Competent Cells for Protein Expression

What packaging works best for you?

We have your competent cells for protein expression. Whatever your application, our cells are engineered for high-efficiency cloning, for removing codon bias and increasing expression levels. Our Custom Services team can package any strain 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 protein expression. For details about genotypes and other cells, see the reverse side of this fact sheet.

Save days of work
BL21-GOLD (DE3)
Ideal for both cloning and protein expression. This strain lacks the EndA1 nuclease, a harmful enzyme that rapidly degrades miniprep DNA, making restriction mapping and DNA sequencing very difficult. Cloning directly into BL21-Gold cells saves two days of work which would otherwise be spent on subcloning procedures in another minus strain. This strain also carries the Hte phenotype* increasing the transformation efficiency 100-fold over the parental BL21-strain.

Improve expression in E.coli
BL21-CodonPlus®(DE3)-RIPL
Codon bias occurs when forced high-level expression of a gene with codons that are rarely used by *E. coli* causes depletion of the internal tRNA pools. This leads to delayed translation of the recombinant RNA resulting in degraded RNA or codon substitutions and misincorporations that destroy the functional characteristics of the protein.

To solve this problem, we increased the supply of E. coli tRNAs for arginine (AGA) and (AGG), isoleucine (AUA), leucine (CUA), and proline (CCC). This modification dramatically improves expression of many proteins that are difficult to express in conventional E. coli due to codon bias.

Increase available soluble protein
ArcticExpress™ (DE3)
Engineered to express cold-adapted chaperonin Cpn60 and co-chaperonin Cpn10 from psychrophilic bacterium, Oleispira antarctica. Chaperonins are known to facilitate proper protein folding by binding to and stabilizing unfolded or partially folded proteins. The chaperonins from the Antarctic isolate, Oleispira antarctica, show high protein refolding activities at temperatures of 4-12°C. When expressed in our ArcticExpress cells, these chaperonins confer an enhanced ability to grow at lower temperatures and properly process recombinant proteins, thus increasing the amount of available soluble protein.

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

Genotypes

Host Strain	
ABLE® C STRAIN	*E. coli* C lac(LacZω⁻) [Kan^r McrA⁻ McrCB⁻ McrF⁻ Mrr⁻ HsdR (r_K^- m_K^-)] [F′ *pro*AB *lac*I^q*ZΔM15* Tn*10* (Tet^r)]
ABLE® K STRAIN	*E. coli* C lac(LacZω⁻) [Kan^r McrA⁻ McrCB⁻ McrF⁻ Mrr⁻ HsdR (r_K^- m_K^-)] [F′ *pro*AB *lac*I^q*ZΔM15* Tn*10* (Tet^r)]
AG1 STRAIN	*recA1 endA1 gyrA96 thi-1* (r_K^- m_K^-) *supE44 relA1*
BL21-GOLD STRAIN	*E. coli* B F⁻ dcm+ Hte *ompT hsdS*(r_B^- m_B^-) *gal endA* Tet^r [a]
BL21-GOLD(DE3) STRAIN	*E. coli* B F⁻ dcm+ Hte *ompT hsdS*(r_B^- m_B^-) *gal λ* (DE3) *endA* Tet^r [a]
BL21-GOLD(DE3)pLysS STRAIN	*E. coli* B F⁻ dcm+ Hte *ompT hsdS*(r_B^- m_B^-) *gal λ* (DE3) [pLysS Cam^r]* *endA* Tet^r [a]
BL21 STRAIN	*E. coli* B F⁻ dcm *ompT hsdS*(r_B^- m_B^-) *gal*
BL21(DE3) STRAIN	*E. coli* B F⁻ dcm *ompT hsdS*(r_B^- m_B^-) *gal λ*(DE3)
BL21(DE3)pLysS STRAIN	*E. coli* B F⁻ dcm *ompT hsdS*(r_B^- m_B^-) *gal λ*(DE3) [pLysS Cam^r]*
BL21-CODONPLUS® (DE3)-RIPL STRAIN	*E. coli* B F⁻ *ompT hsdS*(r_B^- m_B^-) *dcm*+ Tet^r *gal λ*(DE3) *endA* Hte [*argU proL* Cam^r] [*argU ileY leuW* Strep/Spec^r]
BL21-CODONPLUS® RIL STRAIN	*E. coli* B F⁻ *ompT hsdS*(r_B^- m_B^-) *dcm*+ Tet^r *gal endA* Hte [*argU ileY leuW* Cam^r]*,[a]
BL21-CODONPLUS®(DE3)-RIL STRAIN	*E. coli* B F⁻ *ompT hsdS*(r_B^- m_B^-) *dcm*+ Tet^r *gal λ*(DE3) *endA* Hte [*argU ileY leuW* Cam^r]*,[a]
BL21-CODONPLUS® RP STRAIN	*E. coli* B F⁻ *ompT hsdS*(r_B^- m_B^-) *dcm*+ Tet^r *gal endA* Hte [*argU proL* Cam^r]*,[a]
BL21-CODONPLUS® (DE3)-RP STRAIN	*E. coli* B F⁻ *ompT hsdS*(r_B^- m_B^-) *dcm*+ Tet^r *gal λ*(DE3) *endA* Hte [*argU proL* Cam^r]*,[a]
BL21-CODONPLUS® (DE3)-RIL-X STRAIN	*E. coli* B F⁻ *ompT hsdS*(r_B^- m_B^-) *dcm*+ Tet^r *gal λ*(DE3) *endA* Hte *metA::Tn5*(Kan^r) [*argU ileY leuW* Cam^r]*,[a]
BL21-CODONPLUS® (DE3)-RP-X STRAIN	*E. coli* B F⁻ *ompT hsdS*(r_B^- m_B^-) *dcm*+ Tet^r *gal λ*(DE3) *endA* Hte *metA::Tn5*(Kan^r) [*argU proL* Cam^r]*,[a]
ELECTROTEN-BLUE® STRAIN	*Δ(mcrA)183 (mcrB-hsdSMR-mrr)173 endA1 supE44 thi-1 recA1 gyrA96 relA1 lac* Kan^r Hee [*F′ proAB lac*I^q*ZΔM15Tn10*(Tet^r)]**
JM101 STRAIN	*supE thi*-1 Δ(*lac-proAB*) [F′ *traD36 proAB lac*I^q*ZΔM15*]
JM109 STRAIN	e14⁻(McrA⁻) *recA1 endA1 gyrA96 thi-1 hsdR17* (r_K^- m_K+) *supE44 relA1* Δ(*lac-proAB*) [F′ *traD36 proAB lac*I^q*ZΔM15*]
JM110 STRAIN	*rpsL* (Str^r) *thr leu thi-1 lacY galK galT ara tonA tsx dam dcm supE44 Δ(lac-proAB)* [F′ *traD36 proAB lac*I^q*ZΔM15*]
NM522 STRAIN	*supE thi-1 Δ(lac-proAB) Δ(mcrB-hsdSM)*5 (r_K^- m_K^-) [F′ *proAB lac*I^q*ZΔM15*]
SCS1 STRAIN	*recA1 endA1 gyrA96 thi-1 hsdR17* (r_K^- m_K+) *supE44 relA1*
SCS110 STRAIN	*rpsL* (Str^r) *thr leu endA thi-1 lacY galK galT ara tonA tsx dam dcm supE44 Δ(lac-proAB)* [F′ *traD36 proAB lac*I^q*ZΔM15*]
SURE® STRAIN	e14⁻(McrA⁻) *Δ(mcrCB-hsdSMR-mrr)171 endA1 supE44 thi-1 gyrA96 relA1 lac recB recJ sbcC umuC::Tn5* (Kan^r) *uvrC* [F′ *proAB lac*I^q*ZΔM15* Tn*10* (Tet^r)]
SURE® 2 STRAIN	e14⁻(McrA⁻) *Δ(mcrCB-hsdSMR-mrr)171 endA1 supE44 thi-1 gyrA96 relA1 lac recB recJ sbcC umuC::Tn5* (Kan^r) *uvrC* [F′ *proAB lac*I^q*ZΔM15* Tn*10* (Tet^r) Amy Cam^r]*
TG1 STRAIN	*supE thi-1 Δ(lac-proAB) Δ(mcrB-hsdSM)*5(r_K^- m_K^-) [F′ *traD36 proAB lac*I^q*ZΔM15*]
XL1-BLUE STRAIN	*recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac* [F′ *proAB lac*I^q*ZΔM15* Tn*10* (Tet^r)]
XL1-BLUE MR STRAIN	*Δ(mcrA)183 Δ(mcrCB-hsdSMR-mrr)173 endA1 supE44 thi-1 recA1 gyrA96 relA1 lac*
XL1-BLUE MRF′ STRAIN	*Δ(mcrA)183 Δ(mcrCB-hsdSMR-mrr)173 endA1 supE44 thi-1 recA1 gyrA96 relA1 lac* [F′ *proAB lac*I^q*ZΔM15* Tn*10* (Tet^r)]
XL1-BLUE MRF′ KAN STRAIN	*Δ(mcrA)183 Δ(mcrCB-hsdSMR-mrr)173 endA1 supE44 thi-1 recA1 gyrA96 relA1 lac* [F′ *proAB lac*I^q*ZΔM15* Tn*5* (Kan^r)]
XL2-BLUE STRAIN	*recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac* [F′ *proAB lac*I^q*ZΔM15* Tn*10* (Tet^r) Amy Cam^r]*
XL2-BLUE MRF′ STRAIN	*Δ(mcrA)183 Δ(mcrCB-hsdSMR-mrr)173 endA1 supE44 thi-1 recA1 gyrA96 relA1 lac* [F′ *proAB lac*I^q*ZΔM15* Tn*10* (Tet^r) Amy Cam^r]*
XL10-GOLD® STRAIN	Tet^r *Δ(mcrA)183 Δ(mcrCB-hsdSMR-mrr)173 endA1 supE44 thi-1 recA1 gyrA96 relA1 lac Hte* [F′ *proAB lac*I^q*ZΔM15* Tn*10* (Tet^r) Amy Cam^r]*
XL10-GOLD® KAN STRAIN	Tet^r *Δ(mcrA)183 Δ(mcrCB-hsdSMR-mrr)173 endA1 supE44 thi-1 recA1 gyrA96 relA1 lac Hte* [F′ *proAB lac*I^q*ZΔM15* Tn*10* (Tet^r) Tn*5* (Kan^r) Amy]
XL1-RED STRAIN	*endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac mutD5 mutS mutT* Tn*10* (Tet^r)

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The Measure of Confidence

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