Minutes of the

The 21st STRENDA Meeting

September 8, 2025

Hotel Jagdschloss Niedewald
Rüdesheim, Germany

by
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based on the notes by
Hans V. Westerhoff and Carsten Kettner

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The 21st STRENDA meeting took place on Monday, September 8, 2025 from 9 am to 5 pm at the Hotel Jagdschloss Niederwald in Rüdesheim, Germany.
As some members could not travel, the meeting was hosted as a hybrid event allowing the remote members to participate and contribute to the discussions.

List of Participants

- Andreas Bommarius, Georgia Institute of Technology, Atlanta, USA (online)
- Pimchai Chaiyen, VISTEC, Rayong, Thailand
- Antje Jäde, Leibniz Institute – DSMZ, Braunschweig, Germany
- Julia Hauenstein, Leibniz Institute – DSMZ, Braunschweig, Germany
- Matthias Krull, Leibniz Institute – DSMZ, Braunschweig, Germany
- Andrew McDonald, Trinity College Dublin, Ireland
- Peter Halling, Strathclyde University, Glasgow, UK (online)
- Jürgen Pleiss, University of Stuttgart, Germany
- Frank M. Raushel, Texas A&M University, College Station, USA
- Johann M. Rohwer, University of Stellenbosch, South Africa
- Katrin Rosenthal, Constructor University, Bremen, Germany
- Santiago Schnell, Dartmouth College, Hanover, USA
- Hans V. Westerhoff, Universities of Amsterdam, The Netherlands
- Ulrike Wittig, Heidelberg Institute for Theoretical Studies, Germany
- Roland Wohlgemuth, Lodz University of Technology, Poland
- Carsten Kettner (co-ordination), Beilstein-Institut, Frankfurt, Germany

Unfortunately absent (with excuse) but eventually online attending

- Paul Fitzpatrick, University of Texas Health Science Center at San Antonio, TX, USA
- Frank Raushel,
- Robert Goldberg, Bethesda, ML, USA
- Thomas Leyh, The Albert Einstein College of Medicine, Bronx, NY, USA
- Barbara Bakker, University Medical Center Groningen, The Netherlands

Agenda

Tuesday, September 8

9:00	Welcome and Opening Self-introduction, warm-up, organizational topics, “house keeping” Carsten Kettner
9.30	STRENDA - Overview of Activities for new members Projects, general STRENDA Guidelines, STRENDA DB C. Kettner
10:30	Coffee break
11:00	What’s new? • BRENDA - Antje Jäde and colleagues • Task list from 2024 • Organization, STRENDA DB, RDMkit Carsten Kettner
12:30	Lunch
13:30	The Thermotables • Constructing the standard chemical and metabolic potentials • Debugging in Python and why this is important • Analysis of the Thermotable and manuscript • Recommendations of new thermodynamics and manuscript • Thermotable Excel file • The web-based interface to the thermostable Hans Westerhoff and Johann Rohwer
14.00	EnzymeML Carsten Kettner
14:30	Coffee break
15:00	Biocatalysis Guidelines Katrin Rosenthal
16:00	Tasklist and outlook for 2026
17:00	Close

	Additions
	Demanded by Andrew and accepted by the Commission: Stop of support of NCBJ in general and of the EC Commission in particular by IUBMB

STRENDA – news and activities

Withdrawals from the Commission

Professor Ming-Daw Tsai, Academia Sinica, Taipei, Taiwan, is going to retire and thus left the STRENDA Commission. He emphasized his great pleasure to work with the Commission and wishes the project good luck for the future.

New appointments

Professor Pimchai Chaiyen, VISTEC, Rayong, Thailand accepted the invitation to the join the STRENDA Commission. She introduced herself as being very much interested in comprehensive and proper reporting of enzyme and biocatalysis data and making these data publicly available. She did her PhD at the University of Michigan on pre-steady state kinetics of flavoenzymes. Now, at VISTEC, Pimchai is committed to both sides, the academic research and the application of biotechnological products in industry. VISTEC is a research institute located in a village environment which is sometimes faced with wild elephant warnings on the campus.

Dr. Antje Jäde, Leibniz Institute, DSMZ-German Collection of Microorganisms and Cell Cultures, Braunschweig, is the representative of BRENDA and accepted the invitation to become a member of the STRENDA Commission, too. With a PhD in pharmaceutical biology awarded at the University of Cologne, Antje is working for the BRENDA database since many years and is committed to both, the data quality by curation of literature data and the development of the service together with a team of software developers and co-workers. She introduced Mathias Krull as one of the developers and Dr. Julia Hauenstein as one of her team members.

The STRENDA Commission voted unanimously for both being appointed to the STRENDA Commission.

Overview

Carsten introduced the STRENDA project to the new members starting from the early beginnings in 2004 until now, presented the many members, the past and currents ones and described shortly the ongoing projects, i.e. the reporting guidelines for enzymology data (STRENDA Guidelines), STRENDA DB, STRENDA Biocatalysis reporting guidelines, guidelines for reporting thermodynamic data and the proposal of an advanced metabolic potential for biologically active compounds (Thermotables), and last but not least, EnzymeML, a project which is mainly driven by Jürgen Pleiss.

Die STRENDA Enzymology Guidelines are recommended by more than 60 biochemistry journals, STRENDA DB is recommended by more than 30 biochemistry journals. Carsten gave a short overview about the characteristics of STRENDA DB including the workflow, the amount of data that can be acquired, and the benefits for users. He also reported about the challenges which mainly refer to the data rate but also to the technical development and extensions which potentially opens STRENDA DB to a wider community.

STRENDA DB

One big challenge has been recently tackled when the persistency framework, Apache Cayenne, has been replaced by Hibernate. This framework is required for the object-relational mapping, the mapping of the database schema to Java classes and for the creation of SQL statements during runtime. The change to Hibernate extends the capabilities of this framework to the storage of objects along with attributes and methods, creates DataTransferObjects and provided the chance to increase the efficiency of the data handling which in turn accelerates query and display of data. The framework has been replaced and the tests will be finalized by end of October.

Andrew has worked on the extension of the methodologies and split the one text field into a number of dynamic and interactive fields that describe both the methodologies and techniques in a structured way. However, due to the change of the persistency framework Andrew could not continue his work as the techniques of this framework is beyond of his knowledge.

Discussion

Johann: What about future possible extensions such as the acquisition of time course data, equations, EnzymeML, etc.

Carsten: The good news is that there is budget for a developer, the problem is to find a developer as Udo is too busy with the Beilstein Publishing System and thereby has no time left for STRENDA DB. Johann will ask around at department.

Carsten: One aim would be to get more data from the biocatalysis community. In addition, the graphical user interface needs to be improved.

Ulrike asked whether there is a job offer. Carsten responded that there is no job offer but it is a project based job.

There is a rough project specification, but Carsten's user and programmer specifications need to be integrated in this project. It is not just programming but also thinking from the perspective of the user. Work can be done remotely. Possible linking with writingof Msc Thesis.

Roland: Would you want us to search persons?

Carsten: if someone in mind: person should know about (bio)chemistry not just an informatician / developer. Should also have some experience in database programming in Java or other developer frameworks. Involvement of a bioinformatics group to do this in connection with STRENDA.

Johann: Enzyme ML does not precisely map with STRENDA DB. Carsten: This is not necessary as a kind of a middle layer "converts" EnzymeML into STRNEDA DB. If the input data do not map with the database structure, the user will be alerted that additional input is needed.

Data links to Europe PMC

EuropePMC provides users with links from the abstract of the published paper to data stored in repositories and databases. The generation of this link requires the use of a specific metadata template to upload the connections of datasets and EuropePMC identifiers. This needs to be done manually as there is no API or any other automatic process available. An example, how this linking looks like, is a paper of Taylor et al. JACS, 2017, DOI:10.1021/jacs.7b04824, PMID: 28650156, PMC5629633. On EuropePMC scroll down the hit to "Data behind the article".

Almost all data sets in STRENDA DB are now linked with EuropePMC. The update of datasets is carried out twice per year.

Data links to PubMed

Similar to the process of linking datasets from STRENDA DB to EuropePMC, STRENDA DB datasets are now also linked with PubMed using a specific metadata template. The process is the same as for EuropePMC as due to the lack of a API the linking process has to be done manually.

Currently, 85 datasets from STRENDA DB are linked with PubMed. The update process is carried out twice per year.

What is new?

About BRENDA

Antje gave a report about the long history of BRENDA which is now no longer affiliated with the University of Braunschweig. It has moved to DSMZ (German collection of microorganisms and cell culture). It is always difficult to ensure continuity of databases. Hence the move was required and helpful. BRENDA has joined via the SonderTatBestand with Leibnitz institute. New now: DSMZ digital diversity hub combining many scientific data bases form many sciences together. Much more than just links. Each resource to develop knowledge graph. Knowledge graphs will be integrated. Idea is to have one level where one can query multiple databases at the same time. All resources will be at DSMZ. In the future also external resources will be integrated. DSMZ provides continuity. Evaluations every 7 years. Good news BRENDA now in a safe place

Discussion about the safety of databases:

Problems for continuity of SWIS PROT, e.g. NIH funding discontinued? Swiss government will support this. Ulrike is also to have curators for database updates. Roland is confident. Carsten: Pubchem also has this problem.

Ulrike example climate research databases. Important to have the data everywhere. Data should be physically at multiple places.

Metacyc stopped. Antje: Pathway maps initiatives; automatic generation of pathways. BRENDA pathway maps may be used to show how to use standardized data. Standardization of data reactions. Migration from university took a year.

Hans: connect BRENDA and STRENDA through knowledge graphs? Carsten begin with links. Priority is more with making STRENDA DB more attractive to user.

Expiration of EC Commission?

IUBMB wrote letter to members of IUBMB in NCBMB. Therefore there is actually not a formal international Enzyme commission in place. There are however still submissions. And Andrew has been taking care of putting this into ExplorEnz.

IUBMB/FEBS is restructuring this may solve it.

No funding left for Andrew therefore. Therefore impossible to put the link with STRENDA DB in place. Enzyme curation committee is not official anymore. Also no funding for maintaining it.

No support for the nomenclature committee anymore. IUBMB/FEBS did not renew their support of the NCBMB (NC for Nomenclature Committee). They do not use the EC system themselves.

Roland is surprised IUBMB does not put more support in the Enzyme nomenclature committee. Which host organization? Andrew: IUBMB has little money IUPAC is too bureaucratic.

Roland: IUPAC has nomenclature committee. Would that committee be interested? What annual budget would be needed? Andrew: 6 k€, 2 man weeks/year for maintenance.

Ulrike: are you involved with SIB in Switzerland. Would it be possible to get support from SIB?

Hans: It is an activity of the STRENDA commission to try to ensure continuity of important databases. Proclaim (STRENDA commission) us as a commission that we take it upon us to try to maintain important existing databases by trying to find funding. Roland also the biotech are is worried. Let us think of more options to continue the work of the EC. Hans would take it more general.

Carsten: write together with SABI, STRENDA a letter to IUBMB asking for support

Andrew: writing a letter to Beilstein for support of Explorenz.

Or to have combined support of Explorenz from IUBMB and Beilstein. Andrew: there are 6 members of the EC nomenclature commission.

100 new enzymes a year. Example protein kinases.

Pimchai: supports making envelopes of databases for support.

What about a publication? Carsten: better to write letters defining the support needed and for what? Teaming up with organizations like BRENDA, STRENDA and SABIORK might help.

Antje: Make ExplorEnz an ELIXIR supported resource. Ulrike: Become a node of ELIXIR Ireland and then apply for ELIXIR support. Ulrike can help to do this.

Ask researchers how important these data bases are for you. Roland: ESAB may devote a monthly webinar topic to this. Carsten: combine letter (above) with questionnaire to users. Katrin funders like to see the users expressing needs.

Carsten asks Andrew whether we can help. For instance with the questionnaire. With letters of support. Also letter asking for Beilstein support. Part of the action plan of STRENDA.

Pimchai: EC numbers are used in discussion pathways in bioengineering. Writing to ESAB. IUBMB.

ACTION PLAN

- Andrew is task leader. EC numbers; ExplorEnz support; write letters to ask organizations like IUBMB to support the activities themselves or express need for support.
- Write to IUBMB to ask them whether they would allow STRENDA to then help manage the EC committee / nomenclature committee. The committee may wish to be explicit also to be interested in protein kinases and other enzymes working on proteins rather than metabolites (also MAPkinases)

Organization of the STRENDA Commission in working groups

The organization into working groups as negotiated at the previous STRENDA meeting has been approved.

The following suggestions have been made for an update of the organizational structure:

- Roland proposes subgroup for EC Commission. The new work group around Andrew. Support ExplorEnz and EC. Antje, Roland, Ulrike and Carsten with Andrew as lead.
- Pimchai as member of biocatalysis guidelines.

- Enzyme networks put Katrin's name down as member.
- Santiago and Ulrike: will help with STRENDA guidelines.
- Ulrike is already member of Enzyme ML.

The new structure is as following:

Working groups	Aims	Lead	Members
STRENDA Guidelines	Revision of guidelines	CK	UW, SS
STRENDA DB	Feature requests, specifications, test	CK	FR, JR
Biocatalysis Guidelines	Revision of guidelines	DR, KR	CK, PH, RW, JP, AB
EnzymeML	Use case definitions, extensions	JP	CK, KR, DR, AB, JR, SS
Thermodynamics	Finalization concepts and publications	HW	CK, JR, RW, PH
Enzyme networks	Cascades, synthetic pathways	HW	RW, JR
Outreach	Creation of materials, collaborations, networking e.g. RDMkit, flyers, slide, Online course, online training materials,	UW	CK
EC Commission	Continuation of EC Commission, Support of EC Commission and ExplorEnz	AM	RW, AJ, UW, CK

STRENDA DB Status

As of August 25, there are now 115 datasets published in STRENDA DB with 31 additional datasets in the pipeline awaiting to be published. This depends on the publication of the data in a peer-reviewed journal and the notification of Carsten by the authors. Carsten checks all datasets on a regular basis and contacts the users on the status of their datasets and offers help with regards to the finalization of any other step which may stop the finalization of the input.

The user manual is updated to the current STRENDA DB version 1.3.3.

As previously mentioned, the persistency framework has been updated to Hibernate. Before the deployment on version 1.4, the system has to be tested which will be terminated by the end of October.

Discussion

Hans: Create open field for users to insert their kinetic model? Carsten no: too much additional work; he is supported by Johann. Ulrike: the SABIO-RK team is working on an editor to write equations. But this is done by a company. Johann: the idea is that the user has to put in his mechanism if its is not predefined. A subset of users should be able to put in their kinetic equations. Pimchay refers to facility in pre-steady state kinetics that enables this.

Carsten likes the idea of providing a number of pre-defined kinetic equations. Like Copasi. However, he emphasized that he is not a fan of free text fields.

Data links from UniProtKB

Since the beginning of this year UniProtKB links to datasets published in STRENDA DB. The interconnection is carried out by uploading a specific metadata template to UniProtKB. Currently, 75 data sets are now linked with UniProtKB. The upload is planned to be done twice per year.

Data availability statement

More and more datasets which are published in peer-reviewed journals are in STRENDA DB deposited and published. With this, the journals require the authors to provide a data availability statement to ensure that (a) data are deposited and (b) the data can be accessed by the interested community. The STRENDA Commission believes that a template may help the authors to correctly provide all relevant information in the statement. Thus, Carsten made the following proposal:

“The enzymology data in this study have been deposited in Standards for Reporting Enzymology Data (STRENDA) database (https://www.beilstein-strenda-db.org/strenda/) with the following identifier: DOI nnn”

The datasets may appear in the list of references such as

> [x] <authors’ name(s)>, <described enzyme activity or protein name> STRENDA: Standards for Reporting Enzymology Data database. (https://www.beilstein-strenda-db.org/strenda/). Deposited <date of deposition>. <DOI of dataset>.

The wording of the reference entry, however, depends on the policy of the journal.

This proposal has been approved by the Commission.

ACTION PLAN

- Carsten reaches out to the journals and provide them with the template.

RDMkit

Suggested by Ulrike at the previous STRENDA Meeting, we have created a new domain "Enzymology" on RDMkit pages. RDM stands for Research Data Management and provides information on guidelines, initiative, tools, software, data exchange formats as well as databases and repositories for all those who are interested in data deposition and sharing.

Thanks to Ulrike, Jürgen, Hans, Johann and Carsten, the article entitled "Enzymology and biocatalysis" is now accessible at https://rdmkit.elixir-europe.org/enzymology_and_biocatalysis.

Discussion

Ulrike: The focus is on providing guidelines of data management to those who are commited with including librarians (data stewards) but also researchers who are seeking for info. Articles on RDMkit can be modified at any time. There is a GitHub page where one can add content to the individual pages. The RDMkit is well accepted in theuser community (esp ELIXIR). It is recommended by European Commission (for proposal submitters). An editorial board is supervising the content.

Tool assembly: different tools working together in DM process. Perhaps put Enzyme ML here as one of the cases?

Thermodynamics not here. Does it need to be added?

Thermotables

Hans presents the history of the project within STRENDA DB. He shows that the aims have largely been attained:

- paper for *FEBS J* for generating interest (Peter, Hans) and for having the bulleted list as part thereof.

- a Thermodynamic Table with corresponding standard metabolic energies (finished in excel form. Manuscript plus Table to be submitted to the *Beilstein Journal of Organic Chemistry*.

He also showed a number of scientific results that have come form inspecting the Table. One example was showing cases where the group contribution was not quite right compared to the experimental method represented by the new Table. Hans considers that it is better to have the paper with the Thermotable out before the recommendations are published.

The working group for this work is Hans, Peter, Johann, Carsten

Johann then presented a tool based on Python and running in Google that enables getting the data out of the excel sheet.

EnzymeML – Status, progresses and perspectives

Carsten replaced Jürgen and introduced into the status, progresses and perspectives of EnzymeML.

The EnzymeML platform provides

- a data model that helps to organize the domain-specific data and which can be implemented as a schema (xsd, JSON schema) or as software library such as Python or Rust,
- structure of data into this schema (here: tables)
- tools for easy definition and extension of the data model (using Markdown) which can be converted into a data model in e.g. Python,
- standardized data exchange formats such as EnzymeML, ThermoML, etc.,
- tools for data acquisition, analysis and storage
- a modular workflow implemented in Jupyter Notebook,

With this platform, now, AI could be put into place, and there are many ways where AI, in particular LLMs, can support the processes such as

- generating a data model from text,

- extraction of reaction conditions from text and measured data from csv which support data acquisition,
- visualization and analysis by machine learning that apply neural ODE, neural operators and transformers,
- storage in graph database, knowledge graphs and also for querying databases and repositories

The latest development is the EnzymeML Suite, i.e. a desktop application to handle EnzymeML data such as

- document creation and editing,
- local database of documents,
- visualization of measurements and simulations
- mathematical modeling

EnzymeML integrates web-based databases such as PubChem, UniProt, RheaDB and performs cross-database queries within the Suite and imports the hit results into an EnzymeML document. The Suite allows kinetic modelling by assigning a kinetic law using the kinetic law library from SBO. The parameter estimation applies algorithms for local and global optimization with the results automatically transferred into a new EnzymeML document.

The EnzymeML project would not be possible without quiet a number of partner all around the world; those who are contributing with data from real experiments to propose extensions of EnzymeML, those who are contributing with experiences from own modelling projects, those who are running and maintaining databases and repositories and, finally, those who take bring in expertise from the acquisition of data in electronic lab notebooks.

All information on EnzymeML can be accessed via https://enzymeml.org and https://github.com/EnzymeML

Future extensions comprise

Bioinformatics platform for analyzing sequence-function relationships of protein families

- PyEED: *https://github.com/pyeed* (knowledge graphs, embedding by PLM)

Analytics: read in and analyze chromatographic data (HPLC, GC), IR/Raman, and time-resolved NMR spectra

- ChromHandler: *https://github.com/FAIRChemistry/ChromHandler*
- CaliPytion: *https://github.com/FAIRChemistry/CaliPytion*
- NMRPy (Johann Rohwer, Stellenbosch): *https://github.com/NMRPy*
- FAIR VibSpec: *https://github.com/FAIRChemistry/FAIRVibSpec*

Extend toward biocatalysis

- STRENDA Biocatalysis Guidelines: *https://github.com/Strenda-biocatalysis/*
- FAIR Fluids: *https://github.com/FAIRChemistry/Fairfluids* (thermophysical properties of solvent systems)
- Flow chemistry: *https://github.com/FAIRChemistry/FAIRFlow* (P&ID)

Make chemical synthesis AI-ready

- FAIR Synthesis: materials, organic synthesis

Discussion

Question. Use Enzyme ML suite to help submitters to STRENDA DB. Automatic upload from Enzyme ML to STRENDA DB. Johann: the data models do not match 1/1. EnzymeML tool of including measurement data. STRENDA DB requires more information on the methods. Upload of Enzyme ML data into STRENDA DB is on the top of Carsten's list.

Biocatalysis Reporting Guidelines

Katrin reported about the progress of the STRENDA Biocatalysis Guidelines for Cataloging Metadata. The corresponding paper has been published in *Nature Catalysis* (DOI:10.1038/s41929-024-01261-x.).

This contains a catalogue for what might be needed in an experiment in Biocatalysis. Much of this is already in the original STRENDA guidelines. Other parameters are new and part of a new catalogue. The aim is to increase the reproducibility of biocatalysis data and to enhance the communication between users.

The goal also was to define the most essential meta data, in the best way to create a minimum information reporting guideline with seven metadata categories, i.e.

biocatalyst - information required to unambiguously identify the catalyst, its formulation and storage.

- Components – description of the compounds in the assay
- operation mode – batch, fed-batch, continuous
- vessels and mixing - information about the vessel or reaction container
- reaction conditions – description of the environment in which the reaction takes place, such as aqueous reaction solutions, organic solvents, micro-aqueous reaction solutions, gassed reaction solutions and many more. In addition, the conditions can take place either in monoliquid or in multiphasic systems.
- Sampling – description of the capture and documentation of either standard sampling information and/or specialised sampling data
- results – description of the experimental results and documentation of the way of modelling and analysis.

The catalogue is available on the Github system.

//github.com/Strenda-biocatalysis

//w3id.org/strenda/biocatalysis-guideins

Discussion

The guidelines are more than just a guideline. The metadata catalogue aims at serving the basis for modelling. The guidelines have already been tested in a few already existing

publications. When using LLMs for data extraction according to the guidelines revealed that the more complex the experiment is the more explicit the guidelines have to be to avoid mistakes or misunderstandings. The community responded in multiple ways: there were voices for whom the guidelines were not comprehensive enough but others found them too complex. The common question was about the existence of a database (which does not exist yet). How do these guidelines connect to the STRENDA enzymology guidelines? Kathrin: They are not connected because biocatalysis guidelines already are too complex. But the enzymology guidelines are the basis for the biocatalysis guidelines. Carsten: Indeed, it is important to keep the balance between completeness and simplicity. For the enzymology guidelines some aspects are not relevant such as immobilization etc, therefore it is preferred to have individual, but linked guidelines.

Task list and Outlook for 2026

The updated tasklist can be found here:
https://docs.google.com/spreadsheets/d/1WqvlsqhQIy6UyqI5wWjLkB2yOk-IgPYIK14jktTLjsg/edit?usp=sharing

Task	Description	Priority	Responsible	Status	Started	Result	Result (file)	Coworkers
	and sort out the technical requirements							
Thermodynamics project	formulating and publishing recommendations / reporting guidelines on standard metabolic potentials	P1	Hans V. West...	In work	01.09.2022	The bullet list has been finished; has been formatted into manuscript for FEBS J. and presubmitted to FEBS J	Datei	together with Keith Tipton (UCD
Organization	table with projects, subgroups, leads and members	P1	Carsten Kettn...	Finalized	02.12.2024	presented at 21st STRENDA meeting (2025) and being extended by additional members	Datei	Coworkers
Organization	inform other members about these subgroups and ask if and which subgroup they want to join	P1	Carsten Kettn...	Finalized	14.08.2025	Group members requested for comments	Datei	Coworkers
EQUATOR Network	contact network to sort out potential collaborations	P1	Carsten Kettn...	In work	29.08.2025	Prof. Collins, Uni Oxford contacted	Datei	Coworkers
Outreach - Slide	present the three versions of the slide to the other STRENDees and ask for comments	P1	Carsten Kettn...	Not yet sta...	dd.mm.yyyy		Datei	Coworkers
Outreach - Slide	add QR code and STRENDA logo to slide	P1	p.j.halling@strath.a	Not yet sta...	dd.mm.yyyy		Datei	Coworkers
Outreach - Landscape	draft of a landscape based on the list created at the meeting	P1	Carsten Kettn...	Not yet sta...	dd.mm.yyyy		Datei	Coworkers
Collaboration w/w UniProt	establish linking from/to STRENDA and UniProtKB	P1	Carsten Kettn...	Finalized	03.03.2025	procedure for the cross-referencing with UniProtKB established	Datei	Coworkers
RDMkit	review, finalization and publication of the new domain "Enzymology"	P1	ulrike.wittig ulrike.)	Finalized	13.05.2025	https://rdmkit.elixir-europe.org/enzymology	Datei	Coworkers
ExplorEnz / EC Commission	support of database, revive EC Commission	P1	Andrew McDonald	In work	dd.mm.yyyy		Datei	Roland, Antje, Ulrike, Carsten
FAIRSharing Enzymology Collection	combine databases, standards etc. on FAIRSharing.org		Carsten Kettn...	Not yet sta...	dd.mm.yyyy		Datei	Coworkers
STRENDA DB Extension	specifications for extensions	P1	Carsten Kettn...	In work	04.11.2025		Datei	Hans, Johann for kinetics results
STRENDA DB Extension	Im/export EnzymeML	P1	Carsten Kettn...	In work	04.11.2025	first discussion F Mautz (IPB Halle) and JP, indication of interest, next step (CK): matching table STRENDA DB / EnzymeML	Datei	Jürgen, Fabian Mautz
STRENDA DB Extension	find and contact developer		Name	Not yet sta...	dd.mm.yyyy		Datei	Coworkers
Data availability statement	reach out to journals with suggestion/template	P1	Carsten Kettn...	Not yet sta...	dd.mm.yyyy		Datei	Coworkers

The next STRENDA meeting will take place in September 2026. The dates and place will be sorted out soon.