



Competent Cells for Cloning

What packaging works best for you?

We have your competent cells. Whatever your application, our competent cells can make your cloning faster and more efficient—even if you're cloning difficult or unstable DNA. We can customize our strains for you in the following formats:

- 96-well
- SOLOPACK (single-use aliquots)
- Volumes customized for your application

Proven performers

Here are some of our most popular competent cells. For details about genotypes and other cells, see the reverse side of this fact sheet.

Generate large libraries

ElectroTen-Blue[®] Electroporation-Competent Cells ($> 3 \times 10^{10}$ transformants/ μ g)

Created to transform large DNA molecules with high efficiency, these cells exhibit the high electroporation efficiency (Hee) phenotype. The Hee phenotype improves survival of these cells during electroporation treatment, dramatically improving transformation efficiency. The high cloning efficiency makes this strain an ideal host for generating large, more representative libraries.

Transform large DNA with high efficiency

XL10-Gold Ultracompetent Cells ($> 5 \times 10^9$ transformants/ μ g)

Created for transformation of large DNA molecules with high efficiency, these cells exhibit the Hte phenotype, which increases the transformation efficiency of large and ligated DNA molecules. In addition, the XL10-Gold strain allows blue-white color screening, permits cloning of methylated DNA and produces high-quality miniprep DNA. XL10-Gold ultracompetent cells are the host cells of choice for cloning experiments that require high transformation efficiencies.

Clone difficult and unstable DNA

SURE[®] Electroporation-Competent Cells ($> 1 \times 10^{10}$ transformants/ μ g)

Designed to facilitate cloning of DNA containing secondary structures by removing genes involved in the rearrangement and deletion of these DNAs. The UV repair system (*uvrC*) and the SOS repair pathway (*umuC*) are both involved in repairing DNA lesions. Removal of these genes results in a 10- to 20-fold increase in the stability of DNA containing long inverted repeats. Another set of *E. coli* proteins, the *SbcC* and *RecJ* proteins, are involved in certain types of recombination. Mutations in these genes greatly increases stability of Z-DNA structures.

Please visit

www.agilent.com/genomics/custom_manufacturing
for more information or to request a quote.



Genotypes

Host Strain	
ABLE® C STRAIN	<i>E. coli</i> C lac(LacZω ⁻) [Kan ^r McrA ⁻ McrCB ⁻ McrF ⁻ Mrr ⁻ HsdR (r _k ⁻ m _k ⁻)] [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r)]
ABLE® K STRAIN	<i>E. coli</i> C lac(LacZω ⁻) [Kan ^r McrA ⁻ McrCB ⁻ McrF ⁻ Mrr ⁻ HsdR (r _k ⁻ m _k ⁻)] [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r)]
AG1 STRAIN	<i>recA1 endA1 gyrA96 thi-1</i> (r _k ⁻ m _k ⁻) <i>supE44 relA1</i>
BL21-GOLD STRAIN	<i>E. coli</i> B F ⁻ dcm ⁺ Hte <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>gal endA</i> Tet ^{r a}
BL21-GOLD(DE3) STRAIN	<i>E. coli</i> B F ⁻ dcm ⁺ Hte <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>gal λ</i> (DE3) <i>endA</i> Tet ^{r a}
BL21-GOLD(DE3)pLysS STRAIN	<i>E. coli</i> B F ⁻ dcm ⁺ Hte <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>gal λ</i> (DE3) [pLysS Cam ^r]* <i>endA</i> Tet ^{r a}
BL21 STRAIN	<i>E. coli</i> B F ⁻ dcm <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>gal</i>
BL21(DE3) STRAIN	<i>E. coli</i> B F ⁻ dcm <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>gal λ</i> (DE3)
BL21(DE3)pLysS STRAIN	<i>E. coli</i> B F ⁻ dcm <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>gal λ</i> (DE3) [pLysS Cam ^r]*
BL21-CODONPLUS® (DE3)-RIPL STRAIN	<i>E. coli</i> B F ⁻ <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>dcm</i> + Tet ^r <i>gal λ</i> (DE3) <i>endA</i> Hte [argU <i>proL</i> Cam ^r] [argU <i>ileY leuW</i> Strep/Spec ^r]
BL21-CODONPLUS® RIL STRAIN	<i>E. coli</i> B F ⁻ <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>dcm</i> + Tet ^r <i>gal endA</i> Hte [argU <i>ileY leuW</i> Cam ^r]*, a
BL21-CODONPLUS® (DE3)-RIL STRAIN	<i>E. coli</i> B F ⁻ <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>dcm</i> + Tet ^r <i>gal λ</i> (DE3) <i>endA</i> Hte [argU <i>ileY leuW</i> Cam ^r]*, a
BL21-CODONPLUS® RP STRAIN	<i>E. coli</i> B F ⁻ <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>dcm</i> + Tet ^r <i>gal endA</i> Hte [argU <i>proL</i> Cam ^r]*, a
BL21-CODONPLUS® (DE3)-RP STRAIN	<i>E. coli</i> B F ⁻ <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>dcm</i> + Tet ^r <i>gal λ</i> (DE3) <i>endA</i> Hte [argU <i>proL</i> Cam ^r]*, a
BL21-CODONPLUS® (DE3)-RIL-X STRAIN	<i>E. coli</i> B F ⁻ <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>dcm</i> + Tet ^r <i>gal λ</i> (DE3) <i>endA</i> Hte <i>metA::Tn5</i> (Kan ^r) [argU <i>ileY leuW</i> Cam ^r]*, a
BL21-CODONPLUS® (DE3)-RP-X STRAIN	<i>E. coli</i> B F ⁻ <i>ompT hsdS</i> (r _b ⁻ m _b ⁻) <i>dcm</i> + Tet ^r <i>gal λ</i> (DE3) <i>endA</i> Hte <i>metA::Tn5</i> (Kan ^r) [argU <i>proL</i> Cam ^r]*, a
ELECTROTEN-BLUE® STRAIN	Δ(<i>mcrA</i>)183 (<i>mcrB-hsdSMR-mrr</i>)173 <i>endA1 supE44 thi-1 recA1 gyrA96 relA1 lac</i> Kan ^r Hee [F' <i>proAB lac^hZΔM15Tn10</i> (Tet ^r)]**
JM101 STRAIN	<i>supE thi-1 Δ(lac-proAB)</i> [F' <i>traD36 proAB lac^hZΔM15</i>]
JM109 STRAIN	e14 ⁻ (McrA ⁻) <i>recA1 endA1 gyrA96 thi-1 hsdR17</i> (r _k ⁻ m _k ⁺) <i>supE44 relA1 Δ(lac-proAB)</i> [F' <i>traD36 proAB lac^hZΔM15</i>]
JM110 STRAIN	<i>rpsL</i> (Str ^r) <i>thr leu thi-1 lacY galK galT ara tonA tsx dam dcm supE44 Δ(lac-proAB)</i> [F' <i>traD36 proAB lac^hZΔM15</i>]
NM522 STRAIN	<i>supE thi-1 Δ(lac-proAB) Δ(mcrB-hsdSM)</i> 5 (r _k ⁻ m _k ⁻) [F' <i>proAB lac^hZΔM15</i>]
SCS1 STRAIN	<i>recA1 endA1 gyrA96 thi-1 hsdR17</i> (r _k ⁻ m _k ⁺) <i>supE44 relA1</i>
SCS110 STRAIN	<i>rpsL</i> (Str ^r) <i>thr leu endA thi-1 lacY galK galT ara tonA tsx dam dcm supE44 Δ(lac-proAB)</i> [F' <i>traD36 proAB lac^hZΔM15</i>]
SURE® STRAIN	e14 ⁻ (McrA ⁻) Δ(<i>mcrCB-hsdSMR-mrr</i>)171 <i>endA1 supE44 thi-1 gyrA96 relA1 lac recB recJ sbcC umuC::Tn5</i> (Kan ^r) <i>uvrC</i> [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r)]
SURE® 2 STRAIN	e14 ⁻ (McrA ⁻) Δ(<i>mcrCB-hsdSMR-mrr</i>)171 <i>endA1 supE44 thi-1 gyrA96 relA1 lac recB recJ sbcC umuC::Tn5</i> (Kan ^r) <i>uvrC</i> [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r) Amy Cam ^r]*
TG1 STRAIN	<i>supE thi-1 Δ(lac-proAB) Δ(mcrB-hsdSM)</i> 5 (r _k ⁻ m _k ⁻) [F' <i>traD36 proAB lac^hZΔM15</i>]
XL1-BLUE STRAIN	<i>recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac</i> [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r)]
XL1-BLUE MR STRAIN	Δ(<i>mcrA</i>)183 Δ(<i>mcrCB-hsdSMR-mrr</i>)173 <i>endA1 supE44 thi-1 recA1 gyrA96 relA1 lac</i>
XL1-BLUE MRF' STRAIN	Δ(<i>mcrA</i>)183 Δ(<i>mcrCB-hsdSMR-mrr</i>)173 <i>endA1 supE44 thi-1 recA1 gyrA96 relA1 lac</i> [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r)]
XL1-BLUE MRF' KAN STRAIN	Δ(<i>mcrA</i>)183 Δ(<i>mcrCB-hsdSMR-mrr</i>)173 <i>endA1 supE44 thi-1 recA1 gyrA96 relA1 lac</i> [F' <i>proAB lac^hZΔM15 Tn5</i> (Kan ^r)]
XL2-BLUE STRAIN	<i>recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac</i> [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r) Amy Cam ^r]*
XL2-BLUE MRF' STRAIN	Δ(<i>mcrA</i>)183 Δ(<i>mcrCB-hsdSMR-mrr</i>)173 <i>endA1 supE44 thi-1 recA1 gyrA96 relA1 lac</i> [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r) Amy Cam ^r]*
XL10-GOLD® STRAIN	Tet ^r Δ(<i>mcrA</i>)183 Δ(<i>mcrCB-hsdSMR-mrr</i>)173 <i>endA1 supE44 thi-1 recA1 gyrA96 relA1 lac Hte</i> [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r) Amy Cam ^r]*
XL10-GOLD® KAN STRAIN	Tet ^r Δ(<i>mcrA</i>)183 Δ(<i>mcrCB-hsdSMR-mrr</i>)173 <i>endA1 supE44 thi-1 recA1 gyrA96 relA1 lac Hte</i> [F' <i>proAB lac^hZΔM15 Tn10</i> (Tet ^r) Tn5 (Kan ^r) Amy]
XL1-RED STRAIN	<i>endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac mutD5 mutS mutT Tn10</i> (Tet ^r)

This information is subject to change without notice.

For Research Use Only. Not for use in diagnostic procedures.

© Agilent Technologies, Inc., 2011, 2016
 PR7000-0483
 Published in USA, May 3, 2016
 Publication Number 5990-8743EN

