Resource Summary Report

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CREATE

RRID:SCR_006133
Type: Tool

Proper Citation

CREATE (RRID:SCR_006133)

Resource Information

URL: http://www.creline.org/

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Description: The CREATE consortium represents a core of major European and international mouse database holders and research groups involved in conditional mutagenesis, primarily to develop a strategy for the integration and dissemination of Cre driver strains for modelling aspects of complex human diseases in the mouse. Collectively the participants have amassed a significant number of these strains in their respective databases. Therefore one of the goals of CREATE is to provide a unified portal for worldwide access to these critical resources. The portal can either be searched through an advanced BioMart interface, by driver name, or by anatomical site of expression using Embryonic Mouse Anatomy Project (EMAP) and Mouse Anatomy (MA) ontology terms. Search results link back to the original source of the data for more detailed information and to IMSR to order mice if available. The ontology browser is particularly useful as it enables the CREATE consortium to identify cell and tissues that are not currently covered by existing lines. CREATE also aims to coordinate the production of suitable lines by the Cre generation projects described above. Through the CREATE portal, the CREATE consortium aims to develop a strategy for the production, integration and dissemination of new Cre driver strains for modelling aspects of complex human diseases in the mouse. CREATE is also developing a roadmap for harnessing emerging technologies and methods for improving Cre-mediated recombination in vivo through targeted, intensive workshops and discussion forums on the portal. This will entail review of construct design options for classical transgenic constructs (promoter/enhancer used, small size 2025 Kb) vs large transgenic constructs (BAC, P1, YAC etc.); methods used for Cre transgenic lines including random vs targeted integration, position independent expression loci, or replacement of endogenous coding sequences with Cre recombinase under the control of the endogenous locus. CREATE provides a platform for discussion of additional issues specific to inducible Cre strategies including background activity before induction, inducibility (kinetics), efficiency, and protocols used for induction of Cre recombinase activity. Additional components of the technology roadmap will be the cataloguing of other existing methodologies (rtTA, FLP, Dre) of mouse genome modification, sharing

information on validated Cre mutant lines as well as identification and assessment of new methods of mutagenesis such as RNAi and other emerging technologies. Other discussion topics addressed through surveys on the CREATE portal include the characterization of Cre lines (specificity of expression/deletion; efficiency of expression/deletion; reproducibility of deletion from animal to animal for the same floxed allele; reproducibility with different floxed alleles; timing of expression/deletion, etc.), the extent to which Cre expression changes upon backcrossing to specific genetic backgrounds through variegation and silencing; potential phenotypes caused by either integration-mediated mutagenesis or Cre "toxicity"; and other factors affecting the specificity of Cre-mediated expression/deletion. CREATE regularly integrates common fields from the Cre-X, CreZOO and the MGI recombinase portal resources described below. The data in common consists of: * Transgene or Knock-in name. * MGI ID of allele. * Driver. * Anatomical site of expression. * Pubmed ID. * IMSR strain name and link. * Inducibility (YES/NO).

Abbreviations: CREATE

Synonyms: CREATE (Coordination of resources for conditional expression of mutated mouse alleles) project, CREATE - Coordination of resources for conditional expression of mutated mouse alleles, CREATE portal, CREATE (Coordination of resources for conditional expression of mutated mouse alleles)

Resource Type: data or information resource, database, international standard specification, narrative resource, portal, standard specification, topical portal

Defining Citation: PMID:21195764

Keywords: cre driver, mutagenesis, cre, gene, allele, mutant mouse es cell line, mutant mouse, es cell line, phenotype, gene expression, cre recombinase, tissue, organ, cell, mouse mutagenesis, cre line, FASEB list

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Alternate IDs: nlx_151617

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Record Last Update: 20260821T193758+0000

Ratings and Alerts

No rating or validation information has been found for CREATE.

No alerts have been found for CREATE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 51 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

Stephens J, et al. (2025) Factors associated with preeclampsia and the hypertensive disorders of pregnancy amongst Indigenous women of Canada, Australia, New Zealand, and the United States: A systematic review and meta-analysis. Current hypertension reports, 27(1), 10.

Kennel M, et al. (2025) Characterising socially accountable research: a scoping review protocol paper. BMJ open, 15(7), e093101.

Banjoko AW, et al. (2025) High resolution class I HLA-A, -B, and -C diversity in Eastern and Southern African populations. Scientific reports, 15(1), 23667.

Cui X, et al. (2025) CREATE: cell-type-specific cis-regulatory element identification via discrete embedding. Nature communications, 16(1), 4607.

Rosen T, et al. (2025) Developing a screening tool and intervention strategy for elder neglect in persons with dementia in primary care: protocol to use a multistep process. BMJ open, 15(7), e085172.

Qi Y, et al. (2025) CREATE: a novel attention-based framework for efficient classification of transposable elements. Briefings in bioinformatics, 26(6).

Banjoko AW, et al. (2024) High Resolution Class I HLA -A, -B, and -C Diversity in Eastern and Southern African Populations. bioRxiv : the preprint server for biology.

Benatar M, et al. (2024) Prognostic clinical and biological markers for amyotrophic lateral sclerosis disease progression: validation and implications for clinical trial design and analysis. EBioMedicine, 108, 105323.

Ariad D, et al. (2024) Aberrant landscapes of maternal meiotic crossovers contribute to aneuploidies in human embryos. Genome research, 34(1), 70.

Garzke J, et al. (2024) CREATE'ing improvements in first-year students' science efficacy via an online introductory course experience. Journal of microbiology & biology education, 25(1), e0007923.

Martin EA, et al. (2024) Developing a Computational Phenotype of the Fourth Universal Definition of Myocardial Infarction for Inpatients. Journal of clinical medicine, 13(24).

Benatar M, et al. (2024) Prognostic Clinical and Biological Markers for Amyotrophic Lateral Sclerosis Disease Progression: Validation and Implications for Clinical Trial Design and Analysis. medRxiv : the preprint server for health sciences.

Hiyare-Hewage A, et al. (2024) The cultural safety of research reports on primary healthcare use by Indigenous Peoples: a systematic review. BMC health services research, 24(1), 873.

Ariad D, et al. (2023) Aberrant landscapes of maternal meiotic crossovers contribute to aneuploidies in human embryos. bioRxiv : the preprint server for biology.

Rodrigues LF, et al. (2023) Genetic Differentiation of Aedes aegypti (Diptera: Culicidae) in Areas with High Rates of Infestation in Mid-North Region of Brazil. Insects, 14(6).

Landsverk NG, et al. (2023) Instruments measuring evidence-based practice behavior, attitudes, and self-efficacy among healthcare professionals: a systematic review of measurement properties. Implementation science : IS, 18(1), 42.

Mitchell F, et al. (2023) Factors influencing infant feeding for Aboriginal and Torres Strait Islander women and their families: a systematic review of qualitative evidence. BMC public health, 23(1), 297.

Goudsouzian LK, et al. (2023) Reading Primary Scientific Literature: Approaches for Teaching Students in the Undergraduate STEM Classroom. CBE life sciences education, 22(3), es3.

Wang X, et al. (2022) Improved dsDNA recombineering enables versatile multiplex genome engineering of kilobase-scale sequences in diverse bacteria. Nucleic acids research, 50(3), e15.

Ruano ASM, et al. (2022) Design and validity of an instrument to assess healthcare professionals' perceptions, behaviour, self-efficacy and attitudes towards evidence-based health practice: I-SABE. BMJ open, 12(4), e052767.