

Resource Summary Report

Generated by NIF on Sep 7, 2026

Fluxus Engineering

RRID:SCR_008618

Type: Tool

Proper Citation

Fluxus Engineering (RRID:SCR_008618)

Resource Information

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

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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: 20260905T132625+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 636 mentions in open access literature.

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

Cho AY, et al. (2026) Wild birds drive the introduction, maintenance, and spread of H5N1 clade 2.3.4.4b high pathogenicity avian influenza viruses in Spain, 2021-2022. *Virus evolution*, 12(1), veag006.

Kumar L, et al. (2026) The Old Lady spider cave skeletons in Ladakh have diverse maternal genetic origin. *iScience*, 29(6), 116193.

Fontes JT, et al. (2026) Phylogeography of the widely distributed John Dory (*Zeus faber*, Actinopterygii: Zeiformes) reaffirms the prevalence of at least two deeply divergent clades. *Journal of fish biology*, 108(1), 373.

Xu B, et al. (2026) HaploThread: a scalable desktop tool for efficient haplotype network inference and interactive visualization. *Molecular biology and evolution*, 43(3).

Kostro-Ambroziak A, et al. (2026) New Insight Into the Evolutionary Arms Race Between Spider Egg Sac Pseudoparasitoids and Active Maternal Care by the Spiders. *Ecology and evolution*, 16(5), e73581.

Andrus PS, et al. (2026) Population genetic diversity of invasive Pomacea snails and surveillance of *Angiostrongylus cantonensis* in Shanghai, East China. *Parasites & vectors*, 19(1).

Syuhada NI, et al. (2026) Population Genetics of the Moon Crab *Matuta victor* (Fabricius 1781) on Java Island, Indonesia. *Tropical life sciences research*, 37(1), 185.

Lankheet I, et al. (2026) Revisiting the African mtDNA landscape through complete mitochondrial genomes. *Communications biology*, 9(1).

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

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.

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.

De Elias-Escribano A, et al. (2025) Imported Schistosomiasis in Southwestern Europe: Wide Variation of Pure and Hybrid Genotypes Infecting Sub-Saharan Migrants. *Transboundary and emerging diseases*, 2025, 6614509.

Ou Q, et al. (2025) The Divergence History of Two Japanese *Torreya* Taxa (Taxaceae): Implications for Species Diversification in the Japanese Archipelago. *Plants* (Basel, Switzerland), 14(10).

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.

Pilap W, et al. (2025) Unveiling Genetic Variation in the Seed Bug *Spilostethus pandurus* (Scopoli, 1763) (Hemiptera: Lygaeidae) in Thailand Using Mitochondrial CO1 Sequence. *Biology*, 14(8).

Gomontean B, et al. (2025) Island vs. Mainland: Genetic Divergence of *Calotes versicolor* (Daudin, 1802) (Squamata: Agamidae) in Thailand. *Animals : an open access journal from MDPI*, 15(20).

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

Wieczorek K, et al. (2025) Tracing the Invasion of *Takecallis nigroantennatus* (Hemiptera, Aphididae) on Cold-Hardy Bamboo *Fargesia* Using Mitochondrial COI Data. *International journal of molecular sciences*, 26(17).

Tantrawatpan C, et al. (2025) Nuclear intron sequence analysis and its implications for molecular systematics of Asian zoonotic blood flukes (*Schistosoma* spp.) (Trematoda: Schistosomatidae). *Current research in parasitology & vector-borne diseases*, 8, 100338.