<html><head><style type="text/css"></style></head><body> white-space: pre-wrap; ">CLUSTAL 2.1 multiple sequence alignment humanHEXA ---MTS---SRLWFSLLLAAAFAGRATALWPWPQNFQTSDQRYVLYPNNFQFQYDVSSA 53 mouseHEXA ---MAG----CRLWVSLLLAAALACLATALWPWPQYIQTYHRRYTLYPNNFQFRYHVSSA 53 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 mouseHEXA LDTSRHYLPLSSILDTLDVMAYNKFNVFHWHLVDDSSFPYESFTFPELTRKGSFNPVTHI 233 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 zebrafishHEXA

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VLLSAPWYINHITYGQDWRNSYAVQPQNFSGTEEQKKLVIGGEVAMWGEYVDATNLNPRL 475

FYIQTLLDIVSDYDKGYVVWQEVFDNKVKVRPDTIIQVWREEMPVEYMLEMQDITRAGFR 412

FYMESIMNITAALNKTSIVWQDVFDYHERIPQGTVLEIWKGET---YQTELSKMTKAGHR 415

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