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|  | **Request Form \_IMM****N Terminal Sequencing (SEQ)****PRESTATION** |
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| **Website IMM:** https://www.imm.cnrs.fr/plateformes/proteomique/**Website MAP:** http://marseille-proteomique.univ-amu.fr/ | **Twitter :** @Map\_Proteomique |

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| ***Please, carefully fill this form and send back the form to proteomique@imm.cnrs.fr****If any question, do not hesitate to contact the platform by email or by phone +33 4 91 16 45 25. Thank you.* |

*Reserved for the Proteomics Facility*

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| **N Terminal Sequencing** [ ]  **SEQ N°XXX** |
| ***1) Reception :***XX/ XX / XXXX | ***3) Processed :***XX/ XX / XXXX | ***5) Access completed :***XX/ XX / XXXX |
| ***2) Preparation :***XX/ XX / XXXX | ***4) Report :***XX/ XX / XXXX | ***6) Billing sent*:** XX/ XX / XXXX |

*To be completed by the applicant*

**Contact details and analysis request**

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| **Laboratory with address :** click here to write |
| **Manager of the project :** First and last name | email : adress@xxx.xx | **🕿** XX XX XX XX XX |
| **Contact person (user) :** First and last name | email : adress@xxx.xx | **🕿** XX XX XX XX XX |
| **Description of the request according to the scientific question :** click here to write |

**Information about samples**

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| **Genus, Species :** click here to write |
| **Taxonomy Identifier (txID) :** click here to write |
| **Repetition of a previous analysis ?** [ ]  No [ ]  Yes, please indicate the « SEQ N° » and year of your previous analysis : click here to write |
| **Temperature sample storage constraints :** [ ]  +4 °C [ ]  -20 °C [ ]  -80 °C  |
| **Destruction of samples after processed :** [ ]  Yes [ ]  No |
| ***Instructions for sample preparation*** |
| ***1) Electrotransfer to PVDF membrane :****- It is imperative to use* ***Tris-Borate buffer (50 mM Tris, 50 mM Borate, pH 8.3)*** *instead of the commonly used Tris-Glycine buffer.**- After staining the strip (preferably with* ***Ponceau Red****, otherwise with Coomassie Blue), the strip is cut,* ***placed in an ependorf and stored in a freezer at -20 °C****.**- The higher the molecular weight, the more intense the coloring of the strip.**- The size of the strip should* ***not exceed 4x8 mm****.**- /!\ Nitrocellulose membranes are not usable on the sequencer.**-* ***Please, provide a strip of PVDF membrane cut from any location to verify quality.*** | ***2) Protein in solution :*** *- The* ***protein (between 25 and 500 picomoles)*** *must be in solution ideally in a* ***volume between 5 and 500 µL****.* *- It is the responsibility of the user to know the conditions, in time, of stability of the protein : temperature, concentration, buffer. These conditions will determine both the conditions of transport of the sample to the platform (dry ice, ice pack, room temperature) and the conditions of storage at reception (temperature, delay).* |

***Please inform the Proteomics Facility towards harmful chemical or biological risks linked to the samples***

**Sample list**

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| **SEQ N°***(Reserved for the Proteome Facility)* | **Sample name** | **Theoretical Mass** | **Concentration** | **Number of cycles (min. 5)** | **Strains, buffers, salts, detergents, purifications steps…** |
|  | Sample | Mass | Concentration | Nb | Informations |
|  | Sample | Mass | Concentration | Nb | Informations |
|  | Sample | Mass | Concentration | Nb | Informations |
|  | Sample | Mass | Concentration | Nb | Informations |
|  | Sample | Mass | Concentration | Nb | Informations |
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|  | Sample | Mass | Concentration | Nb | Informations |

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| **Time, Cost, Sample treatment, Recognition, Property, Storage****1. The user of the Proteomics Facility is aware of the time which is necessary to process the proteomic analysis from the experiments to the bioinformatic analysis and the email report, and agrees with the cost of the analysis according to the established price by CNRS audit decision on 1st of July 2024 (Journal Official : DEC247567DR12), upon request at MaP-IMM (+33 4 91 16 45 25 or** **proteomique@imm.cnrs.fr****).***Reserved for the Proteomic Facility*

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| **Customers** | **Number of analyses** *(A)* | **Fee per analysis (HT)** *(B)* | **Total (HT)** *(AxB)* |
| Reserved for the Proteomic Facility | Reserved for the Proteomic Facility | Reserved for the Proteomic Facility | Reserved for the Proteomic Facility |

**2. Using the data supplied by the Proteomics Facility, Marseille Proteomique, in a publication or a poster, or in an oral presentation, you agree to recognize the Engineers who participated to the work, as follows :** **as *co-authors in a scientific publication :*** *« name(s) of the Engineer(s) who performed the experiments, from the Proteomics Facility of the “Institut de Microbiologie de la Méditerranée”, Marseille Proteomique -IBiSA and -Aix Marseille Univ labeled. »* in any crucial scientific clue shown by N-ter sequencing, in any contribution to write Materials & Methods/Figure/Table…**OR** **mentioned** **in the *acknowledgements :*** *« name(s) of the Engineer(s) who performed the experiments, from the Proteomics Facility of the “Institut de Microbiologie de la Méditerranée”, Marseille Proteomique -IBiSA and -Aix Marseille Univ labeled, are acknowledged for N-ter Sequencing analysis*. *»***3. Marseille Proteomique and the user are owners of the Raw and Processed data which will be stored two years on a storage server from Marseille Proteomique.** **Date :** XX**/** XX**/** XXXX**User’s Signature :** |

**Appendix 1 : General scientific context**

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| *Please, briefly describe here below the global scientific project in which this request is submitted. We inform you that this scientific project may be used by MaP for sustaining financial requests for purchasing new scientific equipment, with various administrative organisms, including the guardianship and the Scientific Committee. You can add some scietntific references. Thank you very much in advance for your support to MaP.*  |

**Title :** click here to write

**User’s Financials :** click here to write

**PI’s name and grants :** click here to write

**Abstract**

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| click here to write |

**References**

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| click here to write |

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| ***Reserved for the Proteomics Facility*** |

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| **Activities** | **Date** | **Operator** | **Parameters** | **Analysis conditions** | **Comments** |
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| **Reception** | **/ /** |  |  |  |  |  |  |
| **Preparation** | **/ /** |  |  |  |  |  |  |
| **Processed** | **/ /** |  | [ ]  PPSQ-31B Protein Sequencer (Shimadzu) |  |  |  |  |
| **Data analysis** | **/ /** |  |  |  |  |  |  |
| **Report** | **/ /** |  |  |  |  |  |  |
| **Access completed** | **/ /** |  |  |  |  |  |  |
| **Billing sent** | **/ /** |  |  |  |  |  |  |

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| ***Legend  :*** *No anomaly* *Anomaly with no impact on results* *Anomaly with impact on results* |

**Sample analyses :** [ ]  Once only (as originally planned) [ ]  Several times due to :