

NDUF2

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NDUF2.1_FHEP    VTTHALDVGAMNPLFWM...VESPKGEFG...SRKHLLADVPAILGSLDIVFGEVDR
NDUF2.2_FHEP    IGSHILDVGAITPIFWL...IEAPKGEFG...CRGYLLADVVAI---VISSNCDR
NDUF2_SMED      IATHILDVGGLTPIFWL...IESPKGELG...SKGLMLADLVAIIGTLDVVFGEVDR
NDUF2_SMAN      VGSTVLDIGGITPIFWL...VEAPKGEFG...CRGFMLPDVVAVIGTLDIVFGEVDR
NDUF2_HMIC      LGANILDMGAITPFFWL...VEAPKGEFG...CKGYLLADVVSVLGNLDIVFGEVDR
NDUF2_EGRA      LGSNILDMGAITPFFWL...VEAPKGEFG...CKGFLLADVVSVLGNLDIVFGEVDR
NDUF2_EMUL      LGSNILDMGAITPFFWL...VEAPKGEFG...CKGFLLADVVSVLGNLDIVFGEVDR
NDUF2_TMUR      VSSHALDIGALTPIFWL...IEAPKGEFG...SKYHFLADLVAIIGTMDIVFGEVDR
NDUF2.2_OVOL    IVTHALDIGAMTPIFWM...IEAPNGEYG...TYMSMISDVVAVIGTLDIVFGEVDR
NDUF2.2_BMAL    IVTHALDIGAMTPIFWM...IEAPNGEYG...THMSLISDVVAVIGTMDIVFGEVDR
NDUF2.1_OVOL    ITTHALDIGAMTPIFWM...IEAPKGEFG...CHMSLLSDVVAVIGTLDIVFGEIDR
NDUF2.1_BMAL    VTTHALDVGAMTPIFWM...VEAPKGEFG...CHLSMLSDVVAVIGTLDIVFGEIDR
NDUF2_MHAP      ITTHALDVGALTPIFWM...TEAPKGEFG...SYMHMIPDLVAIIGTLDVVFGEIDR
NDUF2.2_ASUU    VTTHALDIGAMTPIFWL...IEAPNGEFG...AYMSLIADVVAIIGTLDIVFGEVDR
NDUF2_SRAT      ITTHALDVGAMTPFFWM...TEAPKGEFG...TYMSLIADVVAIIGTMDIVFGEVDR
NDUF2.1_ASUU    ITTHALDIGAMTPIFWM...VEAPKGEFG...CYMSLIADMVAVIGTLDIVFGEVDR
NDUF2.1_CELE    ITTHALDVGAMTPFFWM...IEAPKGEFG...CYMSLIADIVAVIGTMDIVFGEVDR
NDUF2.2_CELE    ITTHALDVGAMTPFFWM...IEAPKGEFG...CYMSLIADIVAVIGTMDIVFGEVDR
NDUF2_HCON      ITTHALDIGAMTPFFWM...IEAPKGEFG...CYMALIADVVAIIGTLDIVFGEVDR
NDUF2_NAME      ITTHALDIGAMTPFFWM...IEAPKGEFG...CYMSLIADVVAIIGTLDIVFGEVDR
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NDUF7

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NDUF7.2_FHEP    SLWPLTFGLACCAIEMMHFAA
NDUF7.1_TMUR    SLWPLSFGLACCAIEMMHFAA
NDUF7.2_TMUR    SLWPLSFGLACCAIEMMHFAA
NDUF7_OVOL      SLWPMTFGLACCAIEMMHFAA
NDUF7_BMAL      SLWPMTFGLACCAIEMMHFAA
NDUF7_ASUU      SLWPLTFGLACCAIEMMHFAA
NDUF7_SRAT      SVWPLTFGLACCAIEMMHMAA
NDUF7_CELE      SIWPLTFGLACCAIEMMHFAA
NDUF7_NAME      SLWPLTFGLACCAIEMMHFAA
NDUF7_HCON      SLWPLTFGLACCAIEMMHFAA
NDUF7.1_SMED    SIWPMTFGLACCAIEMMHMAA
NDUF7.2_SMED    SIWPMTFGLACCAIEMMHMAA
NDUF7_SMAN      SIYPLTFGLACCAIEMMHIAG
NDUF7.1_FHEP    SLWPLTFGLACCAIEMMHIAG
NDUF7_HMIC      SIWPLSFGLACCAIEMMHMAA
NDUF7_EGRA      SIWPLTFGLACCAIEMMHMAA
NDUF7_EMUL      SIWPLTFGLACCAIEMMHMAA
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Supplementary Figure 3. Alignment of NDUF2 and NDUF7 subunits. The residues that form the quinone-reaction chamber according to Degli Esposti (2015) are highlighted in black. These residues are not all identical in helminth sequences, yet highly conserved. In turquoise is highlighted an unusual K→Y substitution found in nematodes that would be related to RQ-binding according to Degli Esposti (2015). We found that most nematodes encode Y, but some encode H and *T. muris* retained a K. In plathyhelminths this residue is either K or R. The numeration corresponds to *C. elegans* NDUF2-1 and NDUF7 sequences. Reference: Degli Esposti, M. (2015). Genome Analysis of Structure-Function Relationships in Respiratory Complex I, an Ancient Bioenergetic Enzyme. *Genome Biol. Evol.* 8, 126–47. doi:10.1093/gbe/evv239.