

Resource Summary Report

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Fluxus Engineering

RRID:SCR_008618

Type: Tool

Proper Citation

Fluxus Engineering (RRID:SCR_008618)

Resource Information

URL: <http://www.fluxus-engineering.com/>

Proper Citation: Fluxus Engineering (RRID:SCR_008618)

Description: The DNA Alignment software and Network software is used by biologists, anthropologists, medical researchers and students world wide. We carry out phylogeographic consultancy for US, UK and German clients, including legal medical work. We were involved in the tv projects The Real Eve (Discovery Channel) and Motherland (BBC). Our biotechnological director Dr Peter Forster is on the editorial board of the International Journal of Legal Medicine since 1999.

Synonyms: Fluxus

Resource Type: software resource

Resource Name: Fluxus Engineering

Resource ID: SCR_008618

Alternate IDs: nif-0000-31972

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260801T190334+0000

Ratings and Alerts

No rating or validation information has been found for Fluxus Engineering.

No alerts have been found for Fluxus Engineering.

Data and Source Information

Usage and Citation Metrics

We found 589 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Poriswanish N, et al. (2025) Multiple origins and phenotypic implications of an extended human pseudoautosomal region shown by analysis of the UK Biobank. *American journal of human genetics*, 112(4), 927.

Chi L, et al. (2025) HapNetworkView: a tool for haplotype network exploration and visualization. *BMC genomics*, 26(1), 52.

Bunchom N, et al. (2025) Genetic structure and geographical distribution of *Bithynia siamensis* sensu lato from Khong and Mounlapamok districts, Champasak Province, Laos. *Tropical medicine and health*, 53(1), 44.

Tantrawatpan C, et al. (2025) Nuclear Intron Sequence Variation of the *Bulinus globosus* Complex (Mollusca: Planorbidae): Implications for Molecular Systematic Analyses. *Biology*, 14(1).

Dandi-Labou J, et al. (2025) Susceptibility profile of *Anopheles* and target site resistance mechanism against organophosphates in Cameroon. *PloS one*, 20(5), e0321825.

Azzena I, et al. (2025) Conservation hints for *Pinna nobilis* from a century-old genetic time capsule. *Scientific reports*, 15(1), 37660.

Ena GF, et al. (2025) Demographic insights into paternal genetic diversity and regional substructure in the Spanish Roma. *BMC genomics*, 26(1), 1012.

Ali A, et al. (2025) Phylogeography of a dominant desert lizard reveals the synergistic effects of topography and climate dynamics on diversification in arid eastern-Central Asia. *Zoological research*, 46(3), 485.

De Elías-Escribano A, et al. (2025) Wide Variation of *Aedes albopictus* Genotypes First Introduced into Canary Islands Assessed by rDNA Internal Transcribed Spacer Region and mtDNA cox1 Sequencing and Cloning. *Tropical medicine and infectious disease*, 10(2).

Jin WT, et al. (2025) Human Fragmentation Effects Are Genetically Detectable After 6 Years in an Island-Endemic Plant. *Ecology and evolution*, 15(5), e71310.

Bunchom N, et al. (2025) Molecular insights into seasonal trematode infections in *Bithynia* Snails: host lineages, parasite diversity, and *Opisthorchis viverrini* susceptibility in southern Lao PDR. *Tropical medicine and health*, 53(1), 173.

Kutanan W, et al. (2025) Maternal genetic origin of Chao Lay coastal maritime populations from Thailand. *BMC biology*, 23(1), 146.

Quiroga MP, et al. (2025) Everything everywhere all at once? Disentangling the long-lasting riddle of phylogenetic relationships and cryptic hybridization in the amphitropical genus *Larrea*. *AoB PLANTS*, 17(3), plaf024.

Sangthong D, et al. (2025) Molecular characterization of *Rhipicephalus microplus* and *Haemaphysalis bispinosa* ticks from cattle across Thailand: Regional identification and evidence of different genetic sub-structures between mainland and peninsular populations. *PloS one*, 20(11), e0337052.

Wu M, et al. (2024) Phylogeography of *Morella nana*: The Wumeng Mountains as a natural geographical isolation boundary on the Yunnan-Guizhou Plateau. *Ecology and evolution*, 14(7), e11566.

Yu Q, et al. (2024) Demographic patterns of two related desert shrubs with overlapping distributions in response to past climate changes. *Frontiers in plant science*, 15, 1345624.

Kim S, et al. (2024) Genetic analyses of *Anisakis pegreffii* (Nematoda: Anisakidae) from the East Asian finless porpoise *Neophocaena asiaeorientalis sunameri* (Cetacea: Phocoenidae) in Korean waters. *Parasitology research*, 123(11), 365.

Dumidae A, et al. (2024) Population genetic structure of *Indoplanorbis exustus* (Gastropoda: Planorbidae) in Thailand and its infection with trematode cercariae. *PloS one*, 19(1), e0297761.

Liao JY, et al. (2024) Emerging and characterization of a novel fowl adenovirus 4 strain with open reading frame 19 (ORF19) in diseased chickens from China. *Poultry science*, 104(2), 104702.

Suwannahitatorn P, et al. (2024) Study of the population genetic structure of *Opisthorchis*-like eggs in northern Thailand using mitochondrial genes. *PLoS neglected tropical diseases*, 18(8), e0012445.