



Expression of Interest (EOI) - FAQ

Seeking an in-vitro diagnostic (IVD) partner to apply to a Horizon Europe call for the translation of a host-response mRNA signature to a portable point-of-care molecular diagnostic platform and advancing the assay to market in LMICs.

Frequently Asked Questions

Version: 21 OCTOBER 2026

this FAQ will be updated until the 4th of November, 5pm CET

1. Platform eligibility: Is prior experimental demonstration of host-gene expression quantification a mandatory prerequisite, or are commercially available RT-qPCR platforms with demonstrated RNA detection and multiplexing capabilities also eligible?

[FIND RESPONSE]: *No, a prior experimental demonstration of host-gene expression quantification is **NOT** an essential prerequisite, although it would be considered an advantage. Demonstrated RNA detection capability provides confidence in the platform's potential to support mRNA measurement. Applicants should describe the available evidence supporting the platform's compatibility with transcriptomic read-out, as well as their proposed approach for transferring and optimizing the DIAMONDS host-response signature onto the platform.*

2. Gene signature and multiplexing: Is simultaneous measurement of the complete 12-gene signature mandatory or a reduced-gene panel or multiple reactions could be considered?

[FIND RESPONSE]: *No, simultaneous measurement of the complete 12-gene signature is not mandatory. The final signature is not fully locked at this stage, and a reduced number of gene markers may be considered, provided that the resulting assay can meet the required diagnostic performance and operational characteristics. The EOI notes that similar sensitivity and specificity have been achieved with smaller numbers of genes.*

High multiplexing capability is therefore an advantage rather than an essential prerequisite. Applicants should describe the maximum multiplexing capability of their platform and their proposed strategy for implementing the signature, including the use of multiple reactions if relevant. These elements will be considered as part of the overall assessment of the proposed platform and approach.

3. Direct whole-blood workflow: Would an extraction-free approach using a proprietary inhibitor-tolerant chemistry be acceptable for development and evaluation, provided adequate mRNA stability, quantitative performance and clinical accuracy can be established?

[FIND RESPONSE]: *Yes. An extraction-free approach would be acceptable, provided that adequate mRNA stability, analytical and quantitative performance, and clinical performance can be demonstrated (for example through past project on similar molecules) and that the resulting workflow is compatible with the intended point-of-care or near-patient use.*

4. Applicant structure: Would a joint application with two companies meet the industrial-partner eligibility requirements where company A is the original technology developer and manufacturer and company B is responsible for commercialisation and distribution?

[FIND RESPONSE]: *Yes. A joint application from the two companies would be acceptable provided that the proposed partnership clearly covers the capabilities and responsibilities required under the EOI, and that the respective roles of each entity are clearly defined. The original technology developer/manufacturer should have a central role in the application, consistent with the eligibility requirements. The application should clearly describe the governance of the partnership, allocation of responsibilities, and how the two entities will jointly support technology transfer, manufacturing, commercialization, and access in LMICs.*

5. Device maturity: Would a platform that is not yet commercially available, but is progressing toward clinical validation in mid-2027 for regulatory submission by end of 2027, still be considered eligible at its current stage of development?

[FIND RESPONSE]: Yes, your platform may still be considered, especially because the development timeline described suggests that the platform will be at an advanced stage of development or commercially ready by the time the project starts (the Horizon funding award and start of the project are not anticipated before approximately Q1 2028). Applicants should provide evidence of the platform's current development stage and clearly describe the planned development, clinical validation, regulatory and commercialization pathway. The overall maturity of the entity and readiness of the platform, including its expected status at project start, will be considered as part of the evaluation and ranked accordingly.

6. Sample type: What sample type is required for measurement of the mRNA signature? Is the signature intended to be measured from whole blood or plasma, and would a plasma-separation step be compatible with the intended workflow?

[FIND RESPONSE]: The mRNA signature has been evaluated using whole blood, rather than plasma. mRNA was extracted from whole blood collected in PAXgene tubes, which stabilize the RNA and allow samples to be stored for subsequent analysis. The consortium has also evaluated the RNA expression signature using fresh whole blood collected in EDTA tubes. This approach is feasible provided that sample processing, including RNA extraction, is performed within a few hours of sample collection.

As the signature reflects the host immune/inflammatory response, the relevant mRNA is primarily cell-associated, including mRNA from white blood cells. Therefore, a plasma-separation step would not be expected to provide an advantage for this application, as it would separate the plasma from the cells containing much of the target mRNA. In addition, sample-processing steps that physically manipulate or stress blood cells could potentially alter gene expression *ex vivo*, introducing bias into the measured mRNA signature. For this reason, approaches that enable measurement directly from whole blood while minimizing cellular manipulation and preserving the original RNA expression profile would be preferred.

7. Does the RNA signature require precise quantification?

[FIND RESPONSE]: Yes, quantification of the RNA transcripts is required. However, absolute quantification in terms of transcript copy number is not required. The signature relies on relative quantification of the target transcripts against reference ("housekeeping") transcripts. The platform therefore needs to reliably measure relative differences in gene expression, rather than determine the precise number of RNA copies present in the sample.