

Supplementary Figure S1

Ce_ACR-2	MKKTVKILLILITVFLKVHCHNGGHDEAADFLSHTNIDDPNNSDDPNKNSDQGDIMGED	60
HU_alpha3	-----MGSGPLSLPLALSPRLLLLLLLLLPLVARAS-----EAE	35
TOR_alpha	-----MILCSYWHVGLVLLLLFSCCLVLS-----EHE	28
TOR_gamma	-----MVLTLIIIICLALVRS-----NEE	20
	F	
Ce_ACR-2	DRLVIDLFREYNFLIRPVKNVSSPPVVDFGVAMILLINVDEKNQILQTNVWLTMKWDF	120
HU_alpha3	HRLFERLFEDYNEIIRPVANVS-DPVIHFVSMSQLVKVDEVNQIMETNLWLKQIWNQDY	94
TOR_alpha	TRLVANLLENYNKVIRPVEHHT-HFVDITVGLQLIQLINVDEVNQIVETNVRLRQQWIDV	87
TOR_gamma	GRLIEKLLGDYDKRIKPAKTL-DVIDVTLKLTNLISLNEKEEALTTNVWIEIQWQDY	79
	L V F X SS	
Ce_ACR-2	QLAWNPAEYGNISNLHVPSPDRVWLPDIVLFNNADGNYEVSFKSNVFDHHDGVTWVPPAM	180
HU_alpha3	KLKWNPSDYGGAEFMRVPAQKIWKPDIVLYNNAVGFQVDDKTKALLKYTGVTWIPPAI	154
TOR_alpha	RLRWNPADYGGIKKIRLPSDDVWLPDLVLYNNAVGFDAIVHMTKLLLDYTGKIMWTPPAI	147
TOR_gamma	RLSWNTSEYEGIDLVRIPSELLWLPDVVLENNVDGQFEVAYYANLVVYNDGSMYWLPPAI	139
	LX K N F E	
Ce_ACR-2	FKSSCRIDVEWFPFDEQCCTLVFGSWTYNSEVRLHWYNN-----IQAVQLHDYSYSGI	234
HU_alpha3	FKSSCKIDVTYFPFDYQNCMTKFGSWSYDKAKIDLVLIG-----SSMNLKDYWESGE	206
TOR_alpha	FKSYCEIIVTHFPFDQNCMTKLGITWDYGTGKVSISPES-----DRPDLSTFMESGE	199
TOR_gamma	YRSTCIAVTYFPFDWQNCSLVFRSQTYNAAHEVNLQLSAEEGEVVEWHIDPEDFTENGE	199
	S	
Ce_ACR-2	WDVIDVPG-----QLVHKPDLKENKMFVNVVIRRKTLFYTVILIIPTVLMAFLSVMAFYL	289
HU_alpha3	WAIKAPGYKHDIKYNCCEEI-YPDITYSLYIRRLPLFYTINLIIPCLLISFLTVLVFYL	265
TOR_alpha	WWMKDYRGWKHWVYTCPCDTPYLDITYHFIMQRIPLFYVNVVNIIPCLLFSFLTVLVFYL	259
TOR_gamma	WTIRHRPAKKYNWQLTKDDIDFQEIIFLIIQRKPLFYIINIAPCVLISSLVLVFYL	259
	M* I F TM1	
Ce_ACR-2	PVDSG-EKVSLETISLLLALVFLLLVSKILPPTSN-IPLMGKYLLAFVLNITAVVGTVV	347
HU_alpha3	PSDCG-EKVTLCISVLLSLTVFLLVITETIPSTSLVIPLIGEYLLFTMIFVTLISIVTVF	324
TOR_alpha	PTDSG-EKMTLSISVLLSLTVFLLVIVELIPSTSSAVPLIGKYMLFTMIFVISSIIIVTV	318
TOR_gamma	PAQAGGQKCTLSISVLLAQITFLFLIAQKVPETSLNVPLIGKYLIFVMFVSLVIVTNCVI	319
	C	
Ce_ACR-2	IVNIYFRSALSHKMPWTWRKVLEFLPHLLVMKRPERIPIFNGYFVEEYCASEIFDASLV	407
HU_alpha3	VLNVHYRTPPTHTMPSWVKTVFLNLLPRVMFMRP-----	359
TOR_alpha	VINTHHRSPSTHTMPQWVRKIFINTIPNVMFPS-----	351
TOR_gamma	VLNVSLRTPNTHSLSEKIKHLFLEFLPKYLGMHLE-----	354
	R X	
Ce_ACR-2	MPSMTATMLPFLQVTNLLKAASSTSSGQSEHHCNSKWKRLSIRMSKRRAPRARLDDD	467
HU_alpha3	----TSNEGNAQKPRPLYGAELSNLNCFSRAESKCKEGYPCQDGMCGYCHRRRIKISNF	415
TOR_alpha	----TMKRASKEK-----QENK-----IFADDIDISDI	375
TOR_gamma	-PSEETPEKQPRRRSSFGIMIKAEYILKKPRSE-----LMFEEQKDRHGLKRV	403
	S	
Ce_ACR-2	SEDIIDDNTGNHVDS--LQEKISKEMKTVEAIAEYIAEHMKREMSLKKMRDDWKYVAMVL	525
HU_alpha3	SANLTRSSSESVDVAVLSALSPEIKEAIQSVKYIAENMKAQNEAKEIQDDWKYVAMVI	475
TOR_alpha	SG---KQVTGEVIFQTPLIK--NPDVKSIAIEGVKYIAEHMKSDEESSNAAEEWKYVAMVI	430
TOR_gamma	NKMTSDIDIGTTVDLYKDLANFAPEIKSCVEACNFIAKSTKEQNDSGSENENWVLIGKVI	463
	R X	
Ce_ACR-2	DRLILLIFFGVTLGGTLGIICSAPHVDFVDQEAIIISKLNAKYLPSPDMYS---	575
HU_alpha3	DRIFLWVFTLVCILGTAGLFLQP-----LMAREDA-----	505
TOR_alpha	DHILLCVFMLICIIIGTVSVFAGR-----LIELSQEG-----	461
TOR_gamma	DKACFWIALLLFSLGTLAIFLTG-----HLNQVPEFPFPGDPRKYVP	505
	TM4	