About us

CeGaT was founded in 2009 in Tübingen, Germany. Our scientists are specialized in next-generation sequencing (NGS) for genetic diagnostics, and we also provide a variety of sequencing services for research purposes and pharma solutions. Our portfolio is complemented by non-sequencing-based methods such as immunomonitoring.

Our dedicated project management team of scientists and bioinformaticians works closely with you to develop the best strategy for the realization of your project. Depending on its scope, we select the most suitable library preparation and sequencing conditions on our Illumina platforms.

We would be pleased to provide you with our award-winning service. Contact us today to start planning your next project.
Small RNA Sequencing (SRS) focuses on short RNA molecules which play an important role in silencing and post-transcriptional gene expression regulation processes. Sequencing of small RNAs allows the analysis of these molecules in more detail and therefore can be an essential part in the identification of novel biomarkers to obtain more valuable research data.

In addition to our standard library preparation service using 200 ng input material, we also provide a solution for very limited sample amounts.

To offer our customers the best possible technical solution for small RNA sequencing, we are working with the latest Illumina sequencing technologies. Depending on the sample size of a project there are different flow cells available for sequencing on NovaSeq 6000.

CeGaT’s small RNA sequencing service offers reliable and accurate insights into small RNAs from extraction to data analysis. With our long-standing expertise in the diagnostic field, our clients benefit from strict quality control standards, and therefore high quality results.

Explore our small RNA sequencing product portfolio

<table>
<thead>
<tr>
<th>Choose your option</th>
<th>SRS Classic</th>
<th>SRS Premium</th>
<th>SRS Flex</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species</td>
<td>Human</td>
<td>Human</td>
<td>Mammalian Others upon request</td>
</tr>
<tr>
<td>RNA amount</td>
<td>&gt; 200 ng</td>
<td>&gt; 1 ng</td>
<td>&gt; 1 ng</td>
</tr>
<tr>
<td>RNA quality</td>
<td>RIN ≥ 8</td>
<td>Variable RNA quality</td>
<td>Variable RNA quality</td>
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<td>Sequencing technology</td>
<td>Illumina</td>
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<tr>
<td>Output</td>
<td>&gt;10 Mio clusters per sample</td>
<td>&gt;10 Mio clusters per sample</td>
<td>Flexible</td>
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<tr>
<td>Data format</td>
<td>FASTQ</td>
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All products can be combined with RNA isolation service as well as further bioinformatics such as data alignment, counting of miRNAs, normalization (miRge), differential gene expression analysis or annotation (miRbase) for human samples.