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COVER IMAGES

Upper-left image: Network display predicted for COX1. A:Homo sapiens and B: Mus musculus. (vol. 28, iss. 4, fig. 3., p. 187)

Middle far left image: Multiple alignment of MT-CO1 gene in different species. (vol. 28, iss. 4, supplementary fig. 1., p. 187)

Middle first row right image: The 3D structure of MT-CO1 shows twelve transmembrane domains. (vol. 28, iss. 4, supplementary fig. 2., p. 189)

Middle first row left image: Motifs for cytochrome c oxidase proteins. The MEME motifs are shown as different colored boxes. Biochemical properties of the various amino acids indicated: Blue; most hydrophobic, Magenta; acidic, Red; positively charged and Green; polar, non-charged and non-aliphatic residues. (vol. 28, iss. 4, fig. 2., p. 186)

Middle second row right image: The frequency distribution and expression pattern of MT-CO1 based on log 2 in tissues. (vol. 28, iss. 4, fig. 1., p. 185)

Middle second row left image: Land and water classification in a – pre-flooding, b – flooding, and c – post-flooding. (vol. 28, iss. 4, fig. 7., p. 164)

Bottom left image: NDWI a – pre-flooding, b – flooding phase, and c – post-flooding. (vol. 28, iss. 4, fig. 4., p. 162)

Bottom middle image: MNDWI a – pre-flooding, b – flooding phase, and c – post-flooding. (vol. 28, iss. 4, fig. 5., p. 163)

Bottom right image: NDVI a – pre-flooding, b – flooding phase, and c – post-flooding. (vol. 28, iss. 4, fig. 3., p. 162)

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