



Request for Applications (RFA)

Issued by: Multiple Myeloma Research Foundation (MMRF®)

Program: CoMMpassSM Biospecimen Inventory Access 2026-2027

Key Dates:

| RFA Cycle | RFA Due Date | Scientific Review Period | Notification Target Date | Earliest Anticipated Biospecimen Access* |
|-----------|--------------------|--------------------------|--------------------------|--|
| Cycle 1 | September 15, 2026 | October – November 2026 | November 30, 2026 | January 2027 |
| Cycle 2 | December 15, 2026 | January – February 2027 | February 26, 2027 | April 2027 |
| Cycle 3 | March 15, 2027 | April – May 2027 | May 28, 2027 | July 2027 |

*Biospecimen access may depend on scientific review, sample availability, execution of required agreements, and operational feasibility.

1. Background

The MMRF CoMMpass Study (NCT01454297) is a landmark, longitudinal, multi-center research effort designed to comprehensively map the genomic and clinical landscape of multiple myeloma. Launched in 2011, CoMMpass represents one of the most ambitious precision medicine initiatives in cancer and has generated the largest integrated genomic and clinical dataset ever assembled for a single cancer type. The study followed 1,143 multiple myeloma patients over eight years from diagnosis throughout their treatment, while collecting biospecimens and generating a molecular dataset from bone marrow tumor cells and the tumor immune microenvironment. Use of interim clinical and molecular data has redefined the biological heterogeneity of multiple myeloma while illuminating candidate drivers, drug targets, and prognosis. In the past 2 years, the clinical database was locked, and immune and tumor molecular data have been completed¹⁻³, making this a unique patient dataset for a single cancer. The CoMMpass biorepository contains thousands of bone marrow and whole blood tissue samples, including longitudinal samples, that can support new data generation and important

1. Skerget, S. *et al.* Comprehensive molecular profiling of multiple myeloma identifies refined copy number and expression subtypes. *Nat. Genet.* **56**, 1878–1889 (2024).

2. Pilcher, W. C. *et al.* A single-cell atlas characterizes dysregulation of the bone marrow immune microenvironment associated with outcomes in multiple myeloma. *Nat. Cancer* 1–23 (2026).

3. Ohlstrom, D. J. *et al.* Longitudinal profiling of tumor and immune compartments uncovers patterns of dysregulation and associations with response in multiple myeloma. *Blood Cancer Discov.* (2025).

discoveries. New data can be integrated with existing clinical and molecular datasets revealing associations with biological pathways as well as clinical and/or demographic factors.

2. Purpose

The MMRF invites applications requesting access to biospecimens from the CoMMpass Study for rapid, hypothesis-driven research projects. This streamlined RFA is intended to support time-sensitive, high-impact studies while ensuring responsible stewardship of a limited and valuable biospecimen resource.

Applicants must 1) clearly define the scientific question, 2) justify the number and type of biospecimens requested, and 3) commit to generating high-quality data that will be securely uploaded to the MMRF Virtual Lab™ (VLAB). For clarity, VLAB will be the only database data shall be shared through, including for publication purposes. This RFA is explicitly for procuring CoMMpass biospecimens. Applicants must apply separately for access to clinical and genomic data through VLAB.

3. Eligible Research Scope

Proposed projects should address key biological, translational, or clinical questions in multiple myeloma and may include, but are not limited to:

- Biomarker discovery or validation
- Mechanistic studies of disease progression or treatment response
- Molecular or functional profiling linked to clinical outcomes

Eligible biospecimens may include bone marrow aspirates, whole blood and their derived samples, and nucleic acid aliquots, subject to availability.

4. Eligibility

Applications may be submitted by investigators from academic and non-profit institutions. Applicants must demonstrate:

- Appropriate scientific expertise and infrastructure
- Ability to comply with human biospecimen handling requirements
- Experience with proposed assay methodology and funding to complete planned assays
- Commitment to MMRF data sharing and publication policies (see Section 7, Terms of Access)

5. Application Requirements (maximum 4 pages total)

All applications must be submitted as a single PDF and adhere to the page limits below.

5.1 Project Overview (0.5 pages)

- Project title
- Principal Investigator (PI) and institution
- Key collaborators
- Proposed project duration

5.2 Scientific Question and Rationale (1 page)

Describe the primary research question(s) and supporting rationale, including:

- Brief background and significance
- Relevance to multiple myeloma and patient impact
- Alignment with CoMMpass Study objectives

5.3 Study Design and Approach (1-1.5 pages)

Summarize the proposed experimental and/or analytical approach:

- Key hypotheses
- Assays, platforms, or analytical methods
- Feasibility considerations and potential risks
- High-level statistical or power rationale, if applicable

5.4 Biospecimen Request and Justification (0.5 - 1 page)

Clearly specify the biospecimens requested and justify their use. Here's an example:

| Biospecimen Type | Timepoint / Disease Stage | Number of Samples Requested | Volume Requested (per sample) | Additional notes |
|---------------------------|---|-----------------------------|-------------------------------|--|
| Plasma derived from blood | Baseline samples (and samples at additional timepoints) | 317 | 500 ul | Treatment naïve samples that are high risk as defined by IMWG criteria |

Please refer to the biospecimen inventory table at the end of this document.

Applicants should note:

- Whether longitudinal or matched samples are required
- Acceptable flexibility in sample characteristics, if any

5.5 Data Generation and Sharing Plan (0.5 page)

Describe the data that will be generated and shared with MMRF:

- Data types (e.g., bulk RNA-seq, single-cell, WES/WGS, protein, and other outputs)

- Estimated timeline for data generation
- Commitment to sharing raw and/or processed data with appropriate metadata

6. Review and Decision Criteria

Applications will be reviewed on a rolling or batched basis using the following criteria:

- Scientific merit and clarity of the research question
- Appropriateness and efficiency of biospecimen use
- Feasibility within the proposed timeline
- Value of anticipated data to the broader myeloma research community

MMRF reserves the right to recommend modifications to sample numbers or study scope prior to approval, depending on sample volume availability and data types to be generated.

7. Research Agreement Key Terms

Approved projects will be subject to:

| | |
|-------------------------------------|---|
| <p>1. Purpose</p> | <ul style="list-style-type: none"> • MMRF has spent considerable time and resources to conduct its CoMMpass StudySM over the past 15 years, establishing one of the largest longitudinal biorepositories of samples from patients with multiple myeloma. • Recipient desires to access this unique repository of high-quality samples to conduct research. |
| <p>2. Biological Samples</p> | <ul style="list-style-type: none"> • MMRF retains ownership of the biological samples. • MMRF provides the biological samples “AS IS” without any warranty. • Recipient receives a license to use the samples solely for the purpose of the Research Project. • Recipient shall return or destroy the samples, at MMRF’s direction, upon completion of the Research Project. |
| <p>3. Data</p> | <ul style="list-style-type: none"> • Recipient owns the Research Data derived from the Research Project. • MMRF receives an irrevocable, perpetual, world-wide, non-exclusive, royalty-free, sublicensable license to the Research Data. • The only database for public access for any published data resulting from the Research Project shall be the MMRF Virtual Lab. • MMRF can freely share the Research Data through the MMRF Virtual Lab after 18 months embargo period to allow time for publication. |
| | |

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|---------------------------------|---|
| 4. Intellectual Property | <ul style="list-style-type: none"> Requirement to disclose Inventions derived from the Research Project to MMRF. |
| 5. Publication | <ul style="list-style-type: none"> MMRF to receive 30 days prior written notice of any publication. MMRF acknowledgement in any publication shall state “Biological Samples are provided through a collaboration with the Multiple Myeloma Research Foundation (MMRF) CoMMpass StudySM.” |
| 6. Term and Termination | <ul style="list-style-type: none"> Agreement will terminate once Research Project is completed and data is transferred to MMRF. |
| 7. Insurance | <p>Each party is responsible to carry insurance to cover the liabilities under the agreement throughout the term.</p> |
| 8. Indemnification | <p>Mutual indemnification from and against any and all claims, liabilities, damages, losses, and expenses (including reasonable attorneys’ fees) arising out of or resulting from the negligent acts, omissions, or willful misconduct of the Indemnifying Party in connection with this Agreement.</p> |

8. Submission Instructions

Submit applications as a single PDF to research@themmrf.org with subject line “CoMMpass Biospecimen Inventory Access RFA 2026-2027 – PI NAME”.

File name format: *CoMMpassBiospecimenRFA_2026-2027_PIName_ProjectTitle.pdf*

For all scientific and administrative inquiries, please contact Chaitanya (Chuck) Acharya, PhD and Steven Foltz, PhD via email at research@themmrf.org.

CoMMpass Biospecimen Availability

Number of patients

Bone Marrow

| | | Total | Baseline | Relapse | Remission | Base + Rel | Base + Rem | Base + Rel + Rem | Median volume (μ L) |
|-------|--------|-------|----------|---------|-----------|---------------|---------------|------------------------|--------------------------------|
| Cells | CD138- | 714 | 491 | 141 | 82 | 62 | 32 | 11 | 1000 (100-1250) |
| | CD138+ | 261 | 215 | 27 | 19 | 12 | 5 | 0 | 1000 (500-1000) |
| DNA | CD138+ | 609 | 516 | 86 | 7 | 58 | 4 | 1 | 15 (1-321) |
| RNA | CD138+ | 693 | 603 | 85 | 5 | 63 | 3 | 0 | 15 (0.5-150) |

Whole Blood

| | | Total | Baseline | Relapse | Remission | Base + Rel | Base + Rem | Base + Rel + Rem | Median volume (μ L) |
|--------|----------|-------|----------|---------|-----------|---------------|---------------|------------------------|--------------------------------|
| DNA | CD138+ | 21 | 13 | 8 | 0 | 2 | 0 | 0 | 15 (3-115) |
| | CD3+ | 57 | 49 | 8 | 0 | 2 | 0 | 0 | 15 (1-182) |
| | Unsorted | 1024 | 861 | 133 | 30 | 83 | 14 | 1 | 30 (1-222) |
| Plasma | Unsorted | 1216 | 887 | 216 | 113 | 162 | 69 | 42 | 1000 (250-1002) |
| RNA | CD138+ | 19 | 11 | 8 | 0 | 2 | 0 | 0 | 15 (2-50) |

Numbers indicate total patients with biospecimen(s) available.

Total: sum of baseline, relapse, and remission sample collections.

Longitudinal: mutually exclusive counts of patients with baseline plus relapse and/or remission collections.

Volume: median volume per vial (μ L) and (range) with a median of 3 vials per collection event.