Elizabeth Hannah Jenkinson Research Fund

List of Publications

Listed below are some of publications acknowledging funding from the Elizabeth Hannah Jenkinson Research Fund. In some cases the fund will have facilitated part of the work reported.

2021

Dai, Y., Trigueros, S., & Holland, P.W.H. (2021). Compromised Function of the Pancreatic Transcription Factor PDX1 in a Lineage of Desert Rodents. Journal of Mammalian Evolution, 1-13.

2020

Zhong, Y., Herrera-Úbeda, C., Garcia-Fernàndez, J., Li, G., & Holland, P.W.H (2020). Mutation of amphioxus Pdx and Cdx demonstrates conserved roles for ParaHox genes in gut, anus and tail patterning. BMC Biology, 18(1), 1-15.

2019

English, S., & Bonsall, M. B. (2019). Physiological dynamics, reproduction-maintenance allocations, and life history evolution. Ecology and Evolution, 9(16), 9312-9323.

Leung, B., & Shimeld, S. M. (2019). Evolution of vertebrate spinal cord patterning. Developmental Dynamics, 248(11), 1028-1043.

Dai, Y., & Holland, P. W. (2019). The interaction of natural selection and GC skew may drive the fast evolution of a sand rat homeobox gene. Molecular Biology and Evolution, 36(7), 1473-1480.

Davranoglou, L. R., Mortimer, B., Taylor, G. K., & Malenovský, I. (2019). On the morphology and possible function of two putative vibroacoustic mechanisms in derbid planthoppers (Hemiptera: Fulgoromorpha: Derbidae). Arthropod Structure & Development, 52, 100880.

2018

Lai, A. G., Kosaka, N., Abnave, P., Sahu, S., & Aboobaker, A. A. (2018). The abrogation of condensin function provides independent evidence for defining the self-renewing population of pluripotent stem cells. Developmental Biology, 433(2), 218-226.

Lai, A. G., & Aboobaker, A. A. (2018). EvoRegen in animals: Time to uncover deep conservation or convergence of adult stem cell evolution and regenerative processes. Developmental Biology, 433(2), 118-131.

2017

Davranoglou, L. R., Baňař, P., Schlepütz, C. M., Mortimer, B., & Taylor, G. K. (2017). The pregenital abdomen of Enicocephalomorpha and morphological evidence for different modes of communication at the dawn of heteropteran evolution. Arthropod Structure & Development, 46(6), 843-868.

2016

Patthey, C., Clifford, H., Haerty, W., Ponting, C. P., Shimeld, S. M., & Begbie, J. (2016). Identification of molecular signatures specific for distinct cranial sensory ganglia in the developing chick. Neural development, 11(1), 1-20.

Toledo, A., Andersson, M. N., Wang, H. L., Salmón, P., Watson, H., Burdge, G. C., & Isaksson, C. (2016). Fatty acid profiles of great tit (Parus major) eggs differ between urban and rural habitats, but not between coniferous and deciduous forests. The Science of Nature, 103(7), 1-11.

Kao, D., Lai, A. G., Stamataki, E., Rosic, S., Konstantinides, N., Jarvis, E., ... & Aboobaker, A. (2016). The genome of the crustacean Parhyale hawaiensis, a model for animal development, regeneration, immunity and lignocellulose digestion. elife, 5, e20062.

2015

Kenny, N. J., Namigai, E. K., Dearden, P. K., Hui, J. H., Grande, C., & Shimeld, S. M. (2015). The Lophotrochozoan TGF-β signalling cassette-diversification and conservation in a key signalling pathway. International Journal of Developmental Biology, 58(6-7-8), 533-549.

Kenny, N.J., Namigai, E.K.O., Marlétaz, F., Hui, J.H.L. & Shimeld, S.M. (2015). Draft genome assemblies and predicted microRNA complements of the intertidal lophotrochozoans Patella vulgata (Mollusca, Patellogastropoda) and Spirobranchus (Pomatoceros) lamarcki (Annelida, Serpulida). Marine Genomics 24(2): 139-146.

Quah S, Hui J.H.L., Holland P.W.H. (2015). A Burst of miRNA Innovation in the Early Evolution of Butterflies and Moths. Molecular Biology and Evolution (Impact Factor: 9.11). 32(5): 1161-1174.

Isaksson, C., Hanson, M.A. & Burdge, G.C. (2015). The effects of spatial and temporal ecological variation on fatty acid compositions of wild great tits Parus major. Journal of Avian Biology, 46(3): 245–253.

2014

Martin, K.J. & Holland, P.W.H. (2014). Enigmatic orthology relationships between hox clusters of the African butterfly fish and other teleosts following ancient whole-genome duplication. Molecular Biology and Evolution, 31, no. 10: 2592-611.

Perry J.C., Harrison, P.W. & Mank, J.E. (2014). The ontogeny and evolution of sex-biased gene expression in Drosophila melanogaster. Molecular Biology and Evolution, 31: 1206¬1219.

2013

Tan, C.K.W., Pizzari, T. & Wigby, S. (2013). Parental age, gametic age, and inbreeding interact to modulate offspring viability in Drosophila melanogaster. Evolution. 67, 3043-3051.

2012

Werner, G.D.A., Gemmell, P., Grosser, S., Hamer, R. & Shimeld, S.M. (2012). Analysis of a deep transcriptome from the mantle tissue of Patella vulgata Linnaeus (Mollusca: Gastropoda: Patellidae) reveals candidate biomineralising genes. Marine Biotechnology, 15, Issue 2: 230¬243.

Kenny, N. & Shimeld, S.M. (2012). Additive multiple k-mer transcriptome of the keelworm Pomatoceros lamarckii (Annelida; Serpulidae) reveals annelid trochophore transcription factor cassette. Dev. Genes. Evol. DOI 10.1007/s00427-012-0416-6.

2011

McMahon, D.P., Hayward, A. & Kathirithamby, J. (2011). The first molecular phylogeny of Strepsiptera (Insecta) reveals an early burst of molecular evolution correlated with the transition to endoparasitism. PLoS One, 6: e21206.

2009

McMahon, D.P., Hayward, A. & Kathirithamby, J. (2009). The mitochondrial genome of the 'twisted-wing parasite' Mengenilla australiensis (Insecta, Strepsiptera): a comparative study. BMC Genomics, 10: 603.

2006

Mulley, J.F., Chiu, C-H & Holland, P.W.H (2006). Break-up of a homeobox gene cluster after genome duplication in teleosts. PNAS, 103: 10369.