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HsNHA1    1 MHTTESKNEHLEDENFQTSTTPQSLIDPNNTAHEETKTVLSDTEEIKPQT-----------------------KKETYIS
HsNHA2    1 ---MGDEDKRITYEDSEPSTGMNYTPSMHQEAQEETVMKLKGIDANEPTEGSILLKSSEKKLQETPTEANHVQRLRQMLA

HsNHA1   58 CPLRGVLNVIITNGVILFVIWCMTWSILGSEALPGGNLFGLFIIFYSAIIGGKILQLIRIPLVPPLPPLLGMLLAGFTIR
HsNHA2   78 CPPHGLLDRVITNVTIIVLLWAVVWSITGSECLPGGNLFGIIILFYCAIIGGKLLGLIKLPTLPPLPSLLGMLLAGFLIR

HsNHA1  138 NVPFINEHVHVPNTWSSILRSIALTIILIRAGLGLDPQALRHLKVVCFRLAVGPCLMEASAAAVFSHFIMKFPWQWAFLL
HsNHA2  158 NIPVINDNVQIKHKWSSSLRSIALSIILVRAGLGLDSKALKKLKGVCVRLSMGPCIVEACTSALLAHYLLGLPWQWGFIL

HsNHA1  218 GFVLGAVSPAVVVPYMMVLQENGYGVEEGIPTLLMAASSMDDILAITGFNTCLSIVFSSGGILNNAIASIRNVCISLLAG
HsNHA2  238 GFVLGAVSPAVVVPSMLLLQGGGYGVEKGVPTLLMAAGSFDDILAITGFNTCLGIAFSTGSTVFNVLRGVLEVVIGVATG

HsNHA1  298 IVLGFFVRYFPSEDQKKLTLKRGFLVLTMCVSAVLGSQRIGLHGSGGLCTLVLSFIAGTKWSQEKMKVQKIITTVWDIFQ
HsNHA2  318 SVLGFFIQYFPSRDQDKLVCKRTFLVLGLSVLAVFSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAWDIFQ

HsNHA1  378 PLLFGLVGAEVSVSSLESNIVGISVATLSLALCVRILTTYLLMCFAGFSFKEKIFIALAWMPKATVQAVLGPLALETARV
HsNHA2  398 PLLFGLIGAEVSIASLRPETVGLCVATVGIAVLIRILTTFLMVCFAGFNLKEKIFISFAWLPKATVQAAIGSVALDTARS

HsNHA1  458 SAP-HLEPYAKDVMTVAFLAILITAPNGALLMGILGPKMLTRHYDPSKIKLQLSTLEHH-
HsNHA2  478 HGEKQLEDYGMDVLTVAFLSILITAPIGSLLIGLLGPRLLQKVEHQNKDEEVQGETSVQV
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