



# opn2SCREEN: The opnMe molecule library

How would you leverage the entire opnMe molecule library to address new biological questions in the context of human disease as part of screening and profiling activities?

Answers to this [question](#) including a proposal for collaboration can only be considered if they arrive no later than June 17, 2026, 11:59 pm PST.

# Table of contents

Summary .....	2
Background.....	2
What potential proposals could be in scope? .....	3
What potential proposals would be out of scope?.....	4
What benefits do we offer to you in exchange for having submitted a proposal?.....	4
Confidential information.....	5
Key Criteria for the selection of proposals.....	5
Anticipated Timelines.....	5
Submitting a proposal .....	5
Supplementary Data / Technical Specifications .....	6
References.....	7

## Summary

For a limited time, opnMe is sharing its entire molecule-to-order library with scientists worldwide to support systematic screening and profiling approaches for the validation of novel, disease-relevant biological hypotheses. The collection comprises 176 high-quality, well-characterized molecules, including relevant negative controls.

By providing access to this library, opnMe enables researchers to run library-wide phenotypic and profiling screens, compare pathways, and generate robust morphological, functional, and multi-omics signatures. These efforts support the discovery of disease-relevant phenotypes and the development of data-driven biological hypotheses.

We invite innovative research proposals aligned with our current discovery research priorities. Submit your proposal by **June 17, 2026 (11:59 pm PST)** for a chance to access the full opnMe molecule library.

## Background

Through opnMe<sup>1</sup>, Boehringer Ingelheim has championed open innovation by making high-quality, well-characterized preclinical tool molecules available for free. These molecules—originating from our internal discovery research programs or developed together with external collaborators—have enabled scientists worldwide to test and validate their research hypotheses. To date, they have supported more than 250 independent, peer-reviewed publications, highlighting the relevance of offering these molecules for research.

While the core objective of opnMe is to allow independent hypothesis-driven research on specific targets, we recognize that accessing the entire opnMe molecule collection may help to address other objectives.

Access to a well-characterized tool compound library provides a strong foundation for early biological discovery. By enabling controlled perturbation of cellular pathways, the opnMe library enables researchers to run unbiased, scalable screens to generate hypotheses rapidly and uncover disease-relevant phenotypes. Because each compound's mode of action and selectivity are well understood, library-wide responses observed in screening experiments can be interpreted with greater clarity, supporting the identification of novel pathways, signatures, and mechanisms emerging from comparative analyses across the full set.

Well-characterized probes also enable comparative analyses alongside genetic perturbations in screening contexts (e.g., CRISPR-coupled designs), helping to reveal acute cellular responses and gene–compound interaction patterns. In addition, profiling tool compounds across cellular, biochemical, and omics-based readouts supports the systematic exploration of pathway interactions, signaling dependencies, and molecular drivers of disease.

A curated tool compound library further enables researchers to build integrative, cross-compound datasets that helps clarify disease-associated networks and reduces uncertainty in interpreting early functional data generated through screening.

Hence, we are now making the entire opnMe molecule set available as a single, ready-to-screen microtiter plate (MTP) for a short period of time. The library will be shipped in a 384-well MTP, with each tube containing 40 µl of a 10 mM stock solution in DMSO, enabling seamless integration into established screening workflows. In total, the library will comprise 99 active molecules and 77 negative controls, resulting in 176 molecules in total.

We invite scientists to address novel scientific hypotheses with a focus on our current research priorities to address the following [question](#):

### **How would you leverage the entire opnMe molecule library to address new biological questions in the context of human disease as part of screening and profiling activities?**

Please note, we specifically encourage screening and profiling proposals that utilize the entire library rather than single-target or small-subset studies.

Please submit your research proposal no later than **June 17, 2026, at 11:59 pm PST**. All submissions will be evaluated by Boehringer Ingelheim scientists based on novelty, feasibility, and alignment with our current disease priorities (please see below).

The opnMe library contains molecules of the following ten target classes, including:

Target Class	No. of molecules	No. of neg controls
Enzyme	30	24
Epigenetic Target	9	8
GPCR	20	15
Ion Channel	7	6
Kinase	16	9
Membrane Protein	1	1
Membrane Transporter	4	4
Nuclear receptor	1	1
PPI	10	8
RNA target	1	1

The full list of the molecules included in the opnMe library can be downloaded [here](#).

## **What potential proposals could be in scope?**

The following research proposals focusing on the following indications are in scope:

- Cardiovascular–renal–metabolic diseases: kidney, cardiovascular, liver diseases, and obesity

- Immunology & respiratory diseases: chronic inflammatory conditions
- Neuroscience: mental health and neurology
- Oncology: cancer cell-directed agents, immuno-oncology therapies, and combination approaches
- Eye health: disease progression and earlier-stage intervention to prevent vision loss

In addition, proposals focusing on:

- Approaches to evaluate molecular sustainability and environmental impact

And centering on the following approaches and methodologies:

- Phenotypic screening
- High-content or morphological profiling (e.g., cell painting)
- Chemical genomics & CRISPR-coupled screening
- Combination screening
- Computational approaches where access to the opnMe molecule library would be required for validation of the model

Proposals with ideas for using the molecule library for screening and profiling approaches in the next 12 months

## What potential proposals would be out of scope?

- Research proposals without a focus on human disease
- Any target approaches typically requiring only a single or few molecules:
  - Target validation
  - Assay development
  - Biomarker discovery in targeted experiments
  - Mechanistic deep dives
  - Medicinal chemistry or SAR optimization
- Proposals with a primary focus on service improvement and/or delivery, such as proposals from contract research organizations and/or suppliers of laboratory reagents
- Requests with the main purpose of storing compounds without research objectives and definite experimental plan within the next 12 months

## What benefits do we offer to you in exchange for having submitted a proposal?

If your project is selected, you will obtain access to the opnMe molecule library for your own research. The library covers well-characterized molecules with defined selectivity profiles. A set of negative controls that are included in the library will help you to interpret your scientific experiments and increase confidence in your results. It will be provided to you free of charge, but please note that [proforma custom fees](#) may apply to some countries.

Upon receiving the opnMe library, you will be able to pursue your research on your own and publish your results independently. You will also be able to access individual molecules in greater quantity sufficient for follow-up studies upon request.

## Confidential information

For this opnMe call, please do not provide any confidential information as part of your proposal. Please indicate that you have additional confidential information to substantiate your proposal. If Boehringer Ingelheim finds the non-confidential concept proposal sufficiently interesting, they will execute a CDA for confidential discussions.

## Key Criteria for the selection of proposals

We are seeking well-structured research proposals outlining a brief non-confidential description of your research objectives, proposed experiments, anticipated timelines, and planned start of the project. Priority will be given to innovative research hypotheses and ideas.

As this offering is specifically designed to support high-throughput screening, applicants must have direct access to a wet laboratory and have established capabilities for plate-based screening, hit identification, and hit profiling to effectively evaluate the full molecule collection.

The planned experiments in the context of the proposed submission should start within the next 12 months. In addition, the boundary criteria of the call as outlined in the in-scope and out-of-scope sections must be met.

## Anticipated Timelines

Phase 1	Review of the proposals will start after the submission phase, and we aim to finalize our review by mid-August 2026.
Phase 2	Shipments starting Q3/2026.

## Submitting a proposal

- Check the outline of the [opn2SCREEN opnMe molecule library profile](#) on opnMe
- Alternatively, you may click the “Get Submission Template” banner to access the submission document including the material transfer agreement.
- Follow the instructions to upload your submission document (requires login or registration). Please note that the submission includes the material transfer agreement that needs to be signed before submission.
- The upload allows you to attach additional application files if desired.
- You will be able to access your final submitted proposal in your personal dashboard and follow its review status.

- Please also visit the [FAQ section](#) on [opnMe.com](#) to learn more about our opn2SCREENprogram.

## Supplementary Data / Technical Specifications

The 384-well MTP is compatible with typical automation instruments such as e.g. Hamilton, Tecan, or Analytik-Jena pipetting systems. The plates are heat sealed with peelable/piercable seal foil. A data file will be provided including, layout and molecule information.

The active molecules are positioned in columns 3-11 (green) and the negative controls in columns 12-19 (yellow), with a double perimeter of empty wells and remaining cells filled with DMSO (red).

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
A																								
B																								
C			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
D			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
E			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
F			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
G			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
H			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
I			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
J			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
K			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
L			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
M			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
N			●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●	●
O																								
P																								

- 99 actives
- 77 controls
- DMSO Tubes

Features	Molecule library
Formulation	Liquid
Concentration	10 mM stock solution in DMSO
Volume	40 $\mu$ l
Plates	384 deep well microplate, PP, small volume
Plating Layout	Double frame empty (176/plate)

## References

1. Gollner A., Koester M., Nicklin P., Trieselmann T., Klein E., Vlach J., Heine C., Grundl M., Ramharter J., Wyatt D., Chaturvedi M., Ciulli A., Carter K. C., Müller S., Bischoff D., Ettmayer P., Haaksma E., Mack J., McConnell D., Stenkamp D., Weinstabl H., Zentgraf M., Wood C. R., Montel F. opnMe.com: a digital initiative for sharing tools with the biomedical research community *Nat. Rev. Drug Discov.* **2022** 21(7):475-476. DOI: [10.1038/d41573-022-00071-9](https://doi.org/10.1038/d41573-022-00071-9), [PubMed](#).