<html><head><style type="text/css"></style></head><body> white-space: pre-wrap; ">CLUSTAL 2.1 multiple sequence alignment humanHEXA ---MTS----SRLWFSLLLAAAFAGRATALWPWPQNFQTSDQRYVLYPNNFQFQYDVSSA 53 ---MAG----CRLWVSLLLAAALACLATALWPWPQYIQTYHRRYTLYPNNFQFRYHVSSA 53 mouseHEXA zebrafishHEXA MARIAKSPRFCCCLLSVVFVSQFVERVCGVWPLPQEIQQSAESSGLSPQLFTFTYSQDSA 60 .\*::::: \* \*: \* \* \* humanHEXA AQPGCSVLDEAFQRYRDLLFGSGSWPRPYLTGKRHTLEKNVLVVSVVTPGCNQLPTLESV 113 AQAGCVVLDEAFRRYRNLLFGSGSWPRPSFSNKQQTLGKNILVVSVVTAECNEFPNLESV 113 mouseHEXA zebrafishHEXA AOAGCSVLDTAFKRYFSIIFP--DFTKDALHDMWLEPKAFVLSVSVKTRGCDGYPDEDSD 118 \*\*.\*\* \*\*\* \*\*.\*\* \* \* \* \* \* . : . : : . humanHEXA ENYTLTINDDQCLLLSETVWGALRGLETFSQLVWKSAEGTFFINKTEIEDFPRFPHRGLL 173 mouseHEXA ENYTLTINDDQCLLASETVWGALRGLETFSQLVWKSAEGTFFINKTKIKDFPRFPHRGVL 173 zebrafishHEXA ESYNLSVSEGQAVLRSVTVWGALRGLESFSQLVYRDDYGAYFVNKTEIVDFPRFAFRGLL 178 humanHEXA LDTSRHYLPLSSILDTLDVMAYNKLNVFHWHLVDDPSFPYESFTFPELMRKGSYNPVTHI 233 LDTSRHYLPLSSILDTLDVMAYNKFNVFHWHLVDDSSFPYESFTFPELTRKGSFNPVTHI 233 mouseHEXA zebrafishHEXA LDTSRHYLPLHAILKTLDAMAYSKFNVFHWHIVDDPSFPYQSRTFPDLSKKGAFHPFTHI 238 humanHEXA YTAODVKEVIEYARLRGIRVLAEFDTPGHTLSWGPGIPGLLTPCYSGSEPSGTFGPVNPS 293 YTAODVKEVIEYARLRGIRVLAEFDTPGHTLSWGPGAPGLLTPCYSGSHLSGTFGPVNPS 293 mouseHEXA zebrafishHEXA YTQSDVMRVIEHARMRGIRVVPEFDSPGHTQSWGKGQPDLLTPCYKGGKPSGTYGPVDPT 298 humanHEXA LNNTYEFMSTFFLEVSSVFPDFYLHLGGDEVDFTCWKSNPEIQDFMRKKGFGEDFKQLES 353 mouseHEXA LNSTYDFMSTLFLEISSVFPDFYLHLGGDEVDFTCWKSNPNIQAFMKKKGF-TDFKQLES 352 zebrafishHEXA VDTTYRFMERLLKEVKFVFPDSYVHLGGDEVSFACWQSNPSVGKFMEKMGFGRDFTKLES 358 humanHEXA FYIQTLLDIVSSYGKGYVVWQEVFDNKVKIQPDTIIQVWREDIPVNYMKELELVTKAGFR 413 mouseHEXA FYIQTLLDIVSDYDKGYVVWQEVFDNKVKVRPDTIIQVWREEMPVEYMLEMQDITRAGFR 412 zebrafishHEXA FYMESIMNITAALNKTSIVWQDVFDYHERIPQGTVLEIWKGET---YQTELSKMTKAGHR 415 \* \* . . . \* \* \* \* \* \* \*

humanHEXA

mouseHEXA zebrafishHEXA

humanHEXA mouseHEXA zebrafishHEXA </body></html>