Enzymes for molecular biology

For research use only. Not for use in diagnostic procedures.
management of that human being.

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management of that human being.

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management of that human being.
About LGC, Biosearch Technologies and Lucigen

Lucigen® is now part of LGC, Biosearch Technologies, providing an expanded portfolio of products and services for agrigenomics and molecular diagnostics.

Biosearch Technologies is working to improve people’s lives by providing quality products and services to life science and healthcare professionals. Biosearch Technologies offers products and services that enable life-science professionals to perform their research and testing more efficiently and effectively. The company has grown to manufacture and sell over 325 biomedical research products and services to customers worldwide, all under an ISO 13485-certified quality system. Core competencies include protein expression and purification, enzymes and reagents, competent cells and cloning, PCR and isothermal amplification, next gen sequencing, and assay design for molecular diagnostics.

Custom and OEM Solutions

Your needs are unique. Your solutions should be, too.

Biosearch Technologies specialises in custom and OEM manufacture of high-quality enzymes and competent cells for an array of diagnostic and research applications. We can customise our catalog enzyme concentration, formulation, dispensing, packaging and labeling - including private labels. And, we’ll provide knowledgeable scientific support for your project from start to finish.

Here’s why partnering with Biosearch Technologies could be right for you:

Speed your development with responsive manufacturing, rapid order turn-around, and on-time delivery.

• Use our in-house expertise in a broad array of enzyme classes, applications, and technologies.

• Leverage our quality in ISO 13485-certified quality system.

• Proceed with confidence as our scientists support your project at every step.

• Complete your workflow with our diverse offering - from polymerases and proteases to Cas9 Nuclease.
## Enzyme properties

### Mesophilic DNA polymerases

<table>
<thead>
<tr>
<th>Product name</th>
<th>Activity</th>
<th>Optimum temp.</th>
<th>Heat inactivation</th>
<th>Strand displacement</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bis DNA Polymerase, Exonuclease Minus</td>
<td>–</td>
<td>–</td>
<td>55–65 °C</td>
<td>80 °C for 20 minutes</td>
</tr>
<tr>
<td>NvGen phi29 DNA Polymerase</td>
<td>–</td>
<td>++</td>
<td>30 °C</td>
<td>65 °C for 10 minutes</td>
</tr>
<tr>
<td>Eco-Minus Klenta DNA Polymerase (CDS5A, E33TA)</td>
<td>–</td>
<td>–</td>
<td>37 °C</td>
<td>n.d.</td>
</tr>
</tbody>
</table>

*Indicated treatment results in incomplete inactivation under standard reaction conditions; n.d., not determined.

### Thermophilic DNA polymerases

<table>
<thead>
<tr>
<th>Product name</th>
<th>Activity</th>
<th>Optimum temp.</th>
<th>Thermostability</th>
<th>Fidelity</th>
</tr>
</thead>
<tbody>
<tr>
<td>EcoTaq DNA Polymerase</td>
<td>+</td>
<td>70–72 °C</td>
<td>n.d.</td>
<td>n.d.</td>
</tr>
<tr>
<td>MasterAmp 7a DNA Polymerase</td>
<td>+</td>
<td>70–72 °C</td>
<td>10 minutes at 97 °C</td>
<td>0.38–1.82 x 10⁶</td>
</tr>
<tr>
<td>MasterAmp 7h DNA Polymerase</td>
<td>+</td>
<td>68–74 °C</td>
<td>10 minutes at 97 °C</td>
<td>2.2 x 10⁵</td>
</tr>
<tr>
<td>LavaLAMP® DNA Enzyme</td>
<td>n.d.</td>
<td>68–74 °C</td>
<td>n.d.</td>
<td>n.d.</td>
</tr>
<tr>
<td>LavaLAMP® RNA Enzyme</td>
<td>n.d.</td>
<td>68–74 °C</td>
<td>n.d.</td>
<td>n.d.</td>
</tr>
</tbody>
</table>

### RNA polymerases

<table>
<thead>
<tr>
<th>Product name</th>
<th>Activity</th>
<th>Optimum temp.</th>
<th>Heat inactivation</th>
</tr>
</thead>
<tbody>
<tr>
<td>NvGen T7 RNA Polymerase</td>
<td>–</td>
<td>37 °C</td>
<td>n.d.</td>
</tr>
<tr>
<td>T7 RMDNA Polymerase</td>
<td>–</td>
<td>37 °C</td>
<td>n.d.</td>
</tr>
<tr>
<td>Poly(A) Polymerase</td>
<td>–</td>
<td>37 °C</td>
<td>not recommended</td>
</tr>
</tbody>
</table>

*n.d., not determined.

### Reverse transcriptases

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Activity</th>
<th>Substrates</th>
<th>RNase H activity</th>
<th>Optimum temp.</th>
<th>Heat inactivation</th>
</tr>
</thead>
<tbody>
<tr>
<td>MLV High Performance Reverse Transcriptase</td>
<td>Synthesis first-strand cDNA</td>
<td>ssRNA, ssDNA</td>
<td>+</td>
<td>37 °C</td>
<td>85 °C for 5 minutes</td>
</tr>
<tr>
<td>NvGen M-MuLV Reverse Transcriptase</td>
<td>Synthesis first-strand cDNA</td>
<td>ssRNA, ssDNA</td>
<td>+</td>
<td>37–42 °C</td>
<td>85 °C for 10 minutes</td>
</tr>
<tr>
<td>EpiScript RNase H Reverse Transcriptase</td>
<td>Synthesis first-strand cDNA</td>
<td>ssRNA, ssDNA</td>
<td>–</td>
<td>37 °C</td>
<td>85 °C for 5 minutes</td>
</tr>
</tbody>
</table>

### DNA endonucleases

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Substrate</th>
<th>Activity</th>
<th>Products</th>
<th>Applications</th>
<th>Optimum temp.</th>
<th>Heat inactivation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Baseline-ZERO DNase</td>
<td>dsDNA and ssDNA</td>
<td>Digests dsDNA or ssDNA to mononucleotides.</td>
<td>Mononucleotides</td>
<td>Removing DNA from RNA preparations;</td>
<td>37 °C</td>
<td>66 °C for 10 minutes*</td>
</tr>
<tr>
<td>RNase-Free DNase I</td>
<td>dsDNA and ssDNA</td>
<td>Activated by divalent cations. In presence of Mg²⁺, it cleaves each DNA strand of dsDNA randomly and independently.</td>
<td>Oligos and dNMPs with 5’ P and 3’ OH;</td>
<td>Removing DNA from RNA preparations; Random nicking of dsDNA; DNase footprinting;</td>
<td>37 °C</td>
<td>n.d.</td>
</tr>
</tbody>
</table>

*n.d., not determined.

### DNA exonucleases

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Substrate</th>
<th>Activity</th>
<th>Products</th>
<th>Applications</th>
<th>Optimum temp.</th>
<th>Heat inactivation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exonuclease I (E. coli)</td>
<td>ssDNA</td>
<td>5’ → 3’ exonuclease that digests ssDNA in the presence of Mg²⁺.</td>
<td>dNMPs</td>
<td>Removal of ssDNA and oligonucleotides;</td>
<td>37 °C</td>
<td>80 °C for 10 minutes</td>
</tr>
<tr>
<td>Exonuclease III (E. coli)</td>
<td>dsDNA</td>
<td>5’ → 3’ exonuclease that digests duplex DNA from the 3’ end of a nick, or a blunt or 3’-excessed end; not active on thymidylate. Exo III also has RNase H, 3’-DNA-phosphatase, and apurinic DNA endonuclease activities.</td>
<td>dNMPs and ssDNA on the opposite strand. Partial digestion produces ssDNA having 3’ extensions of dsDNA;</td>
<td>Used with S1 Nuclease or Munir Bean Nuclease to make nested deletions; Preparation of ssDNA templates for sequencing; Site-directed mutagenesis; Preparation of labeled strand-specific probes;</td>
<td>37 °C</td>
<td>65 °C for 10 minutes</td>
</tr>
<tr>
<td>Exonuclease VII (E. coli)</td>
<td>ssDNA</td>
<td>Exonuclease that digests ssDNA in both 5’ → 3’ and 3’ → 5’ directions.</td>
<td>dNMPs</td>
<td>Removal of primers and single-stranded oligos;</td>
<td>37 °C</td>
<td>n.d.</td>
</tr>
<tr>
<td>Plasmid-Safe ATP-Dependent DNAse</td>
<td>Linear ssDNA and dsDNA</td>
<td>Selectively digests linear DNA. No activity on nicked or closed-circular dsDNA;</td>
<td>dNMPs</td>
<td>Removal of chromosomal DNA fragments from plasmid, fosmid, and BAC preparations;</td>
<td>37 °C</td>
<td>70 °C for 10 minutes</td>
</tr>
<tr>
<td>Rec J Exonuclease</td>
<td>ssDNA</td>
<td>5’ → 3’ exonuclease that digests ssDNA in the presence of Mg²⁺.</td>
<td>dNMPs</td>
<td>Removal of primers and ssDNA from dsDNA;</td>
<td>37 °C</td>
<td>65 °C for 20 minutes</td>
</tr>
</tbody>
</table>

*Indicated treatment results in complete inactivation under standard reaction conditions; n.d., not determined.

**Values represent half-lives: 50% of the enzymatic activity is retained after the given time at the stated temperature.

*Defined as the average number of correct nucleotides a polymerase incorporates before making an error; n.d., not determined.

**In the presence of the provided Stop Solution; n.d., not determined.
Enzyme properties

Nucleases active on both DNA and RNA

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Substrate</th>
<th>Activity</th>
<th>Products</th>
<th>Applications</th>
<th>Optimum temp.</th>
<th>Heat inactivation</th>
</tr>
</thead>
</table>
| Terminator 5’-Phosphate-Dependent Exonuclease | ssDNA or ssRNA | 5’-3’ exonuclease that digests ssDNA or ssRNA with 5’-monophosphorylated ends, but not with 5’-OH, 5’-triphosphorylated, or 5’-capped ends | dNMPs or NMPs  | • Removal of 5’-monophosphorylated DNA or primers or oligos  
  • Enrichment of ssDNA or ssRNA molecules lacking 5’-monophosphate groups | 30 °C (Buffer A)  
  42 °C (Buffer B) | not recommended |
| OmniCleave Endonuclease          | ssDNA, ssRNA, or RNA | Endonuclease that efficiently digests DNA and RNA | ds-, tri-, and tetra-nucleotides | • Removal of DNA and RNA from protein preparations  
  • Removal of host DNA from plasmid preparations | 25–37 °C | not recommended |

RNA nucleases

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Substrate</th>
<th>Activity</th>
<th>Products</th>
<th>Applications</th>
<th>Optimum temp.</th>
<th>Heat inactivation</th>
</tr>
</thead>
</table>
| RNase A | ssRNA     | Cleaves ssRNA 3’ of pyrimidine residues. | Oligoribonucleotides with 3’-cytidine or 3’-uridine residues | • Removal of RNA from DNA preparations  
  • RNase protection assays  
  • RNA mapping and structure studies | 37 °C (15–70 °C) | not recommended |
| RNase L, E. coli | ssRNA | Cleaves ssRNA between all dinucleotide pairs. | NMPs with 5’-OH and 2’,3’-cyclic monophosphate | • Removal of RNA from DNA preparations  
  • RNase protection assays  
  • Mismatch detection of single basepairs in RNA:RNA or RNA:DNA hybrids | 37 °C | 70 °C for 20 minutes (in presence of 5 mM DTT) |
| Hybridase Thermostable RNase H | RNA in RNA:DNA hybrid | Cleaves RNA in RNA:DNA hybrid without affecting unhybridised RNA or DNA. | Oligoribonucleotides with 5’ phosphate and 3’ OH | High-stringency hybrid selection | 45–70 °C | not recommended |
| RNase R | Linear RNA | Digests linear RNA, including the ssRNA end of telomeric structures, but not circular RNA or dsDNA with 3’ overhangs <7 nt. | Oligoribonucleotides with 5’ phosphate and 3’ OH | • Alternative splicing and gene expression studies  
  • Intronic RNA production  
  • Intronic screening of cDNA libraries | 37 °C | n.d. |

n.d., not determined.

RNA-guided endonucleases

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Modifications</th>
<th>Concentration</th>
<th>PAM preference</th>
<th>Type of edit</th>
<th>Guide RNA length</th>
</tr>
</thead>
<tbody>
<tr>
<td>CRISPRCas9 S. Cas9 Nuclease</td>
<td>One C-terminal NLS, one C-terminal 6× His tag</td>
<td>10 mg/mL (62 µM)</td>
<td>G-rich (NNG)</td>
<td>Blunt double-stranded break</td>
<td>~97 nt</td>
</tr>
<tr>
<td>AsCas13a Nuclease</td>
<td>Two C-terminal NLS, one C-terminal 6× His tag</td>
<td>10 mg/mL (64 µM)</td>
<td>T-rich (TTTV)</td>
<td>Staggered double-stranded break</td>
<td>~41 nt</td>
</tr>
</tbody>
</table>

NLS, nuclear localisation signal. PAM, protospacer-adjacent motif.
**DNA polymerases**

**Enzymes for molecular biology**

**Bst DNA Polymerase, Exonuclease Minus**

Bst DNA Polymerase, Exonuclease Minus,* is a recombinant form of the 67 kDa Badillus stearothermophilus DNA Polymerase protein (large fragment). The enzyme has 5′→3′ polymerase activity and strand-displacement activity, but it lacks 3′→5′ exonuclease activity. It also has reverse transcription activity.

- Strand-displacement amplification
- DNA sequencing through high GC regions
- Rapid sequencing from nanogram amounts of DNA template

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>30027-1</td>
<td>8,000 U/mL</td>
<td>2,000 U</td>
</tr>
<tr>
<td>30027-2</td>
<td>8,000 U/mL</td>
<td>10,000 U</td>
</tr>
<tr>
<td>30028-1</td>
<td>50,000 U/mL</td>
<td>10,000 U</td>
</tr>
</tbody>
</table>

*Note: Some uses for this product may require licenses. Lucigen does not encourage or support the unauthorized or unlicensed use of patented nucleic acid amplification processes for isothermal amplification, whole-genome amplification (WGA), multiplex-displacement amplification (MDA), and next-generation sequencing. It is the sole responsibility of the buyer to ensure that use of the product does not infringe the patent rights of third parties. If the purchaser is not willing to accept these use limitations, Lucigen Corporation is willing to accept return of the product for a full refund.

**NxGen phi29 DNA Polymerase**

NxGen phi29 DNA Polymerase is a highly processive enzyme with exceptional strand-displacement activity. The enzyme also contains a 3′→5′ exonuclease activity that enables proofreading capability.

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>30021-1</td>
<td>10,000 U/mL</td>
<td>2,000 U</td>
</tr>
<tr>
<td>30021-2</td>
<td>10,000 U/mL</td>
<td>10,000 U</td>
</tr>
</tbody>
</table>

**Exo-Minus Klenow DNA Polymerase (D355A, E357A)**

Exo-Minus Klenow DNA Polymerase is a DNA-dependent DNA polymerase that lacks both the 5′→3′ and 3′→5′ exonuclease activities of E. coli DNA Polymerase I, from which it is derived. This N-terminal truncation of DNA Polymerase I also has two mutations (D355A and E357A).

- Random-primer labeling of DNA
- Second-stand cDNA synthesis
- Strand-displacement amplification

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>30031-1</td>
<td>5 U/µL</td>
<td>1,000 U</td>
</tr>
<tr>
<td>30031-2</td>
<td>5 U/µL</td>
<td>5,000 U</td>
</tr>
<tr>
<td>30031-3</td>
<td>5 U/µL</td>
<td>10,000 U</td>
</tr>
</tbody>
</table>

**FailSafe Enzyme Mix**

FailSafe Enzyme Mix is a unique blend of thermostable DNA polymerase and a 3′→5′ proofreading exonuclease that is capable of amplifying most difficult templates. The FailSafe enzyme provides 3-fold higher fidelity than 7α DNA polymerase, with the ability to amplify PCR products up to 20 kb. The error rate of the FailSafe Enzyme Mix is approximately 1 in 27,000–30,000.

- PCR and multiplex PCR
- PCR of difficult templates
- High-sensitivity PCR
- PCR amplification of any sequence up to 20 kb

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>FSE5100</td>
<td>100 U</td>
</tr>
<tr>
<td>FSE510K</td>
<td>1,000 U</td>
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</tbody>
</table>

**EconoTaq DNA Polymerase**

Derived from Thermus aquaticus, this enzyme has optimal activity at temperatures above 70 °C. It has an intrinsic 5′→3′ structure-dependent exonuclease activity but lacks 3′→5′ proofreading exonuclease activity. EconoTaq’s low price is coupled with high quality and performance. It is supplied with a magnesium-containing buffer or a separate tube of MgCl₂.

- PCR and multiplex PCR amplification of DNA templates

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q8205K</td>
<td>5 U/µL</td>
<td>500 reactions</td>
</tr>
<tr>
<td>30035-2</td>
<td>1,000 reactions</td>
<td></td>
</tr>
</tbody>
</table>

**MasterAmp Taq DNA Polymerase**

Derived from Thermus aquaticus, this enzyme has optimal activity at temperatures above 70 °C. It has an intrinsic 5′→3′ structure-dependent exonuclease activity but lacks 3′→5′ proofreading exonuclease activity. The enzyme is provided with the MasterAmp PCR Enhancer, which increases the probability of obtaining the desired amplification product and the reproducibility of PCR. It improves the consistency of PCR product yields in multiple PCR.

- PCR and multiplex PCR amplification of DNA templates

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q8250K</td>
<td>5 U/µL</td>
<td>250 U</td>
</tr>
</tbody>
</table>

**EconoTaq PLUS 2X Master Mix**

EconoTaq PLUS 2X Master Mix is a ready-to-use PCR master mix, containing dNTPs and PCR Enhancer. It offers outstanding performance and value, and is perfect for routine PCR.

- PCR and multiplex PCR amplification of DNA templates

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q8205K</td>
<td>500 reactions</td>
</tr>
<tr>
<td>30035-2</td>
<td>1,000 reactions</td>
</tr>
</tbody>
</table>

**MasterAmp 7Th DNA Polymerase**

This recombinant enzyme from Thermus thermophilus has DNA polymerase activities up to ~95 °C, as well as reverse-transcriptase activity. High reaction temperatures can reduce nonspecific priming and template secondary structure. It is provided with MasterAmp PCR Enhancer.

- PCR amplification of DNA
- Improved PCR of DNA templates having a high degree of secondary structure
- One-step RT-PCR of RNA

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>TTH7250</td>
<td>5 U/µL</td>
<td>250 U</td>
</tr>
</tbody>
</table>

**For optimal results, use with MasterAmp PCR PreMixes.**

---

*For optimal results, use with MasterAmp PCR PreMixes.*

**Activity of NxGen phi29 DNA Polymerase.**

1. Anneal hexamer primers
2. Add 0.2 DNA Polymerase + dNTPs to extend
3. 30°C
RNA polymerases

Enzymes for molecular biology

**NxGen T7 RNA Polymerase**

T7 RNA polymerase catalyses the 5′→3′ RNA synthesis from the T7 promoter. It is a DNA-dependent RNA polymerase cloned from the T7 bacteriophage. It recognises the T7 promoter and terminator sequences with high specificity.

- **Synthesis of RNA for nucleic acid amplification methods or gene expression studies**

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>NxGen T7 RNA Polymerase 30223-1</td>
<td>50 U/µL</td>
<td>25,000 U</td>
</tr>
<tr>
<td>30223-2</td>
<td>50 U/µL</td>
<td>125,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, 10X T7 RNA Polymerase Buffer

---

**Poly(A) Polymerase Tailing Kit**

Poly(A) Polymerase uses ATP as a substrate for template-independent addition of adenosine monophosphate to the 3′-OH termini of RNA molecules. The Poly(A) Polymerase Tailing Kit provides the enzyme and other reagents for quickly and easily adding a poly(A) tail to the 3′ end of any RNA.

- **Addition of a poly(A) tail to RNA synthesised in vitro**
- **Synthesis of polyadenylated RNA for nucleic acid amplification methods or gene expression studies**
- **3′-end-labeling of RNA with radioactive A residues**

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Poly(A) Polymerase Tailing Kit PAP5104H</td>
<td>4 U/µL</td>
<td>50 Reactions</td>
</tr>
</tbody>
</table>

Contents: Poly(A) Polymerase, 10X Reaction Buffer, 10 mM ATP, Sterile RNase-Free Water

---

**T7 R&DNA Polymerase**

This enzyme is a mutant form of T7 RNA polymerase (Y639F mutant). The mutation enables T7 R&DNA Polymerase to incorporate 2′-deoxyribonucleoside triphosphates (dNTPs) into full-length “RNA” transcripts more efficiently than the corresponding wild-type T7 RNA polymerase.

- **Synthesis of “RNA” transcripts of mixed rNMP/2′-dNMP composition**
- **Synthesis of modified “RNA” transcripts that are resistant to RNase A**

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>T7R&amp;DNA01K</td>
<td>50 U/µL</td>
<td>1,000 U</td>
</tr>
<tr>
<td>T7R&amp;DNA05K</td>
<td>50 U/µL</td>
<td>5,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, 5X Reaction Buffer, 100 mM DTT

---

**MMLV High Performance Reverse Transcripase**

MMLV High Performance Reverse Transcriptase (MMLV HP RT) demonstrates significantly greater reverse transcriptase activity than other commercially available MMLV RT enzymes. Typically, just 100 units of MMLV HP RT are required for full-length cDNA synthesis compared to 200 units of MMLV RT enzymes from many other suppliers. The enzyme synthesises full-length cDNA from RNA templates longer than 15 kb, starting with picogram amounts of RNA.

- **cDNA synthesis from total RNA or poly(A)-enriched RNA for subsequent PCR, qPCR, or RNA-Seq library preparation**

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>MMLV High Performance Reverse Transcriptase RT80125K</td>
<td>200 U/µL</td>
<td>25,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, 10X Reaction Buffer, DTT

---

**EpiScript RNase H-Reverse Transcripase**

EpiScript Reverse Transcriptase is highly efficient at producing full-length cDNA from RNA templates up to 12 kb. The enzyme is genetically engineered to substantially reduce RNase H activity. This structural modification eliminates degradation of RNA molecules during first-strand cDNA synthesis and gives EpiScript Reverse Transcriptase superior performance for real-time RT-PCR analysis and other applications.

- **Efficient cDNA synthesis from picogram amounts of total RNA for subsequent PCR, qPCR, or RNA-Seq library preparation**

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>EpiScript Reverse Transcriptase ERT12910K</td>
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<td>10,000 U</td>
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<tr>
<td>ERT12925K</td>
<td>200 U/µL</td>
<td>25,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, 10X Reaction Buffer, DTT

---

**NxGen M-MuLV Reverse Transcriptase**

NxGen M-MuLV Reverse Transcriptase is an RNA-dependent DNA polymerase that shows no measurable 3′→5′ proofreading activity. This enzyme can copy a single-stranded DNA template or perform cDNA synthesis by extending a DNA primer annealed to an RNA template.

- **cDNA synthesis from total RNA or poly(A)-enriched RNA for subsequent PCR, qPCR, or RNA-Seq library preparation**

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>NxGen M-MuLV Reverse Transcriptase 30222-1</td>
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<td>50,000 U</td>
</tr>
<tr>
<td>30222-2</td>
<td>200 U/µL</td>
<td>250,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, 10X M-MuLV RT Buffer

---

**Reverse transcripases**

Enzymes for molecular biology

**MMLV High Performance Reverse Transcripase**

MMLV High Performance Reverse Transcriptase (MMLV HP RT) demonstrates significantly greater reverse transcriptase activity than other commercially available MMLV RT enzymes. Typically, just 100 units of MMLV HP RT are required for full-length cDNA synthesis compared to 200 units of MMLV RT enzymes from many other suppliers. The enzyme synthesises full-length cDNA from RNA templates longer than 15 kb, starting with picogram amounts of RNA.

- **cDNA synthesis from total RNA or poly(A)-enriched RNA for subsequent PCR, qPCR, or RNA-Seq library preparation**

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>MMLV High Performance Reverse Transcriptase RT80125K</td>
<td>200 U/µL</td>
<td>25,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, 10X Reaction Buffer, DTT

---

**EpiScript RNase H-Reverse Transcripase**

EpiScript Reverse Transcriptase is highly efficient at producing full-length cDNA from RNA templates up to 12 kb. The enzyme is genetically engineered to substantially reduce RNase H activity. This structural modification eliminates degradation of RNA molecules during first-strand cDNA synthesis and gives EpiScript Reverse Transcriptase superior performance for real-time RT-PCR analysis and other applications.

- **Efficient cDNA synthesis from picogram amounts of total RNA for subsequent PCR, qPCR, or RNA-Seq library preparation**

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>EpiScript Reverse Transcriptase ERT12910K</td>
<td>200 U/µL</td>
<td>10,000 U</td>
</tr>
<tr>
<td>ERT12925K</td>
<td>200 U/µL</td>
<td>25,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, 10X Reaction Buffer, DTT
Baseline-ZERO DNase
Baseline-ZERO DNase digests dsDNA and ssDNA to mononucleotides more effectively than the commonly used bovine pancreatic DNase I. Following treatment with Baseline-ZERO DNase, even the small DNA oligonucleotides that remain after treatment with DNase I are undetectable. The enzyme provides a true zero baseline for RNA RT-PCR or microarray gene expression experiments.

• Removal of genomic DNA from RNA before RT-PCR, or preparation of target RNA or cDNA for microarray analysis, especially for exon arrays or full-coverage expression analysis
• Removal of small DNA oligonucleotides (e.g., random primers)

### Cat. # | Concentration | Quantity
--- | --- | ---
D66710K | 1 U/µL | 5,000 MBU

Contents: Enzyme, 10X Reaction Buffer, 10X Stop Solution

DNA removal from in vitro transcription reactions using RNase-Free DNase I (bovine pancreas) is an endonuclease useful in removing DNA that might interfere with the characterisation, manipulation, or use of RNA, or for any application requiring highly purified DNase I, such as nick translation. This enzyme efficiently hydrolyses dsDNA and ssDNA to a mixture of short oligonucleotides and mononucleotides.

• Elimination of template DNA following in vitro synthesis of RNA with T7 phage RNA polymerase
• Labeling of DNA by nick translation, in combination with Klenow or other DNA polymerases
• Treatment of RNA before RT-PCR
• Characterisation of DNA-protein interactions by DNase I footprinting

### Cat. # | Concentration | Quantity
--- | --- | ---
D9905K | 1 U/µL | 5,000 MBU
C9910K | 1 U/µL | 10,000 MBU

Contents: Enzyme, 10X Reaction Buffer

Exonuclease VII has high enzymatic specificity for ssDNA and exhibits both 5′→ 3′ and 3′→ 5′ exonuclease activities. It is useful for rapid removal of single-stranded oligonucleotide primers from a completed amplification reaction when different primers are required for subsequent PCR. Exonuclease VII digestion of ssDNA occurs in the absence of magnesium.

• Removal of single-stranded oligonucleotide primers from a completed amplification reaction when different primers are required for subsequent PCR.
• Removal of single-stranded oligonucleotide primers after PCR
• Minimising the effect of primers left over from previous PCRs

### Cat. # | Concentration | Quantity
--- | --- | ---
Exonuclease VII | 10 U/µL | 250 U

Contents: Enzyme, 5X Reaction Buffer

Plasmid-Safe ATP-Dependent DNase
Plasmid-Safe ATP-Dependent DNase selectively removes contaminating bacterial chromosomal DNA from cosmids, BAC, fosmid, and plasmid preparations. The enzyme will processively degrade linear DNA from the ends; closed circular DNA (e.g., a plasmid) does not have free ends and is therefore not degraded. These properties make Plasmid-Safe ATP-Dependent DNase ideal for BAC and fosmid purification protocols, such as for shotgun sequencing, and other applications where high-purity DNA is necessary.

• Removal of contaminating bacterial chromosomal DNA in large-scale plasmid, cosmids, fosmid, and BAC vector or clone preparations

### Cat. # | Concentration | Quantity
--- | --- | ---
E3101K | 10 U/µL | 1,000 U
E3119K | 10 U/µL | 10,000 U

Contents: Enzyme, 1X Reaction Buffer, 2.5 mM ATP

Exonuclease III, E. coli
Exonuclease III digests duplex DNA in a 5′→ 5′ direction from a nick, a blunt end, or a 3′ recessed end, producing stretches of ssDNA on the opposite strand.

• Production of intermediates for site-directed mutagenesis
• Production of strand-specific radiolabelled probes

### Cat. # | Concentration | Quantity
--- | --- | ---
Exonuclease III, E. coli | 200 U/µL | 25,000 U

Contents: Enzyme, 1X Reaction Buffer

Rec J Exonuclease
Rec J Exonuclease, derived from E. coli, catalyses removal of deoxyribonucleoside monophosphates from ssDNA in a 5′→3′ direction. Its activity is dependent on Mg²⁺. Rec J Exonuclease can be heat-inactivated by incubation at 65 °C for 20 minutes.

• Removal of primers from completed PCRs
• Degradation of single-stranded linear DNA in ssDNA and plasmid preparations

### Cat. # | Concentration | Quantity
--- | --- | ---
Rec J Exonuclease | 10 U/µL | 250 U

Contents: Enzyme, 10X Reaction Buffer
### RNA nuclease enzymes

**RNase A**
RNase A is an endonuclease that cleaves ssRNA at the 3' end of pyrimidine residues, forming oligoribonucleotides having 3'-terminal pyrimidine-3'-phosphates. Pyrimidine-3'-monophosphates are also released by RNase A. Cleavage of adjacent pyrimidine nucleotides. Modified RNA containing pyrimidine-2'-fluoro-dNMPs, such as modified RNA made by in vitro transcription using the DuraScribe® T7 Transcription Kit, is completely resistant to cleavage by RNase A.

- Removal of RNA from DNA preparations
- Removal of unhybridised regions of RNA from DNA-RNA or RNA-RNA hybrids

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>RNase A</td>
<td>5 mg/mL</td>
<td>2 mL</td>
</tr>
</tbody>
</table>

**RNase R**
RNase R is a 3' → 5' exonuclease that digests essentially all linear RNAs but will not digest linear or circular RNA structures. Intern RNA can be isolated from total RNA samples by digestion with RNase R. After digestion, only circular RNAs remain.

- Alternative splicing studies
- Gene expression studies
- CircRNA-Seq library preparation
- Intrinsic screening of CDNA libraries

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>RNase R</td>
<td>200 U/µL</td>
<td>250 U</td>
</tr>
</tbody>
</table>

### Hybridase Thermostable RNase H
Hybridase Thermostable RNase H degrades the RNA in a DNA:RNA hybrid, without affecting DNA or unhybridised RNA. In contrast to E. coli RNase H, which is rapidly inactivated at 55 °C, this enzyme has optimal activity above 65 °C, and can be used up to 95 °C. This property allows it to be used at temperatures that give the highest hybridisation stringency for specific DNA:RNA heteroduplexes, maximising sensitivity and selectivity while minimising background due to nonspecific hybridisation.

- High-stringency hybrid selection
- Diagnostic assays of target DNA sequences
- Transcription-based amplification methods
- High-stringency mapping of mRNA structure

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hybridase Thermostable RNase H</td>
<td>5 U/µL</td>
<td>500 U</td>
</tr>
</tbody>
</table>

### Terminator 5'-Phosphate-Dependent Exonuclease
Terminator Exonuclease is a 5' → 3', processive exonuclease that degrades RNAs with a 5' monophosphate. It does not degrade RNAs with a 5' triphosphate, 5' cap structure (such as found on most eukaryotic mRNAs), or a 5' OH. It will also digest DNA with a 5' monophosphate. The enzyme is not inhibited by proteinaceous RNase inhibitors.

- Characterising the 5' termini of RNA transcripts
- Preparing mRNA-enriched samples from eukaryotic or prokaryotic total RNA preparations in 1 hour without the use of oligo(dT), resins, or magnetic beads

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Terminator 5'-Phosphate-Dependent Exonuclease</td>
<td>1 U/µL</td>
<td>40 U</td>
</tr>
</tbody>
</table>

### OmniCleave Endonuclease
This endonuclease digests all forms of DNA and RNA including single-stranded and double-stranded linear, circular, and supercoiled. OmniCleave Endonuclease has the same substrate specificity, and yields the same products as Benzonase®, an enzyme derived from Serratia marcescens.

- Removal of nucleic acids from cell lysates (reduction of viscosity) for improved handling and yield of protein preparations
- Removal of trace contamination by nucleic acids in protein preparations
- Removal of host DNA from phage preparations

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>OmniCleave Endonuclease</td>
<td>200 U/µL</td>
<td>50,000 U</td>
</tr>
</tbody>
</table>
**ActiviOf Ampligase Thermostable DNA Ligase.**

- **Ligation at high temperature**
- **DNA with long, complementary overhangs**
- **DNA with short, complementary overhangs**
- **DNA with long, partially complementary overhangs**
- **Blunt-ended DNA**

**Use of Ready-Lyse Lysozyme Solution to recover recombinant proteins.** A 1 mL sample of induced cells from a recombinant E. coli clone was pelleted by microcentrifugation before induction and at 1 and 3 hours after induction. Ready-Lyse Solution (1 mL) was added to each suspension and cells were incubated at room temperature for 30 minutes. The induced protein is designated by an arrow.

**Ready-Lyse Lysozyme Solution**

ReadLyse Lysozyme Solution is a nonmammalian, nonavian, recombinant lysozyme preparation for the lysis of Gram-negative (e.g., E. coli) and Gram-positive (e.g., Bacillus sp.) bacteria. The specific activity of Ready-Lyse Lysozyme is 200-fold higher than that of egg-white lysozyme. Additionally, it is stable at −20 °C, eliminating the need to prepare a fresh solution for each use. The use of Ready-Lyse Lysozyme results in higher yields of protein or nucleic acids than can be obtained with standard egg-white lysozyme.

- Lysis of Gram-negative or Gram-positive bacteria for protein purification
- Preparation of nucleic acids from bacteria

**Contents:** Enzyme only

**Cat. #** | **Quantity**
---|---
R1804M | 4 × 10^6 U
R1810M | 10 × 10^6 U

**Note:** One unit of Ampligase DNA Ligase is equal to as many as 15 units of other thermostable DNA ligases.

**Ampligase 10X Reaction Buffer**

- **Cat. #** | **Concentration** | **Quantity**
---|---|---
A1905B | 10× | 5 mL

**Enzymes for molecular biology**

**Lysozyme**

Enzymes for molecular biology

**Fast-Link DNA Ligation Kit**

Fast-Link T4 DNA Ligase provides extremely rapid, high-efficiency DNA ligation. Cohesive-end ligations can be performed in 5 minutes at room temperature. In contrast to other ligases, it is not necessary to desalt Fast-Link ligation reactions prior to transformation of electrocompetent or chemically competent cells.

- Blunt-end and TA cloning of PCR products
- Ligation of next gen sequencing adapters to blunt-end DNA
- Genomic and cDNA cloning and subcloning
- BAC/fosmid library construction
- Linker ligation

**Cat. #** | **Quantity**
---|---
LK0705H | 50 Ligations
LK6201H | 100 Ligations

**Contents:** Enzyme, Fast-Link 10X Ligation Buffer, 10 mM ATP

**NxGen T4 DNA Ligase**

NxGen T4 DNA Ligase is a ATP-dependent ligase commonly used for DNA cloning. It covalently joins dsDNA molecules having 5′-phosphorylated and 3′-hydroxylated blunt or compatible cohesive ends produced by restriction enzyme digestion or other enzymatic processes. It has no activity on single-stranded nucleic acids.

- Ligation of blunt or cohesive-ended DNA fragments
- Repair of nicks in double-stranded nucleic acids

**Cat. #** | **Concentration** | **Quantity**
---|---|---
30241-1 | 2 U/µL | 1,500 U
30241-2 | 2 U/µL* | 7,500 U
30243-1 | 10 U/µL | 1,500 U
30243-2 | 10 U/µL* | 7,500 U

**Contents:** Enzyme, 10X T4 DNA Ligase Buffer, 2X Rapid Ligation Buffer

*Weiss units

**Contents:** Enzyme only

**Cat. #** | **Concentration** | **Quantity**
---|---|---
A8101 | 5 U/µL | 1,000 U

**Contents:** Enzyme, 10X Reaction Buffer, Control DNA

**Lysozyme**

Enzymes for molecular biology

**Fast-Link DNA Ligation Kit**

**Contents:** Enzyme, Fast-Link 10X Ligation Buffer, 10 mM ATP

**Cat. #** | **Concentration** | **Quantity**
---|---|---
A32750 | 5 U/µL | 750 U
A3202K | 5 U/µL | 2,500 U
A0102K | 5 U/µL | 2,500 U

**Contents:** Enzyme, 10X Reaction Buffer

**Ampligase DNA Ligase Kit**

**Contents:** Enzyme, Control DNA

**Cat. #** | **Concentration** | **Quantity**
---|---|---
A3210K | 5 U/µL | 10,000 U
A0110K | 100 U/µL | 10,000 U

**Contents:** Enzyme only

**Ampligase 10X Reaction Buffer**

- **Cat. #** | **Concentration** | **Quantity**
---|---|---
A1909B | 10X | 5 mL

**Contents:** Enzyme only

**Cat. #** | **Concentration** | **Quantity**
---|---|---
A3202K | 5 U/µL | 2,500 U
A0102K | 5 U/µL | 2,500 U

**Contents:** Enzyme, 10X Reaction Buffer

**Note:** One unit of Ampligase DNA Ligase is equal to as many as 15 units of other thermostable DNA ligases.
**Enzymes for molecular biology**

### Ligases

#### T4 RNA Ligase 2, Deletion Mutant

T4 RNA Ligase 2, Deletion Mutant, T4Rn2(1-249), ligates single-stranded, adenylated DNA or RNA (App-DNA or App-RNA) oligonucleotides to small RNAs. The preadenylated 5’ ends of DNA or RNA are ligated to the 3’ ends of RNA in the absence of ATP, which prevents circularisation and other undesirable bimolecular reactions.

- Preparation of cDNA libraries for small-RNA transcriptome analysis, such as RNA-Seq
- Optimal linker ligation for mRNA cloning

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>LR2D1132K</td>
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</tr>
<tr>
<td>LR2D11310K</td>
<td>200 U/µL</td>
<td>10,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, 10X Reaction Buffer

#### CircLigase II ssDNA Ligase

This thermostable ligase catalyses intramolecular ligation (i.e., circularisation) of ssDNA templates >30 nt having a 5’ phosphate and a 3’ hydroxyl group. It ligation the ends of ssDNA in the absence of a complementary sequence. Standard reaction conditions produce no detectable single-stranded DNA concatamers or concatameric DNA circles. Due to the low degree of adenylation, CircLigase enzyme has high turnover; it can reversibly and repeatedly act on multiple preadenylated DNA molecules under nonstoichiometric reaction conditions.

- Production of ssDNA templates for rolling-circle replication or rolling-circle transcription experiments
- Production of ssDNA templates for RNA polymerase and RNA polymerase inhibitor assays

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>CL4111K</td>
<td>100 U/µL</td>
<td>1,000 U</td>
</tr>
<tr>
<td>CL4115K</td>
<td>100 U/µL</td>
<td>5,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, CircLigase 10X Reaction Buffer, 1 mM ATP, 50 mM MnCl₂, CircLigase ssDNA Control Oligo, Sterile Water

#### RNA 5’ Polynucleotide Kinase

RNA 5’ Polynucleotide Kinase catalyses the transfer of the γ phosphate from ATP to the 5’ OH of ssDNA and dsDNA, RNA, and nucleoside 3’-monophosphates. The enzyme also removes the 3’ phosphate from 3’-phosphorylated polynucleotides, deoxyribonucleoside 3’-monophosphates, and deoxyribonucleoside 3’,5’-diphosphates to form a 3’-OH group.

- Labeling of 5’ termini of DNA and RNA for DNA sequencing, blot-hybridisation, or transcript mapping
- Phosphorylation of oligonucleotide linkers and other DNA or RNA molecules before ligation, or for use in ligation amplification with Ampligase Thermostable DNA Ligase
- Preparation of labeled DNA or RNA molecular weight markers for gel electrophoresis and chromatography

<table>
<thead>
<tr>
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<th>Concentration</th>
<th>Quantity</th>
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</thead>
<tbody>
<tr>
<td>RP8092H</td>
<td>200 U/µL</td>
<td>3,000 U</td>
</tr>
</tbody>
</table>

Contents: Enzyme, 10X Reaction Buffer without ATP, ATP is available separately.

#### T4 Polynucleotide Kinase, Cloned

T4 Polynucleotide Kinase (PNK) catalyses the transfer of the γ phosphate from ATP to the 5’ OH of ssDNA and dsDNA, RNA, and nucleoside 3’-monophosphates. The enzyme catalyses the transfer of the γ phosphate from ATP to the 5’ OH of ssDNA and dsDNA, RNA, and nucleoside 3’-monophosphates.

- Phosphorylation of oligonucleotide linkers and other DNA or RNA molecules before ligation, or for use in ligation amplification with Ampligase Thermostable DNA Ligase
- Preparation of labeled DNA or RNA molecular weight markers for gel electrophoresis and chromatography

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
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</thead>
<tbody>
<tr>
<td>P3003K</td>
<td>100 U/µL</td>
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</tr>
</tbody>
</table>

Contents: Enzyme, 10X Reaction Buffer without ATP, ATP is available separately.

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**Phosphatases and kinases**

### RNA 5’ Polyphosphatase

RNA 5’ Polyphosphatase is a Mg²⁺-independent polyphosphatase enzyme. It sequentially removes the γ and β phosphates from 5’-triphosphorylated RNA (such as primary RNA transcripts). However, it will not dephosphorylate monophosphorylated or 5’-capped RNA.

- Conversion of 5’-triphosphorylated RNA to 5’-monophosphorylated RNA for use in 5’-RNA ligation-tagging methods using T4 RNA Ligase
- Analysis of 5’-end structures of RNA
- Preparation of substrate RNA molecules for subsequent degradation using Terminator Exonuclease

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>RR8020H</td>
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</table>

Contents: Enzyme, 10X Reaction Buffer

#### End-It DNA End-Repair Kit

The End-It DNA End-Repair Kit is used to convert DNA with damaged or incompatible 5’-protruding and/or 3’-protruding ends to 5’-phosphorylated, blunt-end DNA for the subsequent addition of new DNA sequencing adapters, or for cloning. After treatment of DNA with the End-It Kit, fast and efficient blunt-end ligation can be performed using the Fast-Link DNA Ligation Kit (Lucigen).

- Treatment of enzymatically or mechanically sheared DNA or cDNA before adding next gen sequencing adapters
- Polishing of enzymatically or mechanically sheared DNA, cDNA, or PCR amplicons with A overhangs, before cloning into plasmid, cosmid, fosmid, or BAC vectors

<table>
<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
</tr>
</thead>
<tbody>
<tr>
<td>ER0720</td>
<td>20 Reactions</td>
<td>50 Reactions</td>
</tr>
</tbody>
</table>

Contents: End-It Repair Enzyme Mix, End-Repair 10X Buffer, dNTP Solution, ATP

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**Activity of the End-It DNA End-Repair Kit.**
**CRISPRcraft S.p. Cas9 Nuclease**

CRISPRcraft S.p. Cas9 Nuclease is a purified, recombinant wild-type *Streptococcus pyogenes* Cas9 nuclease produced in *E. coli*, containing a C-terminal 6× His tag and a C-terminal nuclear localisation sequence (NLS) to allow efficient transport to the nucleus. It is provided at high concentration (10 mg/mL; 62 µM) to enable efficient ribonucleoprotein (RNP) delivery and compatibility with multiple delivery methods, including lipid-based transfection and electroporation.

- **CRISPR/Cas9 gene-editing experiments**
- **Sequence-specific, RNA-guided cleavage of dsDNA**
- **Sequence enrichment and depletion**

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<thead>
<tr>
<th>Cat. #</th>
<th>Concentration</th>
<th>Quantity</th>
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<tbody>
<tr>
<td>70020-1</td>
<td>10 mg/mL</td>
<td>120 µg</td>
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<tr>
<td>70020-2</td>
<td>200 U/µL</td>
<td>400 µg</td>
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</table>

Contents: Enzyme only

**CRISPRcraft S.p. Cas9 Nuclease Control Kit**

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<th>Concentration</th>
<th>Quantity</th>
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</thead>
<tbody>
<tr>
<td>70020-1</td>
<td>10 mg/mL</td>
<td>120 µg</td>
</tr>
</tbody>
</table>

Contents: Cas9 Control HPRT Guide crRNA and Cas9 Universal tracrRNA, Control HPRT Forward and Reverse PCR Primers, Control HPRT Substrate DNA, 10X RGEN Buffer (Cas9 Nuclease not included)

*Note: Some uses for this product may require licenses. Lucigen does not encourage or support the unauthorised or unlicensed use of any product. It is the sole responsibility of the buyer to ensure that use of the product does not infringe the patent rights of third parties.

**AsCpf1 Nuclease**

Cpf1 nuclease is an RNA-guided endonuclease (RGEN), with published applications including gene editing, sensitive DNA sequence detection, and cloning and assembling large DNA inserts. Several features distinguish Cpf1 from other RGEN enzymes. Cpf1 prefers an A/T-rich protospacer adjacent motif (PAM) sequence, enabling targeting of DNA sequences with high A/T content. Cpf1 cleaves DNA in a staggered fashion, similar to restriction enzymes. It does not require a tracrRNA, so guide RNAs are short.

AsCpf1 Nuclease is a purified, recombinant *Acidaminococcus* sp. Cpf1 nuclease produced in *E. coli* with two C-terminal nuclear localisation sequences (NLS) and one C-terminal 6× His tag.

Published applications include:

- **CRISPR/Cpf1 gene-editing experiments**
- **Sequence-specific, RNA-guided cleavage of dsDNA**
- **Sequence enrichment and depletion**
- **DNA sequence detection**

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<th>Concentration</th>
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</table>
| Available in bulk quantities with custom dispensing options. Please enquire: bizdev@lucigen.com
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**Schematic overview of the CRISPR-Cas9 genome-editing system**

The CRISPR RNA (crRNA) and transactivating CRISPR RNA (tracrRNA) sequences may be provided as two complexed RNA molecules (dual guide RNA), or combined into a single guide RNA (sgRNA) as shown in this figure. The Cas9:sgRNA complex targets a DNA sequence, provided it contains a protospacer adjacent motif (PAM) directly adjacent to the complementary crRNA sequence. The complex partially unwinds the DNA and interrogates the surrounding sequence for complementarity to the crRNA. If a match is found, the target sequence is cleaved, forming a double-stranded break (DSB).

The DSB is then repaired by one of two pathways. The non-homologous end joining (NHEJ) pathway results in insertions or deletions in the target genomic DNA, while the homology-directed repair (HDR) pathway produces a precise mutation. The donor template for HDR contains a mutation in the PAM sequence to avoid further cleavage of the newly created DNA by the Cas9:sgRNA complex.

**Cas9:sgRNA complex unwinds and cleaves DNA**

- **NHEJ**
- **HDR**
- **Double-stranded break (DSB)**
- **Homology arms**
- **Donor template**
- **Desired mutation**
- **Mutated PAM sequence**
- **Precise mutation**
- **Wild type**
- **Insertion**
- **Deletion**
Integrated tools.
Accelerated science.

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