VOLUNTARY EX ANTE TRANSPARENCY NOTICE

Supplies

Directive 2014/24/EU

SECTION I: CONTRACTING AUTHORITY/ENTITY

I.1) NAME AND ADDRESSES

Official name:
Universiteit Leiden
National ID:
27368929
Postal address:
Kolffpad 1
Town:
Leiden
NUTS code:
NL33
Postal code:
2333BN
Country:
NL
Contact person:
Govert Schipperheijn
Telephone:
+31 715273304
E-mail:
g.m.schipperheijn@ufb.leidenuniv.nl
Fax:
-

Internet address(es)

Main address:
http://www.universiteitleiden.nl
Address of the buyer profile:
https://s2c.mercell.com/buyer/19549

I.4) TYPE OF THE CONTRACTING AUTHORITY

Body governed by public law

I.5) MAIN ACTIVITY

Other activity: Scientific research and higher education

SECTION II: OBJECT

II.1) SCOPE OF THE PROCUREMENT

II.1.1) Title

Mass Spectrometer Orbitrap

Reference number: -

II.1.2) CPV code(s)

Main code:
38433100 - Massaspectrometers
Supplementary code:
FG11 - Voor wetenschappelijke doeleinden

II.1.3) Type of contract

Supplies

II.1.4) Short description

The Leiden Institute of Chemistry (LIC) seeks to purchase a state-of-the-art ultra high-performance liquid chromatography coupled to mass spectrometry (UHPLC-MS) system for the performance of specific proteomic and chemical proteomic experiments.

II.1.6) Information about lots

This contract is divided into lots: no

II.1.7) Total value of the procurement (excluding VAT)

Value: 1 199 995,77

Currency: EUR

II.2) DESCRIPTION

II.2.1) Title

-

Lot No: -

II.2.2) Additional CPV code(s)

Main code:
38433000 - Spectrometers
Supplementary code:
FG11 - Voor wetenschappelijke doeleinden

II.2.3) Place of performance

NUTS code:
NL33 Zuid-Holland

Main site or place of performance:
Leiden, the Netherlands.

II.2.4) Description of the procurement:

(nature and quantity of works, supplies or services or indication of needs and requirements)

The Leiden Institute of Chemistry (LIC) seeks to purchase a state-of-the-art ultra high-performance liquid chromatography coupled to mass spectrometry (UHPLC-MS) system for the performance of specific proteomic and chemical proteomic experiments.
At our institute diverse (chemical) proteomic workflows need to be performed for our research in the field of Chemical Biology. The newly purchased instrument must allow detecting labile peptide modifications and allow streamlining of our mass spectrometric experiments by enabling a high degree of sample multiplexing.

II.2.5) Award criteria

Price
Weighting: -

II.2.11) Information about options

Options: no

II.2.13) Information about European Union funds

The procurement is related to a project and/or programme financed by European Union funds: no

II.2.14) Additional information:

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SECTION IV: PROCEDURE

IV.1) DESCRIPTION

IV.1.1) Type of procedure

Negotiated procedure without prior publication

IV.1.3) Information about framework agreement

-

IV.1.8) Information about the Government Procurement Agreement (GPA)

The procurement is covered by the Government Procurement Agreement: yes

IV.2) ADMINISTRATIVE INFORMATION

IV.2.1) Previous publication concerning this procedure

Notice number in the OJ S: -

SECTION V: AWARD OF CONTRACT / CONCESSION

Contract No: 1
Lot No: 1
Title: Orbitrap Eclipse Tribrid

V.2) AWARD OF CONTRACT / CONCESSION

V.2.1) Date of conclusion of the contract/concession award decision:

04/10/2023

V.2.2) Information about tenders

The contract has been awarded to a group of economic operators: no

V.2.3) Name and address of the contractor/concessionaire

Official name:
Thermo Fisher Scientific BV
National ID:
32059695
Postal address:
Takkebijsters 1
Town:
Breda
NUTS code:
NL41
Postal code:
4817 BL
Country:
NL
Telephone:
-
E-mail:
-
Fax:
-
Internet address:
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The contractor/concessionaire is an SME: no

V.2.4) Information on value of the contract/lot/concession (excluding VAT)

Initial estimated total value of the contract/lot/concession:
1 199 995,77

Total value of the contract/lot/concession: 1 199 995,77

Currency: EUR

V.2.5) Information about subcontracting

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SECTION VI: COMPLEMENTARY INFORMATION

VI.3) ADDITIONAL INFORMATION

This publication is to indicate our intention to award the contract to Thermo Fisher. If no representations are received within 20 days after this publication, the contract will be awarded.

VI.4) PROCEDURES FOR REVIEW

VI.4.1) Review body

Official name:
Rechtbank Den Haag
Postal address:
-
Town:
Den Haag
Postal code:
-
Country:
NL
E-mail:
-
Telephone:
-
Internet address:
-
Fax:
-

VI.4.2) Body responsible for mediation procedures

-

VI.4.3) Review procedure

Precise information on deadline(s) for review procedures:
Within 20 days after this publication.

VI.4.4) Service from which information about the review procedure may be obtained

-

VI.5) DATE OF DISPATCH OF THIS NOTICE

05/10/2023

ANNEX D1 – GENERAL PROCUREMENT: JUSTIFICATION FOR THE AWARD OF THE CONTRACT WITHOUT PRIOR PUBLICATION OF A CALL FOR COMPETITION IN THE OFFICIAL JOURNAL OF THE EUROPEAN UNION

Directive 2014/24/EU

D1.1) Justification for the choice of the negotiated procedure without prior publication of a call for competition in accordance with Article 32 of Directive 2014/24/EU

The works, supplies or services can be provided only by a particular economic operator for the following reason:

- absence of competition for technical reasons

D1.3) Explanation

Please explain in a clear and comprehensive manner why the award of the contract without prior publication in the Official Journal of the European Union is lawful, by stating the relevant facts and, as appropriate, the conclusions of law in accordance with the directive:
The Leiden Institute of Chemistry (LIC) seeks to purchase a state-of-the-art ultra high-performance liquid chromatography coupled to mass spectrometry (UHPLC-MS) system for the performance of specific proteomic and chemical proteomic experiments.
At our institute diverse (chemical) proteomic workflows need to be performed for our research in the field of Chemical Biology. The newly purchased instrument must allow detecting labile peptide modifications and allow streamlining of our mass spectrometric experiments by enabling a high degree of sample multiplexing. Specifically, we need to perform the following experiments:
- Analysis of modified peptides: Our groups are working on the detection of modified peptides, which often contain labile modification. For their analysis, different fragmentation methods give complementary information and often different fragmentation technologies need to be explored to study a certain modification. For this reason, we need to be able to perform fragmentation both with CID, HCD and ETD fragmentation methods.
- Dose-response experiments in one single injection: We have methods in hand to profile the target engagement of inhibitors proteome-wide. In order to get the best information out of these experiments, we need to perform dose- response experiments of eight concentrations plus a control in duplicate. Due to time-constraints and to achieve the best possible data

completeness, these need to be performed in a single injection. For this reason, 18-plex multiplexing is required for these experiments.
- Thermal proteome profiling experiments: The melting curves of proteins can be assessed on a proteome-wide scale and can give important insights into e.g. the interactions of proteins with each other and with small molecules. In order to perform these experiments, the soluble proteome needs to be assessed after treatment at a variety of different temperatures. To perform this with high throughput and most reliably in one single injection, high degrees of multiplexing (11-plex and upwards) are required.
For all of these applications, highly accurate quantification is needed. In order to allow for accurate quantification of samples with high degrees of multiplexing, high resolution of the mass spectrometer is needed and analysis needs to be possible up to at least MS3 to minimize co-isolated ion interference. For this, real-time database searching needs to also be possible to perform optimized ion selection to increase coverage and quantification accuracy.
For all experiments, a UHPLC is needed to separate the underlying peptides regarding the sample amounts available and the flowrates compatible with subsequent mass spectrometric analysis. To further increase the flexibility and allow higher throughput a wide range of flow rates needs to be possible.
Specifically, the following features for an UHPLC-MS are all needed to perform the applications for our research:
- Capability of data-dependent acquisition and data-independent acquisition and
- Possibility to measure MS, MS2 and MS3 spectra and
- Resolution sufficient to perform 18-plex multiplexing on MS2 and MS3 level and
- Possibility to perform fragmentation by CID, HCD and ETD methods and
- Ability to perform real-time database searching for precursor selection in isobaric experiments and
- An UHPLC covering flow rates between 200 nL/min and 100 µl/min and
- Full compatibility of the UHPLC and mass spectrometer in the same software environment and
- Full compatibility with our currently used data analysis softwares Skyline, MaxQuant and FragPipe
In conclusion, the Thermo Eclipse mass spectrometer coupled to a Vanquish neo UHPLC is the only system that offers all of these features, which are necessary for the successful completion of all of these experiments for our diverse research projects.