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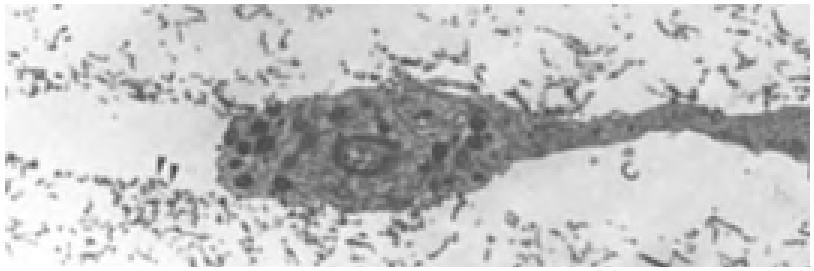


A fibroblast within a tethered lattice, after 13 days, with a cavity surrounding the cell and areas of packed collagen fibrils *(Porter et al. 1998 Wound Rep. Reg. 6: 157-166)*

ISMB NEWSLETTER 52 - April 2026 - Editors: Zoi Piperigkou and Raphael Reuten

NEW EDITORS, SAME MISSION

Dear ISMB Members,

We are delighted to introduce ourselves as the new Editors of the ISMB Newsletter for 2026. It is both an honor and a pleasure to take on this role and contribute to a newsletter that plays such an important part in connecting and informing our society. As we begin this new chapter, we would like to express our sincere gratitude to Prof. Sylvie Ricard-Blum for her outstanding dedication, vision, and hard work during her 9-year term as the Editor of the ISMB Newsletter. Her efforts have shaped the ISMB Newsletter into the engaging and high-quality platform it is today, and we are truly grateful for the strong foundation she leaves behind. We look forward to building on her legacy and bringing fresh perspectives while continuing to serve and inform the ISMB community.

Zoi Piperigkou and Raphael Reuten
Editors of the ISMB Newsletter

FROM THE PRESIDENT'S DESK

Dear ISMB members, friends, and colleagues,

As the new year settles in, we find ourselves surrounded by exciting developments in the ECM field—despite a broader news landscape that is not always as encouraging. We bade farewell to the past year with a spectacular ASMB Biennial Meeting in Baltimore, and the year ahead is already shaping up beautifully, with the GRC Proteoglycans meeting, the FEBS Advanced Lecture Course "Extracellular Matrix in Health and Disease", and—dearest to my heart—Matrix Biology Europe 2026, which will take place under the midnight sun in my hometown of Oulu, Finland.
We also celebrate important changes within the structure of ISMB itself. Our beloved Prof. Sylvie Ricard-Blum steps down from her role as Newsletter Editor, passing the torch to Dr. Raphael Reuten and Dr. Zoi Piperigkou. For the first time, an Early Career Researcher joins the editorial leadership—an important and symbolic step forward. We would like to express our sincere gratitude to Sylvie Ricard-Blum (France) and Gertraud Orend (France), for their dedicated service over the past years. Their commitment, thoughtful contributions, and sustained efforts have been invaluable to the work and development of the Society.

At the same time, we warmly welcome three new council members from Eastern Asia, expanding the reach of our society to include China, Korea, and Taiwan. We are delighted to welcome Luyang Yu (China), Louise Tzung-Harn Hsieh (Taiwan), and Hyeonwoo Kim (South Korea) to the Council and very much look forward to their insights, expertise, and active engagement in shaping the future activities of our vibrant matrix biology community.

All of these developments are clear signs of how lively, inclusive, and forward-looking our community has become. That vitality is perhaps most evident in the steady stream of inspiring ECM research we encounter week after week—across journals, conferences, preprints, and lively scientific discussions. New concepts, technologies, and interdisciplinary bridges continue to reshape how we think about the matrix, its functions, and its roles in health and disease. Just as importantly, this energy is driven by a diverse and growing community: early-career researchers bringing fresh perspectives, established scientists pushing conceptual boundaries, and a truly global network of collaborators strengthening the field as a whole.

I very much look forward to meeting many of you at the upcoming ECM gatherings. I'll very likely be there wanting to hear all about your new findings!

Warm regards,

Valerio Izzi, President (Valerio.Izzi@oulu.fi)

Contents

News from National Societies & ECM Networks

Breaking News from British Society for Matrix Biology

The British Society for Matrix Biology (BSMB) Newsletter (Issue No. 108, January 2026) highlights key developments, opportunities, and community updates within the matrix biology field. The Society introduces new initiatives to support early career researchers (ECRs), including a Tenure-Track ECR Presenter Bursary and a forthcoming "ECR Achievements" section to showcase member successes. The newsletter outlines upcoming scientific events, notably the BSMB Spring Meeting 2026 in Manchester and the Matrix Biology Europe (MBE) 2026 conference in Oulu, alongside details of multiple bursaries and travel awards aimed at supporting researcher participation. It also celebrates excellence in the field, including the 2026 BSMB Medal Award to Professor Joanne Murphy-Ullrich, and announces calls for nominations for the Dick Heinegård Young Investigator Award. Additional content includes updates on new committee members, recent research initiatives such as a special issue on extracellular matrix biology across Cell Press journals, and summaries of recent scientific meetings. The issue also welcomes new members and provides insights into the Society's governance and activities. Finally, the newsletter pays tribute to influential figures in matrix biology, including Professor Allen J. Bailey, recognizing his lasting contributions to connective tissue research and the scientific community.

Breaking News from Danish Society for Matrix Biology

Welcoming the new Chairwoman of the Danish Society for Matrix Biology

The Danish Society for Matrix Biology (DSMB) is entering an exciting new chapter. After six rewarding years of dedicated leadership, Christine Chuang has passed the baton to Andrea Heinz, Associate Professor at the LEO Foundation Center for Cutaneous Drug Delivery, University of Copenhagen.

Andrea's research explores the structure and function of extracellular matrix proteins in the skin and cardiovascular system, with a particular focus on elastin and collagen and how these complex networks change in health, aging, and disease. Her group also develops innovative enzyme-responsive drug delivery systems and protein-based biomaterials to support the treatment of inflammatory skin diseases characterised by extensive extracellular matrix remodelling.
With more than 15 years dedicated to understanding the biology and structural organisation of elastic fibres, Andrea brings deep expertise and enthusiasm for matrix biology. We warmly welcome her as Chairwoman and look forward to seeing DSMB continue to grow, connect researchers, and strengthen the matrix biology community in Denmark and beyond under her leadership.
Andrea will also host the European Elastin Meeting 2026 in Copenhagen (18–21 August 2026), an exciting gathering for the elastin and extracellular matrix research community, which will be preceded by a half-day DSMB annual meeting.

Breaking news from the Hellenic Matrix Biology Section

Hellenic Society of Biochemistry and Molecular Biology

The Hellenic Matrix Biology Section (HMBS), established in 1997 within the Hellenic Society of Biochemistry and Molecular Biology (HSBMB), continues to play a dynamic and expanding role in advancing extracellular matrix (ECM) research in Greece and beyond. Actively engaged with Matrix Biology Europe (MBE) and affiliated with the International Society for Matrix Biology (ISMB), HMBS fosters interdisciplinary collaboration across Biochemistry, Molecular and Cell biology, Medicine, and Biotechnology. Under the coordination of Prof. Nikos Karamanos since 2014, the HMBS has strengthened its international presence by promoting networking, supporting young scientists, and contributing to the development of collaborative research initiatives and training opportunities.

At the forefront of scientific progress, HMBS highlights the pivotal role of the Extracellular Matrix as a dynamic three-dimensional (3D) network that not only provides structural support but also regulates key cellular processes, including adhesion, migration, proliferation, and differentiation. Current research efforts focus on elucidating ECM composition and organization, uncovering structure-function relationships, and defining its regulatory involvement in health and disease. Notably, emerging advances in 3D cell culture systems that closely mimic *in vivo* conditions are transforming disease modelling and translational research, offering new perspectives for diagnostics and therapeutics. Through these activities, HMBS continues to actively contribute to the global matrix biology community and to the dissemination of cutting-edge knowledge in the field.

For more information check out: https://eebmb.gr

Breaking News from Matrix Biology Italy

On January 21, 2026, the new association “Matrix Biology Italy” (MBIta) was officially founded. The founding members, Passi A., Viola M., Forlino A., Besio R., Rossi A., Mongiat M., Gagliano N., Franchi M., Brun P., Masola V., and Onisto M., met in Padua in the presence of a notary. The association's purpose is to promote the advancement of scientific knowledge having to do with the ECM and related topics, to disseminate this knowledge, and to promote studies and research on the ECM and related areas of study.
MBIta association is the natural heir and offshoot of the former Italian Society of Connective Tissue (SISC), which was officially founded in February 1982 in Pavia, in the Aula Magna of the Institute of Zoology. Already in September of the same year, the first scientific meeting of the Society took place in Florence, during which the first Executive Committee was elected (President: Alessandro Castellani, Vice President: Lorenzo Gotte, Secretary: Alberto Calatroni, Treasurer: Giuseppe Cetta, Council Members: Alessandro Ruggeri, Ivonne Pasquali Ronchetti, Cesare Balduini, Ranieri Cancedda, and Vincenzo Chiarugi) and the nomination of Prof. John E. Scott as Honorary Member was unanimously approved.
The first years of the SISC were characterized by the efforts of two fundamental and charismatic figures—namely, Prof. Castellani, founder of the School of Biochemistry of Pavia and leading expert in the biochemistry of the extracellular matrix, and Prof. Gotte, one of the fathers of Italian histology and internationally renowned for his studies on elastin. After their premature deaths (Prof. Castellani in 1988 and Prof. Gotte in 1991), the presidencies of Professors Ruggeri (1991-1997), Calatroni (1998-2004), Pucci Minafra (2005-2010), Rossi (2011-2016), Passi (2017-2022), and Onisto (2023 to date) followed. From its beginning, the SISC organized a scientific meeting every year in various Italian locales to which some of the leading international experts on ECM were invited. Furthermore, in 2004, it applied for and was eventually awarded the privilege of organizing the 19th FECTS Congress in Taormina (9-13 July). Finally, in 2022, the SISC organized the European Matrix Biology Europe 2022 in Florence (28-30 September) at which more than 200 scientists from all over Europe, the U.S.A., Brazil, Canada and Japan successfully participated. The last SISC-MBIta meeting took place from October 2 to 4,2025 in Canizzaro Hall at the University of Messina. It was made up of two intense days of high-level scientific communications, thanks both to the presence of invited speakers Professors N. Karamanos and A. Theocharis (University of Patras) and to the contributions of the many young people present and senior researchers from our association.
MBIta is a member of Matrix Biology Europe (MBE) and also a member of the International Society for Matrix Biology (ISMB).

More information can be found here: www.matrixbiology.it

The founding members (from left to right: Passi A., Viola M., Gagliano N., Franchi M., Mongiat M., Besio R., Masola V., Brun P., Forlino A., Rossi A., and Onisto M.) gathered in Padua for the foundation of MBIta.

Breaking News from The Meshwork

At **The Meshwork**, have put together an open repository of laboratories engaged in extracellular matrix (ECM) research. The aim is to create a go-to resource for our community – making it easier to connect for collaborations, find potential positions, or seek advice from peers working on ECM-related topics.

We already have a starting list, but we know there are gaps and omissions. This is where we need your help!

👉 If your lab works on ECM or you know of a lab that should be included, please take a few minutes to check the list and fill in missing details.

https://docs.google.com/spreadsheets/d/1d2pU1_9lj67AkGveW4VW9PDg1QtQsWrM13W5lC6QGP0/edit?usp=sharing

Together, we can make this a truly comprehensive resource for the community!!!

For more information do not hesitate to contact us: themeshwork2020@gmail.com

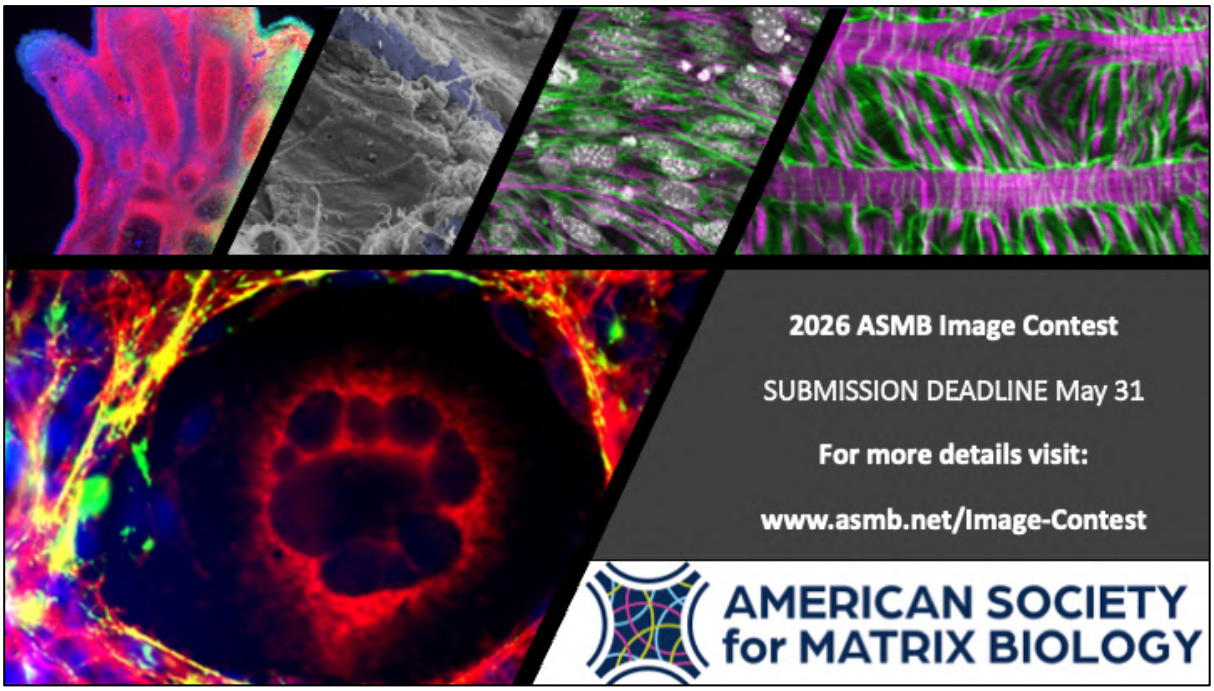
Breaking News from American Society for Matrix Biology

THE AMERICAN SOCIETY FOR MATRIX BIOLOGY HAS CHANGED IT'S LOGO! In 2025 ASMB celebrated our 25th anniversary as a society and introduced a new logo, revealed at the biennial meeting in Baltimore. This logo is designed to reflect the beautiful and diverse extracellular matrix connecting all of us, from the scientific community through to society.
Here are a few words from the designer about their inspiration: "The logo contains a dynamic, interconnected web inspired by the extracellular matrix. The multicolor, intersecting curved lines represent the complexity and interdisciplinary nature of the ECM, the scientific field, and the society as whole. The curved elements enclosing the network evoke a microscopic view of the space between cells, reinforcing ASMB's focus on the ECM and cutting-edge research at the cellular and molecular level. The color scheme of deep blue and vibrant green, pink, and blue, conveys a sense of innovation and trust, aligning with ASMB's mission to foster research, community, and discovery. The bold, professional typography balances this energy with clarity and credibility, positioning ASMB as a forward-thinking, collaborative, and authoritative voice in the scientific community."
Remember to check out our revamped website too https://www.asmb.net/ and keep an eye out for exciting updates (did anyone say '*interviews*'? Shh…watch this space)!

Call for ASMB 2026 e-Symposia proposals - Join Us On-line!

Organize an e-Symposium! ASMB is now accepting proposals for 2026. Members of ASMB and ISMB are invited to submit a proposal to organize an e-Symposia.

E-symposium chair proposals should include the proposed topic title, a brief explanation of why your proposal would be of interest to members of the matrix biology field, the format for the event, and the names and affiliations of the discussion leaders and speakers. Further, please indicate what steps you will take to try and make your session as inclusive and diverse as possible. We will be happy to discuss your proposals with you. Potential chairs must be members of the ASMB or ISMB. We encourage submissions from ASMB or ISMB members at any career stage (including graduate students and post-docs) and welcome proposals from individuals or teams of two. More information can be found on https://www.asmb.net/e-symposia.



Do you have a superb image you'd like to display and showcase your research? Proud of your histology, immunostaining, in situ hybridization, electron microscopy, molecular modeling or 3-D structure data? Is a latent artistic talent hiding within you? Do you have some cool images related to your latest publication that you did not include there? Would you like to call attention to a recent publication from your lab? Submit a matrix-centric image for display on the ASMB website banner, newsletter and social media!!!!

Contest opened February 1st, 2026. ASMB welcomes matrix-centric images. Images should not infringe copyright

and should not have been previously published. Please submit JPG or PNG images of the highest resolution possible, 300 dpi and less than 90 MB in size. Original jpg or png files are preferred; Please upload two versions of the same image. One version must be 980 x 300 px, the other version may be any size. Only one contest entry is permitted per ASMB or ISMB member.

Deadline to submit is May 31st, 2026.

This year, the first 10 submissions will receive a special ASMB travel mug!

Top winners will receive:

- Image featured on the ASMB website and social media
- Invitation to present the science behind the image in an e-Symposium
- Discount registration for a future ASMB workshop or meeting

For more information check out: https://www.asmb.net/image-contest

Breaking News from Matrix South America

Argentina

Hyaluronan as an instructive matrix in stem cell fate definition

Our recent work focuses on hyaluronan-rich extracellular matrices as active instructive systems rather than passive scaffolds. Beyond its structural role, hyaluronan acts as a dynamic regulator of the cellular microenvironment, integrating biochemical cues, matrix organization, and physical properties such as hydration, viscoelasticity, and ligand presentation. We investigate how specific hyaluronan contexts, including molecular weight, sulfation patterns, and matrix architecture, modulate cell–matrix interactions and mechanotransductive signaling, thereby "imprinting" mesenchymal cell phenotypes. In this framework, mesenchymal stem cells are viewed as responsive units whose fate and functional bias are constrained and guided by the surrounding matrix. This hyaluronan-driven regulation of cell behavior provides a conceptual bridge between fundamental matrix biology and translational development. These principles have been formalized and protected through an international patent application (PCT), covering a hyaluronan-based approach to guide mesenchymal stem cell behavior in regenerative contexts, particularly bone repair and complex healing environments. This initiative reflects efforts emerging from Argentina and contributing to the broader South American matrix biology community, bridging extracellular matrix research conducted at the National Scientific and Technical Research Council (CONICET, https://www.conicet.gov.ar/) and the National University of the Northwest of Buenos Aires Province (UNNOBA, https://unnoba.edu.ar/) with GLP-aligned preclinical development through an academic spin-off: https://mesenchyalt.com.ar

🔗 International patent publication (WIPO): https://patentscope.wipo.int

🔗 Project overview (video): https://youtu.be/N-5ukpazaHw?si=-2e9hqHHAOWfE5fm

Dr. Laura Alaniz

Independent Researcher and Professor CONICET-UNNOBA, Argentina | Founder of Mesenchymal-T, an academic spin-off in matrix biology and regenerative medicine

Brazil

Breakthroughs in Marine Glycobiology: UFRJ Group Expands Global Reach and Innovation. Recent weeks have marked a period of significant momentum for the field of marine glycobiology, highlighted by a series of major developments surrounding researcher Mauro Pavão and the Glycobiology Group at the Federal University of Rio de Janeiro (UFRJ). The UFRJ research team, already recognized as a hub of scientific excellence, recently hosted a landmark visit from Prof. John Couchman, a globally renowned expert in the field. This high-level academic exchange underscored the group's growing international influence and fostered strategic discussions that are expected to shape future research directions and international collaborations in glycobiology. In a major structural development, the scientific community also saw the official formation of the Marine EcoGlycan Group. This innovative research consortium was established to bridge the gap between fundamental marine ecology and the vast biotechnological and medical potential of marine sulfated polysaccharides. By uniting these disciplines, the new group aims to build a robust foundation for sustainable marine research and advanced therapeutic discoveries. Adding to this wave of progress, Mauro Pavão is set to participate in the prestigious Maine Blue Biotech Studio. Running from March 9 to March 19, 2026, this fully-funded, two-week accelerator program is held at the renowned Bigelow Laboratory for Ocean Sciences in East Boothbay, Maine. Developed in partnership with Hatch Blue, the premier initiative is specifically designed to accelerate the development of ocean-derived biotech products across sectors such as food, wellness, and advanced materials. Pavão's involvement in the Maine program highlights a critical step in transitioning cutting-edge laboratory research into impactful, real-world applications within the global Blue Economy.

Mauro Pavão, Professor
Instituto de Bioquímica Médica Leopoldo De Meis, Universidade Federal do Rio de Janeiro, Brazil

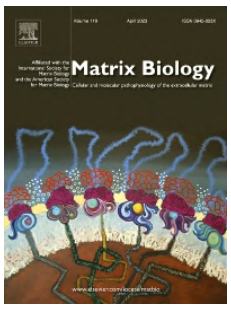
Spotlights on extracellular matrix methods

If you would like to feature in the next newsletter, please email
Julia Etich (julia.etich@uni-koeln.de)

In Focus

Extracellular Matrix Special Issues & Journals

Updates from Matrix Biology and Matrix Biology Plus



It was excellent to see many of you in person at our Editorial Board meeting at the ASMB Biennial Conference in Baltimore in November 2025. We had lively discussions regarding ways that the journals can increase the visibility of ECM to the broader the scientific community and to enhance value to the ECM community. We are in the process of initiating a new Editor's Choice feature to highlight highly novel and significant papers: ASMB and ISMB will be assisting this effort through social media. We are also in discussions with ASMB regarding establishing an early career reviewer program.

We want to thank Lynn Sherrer, our publisher at Elsevier, for her dedication to *Matrix Biology* and *Matrix Biology Plus* from July 2021 to October 2025. Lynn has moved to another position at Elsevier and she will be missed. I am also happy to introduce you to our new Elsevier publisher, Han Xi, who is located at the Shanghai office of Elsevier. Xi has a law degree from the Netherlands and is publisher of other Elsevier pharmacology and toxicology journals. She is eager to meet the ECM community and plans are being made for an Editorial Board meeting at MBE2026 in Oulu.

Special Issues remain an important means of increasing visibility of our science. Our 2024-2025 Special Issues had a great response. We extend our heartfelt gratitude to our Guest Editors for conscientiously leading these efforts. We are still processing some of the more recent submissions for these Special issues, so please keep an eye out for forthcoming publications. "Dynamic regulation of the tissue microenvironment by integrins and the extracellular matrix" (Guest Editor: C. Michael DiPersio, Albany Medical College), "Basement Membranes, biology and pathology" (Guest Editor: Peter Yurchenco, Rutgers Robert Wood Johnson Medical School, Guest Co-Editors: Brian Stramer, King's College London, and Yoshihiro Ishikawa, University of California San Francisco Department of Ophthalmology), and "ASMB 2023 Honors" (Guest Editor, Lynn Sakai, Oregon Health Sciences University).

We are pleased to announce a new Special Issue for *Matrix Biology Plus.* Robyn Shuttleworth, Altos Labs, will be the Guest Editor of a novel special issue on Computational and Mathematical Modeling in ECM Science. Jeff Minor will be Guest Editor of a new *Matrix Biology* Special Issue featuring the honorees of the upcoming 2025 ASMB Biennial Conference. Please watch the journal websites for more details on these two Special issues in the next month.

We welcome new ideas for Special Issues for both journals! Please also suggest new editorial board members.

Elsevier submitted the credentials of *Matrix Biology Plus* to Clarivate this spring to apply for an Impact Factor. The lack of an impact factor has been an issue for some authors and we have been working to get the journal into a favorable position. Hopefully we will receive a decision in 2026.

The *Matrix in Medicine* review series in *Matrix Biology* remains popular and is an ongoing feature. There have been 20 publications since we opened the series in 2023. Please consider submitting a review highlighting the importance of ECM in disease pathogenesis, diagnosis, and/or treatment. Engage your clinically oriented colleagues to expand the reach of this series.

This is a reminder that there are two new types of articles in *Matrix Biology* and *Matrix Biology Plus,* which are described below. The goal of these new features is to make matrix biology attractive and accessible to scientists both within and new to the field of extracellular matrix biology by providing succinct overviews of essential topics regarding the ECM and by providing detailed methodological approaches to studying the ECM. Feel free to reach out to the Editor in Chief or to the Editors regarding potential submissions.

Matrix Biology: **Matrix Essentials**

Matrix Essentials is a new feature of *Matrix Biology* designed to be a resource for both ECM and non-ECM focused scientists. Matrix Essentials articles are short, succinct articles that introduce a specific area of ECM or cell-ECM biology to the general reader, while summarizing the most up to date concepts in the field. This feature contains a single detailed figure and text of no more than 3,000 words, excluding abstract, citations, funding information, and acknowledgements. Citations should be limited to 70 references.

If you wish to submit a Matrix Essentials feature, please contact either the Editor-in-Chief or one of the Editors of *Matrix Biology* regarding your proposal with a short paragraph explaining the content and rationale for this article, including relevant recent references.

https://www.sciencedirect.com/journal/matrix-biology/about/news/announcing-our-new-article-type-matrix-essentials

Matrix Biology Plus: **Protocols and Methods**

Matrix Biology Plus welcomes submissions that advance methods, experimental protocols, or computational approaches for investigating the extracellular matrix. This can include, but is not limited to, new protocols for assessing ECM organization and assembly, determining experimental structures or computational models, post-translational modifications, identifying or validating ECM-related biomarkers, protein and proteoglycan purification, western blotting and immunohistochemical evaluation of ECM components, and biomaterials design and analysis such as for recombinant, targeted, or decellularized matrices. Submissions dealing with statistical protocols, best practices, standards or new tools for handling and analyzing large data sets are welcome.

Submissions should provide a succinct background on the ECM component (if relevant) and a review of the literature on related protocols. Protocols should be formatted to provide specific step by step guidance to the reader.

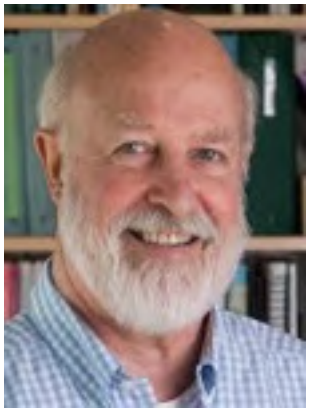
All submissions will undergo the standard peer review process.

https://www.sciencedirect.com/journal/matrix-biology-plus/about/news/protocols-and-methods

Joanne E. Murphy-Ullrich, PhD
Editor-in-Chief of Matrix Biology and Matrix Biology Plus

In Memoriam: Richard O. Hynes (1944–2026), *Matrix Biology*, 2026, 145: 32-28

With the passing of Dr. Richard Hynes on January 6, 2026, the scientific community lost a pioneering leader whose work fundamentally shaped the fields of cell adhesion and extracellular matrix (ECM) biology. As the Daniel K. Ludwig Professor for Cancer Research at MIT and an HHMI investigator, Dr. Hynes made landmark discoveries identifying fibronectin and integrins as key mediators of cell–ECM interactions, thereby establishing core principles of how cells communicate with their surrounding environment. His visionary approach consistently integrated emerging technologies, from gene cloning and knockout mouse models to genomics and proteomics, enabling transformative insights into development and disease, including cancer, fibrosis, thrombosis, and immune disorders. He further advanced the field through large-scale initiatives such as the adhesome and matrisome projects, which defined conserved molecular frameworks of cell adhesion and the extracellular matrix across species. Beyond his scientific contributions, Dr. Hynes played a major role in public policy and research ethics, notably helping establish national guidelines for human embryonic stem cell research. His career was marked by intellectual boldness, interdisciplinary innovation, and sustained influence on generations of scientists, leaving a lasting legacy in biomedical research.



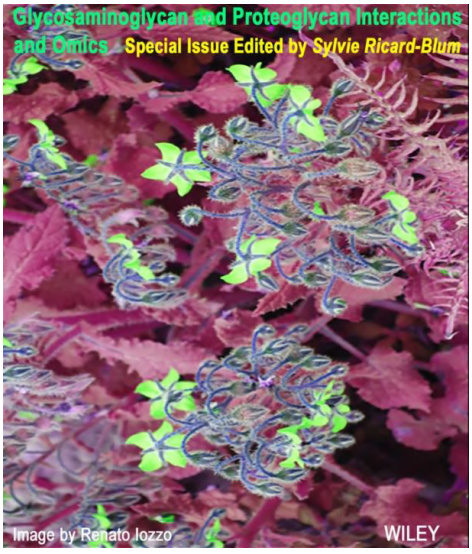
As extraordinary as his scientific and public service achievements were, so too was Dr. Hynes' impact as an intellectual leader and mentor. His intellectual rigor, curiosity, and generosity left an enduring mark on his colleagues and trainees alike. He trained generations of scientists who went on to distinguished careers in academia and industry, many of whom continue to shape the fields of matrix and adhesion biology. The authors had the privilege of knowing Dr. Hynes at different stages of his career, as colleagues and as members of his laboratory. In this tribute, we reflect on his seminal scientific contributions, his leadership and mentorship, and the profound influence he had on our own scientific paths. While no brief account can fully capture his legacy, we hope these reflections —together with testimonials from former trainees – convey the depth of his impact on science and on all who worked with him.

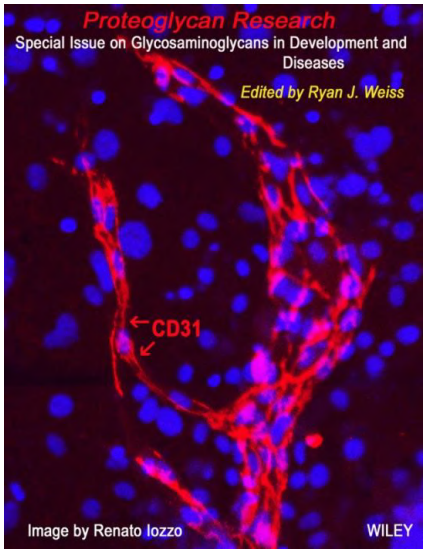
Colleagues have shared a thoughtful tribute highlighting his contributions and legacy. You can read it here: https://doi.org/10.1016/j.matbio.2026.03.002

Updates from Proteoglycan Research

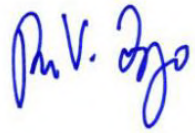
Dear Proteoglycan & Glycosaminoglycan lovers,
I wish a happy and prosperous 2026!

Our journal is thriving this year with an increasing number of high-quality research papers. Proteoglycan Research is now starting its fourth year of publication. We have launched several Special Issues. Indeed, the special issues constitute the driving force of the journal until we reach an international reputation.
The new Special Issues include one edited by Sylvie Ricard-Blum on "Glycosaminoglycans and Proteoglycans Interactions and Omics", and one by Ryan J. Weiss on "Glycosaminoglycans in Development and Disease".
Finally, a new Special Issue to be edited by Makarand Risbud will be focused on "Musculoskeletal Disorders".
We have also applied to Scopus during the past summer and should know the results within a few months from now. We have concurrently applied to PubMed, but this process takes a long time, 12-14 months. So, we should know by the fall of this year.





Please submit your best research to the journal. Proteoglycan Research considers both mechanistic and correlative papers including research articles, research reports, comprehensive reviews, mini-reviews, perspectives, methods papers, and technical advances. Please view the Guide to Authors for more information at https://onlinelibrary.wiley.com/journal/28323556.



Renato V. Iozzo, MD PhD (Honoris causa)
Editor-In-Chief, Proteoglycan Research

International Travel Grants

ISMB provides **international travel grants** (on average 500 Euros) to allow young scientists to attend major meetings in matrix biology anywhere in the world. Please apply several months before the meeting, by one of the following deadlines: January 1, April 1, July 1, October 1.
Follow the link to apply: https://www.ismb.org/copy-of-travel-grants
Check out our list of upcoming matrix-related meetings: https://www.ismb.org/meetings

Opening of the 2026 Rupert Timpl Award competition

The International Society for Matrix Biology created in 2004 a prize dedicated to the memory of the outstanding matrix biologist, Rupert Timpl, who left us on October 20th, 2003. The prize is called the "Rupert Timpl Award". The prize is awarded biannually at the occasion of the Matrix Biology Europe meeting. It is given to a young matrix biologist at an early stage of their independent scientific career who has published the "**Best paper in the field of matrix biology"** during the two years prior to the year of the MBE meeting.
As an integral part of the programme, the laureate will give a plenary lecture, called the Rupert Timpl Lecture, at the MBE2026 meeting to be held in Oulu, Finland, 29 June – 3 July 2026 (https://www.mbe2026.org/).

A prize of EUR 2,000 will be given, which is generously sponsored by Elsevier, the publisher of the journal *Matrix Biology*.

Nominees for the Rupert Timpl Award will have to meet the following criteria:

I. Be an early-stage investigator with no more than 8 years of experience since completion of PhD, at the time of nomination. Eligibility can be extended for reasons such as parental leave, illness, national service, training, natural disasters. These will need to be addressed in the nominee's CV and nomination letter (see below).
II. Have published - as first, co-first, or sole last author - a peer-reviewed primary research paper reporting original findings that have the potential to significantly advance the field of ECM research. The paper should have been published in the past two calendar years, at the time of the opening of the nomination call.
III. Starting out an independent career in ECM research.
IV. ISMB membership at the time of nomination is a requirement.
V. Self-nominations are excluded.

Please provide for your nomination:

I. A letter of support that includes a rationale for the nomination and the specific paper for consideration published over the two preceding calendar years at the time of the opening of the nomination call.
II. A copy of the peer-reviewed primary research paper submitted for consideration, including all supplementary information.
III. The nominee's CV, with 1) complete training and employment history and including the names of all direct research supervisors and institutions to avoid potential conflicts of interest, and 2) a full list of publications with inclusion of names of all co-authors.

ISMB members are invited to send their nominations for the Awardee to the ISMB Secretary (julia.etich@uni-koeln.de) by **April 29th, 2026, at 23:59 Central Europe Time.**

The nominations will be voted on by ISMB Council and the winner will be announced in June 2026.

Dick Heinegård European Young Investigator Award 2026

The ISMB, on behalf of the organizers of the Matrix Biology Europe Conference 2026, is pleased to announce the Dick Heinegård European Young Investigator Award 2026, to be presented at the MBE2026 meeting in Oulu.

In memory of the distinguished matrix researcher Dick Heinegård, this award recognizes **outstanding early-career postdoctoral researchers** in matrix biology.

Each affiliated European Matrix Biology Society is invited to nominate one candidate following their own procedures for national selection. From these nominations, the Young Investigator Award Committee will select six finalists to present their work in a dedicated Award Session at MBE2026. The winner will be chosen based on the **overall scientific excellence and quality of the oral presentation**. **Please send your candidacies to the chair of MBE2026, valerio.izzi@oulu.fi latest by 30 April 2026.**

The award includes a certificate and a monetary prize funded by the Dutch, German, French, British and Finnish Matrix Societies (2000€).

Eligible candidates must have no more than five years of postdoctoral research experience. Applicants should contact their respective national Matrix Biology Society for further details on the nomination process. Applicants working in European Countries that do not have an affiliated Matrix Society may apply directly to the conference organizers.

We warmly **encourage European societies to identify and support** outstanding young investigators for this prestigious distinction. And thanks to those societies who have already activated!

Now Recruiting: ISMB Newsletter Editor and Web Master

These positions offer an excellent opportunity to contribute to the visibility, communication, and community engagement of ISMB.

The Newsletter Editor will:

- Coordinate and release the ISMB newsletter (3 issues per year)
- Solicit and edit content
- Work closely with the ISMB Executive Board and committee chairs
- Support timely communication with the membership

The Web Master will:

- Maintain and update the ISMB website
- Post announcements, meeting information, and society news
- Coordinate with meeting organizers and committees to ensure up-to-date content
- Suggest improvements to website structure and digital communication

Term and Commitment: Both roles are volunteer positions, typically for a 3-year term, with the possibility of renewal. Board interaction is collaborative and supportive, and responsibilities are manageable alongside academic duties.

Interested members are invited to apply by sending a brief CV to the ISMB Secretary (julia.etich@uni-koeln.de) before **May 31st, 2026.**

We strongly encourage early-career and mid-career members to apply and actively contribute to shaping the Society's communication and outreach and look forward to welcoming motivated colleagues to these important roles within ISMB.

Meeting reports from ISMB International Travel Awardees

2025 American Society for Matrix Biology Biennial Meeting, Baltimore, MD, November 2025

With the support of an ISMB travel award, I attended the American Society for Matrix Biology (ASMB) Biennial Meeting 2025*: Matrix Marvels – 25 Years of Pioneering Progress, Infinite Potential Ahead*, held in Baltimore, USA. I travelled from the UK as a PhD student at the University of Surrey, where my research focuses on extracellular matrix (ECM) proteases and their role in cardiovascular disease.

I was honoured to be selected for an oral presentation in the Next-Gen Proteomics concurrent session, where I presented my research on ADAMTS8, a metalloprotease implicated in pulmonary arterial hypertension. Presenting at an international meeting provided valuable feedback from experts in ECM biology and proteomics and helped refine how I communicate interdisciplinary protease research to a broad ECM audience.

The programme covered diverse aspects of matrix biology, including ECM mechanobiology, matrix remodelling in disease, and emerging links between artificial intelligence and ECM research. I particularly appreciated the poster flash talk session, which offered concise insights into a wide range of projects and encouraged follow-up discussions.

Beyond the scientific sessions, the meeting offered excellent networking opportunities. Informal conversations with fellow PhD students and established investigators gave me the chance to exchange ideas, seek advice on future academic career paths, and build new scientific connections.

Overall, ASMB 2025 was a highly enriching experience both scientifically and professionally. The ISMB travel award enabled me to present my work, engage with the international ECM community, and gain new perspectives on the future of matrix biology. The experience strengthened my motivation to pursue an academic career in this field and left me excited about the marvelous matrix and its potential ahead.

Tina Burkhard, PhD Student
Faculty of Health and Medical Sciences
School of Biosciences, University of Surrey, UK

2025 American Society for Matrix Biology Biennial Meeting, Baltimore, MD, November 2025

I am sincerely grateful to the International Society of Matrix Biology (ISMB) for awarding me the International Travel grant, which enabled my participation in the American Society of Matrix Biology (ASMB), 2025, Biennial Meeting in Baltimore, USA. Attending this conference was an invaluable experience, an opportunity to engage with the global matrix biology community and to present my work on "Mapping the Collagen Landscape: Tissue-Specific Chain expression and Modifications in Mice". The breadth of scientific discussions provided a comprehensive view of conceptual advances in the field of matrix biology. I particularly benefitted from sessions focused on ECM proteomics, Post-Translational Modifications (PTMs) and cross-linking chemistry, which is directly related to my research work. These talks deepened my understanding of how structural mapping and inter-disciplinary approaches can shape the future of matrix biology. Giving an oral and poster presentation both and then discussing about my work with experts was an amazing experience. I received constructive feedback that will help my ongoing analyses of collagen PTMs and ECM organization across different tissues of mice. Several discussions opened potential avenues for some in future collaborations and helped me appreciate how my work fits into larger efforts to build community-wide resources such as ECM atlas, PTM databases and integrative computational pipelines. The meeting also allowed me to meet and interact with early-career researchers from several countries, giving me insights into diverse perspectives and career trajectories. Beyond the scientific discussions and programme, attending ASMB 2025 Biennial Meeting strengthened my commitment to pursuing research in Matrix Biology. The meeting highlighted the translational relevance of matrix biology, from developmental biology to fibrosis, some specific diseases such as cardiovascular diseases, and regenerative medicine. This meeting underscored the importance of developing comprehensive analytical tools for ECM characterization. I am deeply appreciative of ISMB's support, which made this experience possible for me. Attending this meeting had a meaningful impact on my scientific growth, and I look forward to contributing to this community in the years ahead.

Ayush Nigam, Project Intern
Cardiometabolic Lab, Indian Institute of Technology Mandi, Himachal Pradesh, India

2025 American Society for Matrix Biology Biennial Meeting, Baltimore, MD, November 2025

Thanks to the generous support of the ISMB Young Scientist Travel Grant, I was able to attend the American Society for Matrix Biology 2025 Biennial Meeting in Baltimore. As a second-year PhD student from the University of Oulu, Finland, this was my first opportunity to engage with the North American matrix biology community, and the experience was both formative and inspiring. The scientific programme offered exceptional sessions on computational methods and machine learning for ECM research, which aligned perfectly with my doctoral work on spatial transcriptomics. Additionally, sessions focused on experimental research provided valuable insights into promising ECM targets and interactions. I presented my poster on MatriSpace, a user-friendly computational tool I developed to analyse and visualise matrisome spatial patterns in healthy and diseased tissues. The poster session was well attended, and I received valuable feedback from leading experts and potential users that will directly inform the tool's continued development. The discussions sparked new ideas for incorporating advanced analysis methods and expanding the curated dataset collection. Beyond the science, the meeting provided invaluable opportunities to build an international network and connect with researchers across the field. The interactions with both established scientists and fellow early-career researchers have opened doors for potential collaborations on matrix-tumour interactions. I am deeply grateful to the ISMB for making this experience possible.

Ayomide Oshinjo, Doctoral Researcher
Izzi Lab, Faculty of Biochemistry and Molecular Medicine
University of Oulu, Finland

Scientific Highlights

We warmly invite members of the International Society for Matrix Biology (ISMB) to share their latest scientific highlights and research advances for dissemination through our newsletter. All the contributions will be prominently featured, providing visibility to cutting-edge work across the global matrix biology community.

Targeting the microbiota-miRNA-protease axis: A new therapeutic avenue in melanoma. Katsoulieris EN, Ioannou P, Afratis NA. *FEBS Journal*, 2026, In Press, 10.1111/febs.70386

Abstract: Modulation of extracellular matrix (ECM) turnover is a critical prerequisite process underlying the onset of melanoma metastasis. ECM proteases are involved in the degradation of matrix components during ECM turnover, which is associated with melanoma cell growth, migration, invasion, extravasation, metastasis, and modulation of melanoma tumor immunogenicity. During these processes, fluctuations in ECM protease activities and concentrations occur in response to complex regulatory mechanisms acting at both the transcriptional and post-transcriptional levels of protease gene expression. In this review, we examine the major factors of epigenetic machinery, specifically protease-regulating microRNAs (miRNAs), with respect to their ability to directly target ECM protease transcripts and influence melanoma progression. Furthermore, given that dysregulation of the intestinal microbiota has been identified as an etiological factor in melanoma resistance to contemporary immunotherapies, this review examines evidence linking gut dysbiosis-induced changes in matrix metalloproteinase-targeting miRNA profiles to the progression of melanoma. In conclusion, we evaluate the therapeutic potential of approaches involving modifications of gut microbiota populations, alongside direct miRNA targeting of ECM proteases. The integration of these strategies may facilitate the development of innovative adjuvant therapies aimed at overcoming resistance to current inhibitor checkpoint immunotherapies.

A guide to types, structures and functions of matrix metalloproteinases, Piperigkou Z, Mangani S, Koletsis NE, Kremmydas S, Karamanos NK. *FEBS Journal*, 2025, In Press, 10.1111/febs.70296

Abstract: Matrix metalloproteinases (MMPs) represent a diverse family of zinc-dependent matrix remodeling enzymes that play critical roles in both physiological and pathological processes, including cancer progression. Their enzymatic activity in matrix remodeling underpins key aspects of cellular physiology; however, uncontrolled remodeling determines several pathological conditions, such as osteoarthritis, fibrosis, and cancer. MMPs guide critical steps during cancer progression, including cell behavior, epithelial-to-mesenchymal transition, pre-metastatic niche formation, angiogenesis, and immune surveillance. However, the roles of MMPs in cancer are complex and context-dependent, with certain family members demonstrating opposing functions that vary with tumor stage, anatomic site, enzyme localization, and substrate specificity. While early clinical trials of MMP inhibitors (MMPIs) yielded disappointing outcomes, advances in preclinical models have improved our knowledge of MMP biology and continue to inform the design of more effective and selective MMPIs. This guide on the types, structures, and functions of MMPs gives an overview of MMP structural domains, matrix substrates, and specific functions, summarizing their main roles in normal and pathophysiological conditions, with a particular emphasis on cancer progression. New insights into pharmacological targeting, diagnostic applications, and progress on clinical trials are also presented here and critically discussed. This guide revisits the concept of the multifaceted biological functions of MMPs, critically examines the limitations of previous therapeutic attempts, and explores future directions for the development of effective MMP-based molecular targeting.

Spheroid-based 3D models to decode cell function and matrix effectors in breast cancer. Mangani S, Koutsakis C, Koletsis NE, Piperigkou Z, Franchi M, Götte M, Karamanos NK. *Cancers*, 2025, 17(21):3512, 10.3390/cancers17213512

Abstract: Traditional two-dimensional (2D) cell cultures are widely used in cancer research but fail to replicate the complex interactions that occur in tumors in vivo. Three-dimensional (3D) models more closely mimic the tumor microenvironment by preserving dynamic cell–matrix communication. In this study, we developed and characterized 3D spheroids from two breast cancer cell lines with distinct metastatic potential (MCF-7 and MDA-MB-231). Significant differences in cell morphology, epithelial-to-mesenchymal transition (EMT) markers expression, and functional behavior compared to 2D cultures were observed. The spheroids also showed the distinct expression of key receptors (ERs, EGFR, IGF1R) and matrix molecules (syndecans and matrix metalloproteinases). Bioinformatic analysis further revealed the clinical relevance of these matrix regulators in breast cancer prognosis. Overall, these findings introduce an informative, matrix-free cell culture platform for studying breast cancer progression and potentially exploring new therapeutic approaches.

Blood Proteomics: Insights from public datasets, accomplishments, and remaining challenges. Larrea-Sebal A, Dai C, Brenes A, Korff K, Neely BA, Geyer PE, Dagley L, Unwin RD, Naba A, MacCoss MJ, Guo T, Deutsch EW, Martin C, Schwenk JM, Perez-Riverol Y. *Genome Biology*, 2026, 27, 81, 10.1186/s13059-026-04027-9

Abstract: The circulating blood proteome comprises soluble and cellular components that reflect physiological and pathological states across tissues. Advances in mass spectrometry and affinity-based proteomics have improved sensitivity and throughput, enabling the generation of public blood proteomics resources. However, comprehensive assessments of these datasets remain limited. This work reviews the cellular and molecular complexity of publicly available blood proteomics data, recent methodological developments, and the complementarity of diverse data sources across the abundance range, while outlining remaining challenges for translating blood proteomics into personalized medicine.

A guide to building the matrisome interactome: From computational prediction to experimental validation. Leverton L, Bains AK, Isa I, Ricard-Blum S, Naba A. *FEBS Journal*, 2025, 293(1):42-70, 10.1111/febs.70344

Abstract: The extracellular matrix (ECM) is a complex meshwork of proteins and polysaccharides found in all multicellular organisms, that provides structural support to cells and organize them into tissues and organs. In addition to its architectural role, the ECM conveys key mechanical and biochemical signals to cells via cell surface receptors that activate biological pathways controlling a plethora of cellular behaviors, including proliferation, stemness, adhesion, migration, or differentiation. The structural integrity of the ECM and its signaling functions are mediated by protein–protein and protein–polysaccharide interactions. Uncovering the mechanisms regulating these interactions is critical to better understand ECM assembly and biology and envision therapeutic strategies targeting the ECM. Here, we provide a comprehensive review of the computational and experimental approaches available to identify and characterize ECM protein interactions, from individual interactions to the interactome of the full matrisome. We first review computational tools currently available to predict interactions and then describe techniques that allow the experimental determination of these interactions and the parameters governing them. Using examples from original research literature, we illustrate how each approach has been applied to identify ECM interactions and has helped advance our understanding of ECM functions in health and disease. To assist researchers interested in the field, we propose a roadmap combining computational and experimental approaches to generate cell-, tissue-, or disease-specific ECM interaction networks. Lastly, we discuss the remaining challenges and perspectives in the field of ECM interactomics.

Comparative proteomic analysis of the ECM composition of the human omentum and mesentery, the main sites of ovarian cancer metastasis. Considine JM, Gomez C, Pally D, Yang N, Taha IN, Sorenson J, Brooks EG, Kreeger PK, Naba A. *iScience*, 2025, 29(1):114461, 10.1016/j.isci.2025.114461

Abstract: Due to its limited symptoms, high-grade serous ovarian cancer (HGSOC) has frequently metastasized extensively throughout the peritoneal cavity prior to its diagnosis, resulting in an overall five-year survival rate of less than 50%. The omentum and mesentery are two of the most common metastatic sites in HGSOC. However, the mechanisms underlying HGSOC metastatic tropism remain unknown. The extracellular matrix (ECM) is a meshwork of proteins that provides biochemical and mechanical signals to cells and has been shown to drive the dissemination of several cancer types to preferential distant sites. Here, combining histological assessment and proteomics, we defined the architectural features and composition of the ECM of paired omentum and mesentery samples from disease-free adult women. We found that over 90% of the proteins detected were shared between the omentum and mesentery, but also identified tissue-specific ECM proteins, including collagen XII and tenascin-C.

The Gene Ontology Consortium. The Gene Ontology Knowledgebase in 2026. *Nucleic Acids Research*, 2025, 54(D1):D1779-D1792, 10.1093/nar/gkaf1292

Abstract: The Gene Ontology (GO) knowledge base (https://geneontology.org) is a comprehensive resource describing the functions of genes. The GO knowledgebase is regularly updated and improved. We describe here the major updates that have been made in the past 3 years. The ontology and annotations have been expanded and revised, particularly in several areas of biology: cellular metabolism, multi-organism interactions (e.g. host-pathogen), extracellular matrix proteins, chromatin remodeling (e.g. the “histone code”), and noncoding RNA functions. We have released version 2 of a comprehensive set of integrated, reviewed annotations for human genes, which we call the “functionome.” We have also dramatically increased the number of GO-CAM models, with over 1500 models of metabolic and signaling pathways, primarily in human, mouse, budding and fission yeast, and fruit fly. Finally, we discuss our current recommendations and future prospects of AI in the use and development of GO.

Dichotomous SMAD2/3 regulation and selective antihypertrophic activity of heparin during in vitro chondrogenesis of mesenchymal stromal cells. Schmidt S, Chasan S, Dietmar HF, Klampfleuthner FAM, Hesse E, Walker T, Freudenberg U, Richter W, Diederichs S. *Cellular & Molecular Biology Letters*, 2026, 31, 51, 10.1186/s11658-026-00899-8

Abstract: Endochondral instead of chondral differentiation hinders mesenchymal stromal cell (MSC) application for clinical cartilage regeneration. We previously showed that heparin–polyethylene glycol (PEG) hydrogels loaded with transforming growth factor TGF-β instructed stable chondral MSC development in vivo. Here, we assessed this approach in vitro, utilizing heparin–PEG hydrogels or the pellet culture system with soluble heparin supplementation of chondrogenic medium. Unlike in vivo, human MSCs differentiated in heparin–PEG hydrogels into type X collagen and alkaline phosphatase-positive hypertrophic chondrocytes in vitro. Interestingly, treating MSC pellets with soluble heparin (10–700 µg/mL) revealed reduced TGF-β-SMAD3 but not SMAD2 activation at unaffected type II collagen and proteoglycan/DNA levels. We propose that the stimulation of the insulin-AKT pathway by heparin aided in maintaining SMAD2 activation, which apparently plays a more prominent role than SMAD3 for MSC chondrogenesis. Heparin treatment inhibited the pro-hypertrophic WNT/β-catenin pathway in vitro but insufficiently silenced TGF-β-SMAD1/5/9 activation and unfortunately reduced antihypertrophic prostaglandin PGE2 levels. Ultimately, treatment with 10 µg/mL heparin reduced the upregulation of several hypertrophy markers (MEF2C, IHH, IBSP messenger RNAs [mRNAs], alkaline phosphatase activity) below control levels, but type X collagen remained unresponsive. Thus, soluble heparin treatment was similarly selective and effective as previous antihypertrophic interventions (PTHrP pulses, WNT inhibition), while offering technical

simplicity, reduced cost, and solvent-free formulation. Taken together, heparin-TGF-β showed a novel dichotomous SMAD2/3 inhibition at maintained chondrogenic differentiation and context-dependent lineage-instructive properties—permitting endochondral commitment in vitro but chondral development in vivo. Thus, environmental contributions are mandatory to allow heparin–PEG-guided chondral versus endochondral lineage commitment of MSCs in vivo, potentially involving SMAD1/5/9 suppressors and PGE2 sources.

Anti-inflammatory macrophages are recruited to keloids that obtain response to intra-lesional injection therapies. Before and After Treatment Biopsies from a Double-Blinded, Randomized, Controlled Trial. Komulainen T, Ylitörmä M, Hietanen KE, Järvinen J, Junttila I, Kaartinen I, Järvinen TAH. *J Invest Dermatol*, 2026, 146(5):1438-1442, 10.1016/j.jid.2025.10.597

Abstract: The authors explored the predictive value of immune cell populations to intralesional injections using biopsies collected from the active border of keloids before and after injections in the double-blinded randomized controlled trial comparing the efficacy of intralesional 5-fluorouracil (5-FU) with that of triamcinolone (TAC) injections in 48 human keloids. Immunohistochemistry using antibodies and quantitative virtual microscopy were used to detect and score immune cell populations in different keloid layers. Double-blinded randomized control trial is an ideal way to assess the clinical response to the therapies. Pre- and post-treatment biopsies provide "window" to explore the biological state of the leading edge of keloid in response to the intralesional injection treatments. To the best of the authors' knowledge, no other material of same scientific rigor has been collected from the keloid randomized control trials. None of the immune cell populations is predictive of the response, but the M2 macrophages accumulate, whereas Tregs almost disappear, in the keloids that obtain response to intralesional injections, especially to corticosteroid.

Keloid vasculature reacts to intralesional injection therapies but does not predict the response to treatment. A double-blinded, randomized, controlled trial. Komulainen T, Hietanen KR, Tolonen T, Parkkila S, Kaartinen IS, Järvinen TAH. *Biochim Biochem Acta*, 2025, 1871(5):167790, 10.1016/j.bbadis.2025.167790

Abstract: Keloids are benign fibroproliferative skin scars that expand beyond the original wound site. Hypoxia and angiogenesis are thought to drive pathological scar formation in keloids. We utilized biopsies collected before, during and after the double-blinded randomized controlled trial (RCT) comparing the intralesional treatments of 5-fluorouracil and triamcinolone injections in 48 human keloids. We could not detect any cells expressing the hypoxia markers (carbonic anhydrase 9 and hypoxia-inducible factor 1α) in the three distinct regions of keloid dermis. The amount of epidermal hypoxia could not predict the response to treatment. The middle dermis of the patients obtaining a clinical response to the intralesional injections showed significant increase in mature blood vessels and in lymphatics after the treatment. Our study does not support hypoxia being the driver behind keloid formation but demonstrates that the patients obtaining a response to intralesional therapies develop more blood vessels and lymphatics in the middle dermis of the keloids during the treatment.

Tenascin-C orchestrates radiotherapy-induced head and neck tumor regression. Loustau T, Mitrentsi I, Wang N, Spenlé C, Pavlidaki A, Tranchant T, Riegel G, Venu A, Oueidat R, Koch M, Dumas M, Wack F, Hirschler A, Carapito C, Paul N, Carapito R, Mörgelin M, Hansen U, Azzi J, Aubergeon L, Salomé N, Dhaouadi S, Grenot P, Bouhaouala-Zahar B, La Cioppa S, Oertle P, Izzi V, Plodinec M, Noel G, Burckel H, Gertraud Orend. *EMBO Mol Med*, 2026, 10.1038/s44321-026-00406-8

Abstract: Given that head and neck squamous cell carcinoma (HNSCC) patients have poor survival outcomes, a better understanding of the therapeutic benefits of ionizing irradiation (IR), the major treatment modality besides surgery, is needed. A confounding factor is the immunosuppressive tumor microenvironment determined by tenascin-C (TNC), a highly abundant extracellular matrix molecule upregulated by IR. We investigated the roles of TNC on radio-induced tumor regression in a murine oral HNSCC model expressing or lacking TNC. While tumors

in a TNC-expressing host were radiosensitive, they were radioresistant in TNC genetically-depleted mice. We identified fibroblast reticular cells (FRCs) as critical regulators. TNC plays a compartmentalized and dual role in regulating tumor radiosensitivity with a detrimental role in the tumor stroma opposed to an essential role in the tumor draining lymph nodes. This is relevant as a high FRC signature and high TNC levels together correlate with shorter HNSCC patient survival. TNC-expressing FRCs may be an excellent novel target to improve radiotherapy-induced tumor eradication, as our TNC targeting MAREMO peptide reduced tumor cell numbers and plasticity upon IR.

The Chloride Channel Regulator, Calcium-Activated-1 Is Expressed in Synoviocytes and Articular Chondrocytes in Health and Disease. Bushe J, Fürstenau J, Bartenschlager F, Dökel S, Jovanovic VM, Rösch G, Jenei-Lanzl Z, Zaucke F, Dietert K, Gruber AD. *J Histochem Cytochem*, 2026, In Press, 10.1369/00221554261423720

Abstract: The chloride channel regulator, calcium-activated-1, CLCA1, acts as a multifunctional secreted glycoprotein in anion channel modulation, mucus homeostasis, immune regulation, and other functions. So far, it has been described in goblet and other mucus-producing cells in mucous membranes, primarily of the respiratory, alimentary, and urogenital tracts. Here, we identify the expression of CLCA1 in fibroblast-like synoviocytes and superficial as well as, to a lesser extent, intermediate zone chondrocytes of diarthrodial articular joints. The expression pattern was found to be conserved in major joints in mice, pigs, and humans. First analyses of degenerate or infectious inflammatory joint conditions in mice or pigs, respectively, suggest rather continuous expression levels in articular disease. We speculate that CLCA1 may be involved in articular anion conductance, proteoglycan homeostasis, and inflammation of articular joints, possibly similar to analogous functions of this molecule as established in mucous membranes of the lungs and intestine.

Identification of novel fibroblast subsets in diffuse cutaneous systemic sclerosis. Rosendahl AS, Bornikoel A, Zeinert I, Keufgens L, Tellkamp F, Kleinenkuhnen N, Baar T, Schönborn K, Krüger M, Tresch A, Brachvogel B, Eckes B, Moinzadeh P, Krieg T. *Ann Rheum Dis*, 2025, S0003-4967(25)04594-7, 10.1016/j.ard.2025.11.027

Abstract: Systemic sclerosis (SSc) is an autoimmune-driven fibrotic disease, characterised by excessive extracellular matrix (ECM) deposition and fibroblast activation. Our study aimed to identify novel fibroblast subpopulations in SSc and determine their functional role. We performed single-cell RNA sequencing on cultured dermal fibroblasts from healthy donors and patients with diffuse cutaneous SSc, verified selected, specific genes at the protein level and used siRNA knockdown experiments to provide evidence for a functional role of these proteins. SSc fibroblasts revealed high heterogeneity and in specific activated subsets strong upregulation of CD9 and four and a half LIM domain 1 (FHL1), previously described as a muscle-related protein. Overexpression of FHL1 and CD9 was also detected in fibroblast subsets in patient skin. CD9 was associated with the regulation of FHL1 expression. Downmodulation of FHL1 in primary skin fibroblasts correlated with downregulation of the vestigial-like family member 3 (VGLL3) gene, which is known to be expressed in myofibroblasts in a stiff and fibrotic environment and to upregulate collagen synthesis. Further, VGLL3 was confirmed to be upregulated in SSc donor skin. Our study identified novel fibroblast subsets in SSc, characterised by CD9 and/or FHL1 upregulation. The data indicate a functional role of FHL1 in fibroblasts and its involvement in the regulation of ECM production and provide a new mechanistic link to VGLL3 regulation. Our findings suggest new avenues for therapeutic exploration targeting the perpetuating fibroblast activation by the fibrotic environment.

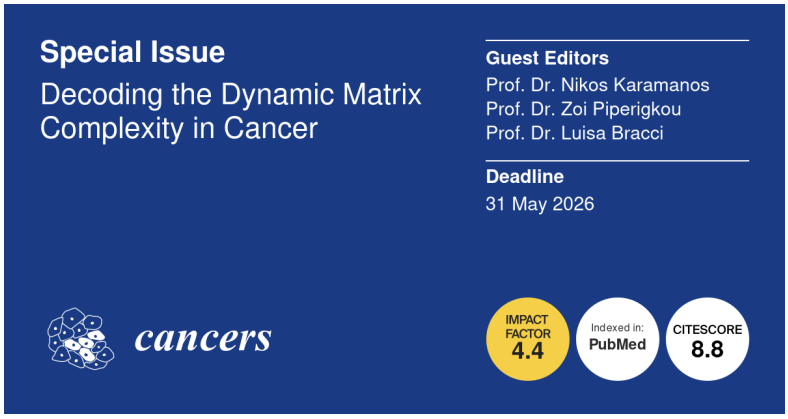
An improved porcine model of infrarenal abdominal aortic aneurysm. Stei M, Arkenberg P, Uebing T, Mazrekaj A, Mulorz J, Mehrkens D, Ahdab M, Barnowski P, Sengle G, Adam M, Lohner V, Hoerr V, Nahardani A, Schubert-Quecke C, Mewes B, Lindemeyer J, Grüll H, Busch A, Zimmer S, Winkels H, Schelzig H, Kelm M, Nickenig G, Baldus S, Wagenhäuser MU, Mollenhauer M. *Scientific Reports,* 2025, 15(1):44059, 10.1038/s41598-025-31690-y

Abstract: Abdominal aortic aneurysm (AAA) remains a significant public health challenge, primarily due to its high mortality rate and the lack of effective preventive and causal strategies. This study aims to establish an improved translational triple-hit porcine model of AAA and to compare it with human AAA disease. AAA was induced in four juvenile domestic pigs by balloon catheter-based aortic dilation, enzyme-mediated extracellular matrix (ECM) degradation, and lysyl oxidase inhibition. The porcine AAA model was characterized by proteomics, histological investigation, and cytokine profiling, and compared with natural occurred human AAA disease. Infrarenal AAA was successfully established with sustained aortic dilation (> 150% of baseline diameter) occurring within 7–14 days post induction and maintained through day 28. Proteomic analysis of porcine AAA tissue identified significant shifts in protein abundance, including downregulation of proteins associated with vascular smooth muscle cell function and ECM integrity, and upregulation of immune-related proteins. Comparative analysis of porcine and human aortic tissues revealed reduced medial elastic fiber content and length, along with increased calcification in porcine AAA, reflecting structural and pathological changes observed in human AAA. Systemic cytokine profiling revealed significant increases in both pro-inflammatory and anti-inflammatory cytokines following AAA induction in pigs, with a cytokine profile largely comparable to that observed in human AAA patients. These findings suggest that the refined porcine AAA model offers a reliable and reproducible platform for investigating AAA progression and evaluating potential therapeutic interventions prior to clinical implementation.

Binding of the elastin peptide VGVAPG and lactose to the human elastin binding protein. Haslak ZP, Belloy N, Debelle L, Dauchez M, Baud S. *J Struct Biol*, 2026, 218(2):108318, **10.1016/j.jsb.2026.108318**

Abstract: Elastin-derived peptides (EDPs) interact with elastin-binding protein (EBP), a key component of the elastin receptor complex, modulating cellular processes such as protease activation, apoptosis, and chemotaxis via regulation of NEU-1 sialidase activity. Despite their therapeutic relevance, the structural basis of EDP-EBP interactions remains poorly understood. Here, we present the first full-length homology model of EBP (residues 29–516), constructed and validated through duplicate 1 microsecond long molecular dynamics (MD) simulations. Molecular docking of VGVAPG (as a representative EDP) and lactose (as a representative galactosugar) followed by MD simulations, allowed us to identify key binding residues: D98, E99, S104, and S136 for VGVAPG; and E99, S101, S104, N116, Q124, E137, and Y139 for lactose. These data reveal a shared binding region within residues 83–139, suggesting a competitive binding between EDPs and galactosugars. Furthermore, EBP residues P233 and I234 were implicated in potential interactions with PPCA or NEU-1, contributing to ERC assembly. These findings offer new insights into the molecular recognition mechanisms of EBP and provide a foundation for the design of EBP-targeted elastin peptide antagonists.

Special Issues Announcements



Cancers Special Issue [Decoding the Dynamic Matrix Complexity in Cancer](https://www.mdpi.com/journal/cancers/special_issues/NN9WDABN0D) seeks to highlight the roles of regulatory extracellular matrix (ECM) macromolecules, including matrix remodeling enzymes, PGs/GAGs, specific types of collagens and matrix (glyco)proteins, the modeling of tumor microenvironment complexity as well as the mechanisms underlying the dynamic cancer-associated cell–matrix interactions that drive cancer development and aggressiveness. Matrix macromolecules form complex networks through which they dynamically communicate with cells and shape the complex tumor microenvironment. ECMs are not merely structural components, but rather active and critical regulators of several homeostatic and pathological processes, such as cancer. Their molecular composition varies among different tissues and undergoes significant modifications and remodeling during cancer progression. The elucidation of the mechanistic aspects governing matrix assembly and modifications, as well as cell–cell and cell–matrix interactions, is of critical importance to fully understand cancer pathobiology and to identify tumor biomarkers and novel therapeutic targets. Moreover, 3D cell culture models and bioscaffolds that mimic native ECM architecture and biophysical properties have emerged as powerful tools to investigate cell–matrix crosstalk and the dynamic interactions within the tumor microenvironment.

Special Issue topics will include but are not limited to the following, which are aligned with the aim of decoding dynamic matrix complexity:

- Proteoglycans and Glycosaminoglycans as Dynamic Regulators of Tumor Plasticity
- Targeting Matrix Remodeling Enzymes in Cancer Progression
- Collagen and Glycoprotein Networks as Biomarkers and Therapeutic Targets
- Cell Surface Matrix Receptors and Effectors in Pre-metastatic Niche Formation
- Matrix-Derived Bioscaffolds for Modeling Tumor Microenvironment Complexity
- 3D Cell Culture Models in Mimicking Tumor Microenvironment

You can find more information here: https://www.mdpi.com/journal/cancers/special_issues/NN9WDABN0D

Prof. Dr. Nikos Karamanos
Prof. Dr. Zoi Piperigkou
Prof. Dr. Luisa Bracci
Guest Editors

The aim of this *JoVE Topical Collection of "Methods for Research in Development, Health, and Disease* is to highlight and facilitate the dissemination of the latest techniques in ECM research and their application across diverse fields of research, including development, cancer, fibrosis, skeletal disorders, tissue engineering, wound healing, and aging.

The Collection will cover, but is not limited to:

- Techniques to profile the global composition of the ECM (*e.g.*, proteomic, mass spectrometry imaging, multiplexed IHC)
- Techniques to image and quantify the physical and mechanical properties of the ECM from in-vitro cell culture systems or in- or ex-vivo samples across model organisms
- Techniques to characterize the mechanisms of ECM assembly and remodeling
- Techniques to probe cell-ECM and ECM protein-protein interactions
- Techniques to engineer *in-vitro* ECMs and ECM mimics with applications to cancer research, wound healing, or tissue regeneration
- Computational approaches to mine -omic datasets to gain insights into genetic, transcriptional, translational, and post-translational regulations of the matrisome.

You can find more information and submit your abstract at: https://app.jove.com/methods-collections/4883

Meetings Announcements

Save the dates!

The Extracellular Matrix Pharmacology Congress

June 15 - 17, 2026 | Copenhagen, Denmark

Fibrogenesis is estimated to contribute to nearly 40% of deaths in the Western world, yet it remains one of the most overlooked therapeutic targets. ECM2026 aims to change this by bringing together experts across disciplines to explore the extracellular matrix (ECM) as a driver of disease and a source of new treatment opportunities.

Selected topics include:

- Obesity and multi-organ fibrosis
- Emerging therapies and target discovery
- Fibroblasts and cancer
- Autoimmunity and chronic inflammation
- Lung and liver fibrosis
- Fibroaging
- Precision medicine

Sign up for news and updates: https://ecm-congress.org/

The Matrix Biology Europe (MBE) Conference
29 June – 3 July, 2026 | Oulu, Finland

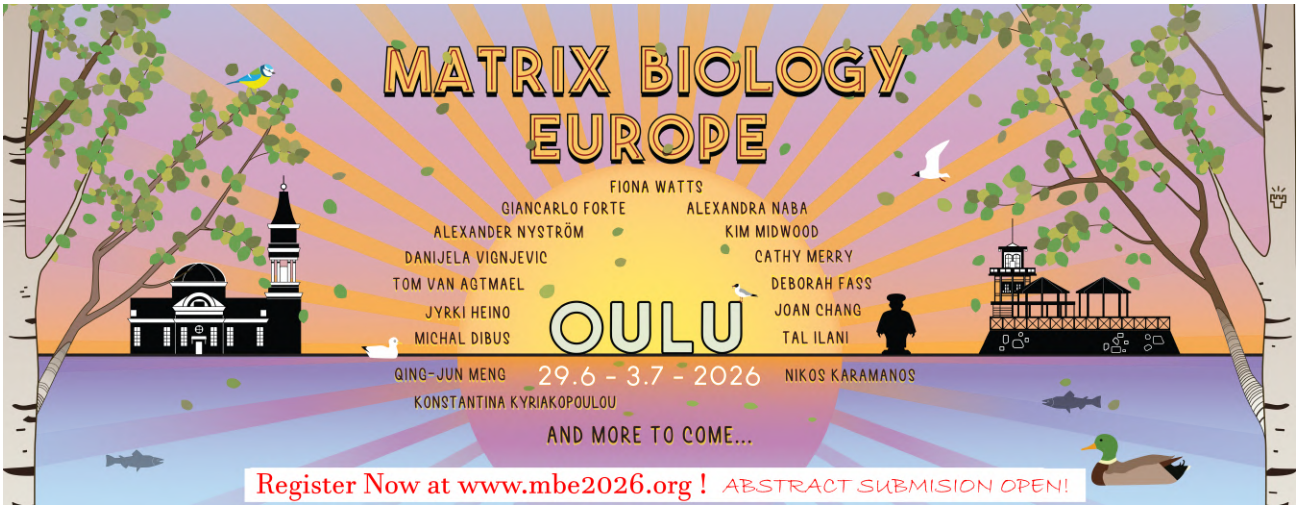
Matrix Biology Europe (MBE) is the main European scientific event for the extracellular matrix research community that takes place every other year in a different European city, where hundreds of extracellular matrix aficionados gather to discuss the latest findings in the field.
20 years past the XXth Meeting of the Federation of European Connective Tissue Societies, matrix biology returns to Oulu, Finland, from 29 June to 3 of July 2026 to bring together scientists from academia and industry. In addition to cutting-edge research, MBE2026 will celebrate excellence across the matrix biology community by hosting the prestigious Rupert Timpl Award and the Dick Heinegård Young Investigator Award. These awards recognize outstanding scientific contributions and emerging talent, underscoring MBE's commitment to scientific excellence, mentorship, and the next generation of leaders in extracellular matrix research.
We envision this meeting as a catalyst for the future of matrix biology, uniting generations of researchers to welcome new perspectives and to ignite the exchange of bold, cutting-edge discoveries.

EARLY-BIRD DEADLINE FOR ABSTRACT SUBMISSION AND HOTEL DEALS IS 29.4! ACT FAST!!!

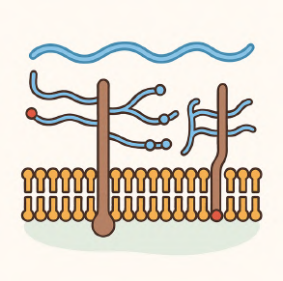
Info and submissions at https://www.mbe2026.org/.

Come and join us in Oulu for this unique scientific adventure!

Valerio Izzi
Conference Chair



2026 Gordon Research Conference (GRC) and Gordon Research Seminar (GRS) on Proteoglycans
June 28 - July 3, 2026
Proctor Academy, Andover, New Hampshire, USA



We are delighted to announce the upcoming **2026 Proteoglycan Gordon Research Conference**, to be held from **June 28 to July 3, 2026**, at **Procter Academy** in **Andover, New Hampshire, USA**.

This international conference will convene leading scientists and emerging researchers to explore the latest advancements in the biology and biochemistry of proteoglycans. Topics will include the synthesis, analysis, and function of **heparan sulfate**, **chondroitin sulfate**, and **hyaluronan**, with a particular emphasis on their roles in health and disease -including **cancer**, **infectious diseases**, and **neurological disorders**.

Confirmed speakers: Jochen Zimmer (U of Virginia); Peng Wu (Scripps); Salvatore Santamaria (U of Surrey); Linda Hsieh-Wilson (Cal Tech); Steven Pals (U of Amsterdam); Nick Riley (U of Washington); Digankumar Chapla (U of Georgia); Renato Iozzo (Thomas Jefferson U); Stavros Garantziotis (NIH/NIEHS); Marco Guerrini (Ronzoni Inst); Maurizio Pacifici (CHOP, Philadelphia); Baohong Zhao (Cornell U); Ding Xu (Emory U); Makarand Risbud (CHOP, Philadelphia); Garron Dodd (U of Melbourne); Peng Zhang (Case Western Reserve U); Clemence Blouet (Cambridge U); Lianchun Wang (U of S Florida); Riccardo Gottardi (CHOP, Philadelphia); Chunyu Wang (Rensselaer Polytech Inst); Jessica Kwok (U of Leeds); Joe Hippensteel (U of Colorado); Andrea Reszegi (U of Florida); Alice Brown (NIH/NCI); Christina Sigurdson (UCSD); Wantong Yao (M.D. Anderson); Hiroshi Nakato (U of Minnesota); Xuefei Huang (Michigan St U); Janice Walker (Thomas Jefferson U); Akankshi Mujal (Duke U); Pyong Woo Park (Harvard Med Schl); Aaron Petry (U of Utah).
And, back by popular demand, our last night party on July 2nd, 2026, will host Nick's Other Band, the live band that has been a huge hit in previous conferences!

We look forward to welcoming you to an exciting and inspiring conference.

Jian Liu (U of North Carolina) and Rashmin Savani (U of Florida)
Meeting Chairs

Vice Chairs: Melanie Simpson and Martin Götte
Venue: Proctor Academy, Andover, NH (USA)
Website: https://www.grc.org/proteoglycans-conference/2026/

Danish Society for Matrix Biology Annual Meeting 2026

We are delighted to announce the date for the DSMB Annual Meeting, to be held on Monday 17 August at the Mærsk Tower, University of Copenhagen.
Our keynote speaker will be Professor Dieter Reinhardt (McGill University), who will present a talk with the preliminary title: "Extracellular Matrix Dynamics Across Tissues: Insights from Adipose Tissue and Bone".

Registration will open in 1 May and will be free for DSMB members [annual membership (period June 2026-May 2027): 300 DKK].

Abstract submission for oral and poster presentations will open alongside registration, with prizes awarded for outstanding presentations. Further details and the full programme will follow in due course.

Abstract deadline 6 July.
Registration deadline 7 August.

Please save the date and share with your colleagues.

The 13th European Elastin Meeting (EEM2026)
August 18-21, 2026 | Copenhagen, Denmark

EEM 2026 will bring together leading experts from across the life and physical sciences to explore the latest advances in elastin and elastic fiber biology – from molecular structure to clinical application. One of the key themes of the programme is diagnosis, damage repair, and treatment of elastin-related diseases.

Sessions will cover:

- Elastic fiber structure and function in tissues like skin, lungs, and blood vessels
- Age-related degeneration and diseases such as atherosclerosis, emphysema and skin aging
- Elastin-mediated signaling pathways in inflammation and tissue remodeling
- Elastin-derived biomaterials for regenerative therapies
- Cutting-edge techniques to study elastin and related ECM proteins at the molecular and tissue level

Join us in Copenhagen, Denmark | 18–21 August 2026, to connect research, clinical insight, and innovation in the field of extracellular matrix biology.

Chair: Andrea Heinz

Local Organizing Committee
Michael Davies
Christine Chuang

Website: https://eem2026.org/


FOR 2722
MUSCULOSKELETAL
EXTRACELLULAR
MATRIX
International Symposium
ECM Dynamics: Shaping Tissues And Disease
September 9-10, 2026
Cologne
https://for2722.uni-koeln.de/
UNIVERSITÄT
ZU KÖLN
UNIKLINIK
KÖLN
DFG

FEBS Advanced Lecture Course "Extracellular matrix in health and disease: Structural dynamics, cell–cell communication, and microbiome crosstalk"
22 – 27 September, 2026 | Eretria, Greece

We are pleased to announce the FEBS Advanced Lecture Course "Extracellular matrix in health and disease: Structural dynamics, cell–cell communication, and microbiome crosstalk", which will take place in Eretria, Greece from 22-27 September 2026. This interdisciplinary course will bring together leading international experts and early-career researchers to explore the extracellular matrix and its dynamic interplay with the immune system and the tissue-associated microbiome—three tightly interconnected systems that collectively regulate tissue homeostasis, regeneration, aging, and disease.

The course will provide participants with exposure to cutting-edge concepts and methodologies through a combination of introductory and advanced lectures, interactive discussions, and meet-the-expert sessions. Key topics include ECM structure-function relationships, matrix remodeling and immune regulation, microbiome-driven modulation of inflammation, stem cell niche dynamics, and advanced experimental models such as organoids and decellularized scaffolds. Complemented by poster sessions, mentoring, and networking opportunities, the course offers a highly collaborative environment. Building on the strong legacy of previous FEBS Advanced Lecture Courses on ECM courses (2007–2023), this event adopts a uniquely integrative perspective on ECM-immune-microbiome crosstalk and aims to equip participants with the tools needed to advance research in this rapidly evolving field. FEBS Youth Travel Fund (YTF) grants will be available.

Nikolaos Afratis, Nikos Karamanos, Martin Götte, Laurent Duca, Valerio Izzi
Course Organizers

Website: https://extracellularmatrix2026.febsevents.org

ASMB 2026 Workshop on Basement Membranes
December 2-5, 2026
The University of Manchester in Manchester, United Kingdom

The ASMB and the University of Manchester will once again offer a Basement Membrane Worksop. Please save the date in your diaries and check back here for more details very soon!

Job Positions

Faculty Position in Arthritis Research

Cleveland Clinic
DEPARTMENT OF BIOMEDICAL ENGINEERING
FACULTY POSITION IN **ARTHRITIS RESEARCH**

Cleveland Clinic's Department of Biomedical Engineering (BME) in collaboration with the Department of Orthopaedic Surgery, invites applications for a faculty position to lead a cutting-edge research program focused on biology or therapeutics of arthritis. Areas of particular interest, include, but are not limited to cellular and molecular mechanisms of joint disease in humans and/or animal models, inflammation, aging and microbiome as they relate to OA, biochemical and genetic biomarkers for diagnosing and predicting disease progression, and identifying therapeutic targets and drug discovery.

This hire will be expected to build an independent, yet highly collaborative, extramurally funded research program at the frontiers of joint disease. The primary appointment will be within the Department of Biomedical Engineering with a secondary appointment in the Department of Orthopaedics. The recruited research program is expected to complement existing strong research programs spanning both departments, including advanced musculoskeletal imaging, arthroplasty, sports, shoulder, computational modeling, extracellular matrix and proteases and clinical research including patient reported outcomes. Cleveland Clinic has operated for over 100 years on the principle of bringing innovative teams together to advance care for patients. Today, we are a world leader in science-based healthcare. The Department of Biomedical Engineering (BME) is situated within Cleveland Clinic Research, which is home to the organization's basic, translational and clinical research activities (https://www.lerner.ccf.org/). With total annual research funding of $479 million in 2025, over 1,800 people (including about 235 principal investigators and 650 trainees) participate in research programs focusing on heart and vascular, cancer, brain, eye, metabolic, microbiome, musculoskeletal, inflammatory and fibrotic diseases. We are currently constructing over 400,000 square feet of new research space, housing state-of-the-art laboratories, technologies and computational resources. In addition, Cleveland Clinic's global footprint provides a wealth of resources to support research throughout the enterprise, including at our locations in Northeast Ohio, Florida, London and Abu Dhabi.

Exceptional core services (https://www.lerner.ccf.org/cores/) provide support in microscopy and other imaging methods; genomics and transcriptomics; proteomics and metabolomics; biostatistics and bioinformatics; gnotobiotic facility & others. Other state-of -the-art resources and facilities include the Global Center for Pathogen & Human Health Research, the Center for Therapeutics Discovery, which operates like an in-house pharmaceutical company and is one of the largest drug discovery initiatives in Northeast Ohio, the institution's Biosafety Level 3 (BSL-3) research laboratory dedicated to studying highly pathogenic infectious diseases, and healthcare's first on-premises IBM Quantum System One supercomputer.

Cleveland Clinic's clinical departments of Orthopaedics and Rheumatology are ranked among the top in the US. As a result, in addition to robust laboratory resources musculoskeletal scientists have access to strong clinical collaborators, data and samples from thousands of patients receiving musculoskeletal care annually. Institutional data and computing infrastructure integrate system-wide demographic, socioeconomic, disease, surgical, treatment, imaging and patient experience data, as well as healthcare utilization and cost. In 2022, a central biorepository was founded that enables systematic prospective banking of synovial fluid, fat, cartilage, and bone from patients undergoing surgery for knee and shoulder conditions. Our Musculoskeletal Research Center brings together our robust musculoskeletal research

community and supports programmatic initiatives including the Cleveland Clinic Center of Excellence in Osteoarthritis and the Arthritis Foundation (AF) Osteoarthritis Imaging Center.
Although not required, teaching opportunities are available through our Department of Molecular Medicine and the Cleveland Clinic Lerner College of Medicine (CCLCM) of Case Western Reserve University (CWRU). Collaborations and appointments are possible at one of our neighboring academic (CWRU, Cleveland State University, Kent State University, University of Akron) or federal institutions (Louis Stokes Cleveland VA Medical Center, NASA Glenn Research Center). A full secondary faculty appointment and teaching opportunities are available in the CWRU Department of Biomedical Engineering through the CC-CWRU BME Alliance (https://engineering.case.edu/ebme/about/alliance). These arrangements provide access to a diverse portfolio of graduate and undergraduate trainees.
We desire an individual with proven skills in grant writing, leadership, organization, innovation, and interpersonal communication. Competitive candidates will hold a doctorate in an appropriate scientific or medical discipline, have a publication record in high-quality peer-reviewed journals, demonstrate established or high potential for funding and be enthusiastic about translation of their research. Applications will be considered at all faculty ranks (Assistant, Associate, and Full).
A generous start-up package is available to support this recruitment, including financial resources for salary, operations, and equipment commensurate with the rank of the individual. Ongoing financial support and commitment beyond the start-up period is provided for all Cleveland Clinic Research faculty.
Salary range: $135,000 - $309,000
The pay range displayed on this job posting reflects the anticipated range for new hires. A successful candidate's actual compensation will be determined after taking various factors into consideration such as the candidate's work history, experience, skill set, and board certification. This is not inclusive of the value of Cleveland Clinic's benefits package, which includes among other benefits, healthcare/dental/ vision, and retirement.
Interested applicants should submit:
• A letter of application
• Complete curriculum vitae
• 1- to 2-page research plan and statement of current and future research goals
• Contact details of three references

Send (preferably by email) the above materials and direct any inquiries to:

Kathleen Derwin, PhD
Chair, Arthritis Research Search Committee
Department of Biomedical Engineering / ND20
Cleveland Clinic
9500 Euclid Avenue
Cleveland, OH 44195
E-mail: BMEJointDisease@ccf.org Phone: 216-408-7930

The Cleveland Clinic is a not-for-profit, multi-specialty academic medical center that integrates clinical and hospital care with research and education. Cleveland Clinic is nationally ranked and globally recognized as a world leader. More information about the Cleveland Clinic and its relevant institutes, departments and resources is provided at https://my.clevelandclinic.org/.
Cleveland Clinic is pleased to be an equal employment opportunity employer.
Smoke/drug free environment.

Postdoctoral or Engineer Position in Radio-Onco-Immunology

Head and neck tumors are still a deadly disease where ionizing irradiation is a major pilar of treatment. However, radiotherapy can also induce an immunosuppressive tumor microenvironment where the extracellular matrix molecule tenascin-C recently was shown to play several roles promoting tumor regrowth (Loustau et al., 2026, EMBO Mol Med). We have developed the novel MAREMO peptide to target tenascin-C and have found that it activates anti-tumor immunity, which subsequently induces tumor regression and supports radiotherapy effects in spheroid cultures. Here we like to determine in more detail in 3D cell culture and in vivo tumor models how targeting tenascin-C with the MAREMO peptide impacts tumor immunity. Recent publications: Li 2024, PNAS; Benn 2023, Sci Adv, Fonta 2023, Matrix Biol; Loustau 2022, Matrix Biol; Yilmaz 2022, J Cell Sci; Murdamoothoo 2021, EMBO Mol Med; Deligne 2020, Cancer Immun Res; Spenle 2020, Cancer Immun Res.

Our international laboratory (https://orend-tme-group.com) is located in the center of Strasbourg and belongs to the INSERM unit 1109 dedicated to immunology research on autoimmune diseases, virology and cancer.

This position is offered for 12 months with a potential renewal.
Keywords: onco-immunology, tumor immunity, tumor microenvironment, tenascin-C targeting.

Candidate profile: We are seeking a highly motivated PhD or research engineer who wants to develop his/her own research project in a good team-working spirit. The candidate must be strongly motivated for comprehensive research using multiple technologies. The candidate should speak English and have knowledge and experience in cancer immunology, particularly in murine tumor models, histology, cell culture, biochemistry and flow cytometry. Specific expertise in bioinformatics is a plus.

Application: Please send a concise cover letter with a statement of research interests and a summary of previous research activity and achievements along with a detailed curriculum vitae and two reference letters to Gertraud Orend: gertraud.orend@inserm.fr.

ISMB Membership: Become a Member of ISMB

ISMB is dedicated to promoting matrix biology research on a global scale and to facilitating communication among matrix-related organizations and researchers from different countries. Junior members are eligible for discounted registration fees at matrix biology meetings supported by ISMB. The Society sends out newsletters highlighting recent research advances, descriptions of matrix biology resources, new appointments and awards, together with announcements of relevant meetings.
Every two years, the Society presents the Rupert Timpl Award to a young scientist (<40 years old), who is starting on their independent career, for the best paper related to matrix biology published in the previous two years and gives the Distinguished Investigator Award for lifetime achievement in the field of matrix biology. ISMB sponsors travel grants for young scientists to attend international matrix meetings. If you work in the matrix biology area, consider becoming a member of ISMB to support the international matrix community and give your input on ways to improve interactions and communication.

Message from ISMB Treasurer

Dear ISMB member,

At the beginning of each year, ***we kindly ask you to pay your annual 2026 ISMB membership subscription fee.***

As you know, ISMB supports matrix biology activities worldwide. Thanks to membership subscriptions, last year we were able **to sponsor five matrix biology conferences in Europe, Australia and the USA**, and **provide seven international travel grants to help young scientists attend meetings** in the USA.

In 2025 we sponsored the Matrix Nexus (joint German-Nordic-Belgian Matrix Biology Societies) Meeting (26-28 March, Freiburg, Germany), the 15th Conference of the International Society for Hyaluronan Sciences (08-12 June, St. Charles, Illinois, USA), the Collagen Gordon Research Conference (06-11 July, Colby Sawyer College, New London, USA), the 13th International Proteoglycan Meeting (27-31 October at Lorne, Victoria, Australia), and the ASMB 2025 Biennial Meeting (16-19 November, Baltimore, Maryland, USA).

We also granted seven international travel awards to attend the Collagen Gordon Research Conference and Seminar (05-11 July, New London, USA), the Elastin, Elastic Fibers and Microfibrils Gordon Research Conference and Seminar (26 July – 1 August, Manchester, New Hampshire, USA), and the ASMB 2025 Biennial Meeting (16-19 November, Baltimore, Maryland, USA).

In addition, we provide information on our web site (www.ismb.org), and ISMB continues to produce regular newsletters packed with news about developments in the field (the next issue will be released shortly).

Of course, ISMB will continue to support matrix biology worldwide in 2026 by sponsoring meetings and providing international travel grants to young scientists (full details on the web site: www.ismb.org). However, in order to do so, **we need your continued support**.

Please renew your membership right now, by using our convenient online payment system: **https://www.ismb.org/join**.

Annual membership fees are:

- 70 euros for regular members,
- 40 euros for postdoc members (5-8 years after Ph.D. and without a faculty position),

- 20 euros for junior members (graduate students and postdocs up to 5 years after Ph.D.),
- 20 euros for retired members.

For those who also wish to subscribe to the *Matrix Biology* journal via the ISMB website using the special rates for ISMB members, subscriptions are now 78 euros for the on-line version of *Matrix Biology* and 136 euros for both the print and on-line version of *Matrix Biology*.

Membership runs from **January 1 to December 31**.

Finally, if you no longer wish to remain a member of ISMB, please let me know.

Best wishes,

Ulrich VALCOURT
ISMB Treasurer

ISMB Council Subcommittees

Meetings and travel grants
Ruud Bank (The Netherlands, chair)
Alexandra Naba, Suneel Apte (USA)
Tom Cox, Hiromi Yanigasawa (Pan-Pacific)

Outreach committee
Valerio Izzi (Finland)
Zoi Piperigkou (Greece)
Konstantina Kyriakopoulou (Germany)
Chloé Yeung (Denmark)

Follow the ISMB on Twitter
ISMB@IntSocMatBio https://twitter.com/intsocmatbio

𝕏 ISMB Correspondents of National Societies for Matrix Biology

The ISMB together with National Societies for Matrix Biology continues to strengthen the visibility of Matrix Biology Research on social media. **Please include @IntSocMatBio on your posts or contact the representatives of the Societies** (see below). We would be happy to share your announcements with the #MatrixBiology world!

International Society for Matrix Biology (ISMB) – 𝕏 @IntSocMatBio
Valerio Izzi, University of Oulu (Finland) valerio.Izzi@oulu.fi

American Society for Matrix Biology (ASMB) – 𝕏 @amsocmatbio
Alexandra Naba, University of Illinois, Chicago (USA) anaba@uic.edu

British Society for Matrix Biology (BSMB) – 𝕏 @BSMB1
Michal Dudek, University of Manchester (UK) michal.dudek@manchester.ac.uk

Danish Society for Matrix Biology (DSMB) – 𝕏 @DSMB_dk
Christine Chuang, University of Copenhagen (Denmark) cchuang@sund.ku.dk

Finnish Connective Tissue Society (FSMB) – 𝕏 @FinnSocMatBio
Valerio Izzi, University of Oulu (Finland) Valerio.izzi@oulu.fi
Piia Takabe, University of Eastern Finland, Kuopio (Finland) piia.takabe@uef.fi

French Society for Matrix Biology (SFBMec) – 𝕏 @SFBMEc
Patricia Albanese, University of Créteil (France) albanese@u-pec.fr

German Society for Matrix Biology (DGMB) – 𝕏/Twitter @Matrixbiologie
Julia Marzi, Eberhard Karls University Tübingen (Germany) julia.marzi@uni-tuebingen.de

Hellenic Society of Biochemistry and Molecular Biology (HSBMB) – 𝕏/Twitter @HSBMB_official
Achilleas Theocharis, University of Patras (Greece) **atheoch@upatras.gr**

Matrix Biology Ireland (MBI) – 𝕏/Twitter @MBIreland
Alexandre Trotier, National University of Ireland, Galway (Ireland) A.TROTIER1@nuigalway.ie

Matrix Biology Society of Australia and New Zealand (MBSANZ) – 𝕏/Twitter @MatrixBioANZ
Luise Kung, Murdoch Childrens Research Institute, Melbourne (Australia) louise.kung@mcri.edu.au

Swiss Society for Matrix Biology (SSMB) – 𝕏/Twitter @SwissMatrixBio
Collin Ewald, ETH Zurich (Switzerland) collin-ewald@ethz.ch

Recent articles published in Matrix Biology

Transmembrane and multiplexin collagens in development and pathobiology, Pihlajaniemi T, *Matrix Biology*, 2025, 142, 11-20, 10.1016/j.matbio.2025.09.005

Abstract: At its best, it is exhilarating to make unexpected discoveries when addressing carefully formed scientific hypotheses. This review depicts my scientific journey in the field of extracellular matrix biology, and more specifically in collagen research, starting in 1978 and continuing with exciting findings up to the present day. While recounting my early work on the enzymes of collagen biosynthesis, the focus will be on our discoveries of new types of nonfibrillar collagen: type XIII collagen, belonging to the MACIT subgroup among the collagen family of proteins, and types XV and XVIII collagens, constituting the multiplexin subgroup. We have investigated these collagens through molecular biological approaches in order to define their primary structures, and through biochemical and cell biological work to understand their special molecular properties. Furthermore, the generation of many mouse models has led us to exciting studies of the roles of these collagens in adipose tissue, bone, eye, heart, kidney, liver, peripheral nerves, skin, and cancer models, although it has of course also been rather daunting in terms of choosing the correct approach for each tissue. The work on animal models has nevertheless resulted in a broad understanding of the *in vivo* significance of these collagens, forming a fruitful basis for studying their relevance to human diseases, including malignant processes. Our conclusions have been that these collagens can contribute to the stability of the extracellular matrix and tissue structures, *e.g.,* the basement membrane and the adjacent fibrillar matrix in the case of the multiplexins and the motor synapse in the case of the MACIT type XIII collagen, and more unexpectedly, that they possess major roles as extrinsic regulators of the fates and functions of cells.

FAM20C and FAM20A in normal and ectopic mineralization: A focus on oro-renal syndromes, Baker A, Al Tarrass M, Chatziantoniou C, Kozyraki R, *Matrix Biology*, 2025,142, 58-85, 10.1016/j.matbio.2025.11.002

Abstract: FAM20C is part of the FAM20 family and is crucial for phosphorylating secreted proteins. It plays roles in various biological processes, including cellular calcium regulation and cardiovascular function. Pathogenic variants of *FAM20C* cause Raine syndrome, resulting in osteosclerotic dysplasia or hypophosphatemic rickets. Its paralog, FAM20A, is a secreted pseudokinase needed for optimal FAM20C activity. Mutations in *FAM20A* cause Enamel-Renal Syndrome. Common features in both syndromes include Amelogenesis Imperfecta, gingival fibromatosis and ectopic mineralization. We summarize current knowledge about the activity, interactions and regulation of FAM20C and FAM20A, with a focus on the possible role of bioactive lipids like sphingosine in activating FAM20C. We highlight the involvement of FAM20A and FAM20C in gingival fibromatosis, a fibrocalcifying disorder directly linked to the dysfunction of these proteins and the underlying molecular mechanisms. Additionally, we provide an overview of how FAM20C and FAM20A influence calcium homeostasis and mineralization. Since FAM20C-mediated phosphorylation is crucial in oral health, we detail how specific substrates such as osteopontin, periostin, or fetuin contribute to normal and ectopic mineralization and periodontal health. Although many questions about the roles of FAM20A and FAM20C in both oral and systemic diseases remain unresolved, targeting their activities could offer promising therapeutic options.

Laminin-511-functionalized fibrin gel enables in-gel proliferation of human induced pluripotent stem cells, Taniguchi Y, Takizawa M, Hada A, Ishimaru A, Sekiguchi K, *Matrix Biology*, 2025, 142, 21-32, 10.1016/j.matbio.2025.10.003

Abstract: Fibrin is a biocompatible hydrogel that is widely used as a surgical sealant and as a scaffold for in vitro cell culture. Here, we engineered a heterotrimeric chimera between fibrinogen and laminin-511 by connecting the N-terminal self-polymerization domain of fibrinogen with the C-terminal integrin-binding domain of laminin-

511 via their coiled-coil regions. The resulting chimeric protein, designated Chimera-511, binds to fibrinogen in a thrombin-dependent manner and exerts integrin-binding activity in a fibrin(ogen)-bound form. Chimera-511 co-polymerizes with fibrinogen to form a fibrin gel endowed with the potent integrin-binding activity of laminin-511, thereby enabling robust three-dimensional proliferation of human induced pluripotent stem cells while maintaining their pluripotency marker expression and trilineage differentiation potential. This functionalized, biodegradable fibrin gel provides a defined and clinically compatible three-dimensional scaffold for stem cell culture, with potential applications in both basic research and regenerative medicine.

Phosphorylation of UDP-glucose dehydrogenase increases glycosaminoglycan biosynthesis and promotes tumor cell motility, spheroid growth, and therapeutic resistance, Utz AR, Ma L, Hilovsky D, Zimmer BM et al., *Matrix Biology*, 2025, 142, 33-45, 10.1016/j.matbio.2025.10.004

Abstract: UDP-glucose 6-dehydrogenase (UGDH) is an essential enzyme that catalyzes the oxidation of UDP-glucose to UDP-glucuronate. UGDH is elevated in multiple cancers, including prostate cancer, and is functionally implicated in castration resistant recurrence. UGDH is composed of three dimeric units that associate stably as a hexamer in cellular conditions. The dynamic reorganization of noncovalent interactions at the dimer contact interfaces is essential for UGDH activity. In this study, we examined the functional relevance of a putative AGC kinase motif located at the dimer-dimer interface. We demonstrated that UGDH is phosphorylated in LNCaP cells, specifically at serine 316, by RSK2, p70S6K, and SGK1. To determine the functional implications of UGDH S316 phosphorylation, we generated and characterized phosphomimetic (S316D) and phosphodeficient (S316A) point mutations. Intrinsic properties of the purified recombinant proteins were only modestly affected by the substitutions. The stable overexpression of UGDH S316D in LNCaP cells significantly increased the rate of N- and O-glycan synthesis, as well as the production of hyaluronan and sulfated glycosaminoglycans, while reducing DHT glucuronidation, resulting in significant increases in growth of tumor spheroids, cell proliferation and motility, and resistance to enzalutamide. In contrast, UGDH S316A expression reduced the production of glycans and glycosaminoglycans, restored DHT glucuronidation, and impaired growth and motility. Overall, our results support UGDH phosphorylation as a point of control for intracellular and cell surface glycan production, thereby regulating cell proliferation, anchorage dependence, motility, and tumor cell therapeutic resistance.

Matrix metalloproteinase 13 (MMP-13) processing of type II collagen is altered by antibodies and citrullination found in the early stages of rheumatoid arthritis, Knapinska AM, Tokmina-Roszyk D, Haag S, Lauer-Fields JK, Singh C, Stawikowska R, He Y, Askling J, Holmdahl R, Fields GB, *Matrix Biology*, 2025, 142, 46-57**,** 10.1016/j.matbio.2025.11.001

Abstract: A subset of rheumatoid arthritis (RA) is the production of autoantibodies, including antibodies to citrullinated proteins (ACPA) and antibodies to type II collagen (AC2A). Type II collagen (COL2) is the major protein in joint cartilage and is a target of arthritogenic autoantibodies. We could confirm that sera from RA patients react with both citrullinated and native triple-helical COL2 epitopes. We examined the modulation of COL2 processing by matrix metalloproteinase 13 (MMP-13), the main collagenase responsible for degradation of articular cartilage. Anti-COL2 antibodies (AC2A) targeting the C1 epitope (residues 359–363) partially inhibited intact COL2 and fragment hydrolysis, resulting in two distinct fragments in the 25–30 kDa range. The AC2A targeting the E10 epitope (residues 777–783, the region where MMP-13 initially cleaves COL2) partially inhibited intact COL2 and fragment hydrolysis, resulting in a distinct fragment of ∼30 kDa. The AC2As targeting the F4 epitope (residues 932–936) partially inhibited collagen fragment hydrolysis, resulting in four distinct fragments in the 20–30 kDa range. Sequencing of isolated fragments revealed 14 terminated cleavage sites. Citrullination of the COL2 cleavage site reduced MMP-13 efficiency, which should further exacerbate fragment production rather than complete digestion. The results indicated that, under normal maintenance, MMP-13 cleaves COL2 initially at the 775–776 bond, followed by further digestion of COL2 fragments. Citrullination slows the initial processing

of COL2 by MMP-13. In concert, AC2As inhibit the action of MMP-13 at different stages, resulting in production of collagen fragments differing in composition encountered under normal circumstances. The abnormal COL2 fragments could activate the immune system to be more pathogenic or regulatory as well as modify chondrocyte functions, and thereby play a role in the initiation of RA.

Follow the science: How fat cells taught us about scarring and ECM homeostasis, Horsley V, *Matrix Biology*, 2026, 143, 89-91, 10.1016/j.matbio.2025.12.004
Abstract: This article describes the journey of my laboratory team as we became fascinated with the dynamic changes that occurred to adipose tissue in the skin during tissue injury and fibrosis. I discuss how lineage tracing and molecular manipulation of adipocyte lineage cells led us to discover novel ways that fat cells contribute to ECM homeostasis in the skin. This work revealed the importance of adipocyte plasticity and cell communication during tissue repair and as they respond to fibrotic stimuli.

Zebrafish *col4a1* loss-of-function models mirror key neurovascular and ocular features of COL4A1/A2 syndrome and enable human variants assessment *in vivo*, Paradisi G, Bonavolontà V, Venditti M, Fasano G, Pedalino C, Del Bene F, Tartaglia M, Lauri A, *Matrix Biology*, 2026, 143, 63-82, 10.1016/j.matbio.2025.11.004
Abstract: Pathogenic variants in *COL4A1* and *COL4A2*, encoding type IV collagen α1 and α2 chains—core components of all basement membranes—cause a multisystem disorder with variable expressivity. Affected individuals commonly present with cerebral small vessel disease (cSVD), unmanageable intracerebral haemorrhage (ICH), drug-resistant epilepsy, microphthalmia, and congenital cataract. Severe phenotypes are often linked to glycine substitutions that disrupt α1/α2 heterotrimer assembly, though insertions, deletions, and haploinsufficiency seem to also be pathogenic. Limited insight into collagen IV α1 and α2 biology and how specific variants affect their functions—coupled with a lack of rapid *in vivo* assays for functional variants classification—hampers patient stratification and therapy development. Here, we established and characterized two complementary *col4a1* knockdown (KD) models in zebrafish. Taking advantages of their transparency and rapid development we set-up *in vivo* assays for neurovascular and ocular phenotyping. Both models reproduced key features of human disease, including ventriculomegaly, vascular fragility with spontaneous and trauma-induced ICH, microphthalmia, and cataracts. Notably, expression of human wild-type COL4A1 partially rescued most of the observed defects, while pathogenic glycine-substitution variants failed to do so. These findings validate *col4a1* KD in zebrafish as a robust *in vivo* model of some aspects of COL4A1/A2 syndrome, highlighting a conserved role of collagen IV α1 in neurovascular and ocular development. Our results also support haploinsufficiency as a contributing pathogenic mechanism, alongside dominant-negative effects. This work lays the foundation for the use of zebrafish to support rapid *COL4A1* and *COL4A2* variants pathogenicity assessment and mechanistic studies, with the potential to accelerate development of targeted therapies.

Furin-like cleavage at the C1-C2 linker region of the α3 chain is not required for collagen VI assembly, Pasanen-Zentz AL, Zhu M, Schmitz S et al., *Matrix Biology*, 2026, 143, 1-13, 10.1016/j.matbio.2025.11.003
Abstract: Collagen VI is a heterotrimeric, ubiquitously expressed microfibrillar collagen with a complex intracellular and extracellular assembly process. In addition to a short collagenous region, it is primarily composed of von Willebrand factor A (VWA) domains. Notably, only the C-terminal end of the α3 chain contains other domain types, including a Kunitz-like C5 domain, which has been reported to be necessary for microfibril formation, to function as a matrikine and exhibit biomarker properties. This region of the α3 chain undergoes proteolytic processing, with cleavage sites identified for proprotein convertases, matrix metalloproteinases (MMPs), and bone morphogenetic protein 1 (BMP1). Cleavage by furin-like convertases results in the generation of a mature collagen VI α3 chain lacking its 70 kDa C2-C5 domains. Here, we provide the first characterization of the functional significance of the furin-like cleavage site, demonstrating that while it is constitutively used, it is

not essential for collagen VI assembly, microfibril formation, or skeletal muscle function under physiological conditions, likely due to the presence of redundant cleavage sites. We also present an initial characterization of the biological activity of the released fragments on myoblast cultures showing that they do not affect C2C12 myoblast behaviour or differentiation. These findings deepen our understanding of α3 chain processing and highlight its potential significance for collagen VI assembly and function, including the generation of peptides with potential biomarker and biological activity properties.

High hyaluronan binding and RHAMM expression identify an invasive and metastatic subpopulation in androgen-resistant prostate cancer cells, Tolg C, Price M, Leith S, Miller T, Pavanel H, Nelson AC , Hill KA, McCarthy JB, Turley EA, *Matrix Biology*, 2026, 143, 23-35, 10.1016/j.matbio.2025.11.006

Abstract: Hyaluronan (HA) metabolism in prostate cancer associates with androgen resistance and metastasis. We showed that binding of low molecular weight HA (≤250 kDa) to castration-resistant prostate cancer cells was heterogeneous with most cells binding low amounts of HA (HA^{low}) while a minor subset bound higher amounts of this polysaccharide (HA^{high}). HA^{high} subsets, which were separated by FACS, were stably more metastatic in vivo than HA^{low} comparators. Multiplexed flow cytometry analyses indicated that both subsets displayed similar expression of the HA receptor CD44 while an elevated RHAMM cell surface display was unique to HA^{high} subsets. Genomic deletion of *RHAMM* using CRISPR-Cas9 editing reduced the detection of HA^{high} subsets by 6mer but not 250 kDa HA fluorescent probes, and phenocopied the lower aggressive properties of HA^{low} tumor cells. Few differences in the mutation landscape of $RHAMM^{+/+}$ vs. $RHAMM^{-/-}$ tumor cells were detected but pathway analyses of differentially expressed genes predicted *RHAMM*-loss altered extracellular matrix signaling. Transcriptomic analyses revealed that HA^{high} subsets and $RHAMM^{+/+}$ PC3MLN4 cells shared high expression of follistatin (FST), an activin member of the TGF-β family that is clinically linked to metastases in PCA patients. A causal role for FST in $RHAMM^{+/+}$ tumor cell aggression was assessed using motility as a surrogate marker of invasive capability. FST antibodies blocked $RHAMM^{+/+}$ PC3MLN4 cell migration while conversely, recombinant FST protein rescued the migration deficit of $RHAMM^{-/-}$ comparators. These results define a novel form of prostate cancer cell heterogeneity, identify a method for detecting and isolating highly metastatic subsets and highlight a novel RHAMM-regulated pathway that may be targeted to improve patient management by limiting metastasis.

α-Dystroglycan at the ECM-Cell crossroad: emerging functions of its N-terminal domain, Bigotti MG, Brancaccio A, *Matrix Biology*, 2026, 143, 83-88, 10.1016/j.matbio.2025.12.002

Abstract: Dystroglycan plays a crucial role for cell to extracellular matrix (ECM) adhesiveness in a plethora of different tissues and physio-pathological conditions. It belongs to the dystrophin-glycoprotein complex, whose overall structure has been recently solved, providing fundamental insight into the assembly of its various protein components, including the dystroglycan complex. This inspired us to embark in a timely "recollection journey" of our studies on the dystroglycan domain organization, mainly focusing on the targeted mutagenesis analysis of the α-dystroglycan's N-terminal domain (α-DGN) that we have carried out during the last 30 years. The account of such a journey also reinforces a crucial notion in protein biochemistry: a single amino acid substitution can lead to a significantly improved stability of the whole protein. Over-stabilizing matrix proteins, and proteins in general, has positive repercussions for the study of their structural and functional properties, and it is a crucial tool for developing biotechnological applications. Here we discuss newly emerged data along a series of yet unresolved points concerning the biochemical features and biological role of α-DGN, as well as the possible biomedical use recently emerged for a stabilized single site-directed variant of this protein domain.

Evolutionary constraints on positional sequence, collective properties and sequence style of tropoelastin dictated by fundamental requirements for formation and function of the extracellular elastic matrix, Keeley FW, *Matrix Biology Plus*, 2025, 28, 100183, 10.1016/j.mbplus.2025.100183

Abstract: Elastin is the extracellular matrix protein responsible for properties of extension and energy-efficient elastic recoil in large blood vessels, lung parenchyma and other vertebrate tissues. Monomeric tropoelastin assembles by phase separation into an extended polymeric matrix covalently cross-linked through lysine residues, producing a robust biomaterial able to withstand hundreds of millions of cycles of extension and recoil. Elastin functions as an entropic elastomer, whose properties are the direct result of the inability of the protein to fold into a fixed, stable structure. Most investigations of how the unusual properties of polymeric elastin arise from the sequence of tropoelastin have utilized molecular biological/biophysical methodologies. This study takes an alternative approach, using a comprehensive, well-curated database of Amniote tropoelastin sequences to identify characteristics conserved through >300 million years of evolution. Conserved characteristics included preservation of not only regions of positional sequence but also collective or compositional characteristics derived from but not strictly dependent on positional sequence. A plausible overall consensus sequence for Amniote tropoelastins allowed quantification of residue-by-residue, domain-by-domain and region-by-region levels of sequence conservation. Regions of low positional sequence conservation nevertheless maintained a recognizable sequence style characterized by tandem repeats and partial repeats of short, non-polar motifs. Motif analysis suggested hPGhGG, with numerous insertions and deletions, as the underlying repeating unit in all Amniote tropoelastins. The data identify significant evolutionary constraints dictated by fundamental requirements for formation and functionality of the extracellular elastin matrix, and suggest a rich source of evolutionarily permitted opportunities for modulating properties to meet specific species requirements.

Loss of fibronectin fiber tension is inherent to ECM remodeling in human myocarditis and post-inflammatory fibrosis, Sridhar K, Mehl J, Klingel K, Thiele M, Van Linthout S, Tschöpe C, Duda GN, Vogel V, *Matrix Biology Plus*, 2025, 28, 100182, 10.1016/j.mbplus.2025.100182

Abstract: Viral myocarditis (MC) is associated with extracellular matrix (ECM) remodeling and involves excessive deposition of collagen and other ECM proteins by cardiac fibroblasts, potentially leading to scarring and ECM stiffening, which may subsequently contribute to impaired cardiac functions. Clarifying whether changes in ECM fiber tension are detectable during either the acute or scarring phase could provide a novel, mechanistically relevant mechanobiological signature. Our goal was to ask whether ECM mechano-markers can be identified in the myocardium, beyond excessive collagen fiber deposition, that are associated with the acute infection or the pathological scarring of the human heart, and how this might be associated with the infiltration of macrophages. Left-ventricular (LV) endomyocardial biopsies were obtained from patients (N = 39) with acute myocarditis MC (N = 21) including COVID-19 (N = 4) patients suspected with myocarditis MC and/or impaired LV function, dilated cardiomyopathy (N = 6), inflammatory dilated cardiomyopathy (N = 12) to specify diagnosis and treatment options. Endomyocardial biopsies were analyzed for viral genomes, immune cells infiltration and ECM remodeling. Fibronectin fiber tension was assessed using the fibronectin-binding tension-sensor (FnBPA5), while collagen fiber deposits were visualized using second harmonic generation (SHG) microscopy. While fibronectin fibers were tensed in healthy hearts, histological staining with our novel tension probe FnBPA5 showed that fibronectin fibers had lost their tension in distinct loci in all patient groups. In the acute inflammatory phase (MC), loci with untensed fibronectin fibers were found in close proximity to infiltrated macrophages. In already dilated hearts, biopsies which presented low densities of infiltrated macrophages, thick collagen I/III fiber bundles as visualized by SHG were found in proximity to untensed fibronectin fibers and myofibroblasts, which together are indicative of fibrotic ECM niches where the inflammation has subsided. Comparison of clinical diagnostic and experimental histological data showed clear correlations between altered ECM niche properties and cardiac function deterioration. Our data suggest that relaxed fibronectin fibers are a recurrent feature of myocarditis and associate with measures of cardiac dysfunction. These findings suggest that fibronectin fiber tension might be a mechanobiological signature that warrants validation in larger, longitudinal cohorts and evaluation of in-vivo measurability.

Latent-Transforming growth factor – β Binding protein 1 (LTBP1) in corneal stroma, Poonen-Honig I, Acosta AC, Sun M, Emerick V, Avila MY, Margo CE, Espana EE, *Matrix Biology Plus*, 2025, 28, 100185, 10.1016/j.mbplus.2025.100185

Abstract: We aim to determine the presence and function of LTBP1 in the corneal stroma. We investigated the temporal and spatial corneal expression of LTBP1, and microfibril-associated glycoprotein 1 (MAGP1), known components of the elastic system and regulators of TGF-β storage and latency. Protein quantification −blotting and proteomics-, immunofluorescence microscopy, mRNA analysis and a luciferase assay were used to study the regulation of transforming growth factor β (TGF-β) by LTBP1 in cornea derived fibroblasts and myofibroblasts. Expression of LTBP1 and MAGP1 was found in adult corneas, and absent or minimal in the scleral stroma. Quantitative polymerase chain reaction and protein blotting analyses showed upregulation of these proteins during early postnatal development and deposition in the corneal matrix with tissue maturation. In vitro, LTBP1 regulated the conversion of fibroblasts to myofibroblasts and maintained TGF-β latent in the matrix. This study shows that LTBP1 and MAGP1, regulators of TGF-β activation and elastic fiber components, are found in adult stroma. LTBP1 is a regulator of TGF-β storage and latency and controls conversion of fibroblast to myofibroblast.

Generation of a conditional *Adamts6* mouse allele reveals roles in lung maturation in addition to cardiac and musculoskeletal development, Sirek JM, Rush EH, Darodkar A, Apte SS, Mead TJ, *Matrix Biology Plus*, 2025, 28, 100186, 10.1016/j.mbplus.2025.100186

Abstract: Prior analysis of mouse embryos homozygous for a point mutation (p.Ser149Arg) that abrogated secretion of the protease, ADAMTS6, showed that it is essential for cardiovascular and limb development. Because *Adamts6*$^{S149R/S149R}$ mice do not survive past birth, it is currently not feasible to investigate ADAMTS6 in specific cellular lineages postnatally. Therefore, we generated a conditional allele using CRISPR-Cas9-mediated genome editing to insert unidirectional loxP sites flanking the first coding exon in *Adamts6*, resulting in a frameshift mutation after loxP recombination. Mice homozygous for the unrecombined floxed allele (*Adamts6*$^{fl/fl}$) are viable, fertile, and without overt phenotype. *Adamts6*$^{del/del}$ embryos, generated upon constitutive recombination induced by a *CMV*-Cre transgene, also do not survive past birth and have identical defects in the heart and limbs as *Adamts6*$^{S149R/S149R}$ embryos, demonstrating efficient transgene recombination. In addition to previous defects in cardiovascular and limb development, *Adamts6*$^{del/del}$ embryos have reduced airway branching, thereby identifying a role for ADAMTS6 in lung maturation. This newly generated *Adamts6*^{fl} allele makes feasible analysis of ADAMTS6 secreted by cells of different lineages and during specified temporal windows during developmental processes as well as in disease models.

Revealing sex-specific changes across protein structure in the aging bone extracellular matrix, Tudor J, Eckersley A, Buckley M, *Matrix Biology Plus*, 2026, 29, 100189, 10.1016/j.mbplus.2025.100189

Abstract: The process of aging is an integral but complex component of life that has been intensely studied for decades, from the molecular level to whole organisms. At the tissue level, bone is one of the most difficult to study due to its composite nature of inorganic and organic phases, but advancements in proteomics are enhancing our understanding of the latter, improving our understanding of skeletal aging through identifying temporal changes across the bone proteome. The relative longevity of extracellular matrix (ECM) proteins can make them more susceptible to accumulating damage modifications over time. In addition, their informational density, including their 2D and 3D structure, protein folding, post translational modifications and proteomic composition, as well as their functional importance, has made them a target of interest in the study of aging and medical conditions such as osteoporosis and arthritis. ECM proteins are also increasingly utilised in forensic science for determining biological sex/age because of their longevity. Following recent developments in peptide location fingerprinting methods that improve capabilities of identifying regional changes in protein structure, this

study aimed to identify age-associated regional changes along protein structures in *Rattus norvegicus* from whole limb LC-MC/MS data. Regional changes in protein structure were identified in a variety of collagenous and non-collagenous ECM proteins, providing evidence for increased remodeling in juvenile rats and a reduced ability in adult rats, alongside damage accumulation in the adult ECM. This research highlights the importance of fibrillar collagen remodeling but is also indicative of potential new roles for osteopontin, thrombin, apolipoproteins and wider ECM regulators such as cartilage oligomeric matrix protein. This demonstrates, in this case, the utility of peptide location fingerprinting as a screening tool to identify biomarker candidates of bone aging between juvenile and adult rats.

P-LM421E8, the heparan sulfate chain-conjugated laminin-421-E8 fragment, drives differentiation of human induced pluripotent stem cells into hematopoietic progenitor cells comparable to basic fibroblast growth factor in a chemically defined system, Ninomiya N, Sasaki K, Katori R et al., *Matrix Biology Plus*, 2026, 29, 100188, 10.1016/j.mbplus.2025.100188

Abstract: Human induced pluripotent stem cells (hiPSCs) are a promising source for cell-based and regenerative therapies. In this study, we developed and optimized a chemically defined differentiation protocol to generate hematopoietic progenitor cells (HPCs) from hiPSCs. We demonstrated that basic fibroblast growth factor (bFGF) plays a crucial role in enhancing HPC differentiation, particularly when applied during both the mesoderm (ME) and hematopoietic endothelial (HE) induction stages. Additionally, we explored the use of P-LM421E8, a recombinant fusion protein of laminin421-E8 fragment with domain 1 (D1) of perlecan possessing heparan sulfate (HS) chains. Our findings indicate that P-LM421E8 effectively supports HPC differentiation, generating stable CD34-high/CD117^{+} populations comparable to those produced with bFGF treatment. Furthermore, we observed that HPCs generated on P-LM421E8-coated surfaces exhibited superior natural killer (NK) cell differentiation potential. Although both P-LM421E8 and bFGF supported HPC differentiation, no significant additive effects were observed when used together. This suggests that P-LM421E8 can effectively support HPC differentiation without the need for exogenous bFGF, possibly through enhanced interaction with endogenous FGFs. The structural properties of P-LM421E8, which facilitate retention and presentation of FGFs via HS chains on its D1, may contribute to its effectiveness in promoting HPC development. Our findings establish P-LM421E8 as a potent matrix for HPC differentiation and highlight its promise for refining hematopoietic protocols and advancing cell-based immunotherapies.