MK - - - KKCLLT	I ILL -	SLVSC	GLSSKNKNSE	TSLL - NIETN	36	
			60			80		
	CbiA	I I SSDL	SNQK	QAL I	SFKNLV	NNKQYSKDL	E QASKSYLEDL	76
	HcpA	LESNI	DDGQK	QALAFF	QESL	QDNKHL	DALK QAQSALLKDI	72
	BhCRASP-1	- LKTLD	NNQK	QAL I	YFKDTL	QDKKYLS	YLT TSQKNFLDDL	72
	BpcA	- LNTLD	NNQK	QAL I	TFKDLL	QDKNHRS	I LE KQQKS I LKDL	69
	BtcA	LLNTLD	DDNQK	QAL I	TFKDLL	QDKKHLS	I LE KQQKS I LEDL	76
			100			120		
	CbiA	KKNNQDL	NLQ	NKLNQ	ELNCD	YDDSKI	EKLF AQLGNDKMKK	116
	HcpA	K - - - - -	- - - - -	DKPQK	TLNFK	YNKTK	LEQLF RKLGNDKTKQ	103
	BhCRASP-1	EKNKK	A PGLQ	YK LK	K T L S S E	YDESQ	F N K L L N E L G N A K A K Q	112
	BpcA	EKHQ	ENS NLQ	DKL	K T L N S E	YDKT	Q L N K L F D E L G N I K T K Q	109
	BtcA	KANQ	K N Y N L Q	DKL	K T L N S E	YDKN	Q L N K L F D E L G N I K T K Q	116
			140			160		
	CbiA	FLQQL	H L M L K	S I N D	G T L I S F	S S S N F R	D T T - T L S Q K K K E R A L	155
	HcpA	FLK	N L H V T I K	F I N N	G S F Q S F	S S A N F N	D L D - T L E K K Q E R A I	142
	BhCRASP-1	FLQQL	H I M L Q	S I K D	G T L T S F	S S A N F N	D L - Q N L E Q K K K E R A L	151
	BpcA	FLQ	K L H I M L K	S I N N	G T L T S F	S S S N F K	D S N Q T L E Q K K K E Q A L	149
	BtcA	FLQQL	H I I L Q	S I K D	G K P T N F	A S S N F N	N L N Q T L E Q K K K E Q A L	156
			180					
	CbiA	EY I	K R Q L Y I E	F Y F H	S N D I S D	T E F F F Q	R T I K L L E T Q S	191
	HcpA	NS I	K E E L Y V N	Y Y L Y	T N E L V D	L D Y F F Y	R A M N Y L - - - S	175
	BhCRASP-1	Q S I	N G E L Y V E	Y Y F Y	I N G I S N	P D N F F E	K I M Q N L K T - -	185
	BpcA	Q Y I	K G Q L Y T D	Y Y L Y	I N G I Q D	A N Y F F E	R I M S V L E I - -	183
	BtcA	K Y I	K D K L Y T D	Y Y L Y	I N G I Q D	A N Y F F E	R I M S L L E - - S	190

Supplementary figure 3. Alignment of proteins of relapsing fever spirochetes.

Deduced amino acid sequences of CbiA, BhCRASP-1, BpcA, HcpA, and BtcA were aligned using CLC Sequence Viewer, Version 8.0 (Qiagen, Aarhus). Lysine residues at the C-termini are highlighted in light grey.