

PC008_v2_3_comp5_c0_seq13	1	MLLISNPRHLGHPMSPGNWKRLIILLSCVFGGAEMNQQHNNPHQPMTLTWQVLSQTGSVVWEKKAVEPPWTWWPSLEPDV	80
AGO86848	1	MLLISNPRHLGHPMSPGNWKRLIILLSCVFGGAEMNQQHNNPHQPMTLTWQVLSQTGSVVWEKKAVEPPWTWWPSLEPDV	80
PC008_v2_3_comp5_c0_seq13	81	CALVAGLESWDIPELTASDSQRPKPPGSSCGVSYSQVGRGLVRQTSYGTLCRCRCPKDRARFSGFGFYVCPRDGRTLSEAR	160
AGO86848	81	CALAAGLETWGIPLHTAPESSQQSAPP-DGCGVLYSQVGRGLVRQS SYGTLCRCRCP RDRNR LAQSQ FYVCPRDGRS LSEAW	159
PC008_v2_3_comp5_c0_seq13	161	RCGGLES LYCKE WGCETAGNAYWQPRSSWDLITVGGHPTGTCE RTGWCNPKIEFTEPGKQFRNWLQGRTWGLRFYVTG	240
AGO86848	160	RCGGFES LYCKE WGCETTGTAYWQPRSSWDLITVGLGHPTGTCEHTGWCNPKIEFTEPGKRFRNWLQGRTWGLRFYVTG	239
PC008_v2_3_comp5_c0_seq13	241	HPGVQLTIRLVITSPPPVVVGPDPLAEQGP RKIPFLPRVPVPTLSPPASPIPTVQASPPAPSTPSPTTGDR L FGLVQG	320
AGO86848	240	HPGVQLTIRLVITSPPPVVVGPDPLAEQGP RKIPFLPRVPVPTLSPPASPIPTVQASPPAPSTPSPTTGDR L FGLVQG	319
PC008_v2_3_comp5_c0_seq13	321	AFLALNATNPEATESCWLCLALGPPYYEGIATPGQVTYASTDSQCRWGGKGLTLTEVSGLGLCIGKVPPTHQHLC S	400
AGO86848	320	AFLALNATNPEATESCWLCLALGPPYYEGIATPGQVTYASTDSQCRWGGKGLTLTEVSGLGLCIGKVPPTHQHLC N	399
PC008_v2_3_comp5_c0_seq13	401	PLNASHTHKYLLPSNHSWWACNSGLTPCLSTSVFNQSNDFCIQIQLVPRIYYHPDGTLLQAYESP HPRNKREPVS LTLAV	480
AGO86848	400	PLNASHTHKYLLPSNHSWWACNSGLTPCLSTSVFNQSNDFCIQIQLVPRIYYHPDGTLLQAYESP HPRNKREPVS LTLAV	479
PC008_v2_3_comp5_c0_seq13	481	LLGLGVAAGIGTGSTALIKGPIDLQQGLTSLQIAMDTDLRALQDSISKLED SLTSLSEVVLQNRRGLDLLFLKEGGLCAA	560
AGO86848	480	LLGLGVAAGIGTGSTALIKGPIDLQQGLTSLQIAMDTDLRALQDSVSKLENSLTSLSEVVLQNRRGLDLLFLKEGGLCAA	559
PC008_v2_3_comp5_c0_seq13	561	LKEECCFYVDHSGAVRDSMRRLKERLDKRQLEHQKNLSWYEGWFNRSPWLTTLLSALAGPLLLLLLLLLLT LGPCVINKLVQ	640
AGO86848	560	LKEECCFYVDHSGAVRDSMRRLKERLDKRQLEHQKNLSWYEGWFNRSPWLTTLLSALAGPLLLLLLLLLLT LGPCVINKLVQ	639
PC008_v2_3_comp5_c0_seq13	641	FINDRVSAVRILVLRHKYQTLDNEDNL	667
AGO86848	640	FINDRVSAVRILVLRHKYQTLDNEDNL	666