

Resource Summary Report

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SMART

RRID:SCR_005026

Type: Tool

Proper Citation

SMART (RRID:SCR_005026)

Resource Information

URL: <http://smart.embl.de/>

Proper Citation: SMART (RRID:SCR_005026)

Description: Software tool for identification and annotation of genetically mobile domains and analysis of domain architectures.

Abbreviations: SMART

Synonyms: Simple Modular Architecture Research Tool

Resource Type: analysis service resource, data access protocol, data analysis service, data or information resource, database, production service resource, service resource, software resource, web service

Defining Citation: [PMID:18978020](#), [PMID:16381859](#), [PMID:14681379](#), [PMID:10592234](#), [PMID:9847187](#), [PMID:9600884](#)

Keywords: extracellular, gene, genetic, genetically, genome, architecture, chromatin, domain, mobile, phyletic, protein, proteome, signaling, structure, taxonomic, tertiary, bio.tools, FASEB list

Funding: European Union

Availability: Free, Freely available

Resource Name: SMART

Resource ID: SCR_005026

Alternate IDs: nif-0000-03471, biotools:smart

Alternate URLs: <http://smart.embl-heidelberg.de/>, <https://bio.tools/smart>

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260903T234737+0000

Ratings and Alerts

No rating or validation information has been found for SMART.

No alerts have been found for SMART.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8432 mentions in open access literature.

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

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Yue Y, et al. (2026) ADA2 Forms Nuclear Condensates with GCN5 and ATP-Citrate Lyase (ACL) to Modulate H3K9 Acetylation at Genes Functioning in Rice Meristems. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(5), e13169.

Chen P, et al. (2026) *Bombyx mori* Jun gene is involved in endoreplication of silk gland cells by regulating S-phase cell cycle genes. *Journal of advanced research*, 82, 367.

Guo R, et al. (2026) Metabolo-Transcriptomics Analyses Reveal Alfalfa Adaptation to Combined Saline-Alkali and Low-Temperature Stress in the Field. *Plant biotechnology journal*, 24(2), 504.

Streit TN, et al. (2026) 4-Fold Protonation of Tetracyanometalates in Superacids: Hydrogen and ??-Hole Bonding in the Solid State. *Inorganic chemistry*, 65(1), 892.

White WL, et al. (2026) Design of solubly expressed miniaturized SMART MHCs. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2505932123.

Zada D, et al. (2026) Convergent thyroid-ATPase interactions regulate collective behavior in *Danionella*. *Cell reports*, 45(1), 116730.

Zhang T, et al. (2026) Multi-omics analyses shed lights on the evolution and fruit development of Chinese raspberries (*Rubus* spp.). *Journal of integrative plant biology*, 68(4), 1032.

Wu L, et al. (2026) High-quality genome assembly and annotation of the white-cheeked goby, *Rhinogobius duospilus* (Herre, 1935) (Gobiiformes: Oxudercidae). *G3* (Bethesda, Md.), 16(2).

Yuasa-Kawada J, et al. (2026) Neuronal guidance signaling in neurodegenerative diseases: Key regulators that function at neuron-glia and neuroimmune interfaces. *Neural regeneration research*, 21(2), 612.

Gao J, et al. (2026) Genome-wide identification of HXK gene families in cucumber and watermelon: CsHXK1 and ClHXK6 play key roles in responding to multiple stresses. *BMC plant biology*, 26(1), 200.

Liang W, et al. (2026) HSPA8 is a biomarker associated with prognosis and immunity in skin cutaneous melanoma. *Discover oncology*, 17(1), 100.

Liu X, et al. (2026) Evolutionary and functional characterization of BBX genes in the barley pangenome. *BMC plant biology*, 26(1).

Zhang L, et al. (2026) Quercetin upregulates steroid hormone biosynthesis to enhance reproductive performance in roosters. *Poultry science*, 105(4), 106590.

Ying J, et al. (2026) Genome-wide identification, characterization and expression analysis of the HSP70 gene family in seagrass *Zostera marina* under abiotic stress. *BMC plant biology*, 26(1).

Chosyang S, et al. (2026) Comparative analysis of the Aquaporin gene family in Cucurbitaceae: insights into evolutionary patterns and functional diversity. *BMC plant biology*, 26(1), 297.

Nawrocka WI, et al. (2026) Nematode extracellular protein interactome expands connections between signaling pathways. *Cell genomics*, 6(5), 101161.

Hu QL, et al. (2026) Chromosome-level genome assembly of the predatory stink bug, *Eocanthecona furcellata* (Wolff). *Scientific data*, 13(1), 6.

Yuan Y, et al. (2026) Genome-wide identification of the GT transcription factor family in alfalfa and functional characterization of MsGT16 in salt stress tolerance. *BMC genomics*, 27(1), 145.

Khanzada H, et al. (2026) Comprehensive Genome-Wide Identification and Expression Analysis of the N6-Methyladenosine (m6A) Regulatory Network Influences Rapid Stress Adaptation With Exogenous Melatonin in Rice. *Journal of pineal research*, 78(1), e70109.