

(A)

		7	11	17	23	27	
AgsA	1	M-MALRTL-----SALPVFADSLFSDRFN--RID-RLFSQLTG-----DTPVAATPAYDL					
IbpB	1	M----RNF-----DLSPLMRQWI-----GFD-KLANALQN-----AGESQSFPPYNI					
IbpA	1	M----RNF-----DLSPLYRSAI-----GFD-RLFNHLENN-----QSQSNGGYPYINV					
HSP16.9	1	M-SIVRRS-----NVFDPFAD-LWADPFD--TFR-SIVPAISGG-----GSETAAAFANARM					
αA-crystallin	1	MDIAIQHPWFKRTLGPFIYPSRLFDQFFGEGLEFYDLLPFLSSTISPIYRQSLFRTVLDSGI					

47	Q--KRDANNYLLTVSV	PGWKEEELEIETVGGN-LNITGKHTEETVEDQTHWIYRGIRKADF
38	E--KSDDNHYRITLALAGFRQEDLEIQLEGTR-LSVKGTP EQPKEEK--KWLHQGLMNQPF	
40	E--LVDENHYRIAIAVAGFAESELEITAQDNL-LVVKGAHADEQKER--TYLYQGIAERNF	
47	D-WKETPEAHVFKADLPGVKKEEVKVEVEDGNVLVVS GERTKEKEDKNDKWHRVERSSGKF	
62	SEVRSDRDKFVIFLDVKHFSPEDLTVKVQEDF-VEIHGKHNERQDDH-----GYISREF	

		24	11
105	QLSFSLPEHAKVNNAK--L-EQGILLVE---	IYQEIPSEKPKKIAIESKPK-AIEHKS	
94	SLSFTLAENMEVSGAT--F-VNGLLHID---	LIRNEPEPIAAQRIASERP----ALNS	
96	ERKFQLAENIHVRGAN--L-VNGLLYID---	LERVIPEAKKPRRIEIN-----	
107	VRRFRLLLEDAKVEEVKAGL-ENGVLTVT---	VPKAEVKKPEVKAIQIS-----G	
115	HRRYRLPSNV DQSALSCSLSADGMLTFSGPKIPSGVDAGHSERAIPVSREEKPSSAPSS		

(B)

