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Lee, Min-Ho, Mitsue Ohmachi, Swathi Arur, Sudhir Nayak, Ross Francis, Diane Church, Eric Lambie and Tim Schedl, Multiple functions and dynamic activation of MPK-1 extracellular signal-regulated kinase signaling in Caenorhabditis elegans germline development.................................................................................................................................................. 2039—2062

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Tanaka, Keita, Yusuke Takehana, Kiyoshi Naruse, Satoshi Hamaguchi and Mitsuru Sakaizumi, Evidence for different origins of sex chromosomes in closely related Oryzias fishes: Substitution of the master sex-determining gene ........................................................................................................................................... 2075—2081

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