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.
CeGaT offers sequencing of Illumina compatible Ready to Load next-generation sequencing (NGS) libraries. As starting material, we accept any Illumina-compatible library. Illumina index sequencing primers, as well as custom primers may be used during the sequencing process at CeGaT.

Flexible sequencing options, including different flow cells and read modes are available (see table below). Read lengths can also be adapted according to your needs. We will be glad to assist you in selecting the ideal sequencing conditions.

**Explore our Ready to Load sequencing product portfolio**

<table>
<thead>
<tr>
<th>NovaSeq 6000 platform (Illumina)</th>
<th>Output [Gb]</th>
<th>Single reads CPF [million]*</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>SP flow cell</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SR / PE 100 cycles</td>
<td>65</td>
<td>650</td>
</tr>
<tr>
<td>SR / PE 300 cycles</td>
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<td>PE 500 cycles</td>
<td>325</td>
<td>650</td>
</tr>
<tr>
<td><strong>S1 flow cell</strong></td>
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<td></td>
</tr>
<tr>
<td>SR / PE 100 cycles</td>
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<td>1330</td>
</tr>
<tr>
<td>SR / PE 200 cycles</td>
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<td>1330</td>
</tr>
<tr>
<td>SR / PE 300 cycles</td>
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<tr>
<td><strong>S2 flow cell</strong></td>
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<tr>
<td>SR / PE 100 cycles</td>
<td>333</td>
<td>3335</td>
</tr>
<tr>
<td>SR / PE 200 cycles</td>
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<td>SR / PE 300 cycles</td>
<td>1000</td>
<td>3335</td>
</tr>
<tr>
<td><strong>S4 flow cell</strong></td>
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<tr>
<td>SR / PE 200 cycles</td>
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<td>8000</td>
</tr>
<tr>
<td>SR / PE 300 cycles</td>
<td>2400</td>
<td>8000</td>
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<table>
<thead>
<tr>
<th>MiSeq platform (Illumina)</th>
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<th>Single reads CPF [million]*</th>
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</thead>
<tbody>
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<tr>
<td>SR / PE 300 cycles</td>
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</tr>
<tr>
<td>PE 500 cycles</td>
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<td>1</td>
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<tr>
<td><strong>V2 Micro flow cell</strong></td>
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<tr>
<td>SR / PE 300 cycles</td>
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<td>4</td>
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<tr>
<td><strong>V2 flow cell</strong></td>
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<tr>
<td>SR / PE 50 cycles</td>
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<tr>
<td>SR / PE 300 cycles</td>
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<td><strong>V3 flow cell</strong></td>
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<tr>
<td>SR / PE 150 cycles</td>
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<tr>
<td>PE 600 cycles</td>
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<td>22</td>
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</tbody>
</table>

*In case of PE sequencing, they will be twice as much.