Datu kuratoru atbalsts AIPP projektu īstenotājiem



Liene Muzikante

Augstākās izglītības un zinātnes IT koplietošanas pakalpojumu centrs (VPC)

04.11.2026

VPC
AUGSTĀKĀS IZGLĪTĪBAS UN ZINĀTNES IT KOPLIETOŠANAS PAKALPOJUMU CENTRS

Izglītības un zinātnes ministrija

Deleģēšanas līgums "Par pētniecības datu pārvaldības pakalpojumu nodrošināšanu un tehniskās infrastruktūras DataverseLV uzturēšanu 2026.–2028"

Projekta īstenošanas laika līnija



Projekta pieteikums



Plānošana



Projekta realizācija



Projekta noslēgums

Datu pārvaldības plāns (DPP)

Dokuments, kurā aprakstīts, kā tiks pārvaldīti pētījuma dati projekta laikā un pēc tā beigām.

- DPP apraksta, kā datus **iegūst**, **glabā**, **aizsargā** un ar kādiem nosacījumiem tos **kopīgo**.
- Plānā nosaka atbildīgos, nepieciešamos resursus un termiņus. To precizē, mainoties datiem vai projekta risinājumiem.

DPP ir praktisks darba dokuments visai projekta komandai.

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Ko ietver DPP?

Vispārīgais projekta apraksts

- Projekta nosaukums, mērķis, termiņi
- Finansētājs un projekta identifikators
- Iesaistītās institūcijas un atbildīgie

Aizpilda vienu reizi par projektu

Datu kopu apraksti

- Datu avoti, veidi, formāti un apjoms
- Datu organizēšana, kvalitāte, metadati
- Glabāšana, drošība un rezerves kopijas
- Ētika, personas dati un licences
- Kopīgošana, ilgtermiņa saglabāšana

Rīki DPP izveidei

DMPONLINE

dmponline.dcc.ac.uk

DSW

DATA STEWARDSHIP WIZARD

ds-wizard.org

argos

argos.openaire.eu

Kā izvēlēties DPP izveides rīku?

- Bezmaksas lietošanas iespējas
- Finansētājam atbilstošas veidnes
- Kopīga rediģēšana, komentāri un versijas
- DPP publicēšana un DOI piešķiršana
- Publiski DPP piemēri iedvesmai

- Pieejami LCS FARP veidne
- Argos pamācība latviski
- Datu kuratoru atbalsts
- Publicēti DPP iedvesmai



Argos mājaslapa

Preview of blueprint: Latvian Council of Science Blueprint

Main Info

Title of DMP

Description
Briefly describe the context and purpose of the DMP

Language
Select the language of your DMP

Contact

Researchers
Add here the names of people that have produced, processed, analysed the data described in the DMP.

Organizations
Add here the names of the organizations contributing to the creation and revision of the DMPs

Funding

Funding organizations
Select a funder of your research or add new

Grants
Find the grant of your research or add new

Project
Projects in Argos are perceived as distinct activities falling under a grant or common activities under different grants in collaborative schemas, eg open call for contributions. Please complete it for the grant associated to your organization if your project falls under this category. In all other cases, please leave blank and it will be autocompleted.

License

Access Rights
Choose how the DMP is displayed after is published on Zenodo. By choosing Open Access, the DMP will be open on Zenodo after the Publication Date. By choosing Restricted Access, the DMP will be restricted after the publication is made.

Publication Date
If Open Access is selected, please indicate the date that the DMP will be made available on Zenodo.

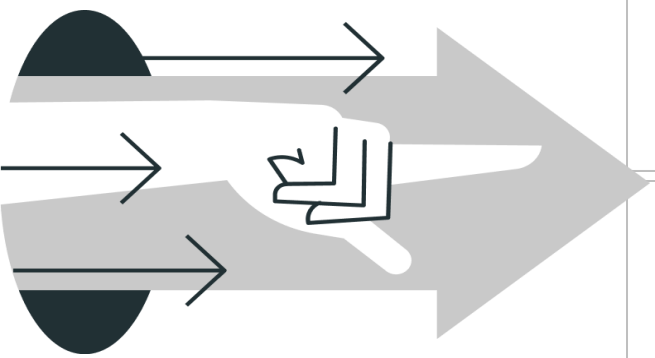
License
Assign a license to your DMP by selecting the most appropriate from the list.

Templates

Use the templates provided by the blueprint or select any of the available description templates.

LCS FARP

1. Data Summary
2. Research Data Management
3. Resources and Security



Genetic Tools for Feed-Efficient and Sustainable Meat Production in Latvian Sheep Breeds

Version 2

Description

1. Scientific Excellence

1.1. Background, hypothesis, aim.

Livestock production involves many global sustainability issues: animal health and welfare, greenhouse gas emissions, use of natural resources, food safety and public health, and production efficiency. Breeders can positively contribute to these challenges, by including them in their breeding programs (Food and Agriculture Organization of the United Nations (Fao)). Innovative strategies to improve sheep production efficiency can have a significant impact on the sustainability, resilience, and overall success of the livestock industry.

This proposal argues in support of the need for sustainable use of native animal genetic resources in sheep husbandry. In our study, we address genetic improvement related to production efficiency, particularly through the selection for breeding the most feed-efficient of animals in the Latvian native sheep breed. This project proposal addresses key challenges: maintaining genetic diversity, increasing environmental sustainability, and increasing product efficiency in the sheep industry.

1. Livestock production involves the use of natural resources such as water and feed and is associated with environmental emissions such as greenhouse gases and manure.

The challenge of feeding a growing population requires an increase in agricultural productivity by 70% by 2050 [1]. We are at a critical juncture where food systems must balance the need for sufficient, healthy, and affordable food with the need to preserve ecosystems essential to life [1]. Therefore, the use of natural resources for livestock production is one of the major aspects causing stress on the environment. To solve this problem, new technologies are needed to increase production while ensuring environmental sustainability. The goal is to produce food more economically and environmentally efficiently than current practices.

Feed costs are high due to poor grain-growing conditions in major grain-producing countries, the use of feed grains in ethanol production, and increased competition for land for crop production relative to urban development [2]. **Feed efficiency (FE)** in growing lambs (i.e. the animal's ability to reach a market or adult body weight (BW) with the least amount of feed intake), is a key factor in the sheep industry. Improving FE reduces production costs. Given that feed costs account for more than two-thirds of total meat production costs, reducing them can have huge profit margins for the manufacturer [3]. The results indicate that the selection of FE in sheep could reduce feed consumption without affecting the growth performance of sheep [4].

In addition to management methods that optimise productive efficiency, it is important to select more genetically efficient sheep. Efficient animals that require fewer natural resources, are more environmentally friendly and economically viable [5]. Thus, there is a need to develop innovative approaches for optimal use of existing genetic variations both between and within animal populations. Traditionally, meat breeding programs have focused on outputs, due mainly to the routine availability of phenotypic data on outputs or correlated traits.

Marker-assisted selection (MAS) offers a valuable tool for identifying desirable traits, including carcass composition characteristics. Assessing carcass characteristics can be challenging, as it often requires post-feeding measurements [6]. To overcome this challenge, MAS relies on established relationships between DNA regions and specific quantitative trait loci (QTL) within a breed [6]. The SheepQTLdb database (December 2023, https://bioregistry.io/registry/sheepqtldb) contains limited QTL information for sheep breeds, hindering its direct use in MAS. Nonetheless, assessing the variability of single nucleotide polymorphisms (SNPs) in local sheep breeds holds promise for selective breeding efforts [7]. Studies have identified the period from weaning to six months of age as critical for maximising lamb growth rates [8]. This phase presents an opportunity to identify animals suitable for breeding purposes or meat production. MAS can be strategically employed in two ways [9]. Firstly, it can assist in selecting crossbred offspring with desired genetic profiles and estimated breeding values (EBVs) for carcass quality traits, optimising crossbreeding outcomes. Second, analysing the genetic markers of

1. Main Info

Title of DMP: Genetic Tools for Feed-Efficient and Sustainable Meat Production in Latvian Sheep Breeds

Description:

1. Scientific Excellence

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Grants: Genetic Tools for Feed-Efficient and Sustainable Meat Production in Latvian Sheep Breeds (lzp-2024/1-0092)

Project: Genetic Tools for Feed-Efficient and Sustainable Meat Production in Latvian Sheep Breeds (lzp-2024/1-0092)

3. License

License: CC-BY-4.0

Access Rights: Public

Publication Date: 2025-03-01

4. Templates

Descriptions

5_Database of association analysis results of DNA loci or SNP genotyped in the SNP chip with feed efficiency indicators

Genome-wide sequencing methodologies (GWAS, Genome-wide association studies) are used to find specific QTL traits, related to productive characteristics in sheep genome. Genetic variations found in specific QTL regions in association with sheep productive tracts can be used as molecular markers for MAS (Marker-assisted selection) selection for sheep breeding.

MAS relies on established relationships between DNA regions and specific quantitative trait loci (QTL) within a breed. Marker-assisted selection offers a valuable tool for identifying desirable traits. Firstly, it can assist in selecting crossbred offspring with desired genetic profiles and estimated breeding values (EBVs) for carcass quality traits, optimising crossbreeding outcomes. Second, analysing the genetic markers of already-born lambs enables the prediction of their productive potential, aiding decisions about their inclusion in breeding programs.

Analyse the association between the value of the above phenotypic and FE-related characteristics and genetic variations. Develop a panel of molecular markers associated with the FE-related parameters.

Template: LCS FARP

Type: Dataset

1 Data Summary

1.1 Data Summary

1.1.1 What is the purpose of the data collection/generation?

By performing a statistical or association analysis between Feed efficiency parameters and the SNPs genotyped as a result of GWAS, data will be obtained for each of the Fe indicators. The results will include both information about a possible QTL region in the sheep genome and a statistically reliable association between a specific SNP and the Fe trait.

The database will collect SNPs or DNA loci for which an association has been established with a statistical reliability of P<0.05 and/or P<1x10-6.

The information contained in the database will be used for further studies: (1) to develop a manual genotyping method; (2) to validate the obtained association in DNA samples of intensively fattened lambs in 2020; (3) to develop know-how and provide recommendations for sheep farmers.

1.1.2 Type of data generated/collected

• Aggregate data

• Process produced data

• Other

Association analyze data

1.1.3 Format of data generated/collected

• XML

• PDF

• CSV

1.1.4 Expected size of the data - give expected size and choose unit of measurement

1

MB

1.1.5 Are you re-using this data set?

No

1.1.6 If No, please describe, if you have considered re-using any of existing data?

It is not possible to use previously created data, as WGS analysis of 54k SNP genotypes has not been performed on samples from the Latvian sheep population.

It is also not possible to use data from analyses of other breeds/populations, as scientific studies have shown that an association in one population/breed may not be repeated in another.

1.1.8 To whom the data might be useful ("data utility")? Other relevant remarks)

The resulting database and its processing results could be useful for molecular biologists and/or sheep farmers, more precisely sheep breeders, to (1) compare data with other breeds and (2) create a MAS tool for breed improvement.

2 Research Data Management

2.1 Metadata and documentation

2.1.1 Will data be attributed with standard identification mechanism (e.g. persistent and unique identifiers such as Digital Object Identifiers – DOI)?

Yes

DOI

2.1.2 Do you plan to provide metadata for your data?

Yes

2.1.3 Will you use any metadata standard?

No

2.1.4 Will search keywords be provided that optimize possibilities for re-use?

Yes

2.1.5 Will you follow any naming conventions for keywords?

No

2.1.6 Will you provide clear version numbers?

Yes

2.2 Making data openly accessible

2.2.1 What type of access the data generated/produced will have (choose one)?

open (anyone is able to access data without restrictions)

2.2.2 Will you apply embargo period to access for your data?

Yes

Comment:
The data will become open data after full data publication.

2.2.3 Will data, associated metadata, documentation and code be made accessible with means of a repository?

Yes

DataVersaLV

https://dataverse.lv/

2.2.4 What methods or software tools are needed to access the data?

R, Excel, notpad

2.2.5 Will documentation about the software needed to access the data included?

No

2.2.6 Is it possible to include the relevant software (e.g. in open source code)?

Yes

P3_Database of previously significant 57 SNP genotypes of DNA samples of sheep breeds and intensively fattened lambs created before the project.

LZP-2021/1-0489 project data on lamb samples of the year 2022, or the A22 group, and year 2023, or th A23, which consists of 76 + 92 intensively fattened lambs from eight breeds.

The database contains genotyping results for 57 SNPs, for which a statistically significant association with one of the feed efficiency indicators was established within the project, using NGS methodology and association statistical methods. The specific SNPs were selected for further work as the first DNA molecular markers for future sheep breeding programs in Latvia.

In the database, SNPs are coded with a laboratory code and an rs ID number. The gene in which the SNP is located is also indicated. The genotypes of each SNP are presented using standard IUB/IUPAC nucleic acid codes, representing the genotype of two alleles at a single locus with a single letter.

Template: LCS FARP

Type: Dataset

1 Data Summary

1.1 Data Summary

1.1.1 What is the purpose of the data collection/generation?

Genotypic characteristics of intensively fattened lambs are collected in a database so that association analysis can then be performed in relation to feed efficiency and other fattening characteristics.

1.1.2 Type of data generated/collected

• Observation data

• Process produced data

• Other

Molecular analysis data

1.1.3 Format of data generated/collected

XML

1.1.4 Expected size of the data - give expected size and choose unit of measurement

100

KB

1.1.5 Are you re-using this data set?

Yes

1.1.7 If Yes, please indicate what data set are you re-using?

Zenodo

https://zenodo.org/

id: https://doi.org/10.5281/zenodo.14224369, Type: doi

1.1.8 To whom the data might be useful ("data utility")? Other relevant remarks)

The resulting database and its processing results could be useful for molecular biologists for more analysis on other type of breeds in different populations.

2 Research Data Management

2.1 Metadata and documentation

2.1.1 Will data be attributed with standard identification mechanism (e.g. persistent and unique identifiers such as Digital Object Identifiers – DOI)?

Yes

DOI

cost-effective and rapid tool for genetic selection or management decisions. By improving native agricultural genetics without introducing external genetic material through crossbreeding, we aim to enhance the intrinsic qualities of these breeds.

The objective of this study is to determine if molecular markers were previously associated with FE-related characteristics in a training population of Latvian lambs when fed the same diet and can accurately predict these traits in L7 sheep breeds. Novelty: we set out to develop an effective method for determining markers of FE-related traits based on molecular markers obtained from the blood of live lambs.

In addition, we believe that through the identification and selection of specific molecular markers, this project will pave the way for more sustainable and efficient sheep farming practices in the Baltic region, as our goal is also to increase cooperation between the Baltic countries and attract new partners to promote comprehensive research into sheep farming practices in the region. By working collaboratively and sharing our findings, we can contribute to the advancement of sheep breeding and promote the conservation of local sheep breeds for future generations.

To achieve our aim, we will use our multidisciplinary expertise in molecular biology, genetics, agriculture, and biotechnology, as well as unrestricted access to samples of lambs in feeding trials—peripheral blood, phenotyping, and FE-related parameters.

Animals with predicted performance associated with the main economic pathways (Feed efficiency traits) can be used for further breeding, thus providing synergy between the two topics: LZP Nr. lzp-2021/1-0489, (2022-2024), related to our pilot study, and LZP Nr. lzp-2024/1-0092, current proposal.

Continued research in this area is critical due to the significant results already obtained and the potential for further development. The LZP project No. lzp-2021/1-0489 has yielded valuable insights into molecular markers related to mitochondrial biogenesis and associated with favourable FE-related parameters in Latvian sheep breeds. Expanding our research builds upon past successes, ensuring sustained impact on sheep farming practices. We aim to refine initial findings, providing reliable molecular markers for practical use. Addressing knowledge gaps in sheep genetics, our future research will enhance understanding and contribute to developing sustainable farming practices amidst evolving agricultural and environmental challenges.

Prasība DPP izstrādei VPP "Aizsardzības inovāciju pētījumu programma 2026-2029" projektu pieteikumos



Projekta pieteikums



Plānošana



Projekta realizācija



Projekta noslēgums

- Līguma **2.6.3. punktā** noteikts, ka projekta īstenotāji ne vēlāk kā **3 mēnešu laikā** no projekta īstenošanas uzsākšanas:
  - izveido **pētniecības datu pārvaldības plānu (DPP)**
  - **aizpilda NZDIS** informācijas sistēmā laukus:
    - kādā informācijas platformā ir izveidots un tiek uzturēts DPP,
    - DPP pieejas saiti,
    - Norāda vai ir plānota piekļuve pētniecības datiem.
  - DPP **var aktualizēt un pielāgot** projekta īstenošanas laikā, kā arī **1 mēnesi** pēc projekta īstenošanas noslēguma.

Projekta īstenošasnas laika līnija



Projekta pieteikums



Plānošana



Projekta realizācija



Projekta noslēgums

Datu:

- Ievākšana
- Apstrāde
- Organizēšana
- Glabāšana
- Uzturēšana

DataverseLV repozitorijs

Pieejamas Latvijas zinātnisko institūciju kolekcijas

Bez maksas visiem pētniekiem Latvijā

Hārvarda Universitātē izstrādāta programmatūra

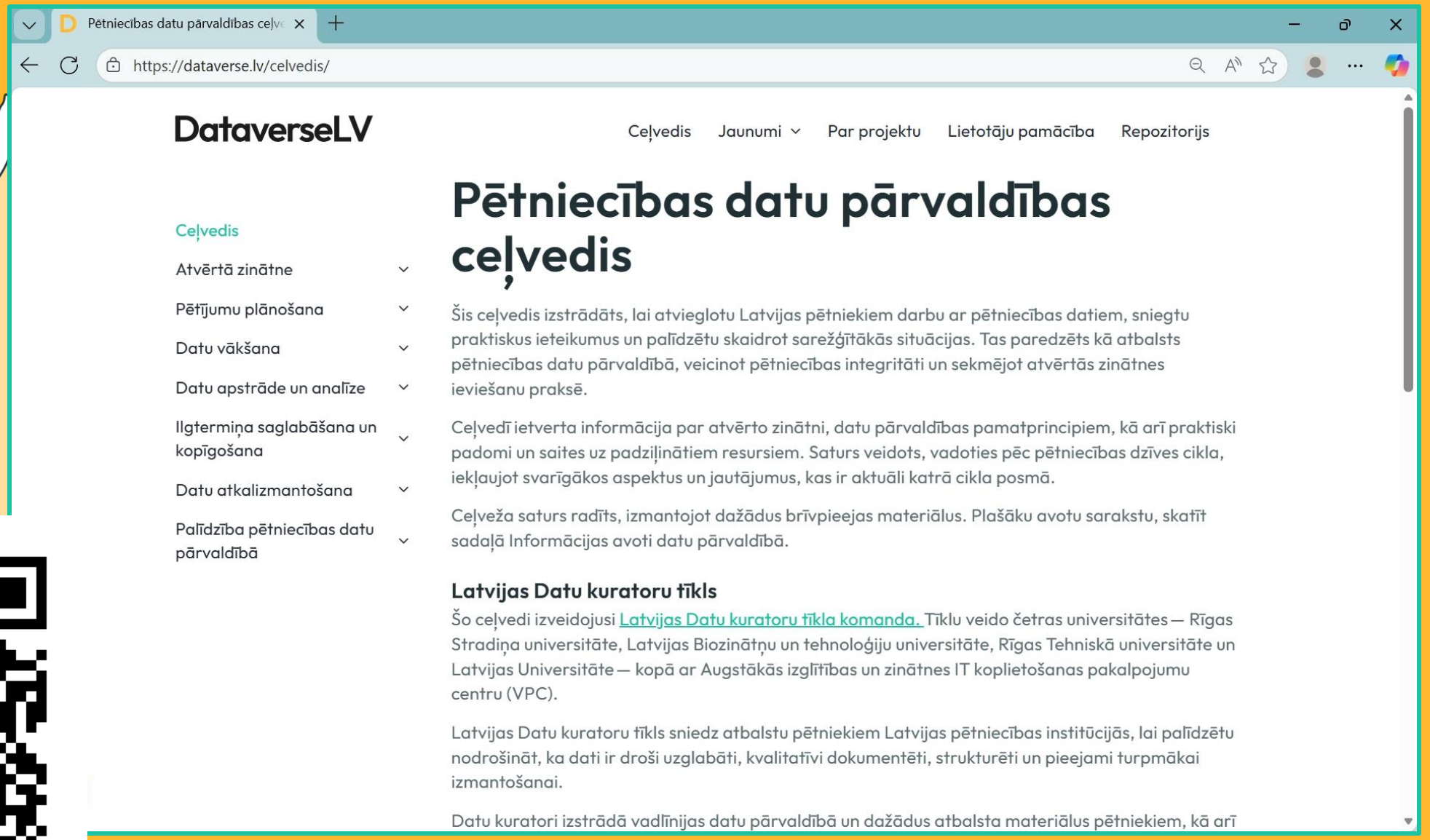
Datu kopām tiek piešķirts DOI

CoreTrustSeal sertificēts

Pieejams datu kuratoru atbalsts

dataverse.lv





dataverse.lv/celvedis

Datu kuratoru atbalsts

Datu kuratori sniedz konsultācijas pētniekiem:

- **DPP konsultācijas, atbalsts**

  (LZP, HORIZION u.c., Argos instrukcija)

- **Citi datu jautājumi**

  (licences, ētikas prasības, sensitīvie dati, IT rīki u.c.)

- **Datu kopu sagatavošana, aprakstīšana, ievietošana repozitorijos**

LATVIJAS UNIVERSITĀTE — datu.kuratori@lu.lv

RTU — datukuratori@rtu.lv

Latvijas Biozinātņu un tehnoloģiju universitāte — datukuratori@lbtu.lv

RSU — datukuratori@rsu.lv

VPC — datukuratori@vpc.lv

Paldies par uzmanību!



VPC
AUGSTĀKĀS IZGLĪTĪBAS UN ZINĀTNES IT KOPLIETOŠANAS PAKALPOJUMU CENTRS

Izglītības un zinātnes ministrija

Deleģēšanas līgums "Par pētniecības datu pārvaldības pakalpojumu nodrošināšanu un tehniskās infrastruktūras DataverseLV uzturēšanu 2026.–2028"