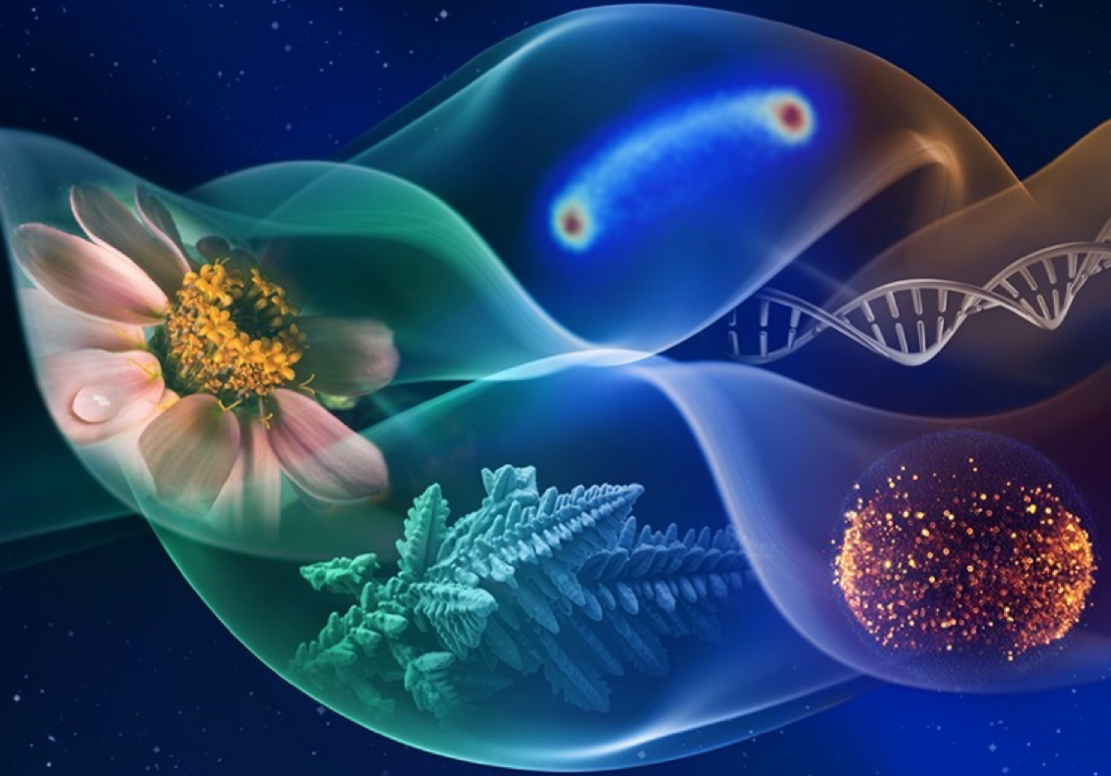


Introduction to open science at NASA

Kris Peach, PhD (she/her)
Space Biosciences
NASA GeneLab AMES Research Center
Contractor: Bionetics



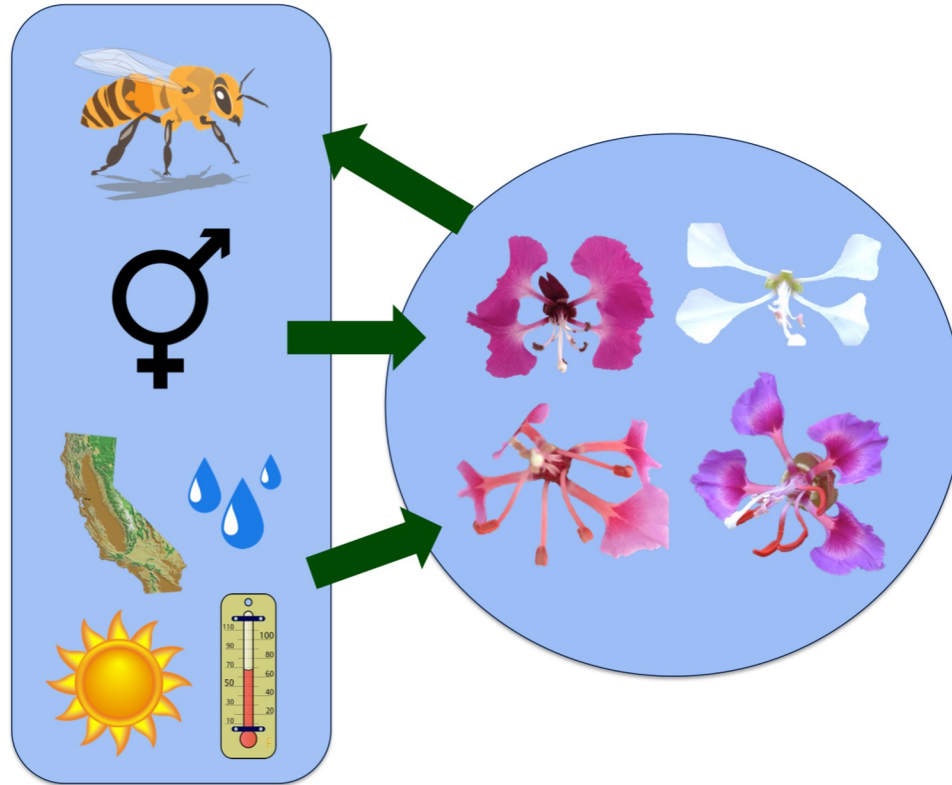
Research relies on open source data and tools

- Herbaria and scientific collections (ex. CCBER, SBBG)
- Long-term climate data (ex. PRISM, ClimateNA, NOAA)
- Plant occurrence data (ex. GBIF)
- Repositories of multi-source observations (ex. Calflora)
- Citizen science apps (ex. CPN, iNaturalist)
- Research data repositories (ex. Dryad, GeneLab)
- Open access data tools and platforms (ex. ImageJ, R, Github)

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My PhD research: The ecology of evolution of floral form and function in *Clarkia unguiculata*



R Studio
Python
ImageJ
ClimateNA
Calflora
Github

My PhD research: The ecology of evolution of floral form and function in *Clarkia unguiculata*

Heteranthery in *Clarkia*: pollen performance of dimorphic anthers contradicts expectations

Kristen Peach^{1,2}  and Susan J. Mazer¹

Climate Predicts UV Floral Pattern Size, Anthocyanin Concentration, and Pollen Performance in *Clarkia unguiculata*

Article

Full-text available

June 2020 · Frontiers in

 Kristen Peach ·  Jasen W. Liu ·  Susan J. Mazer

Floral traits influence the opportunity for selection among male gametophytes: independent and combined effects of style length and petal area

Susan J. Mazer^{1,2} , Joseph P. Chellaw¹, and Kristen Peach¹ 

Mating system and historical climate con

P
C

nature portfolio

Scientific Reports

SI
A

Dioecious hemp (*Cannabis sativa* L.) plants do not express significant sexually dimorphic morphology in the seedling stage

Article

Full-text available

August 2021 · Scientific Reports

 Lesley Geills Campbell ·  Kristen Peach ·  Sydney B. Wizenberg

reaction traits in a sequentially hermaphroditic species

able

February 2020 · Ecology and Evolution

sen W. Liu ·  Kristen Klitgaard ·  Susan J. Mazer

Postdoctoral fellowship in data science

National Center for Ecological Analysis and Synthesis

Open access data tools

- R, SQL, Python, Unix/Bash, XML, Java
- Co-authored several R packages
- Expanded use of Github for collaboration
- Improved DataOne repositories to FAIR standards

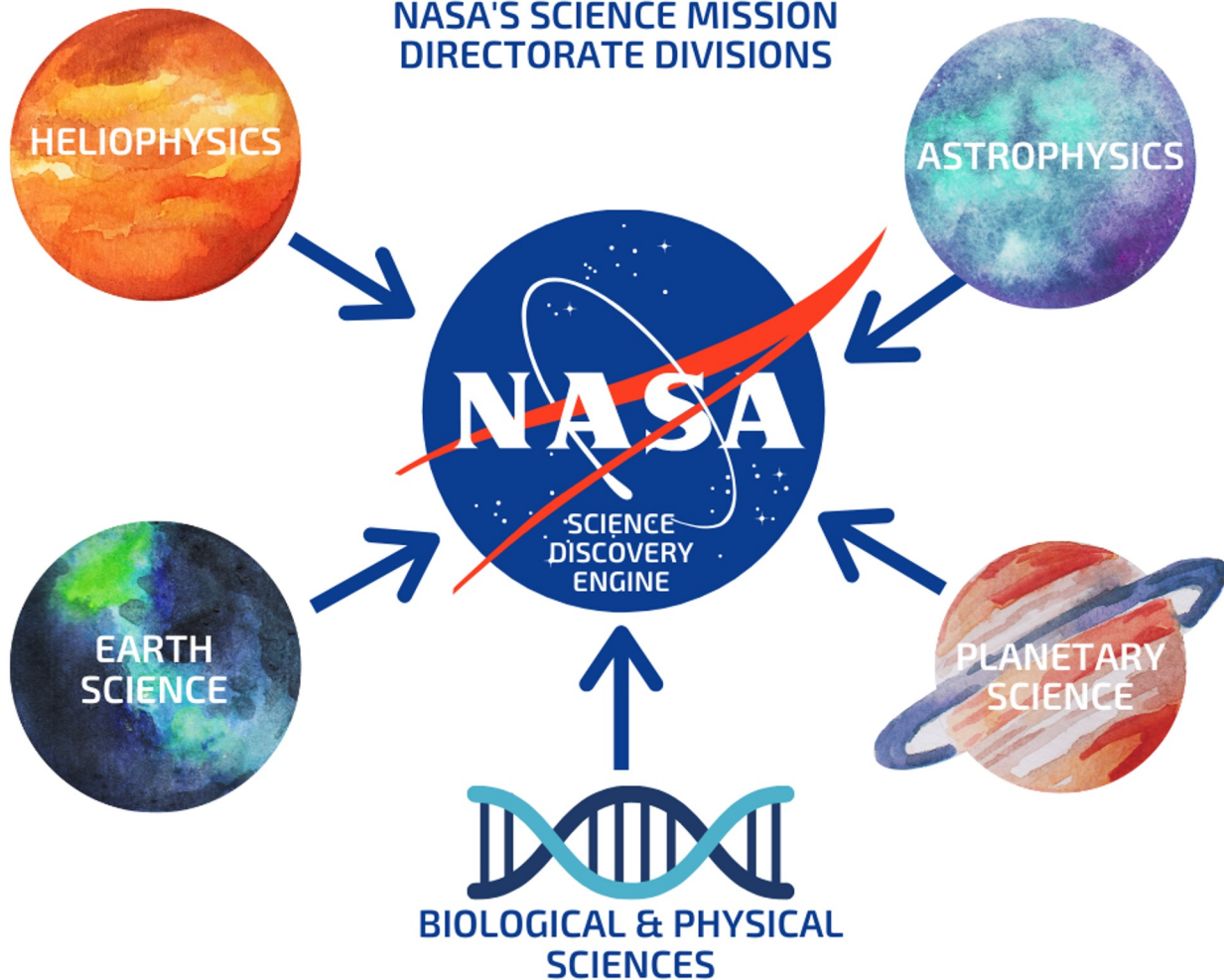
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Open Source Science at NASA

NASA'S SCIENCE MISSION
DIRECTORATE DIVISIONS





What is Open Science?

We define **Open Science** as:
a **collaborative culture enabled by technology** that empowers the **open sharing of data, information, and knowledge** within the **scientific community and the wider public** to accelerate scientific research and understanding.

Biospecimen Sharing Program (BSP)



- *Dissects and preserves* rodent tissues from Flight and Ground investigations
- *Coordinates* internal tissue sharing



NASA Biological Open Science Resources

Biospecimen Sharing Program (BSP)



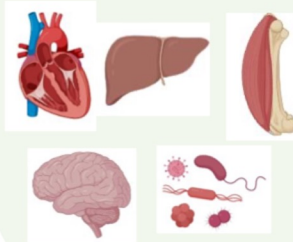
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NASA Biological Institutional Scientific Collection (NBISC)



- *Collection* of non-human specimens and space microbial culture



NASA Biological Open Science Resources

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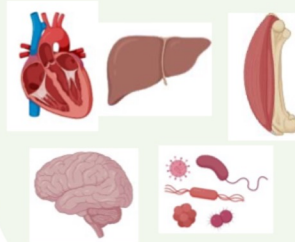
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- *Collection* of non-human specimens and space microbial culture



Ames Life Sciences Data Archive (ALSDA)



- *Collects and curates* physiological, mission, project and imaging data



NASA Biological Open Science Resources



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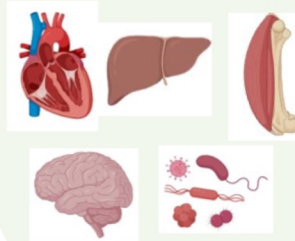
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- *Collects and curates* physiological, mission, project and imaging data



GeneLab (GL)



- *Collects and curates* omics data





Open Science for Life in Space

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Search Filters

Data Source

- ☒ GeneLab
- ☐ NIH GEO
- ☐ EBI PRIDE
- ☐ ANL MG-RAST

GeneLab Search Filters

Project Type

- ☐ Ground
- ☐ Spaceflight
- ☐ High Altitude

Assay Type

- ☐ Microarray
- ☐ RNA Sequencing (RNA-Seq)
- ☐ Single-Cell RNA Sequencing
- ☐ miRNA Sequencing (miRNA-Seq)
- ☐ Nucleotide Sequencing

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Tissue

GeneLab Data Repository Search

Search Datasets



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GLDS-524

[Ionizing radiation induces transgenerational effects of DNA methylation in zebrafish](#)

Organisms	Factors	Assay Types	Release Date	Description
Danio rerio	Ionizing Radiation Generation	DNA methylation profiling	31-Aug-2023	Ionizing radiation is known to cause DNA damage, yet the mechanisms underlying potential transgenerational effects of exposure have been scarcely studied. Previously, we observed effects in offspring ...



GLDS-520

[Changes in DNA Methylation in Arabidopsis thaliana Plants Exposed Over Multiple Generations to Gamma Radiation](#)

Organisms	Factors	Assay Types	Release Date	Description
Arabidopsis thaliana	Generation Ionizing Radiation	DNA methylation profiling	31-Jan-2021	Previous studies have found indications that exposure to ionising radiation (IR) results in DNA methylation changes in plants. However, this phenomenon is yet to be studied across multiple generations...



GLDS-519

[PUCHI represses early meristem formation in developing lateral roots of Arabidopsis thaliana](#)

Organisms	Factors	Assay Types	Release Date	Description
Arabidopsis thaliana	Genotype Organism Part Treatment Time	transcription profiling	25-Mar-2022	Time-series RNAseq analysis following lateral root induction by gravistimulation. Lateral root organogenesis is a key process in the development of a plant's root system and its adaptation to the envi...

Example Study from GeneLab

<https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-520>



Open Science for Life in Space

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Version 2



Description



Version History



Protocols



Samples



Assays



Publications



Study Files



Visualization



130.00 GB

GLDS-520 **Version 2**

Changes in DNA Methylation in Arabidopsis thaliana Plants Exposed Over Multiple Generations to Gamma Radiation

DOI: [10.26030/7q4w-ej22](https://doi.org/10.26030/7q4w-ej22)

Source Accession: [GSE157965](#)

[Cite this Study](#)



Description

Study Description

Previous studies have found indications that exposure to ionising radiation (IR) results in DNA methylation changes in plants. However, this phenomenon is yet to be studied across multiple generations. Furthermore, the exact role of these changes in the IR-induced plant response is still far from understood. Here, we study the effect of gamma radiation on DNA methylation and its effect across generations in young Arabidopsis plants. A multigenerational set-up was used in which three generations (Parent, generation 1, and generation 2) of 7-day old Arabidopsis thaliana plants were exposed to either of the different radiation treatments (30, 60, 110, or 430 mGy/h) or to natural background radiation (control condition) for 14 days. The parental generation consisted of previously non-exposed plants, whereas generation 1 and generation 2 plants had already received a similar irradiation in the previous one or two generations, respectively. Directly after exposure the entire methylomes were analysed with UPLC-MS/MS to measure whole genome methylation levels. Whole genome bisulfite sequencing was used to identify differentially methylated regions (DMRs), including their methylation context in the three generations and this for three different radiation conditions (control, 30 mGy/h, and 110 mGy/h). Both intra- and intergenerational comparisons of the genes and transposable elements associated with the DMRs were made. Taking the methylation context into account, the highest number of changes were found for cytosines followed directly by guanine (CG methylation), whereas only limited changes in CHG methylation occurred and no changes in CHH methylation were observed. A clear increase in IR-induced DMRs was seen over the three generations that were exposed to the lowest dose rate, where generation 2 had a markedly higher number of DMRs than the previous two generations (Parent and generation 1). Counterintuitively, we did not see significant differences in the plants exposed to the highest dose rate. A large number of DMRs associated with transposable elements were found, the majority of them being hypermethylated, likely leading to more genetic stability. Next to that, a significant number of DMRs were associated with genes (either in their promoter-associated region or gene body). A functional analysis of these genes showed an enrichment for genes related to development as well as various stress responses, including DNA repair, RNA splicing, and (ab)iotic stress responses. These observations indicate a role of DNA methylation in the regulation of these genes in response to IR exposure and shows a possible role for epigenetics in plant adaptation to IR over multiple generations.

Factor(s)

Submitted Date:
15-Sep-2020
Initial Release Date:
31-Jan-2021





Data Portal

- First multi-omics space related database
- 371 publicly available studies
- High-order data for transcriptomics and metagenomics studies
- Spaceflight environmental data associated with sample metadata (radiation dosimetry, temperature, humidity)
- Interactive **visualization portal** to explore changes in gene expression

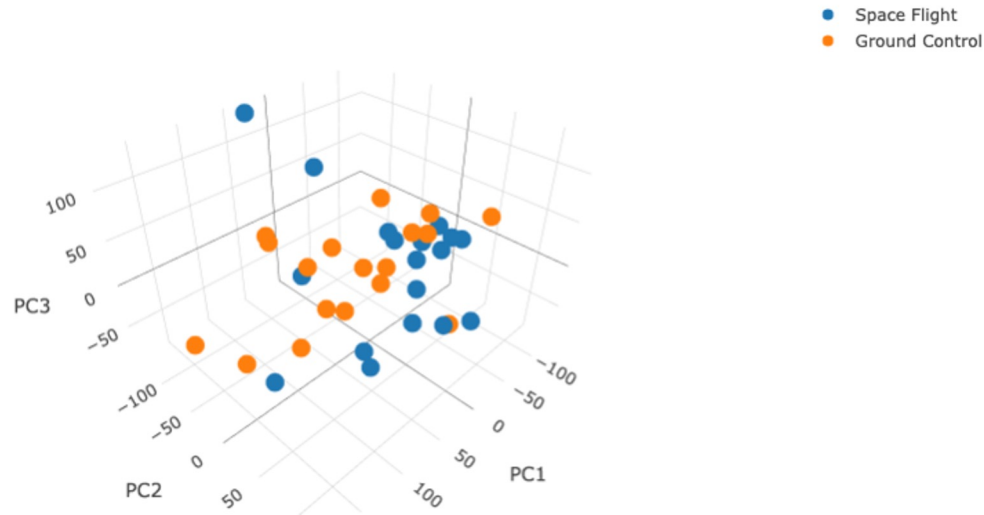


Data Portal

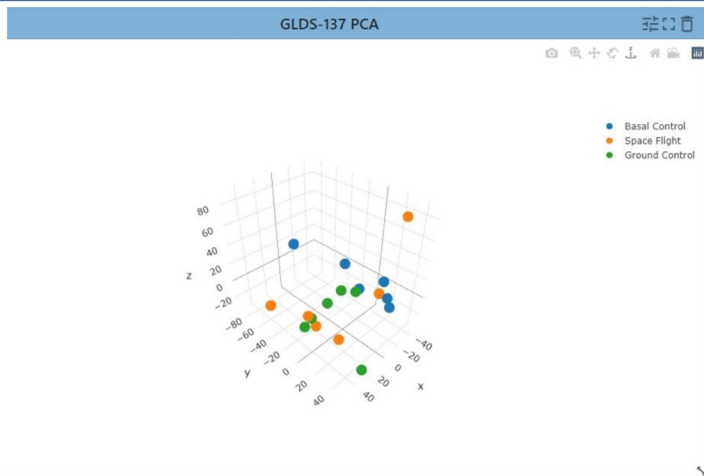
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Example from GLDS-120: Genetic dissection of the Arabidopsis spaceflight transcriptome: Are some responses dispensable for the physiological adaptation of plants to spaceflight?

<https://visualization.genelab.nasa.gov/data/GLDS-120>



GeneLab: Data Visualization Portal



GLDS-137 DGE

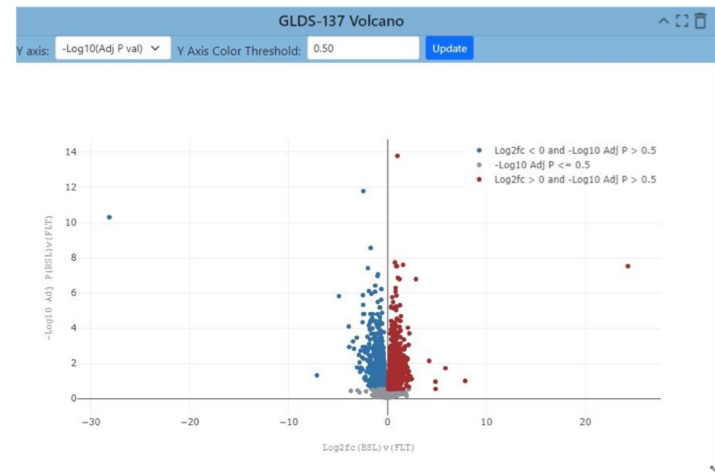
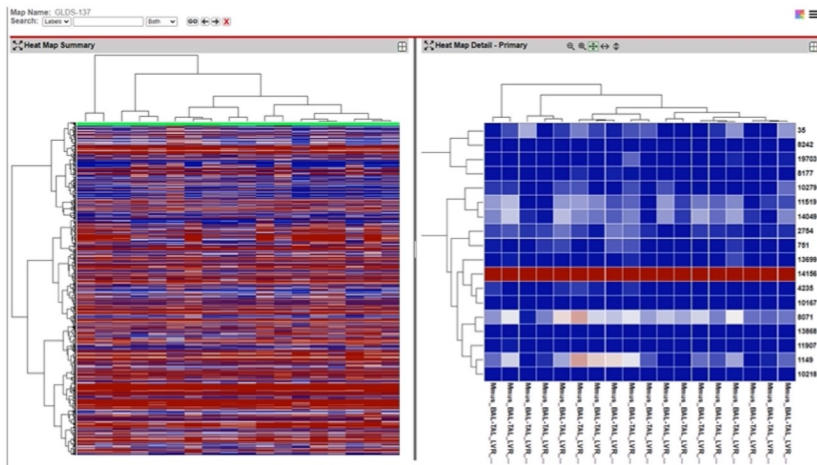
Maximum p-value:
Maximum adjusted p-value:
Search:

Copy CSV Excel PDF Print

ENSEMBL	Symbol	LOG2FC	PVAL	ADJP
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Pvalb	Pvalb	-6.29773327428316		
Actn3	Actn3	-5.97815189279096		
Casq1	Casq1	-3.95963363476749		
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Eef1a2	Eef1a2	-4.65720049798742		
Trnc2	Trnc2	-6.08619947458785		
Jph2	Jph2	-0.8961587251770401		
Trdn	Trdn	-3.2468444937389904		
Ddit4	Ddit4	-0.951185504460951		
Pgcm2	Pgcm2	-5.63776597708189		

Showing 1 to 10 of 22,228 entries

Previous **1** 2 3 4 5 ... 2,223 Next





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Tools

- User friendly submission portal to submit and publish data
- Analysis platform to tools and workflows to analyze your own data or data from the GeneLab repository.
- Tutorials and online resources to learn how to analyze RNA-Seq data
- Workspace to store, share, and organize data files



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<https://github.com/AstroBioMike/genelab-utils>

https://kristenpeach.github.io/GeneLab_Training/



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Sequencing

- State-of-the-art sequencing facility to process spaceflight samples
- Optimized SOPs with standard processing workflow
- Provide sequencing service for NASA funded PI without any university overhead
- Generate high quality data from shared tissues for open science access

https://github.com/nasa/GeneLab_Data_Processing



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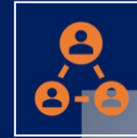
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Community

- Analysis Working Groups comprised of over 250+ scientists worldwide collaborating and analyze space omics data.
- Education Working Group focused on providing resources to educators and students to learn about space biology and bioinformatics

Reuse of data and enabling new discoveries

Re-use of Data and Enabling New Discoveries



46 | enabled publications (10 publications produced by the AWGs) using data available in GeneLab.

Mammalian and Invertebrate Models as Complementary Tools for Gaining Mechanistic Insight on Muscle Responses to Spaceflight

by Thomas Cahill ¹ Henry Cope ² Joseph J. Bass ³ Eliah G. Overbey ⁴ Rachel Gilbert ^{5,6} William Abraham da Silveira ^{1,7} Amber M. Paul ^{5,8,9} Tejaswini Mishra ¹⁰ Raúl Herranz ¹¹ Sigrid S. Reinsch ⁵ Sylvain V. Costes ⁵ Gary Hardiman ^{1,12} Nathaniel J. Szewczyk ^{3,13} and Candice G. T. Tahimic ^{5,14,*}

An Integrative Network Science and Artificial Intelligence Drug Repurposing Approach for Muscle Atrophy in Spaceflight Microgravity

Vidya Manian*, Jairo Orozco-Sandoval and Victor Diaz-Martinez

Article

Knowledge Network Embedding of Transcriptomic Data from Spaceflown Mice Uncovers Signs and Symptoms Associated with Terrestrial Diseases

Charlotte A. Nelson ¹ Ana Uriarte Acuna ^{2,3} Amber M. Paul ^{2,4} Ryan T. Scott ^{2,3} Atul J. Butte ^{5,6} Egile Cekanaviciute ² Sergio E. Baranzini ^{1,5,7,*} and Sylvain V. Costes ^{2,*}

Cell: The biology of spaceflight package

A coordinated package of 29 scientific papers published in five *Cell Press* journals featuring 9 papers utilizing data or resources in GeneLab. *High impact research highlights:*

- [Comparative Transcriptomics Identifies Neuronal and Metabolic Adaptations to Hyper gravity and Microgravity in *Caenorhabditis elegans*](#), *iScience*
- [Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact](#), *Cell*
- [NASA GeneLab RNA-seq consensus pipeline: standardized processing of short-read RNA-seq data](#), *iScience*



Computational and Structural Biotechnology
Journal

Volume 19, 2021, Pages 2223-2235



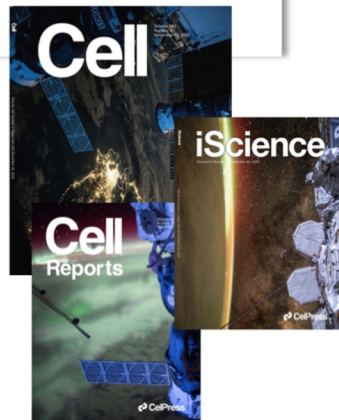
Reanalysis of the Mars500 experiment reveals common gut microbiome alterations in astronauts induced by long-duration confinement

N.J.B. Brereton ^{a,1} , F.E. Pitre ^{a,1} , E. Gonzalez ^{b,1}

Rad-Bio-App: a discovery environment for biologists to explore spaceflight-related radiation exposures

Richard Barker Sylvain V. Costes, Jack Miller, Samrawit G. Gebre, Jonathan Lombardino & Simon Gilroy

npj Microgravity 7, Article number: 15 (2021) | [Cite this article](#)



GeneLab Enabled Publications – 40+



genes



Article

Detection of Genes in *Arabidopsis thaliana* L. Responding to DNA Damage from Radiation and Other Stressors in Spaceflight

Vidya Manian ^{1,2,*}, Jairo Orozco-Sandoval ¹ and Victor Diaz-Martinez ¹



International Journal of
Molecular Sciences



Article

Mammalian and Invertebrate Models as Complementary Tools for Gaining Mechanistic Insight on Muscle Responses to Spaceflight

Thomas Cahill ¹, Henry Cope ², Joseph J. Bass ³, Eliah G. Overbey ⁴, Rachel Gilbert ^{5,6}, William Abraham da Silveira ^{1,7}, Amber M. Paul ^{5,8,9}, Tejaswini Mishra ¹⁰, Raúl Herranz ¹¹, Sigrid S. Reinsch ⁵, Sylvain V. Costes ⁵, Gary Hardiman ^{1,12}, Nathaniel J. Szewczyk ^{3,13} and Candice G. T. Tahimic ^{5,14,*}

iScience



Article

Comparative Transcriptomics Identifies Neuronal and Metabolic Adaptations to Hypergravity and Microgravity in *Caenorhabditis elegans*

Craig R.G. Willis, ¹ Nathaniel J. Szewczyk, ^{2,3} Sylvain V. Costes, ⁴ Ingrid A. Udranszky, ⁵ Sigrid S. Reinsch, ⁴ Timothy Etheridge, ^{1,7,*} and Catharine A. Conley ²

npj | Microgravity

www.nature.com/npjmgrav

ARTICLE OPEN

Comparison of *Bacillus subtilis* transcriptome profiles from two separate missions to the International Space Station

Michael D. Morrison ¹, Patricia Fajardo-Cavazos ¹ and Wayne L. Nicholson ¹

SCIENTIFIC
REPORTS

nature research

Corrected: Author Correction

OPEN

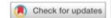
Multi-omics analysis of multiple missions to space reveal a theme of lipid dysregulation in mouse liver

Afshin Beheshti ^{1,8,*}, Kaushik Chakravarty ^{2,8}, Homer Fogle ¹, Hossein Fazelinia ¹, William A. da Silveira ⁴, Valery Boyko ¹, San-Huei Lai Polo ¹, Amanda M. Saravia-Butler ², Gary Hardiman ⁴, Deanne Taylor ⁶, Jonathan M. Galazka ⁷ & Sylvain V. Costes ^{7,*}

npj | Microgravity

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COMMENT OPEN



Rad-Bio-App: a discovery environment for biologists to explore spaceflight-related radiation exposures

Richard Barker ^{1,2}, Sylvain V. Costes ³, Jack Miller ^{3,4}, Samrawit G. Gebre ⁴, Jonathan Lombardino ⁵ and Simon Gilroy ^{1,2}

Cell



Article

Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact

William A. da Silveira, ^{1,23} Hossein Fazelinia, ^{2,23} Sara Brin Rosenthal, ^{3,23} Evagelia C. Laiakis, ^{4,23} Man S. Kim, ^{2,23}