1. The Purchaser commissions the Contractor to perform a RBP-eCLIP service.
2. The service will be performed using the material provided by the purchaser with the following parameters:

|  |  |
| :--- | :---: |
| Sample type | Parameters |
| Sample number | cells |
| Cells amount | 20M per 1 sample |
| Sequencing <br> Configuration | SE50, Illumina Platform |
| Estimated Data <br> Output | $\sim 20 \mathrm{M}$ raw reads per sample |
| Turnaround Time | Provided QC metrics for each sample: Input RNA yield, immunoprecipitation <br> success (western blot), library success (yield and size distribution), <br> sequencing metrics |
| Quality Guarantee |  |

## 3. Description of Service:

| No. | Description of Service * | Units | Unit Price |
| :---: | :---: | :---: | :---: |
| 1 | RBP-eCLIP control Service (Control sample): <br> - 1 IP and 1 input library, sequenced to average 20 million raw reads <br> - Basic data processing (read mapping and input-normalized peak calls) <br> - Fastq files of raw sequencing reads Adapter trimmer fastq files of reads UMI and adapter sequences removed <br> - Bam files containing PCR-deduplicated read alignments to the genome <br> - Bigwig files which can be uploaded to a genome browser to view read density of sample <br> - Bed file of input-normalized peaks containing the location of each peak in the genome, along with the $\log 2$ fold change vs. pvalue <br> - HTML report with figures related to significantly enriched peaks | 2 | To be priced Please provide the unit price for 1 sample: $\qquad$ or; $2 x$ $\qquad$ (unit price.) = |
| 2 | RBP-eCLIP Services (Test sample): <br> - 1 IP and 1 input library, sequenced to average 20 million raw reads <br> - Basic data processing (read mapping and input-normalized peak calls) Fastq files of raw sequencing reads Adapter trimmer fastq files of reads UMI and adapter sequences removed | 2 | To be priced Please provide the unit price for 1 sample: $\qquad$ <br> or; $\qquad$ (unit price.) = |


|  | Bam files containing PCR-deduplicated read alignments to the <br> genome <br> Bigwig files which can be uploaded to a genome browser to view <br> read density of sample <br> Bed file of input-normalized peaks containing the location of <br> each peak in the genome, along with the log2 fold change vs. p- <br> value <br> HTML report with figures related to significantly enriched peaks <br> O |  |
| :---: | :---: | :---: | :---: |
| Total value: | (data) |  |

* The purchaser does not agree to changes in the description of the subject of the service.


## 4. The correct performance of the service is considered to be:

4.1. Performing eCLIP procedure.
4.2. Generating eCLIP libraries for controls and test samples.
4.3. Performing next-generation sequencing ( $\sim$ average 20 million raw reads per sample).
4.4. Comprehensive bioinformatics and data analysis with final report.
4.5. The Contractor does not claim any copyrights to the generated data and will not use them in any way for its own purposes (e.g. database construction). All generated data constitute the entire intellectual property of the Purchaser. The service constituting the subject of the tender will not be performed in collaboration with other entities or with the use of subcontractors or intermediaries.
4.6. The payment for a properly performed service will be made within 30 days from the delivery of the Invoices by the Contractor. If there will be issues with the sample preparation, and it will show in the QC metrics prior to sequencing, then the Contractor will contact Purchaser to make a decision about sequencing. If the Purchaser will decide not to sequence, the Contractor will only charge $25 \%$ of the total project price to cover labor.
4.7. The Contractor is entitled to payment only the actual performed part of the service.
4.8. The Contractor agrees to issue two invoices - one for the position No. 2 (Units: 1), the other together for the position No. 2 (Units: 2) and No. 1 (quantity: 2). If only $25 \%$ of the total price of the service is charged, the Contractor will issue one invoice.

