E. coli Strains Supplied by NEB

The following *E. coli* strains are available upon request from New England Biolabs at no charge with an order or for the cost of shipping if ordered separately. They are supplied in vials containing approximately 200 µl of a 50% glycerol suspension. The strains are **not** competent.

The table summarizes relevant characteristics and recommended applications for each strain. Strain genotypes and brief descriptions are listed below. Genotypes of additional *E. coli* strains (not supplied by NEB) can be found here.

	ER1793	ER1821	ER2267	ER2738	GM2163 ER2925	JM101	JM109	NM522	ER2507	TB1	CAG597	CAG626	CAG629	PR1031	ER2508	KS1000	UT5600	CJ236
Library Construction[1]	+	+	+															
Plasmid Preparation[2]		+	+		+		+											
Cloning/Subcloning	+	+	+	+			+	+	+	+								
Dam⁻/Dcm⁻					+													
Single-stranded Phage[3]			+	+		+	+	+								+		+
Blue/White Screening			+	+		+	+	+		+								
RecA⁻			+				+											
Protease-deficient[4]											+	+	+	+	+	+	+	
LacI^q (for P*lac* regulation)			+	+		+	+	+								+		
Kunkel Mutagenesis																		+
Drug Resistance[5]	str	none	kan	tet	cam str	none	nal	none	kan str	str	tet str	str	tet str	tet	kan str tet	kan nal tet	str	cam

Footnotes

1. Restriction-deficient strain.
2. Strain has a mutation in the *endA* gene which eliminates the major nonspecific endonuclease.
3. Strain contains F´.
4. See strain description for details.
5. cam = chloramphenicol; kan = kanamycin; nal = nalidixic acid; str = streptomycin; tet = tetracycline

Strains for CLONING and SUBCLONING

ER1793 (#E4101S)
F⁻ *fhuA2* Δ*(lacZ)r1 glnV44 e14*⁻(McrA⁻) *trp-31 his-1 rpsL104*(Str^R) *xyl-7 mtl-2 metB1* Δ*(mcrC-mrr)114::IS10*

Lacks native *E. coli* restriction systems; good general cloning strain (1). Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11.

ER1821 (#E4102S)
F⁻ *glnV44 e14*⁻(McrA⁻) *rfbD1? relA1? endA1 spoT1? thi-1* Δ*(mcrC-mrr)114::IS10*

Lacks native *E. coli* restriction systems; good general cloning strain. Different strain background from ER1793. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11.

ER2267 (#E4103S)
F´ *proA*$^+$*B*$^+$ *lacI*^{q} Δ*(lacZ)M15 zzf::mini-Tn10* (Kan^R)/ Δ*(argF-lacZ)U169 glnV44 e14*⁻(McrA⁻) *rfbD1? recA1 relA1? endA1 spoT1? thi-1* Δ*(mcrC-mrr)114::IS10*

Lacks native *E. coli* restriction systems; good strain for cloning repetitive DNA (RecA⁻); can be used for blue/white screening. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11.

ER2738 (#E4104S)
F´*proA*$^+$*B*$^+$ *lacI*^{q} Δ*(lacZ)M15 zzf::Tn10*(Tet^R)/ *fhuA2 glnV* Δ*(lac-proAB) thi-1* Δ*(hsdS-mcrB)5*

This strain is provided with the Ph.D. Phage Display Kit. Can also be used for M13 cloning/sequencing and blue/white screening. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11.

ER2925 (#E4109S)
ara-14 leuB6 fhuA31 lacY1 tsx78 glnV44 galK2 galT22 mcrA dcm-6 hisG4 rfbD1 R(zgb210::Tn10)TetS endA1 rpsL136 dam13::Tn9 xylA-5 mtl-1 thi-1 mcrB1 hsdR2

Strain is both Dam⁻ and Dcm⁻, so it is useful for production of DNA to be cut with Dam or Dcm-sensitive restriction enzymes (2,3). Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of, λ, e.g., λgt11. This strain is resistant to chloramphenicol. Strain is identical to our previous Dam⁻ Dcm⁻ strain GM2163 except that the activity of nonspecific endonuclease I has been abolished, dramatically improving plasmid prep quality in many cases.

GM2163 (#E4105S) replaced by **ER2925** (#E4109)

JM101 (#E4106S)
F´*traD36 proA*$^+$*B*$^+$ *lacI*^{q} Δ*(lacZ)M15/* Δ*(lac-proAB) glnV thi*

The original blue/white strain (4,5). Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11. Has all *E. coli* restriction systems.

JM109 (#E4107S)
F´*traD36 proA*$^+$*B*$^+$ *lacI*^{q} Δ*(lacZ)M15/* Δ*(lac-proAB) glnV44 e14*⁻ *gyrA96 recA1 relA1 endA1 thi hsdR17*

Partly restriction-deficient; good strain for cloning repetitive DNA (RecA⁻). Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11. Can also be used for M13 cloning/sequencing and blue/white screening (4).

NM522 (#E4108S)
F´*proA*$^+$*B*$^+$ *lacI*^{q} Δ*(lacZ)M15/* Δ*(lac-proAB) glnV thi-1* Δ*(hsdS-mcrB)5*

Partly restriction-deficient. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11. Can also be used for M13 cloning/sequencing and blue/white screening (2,6).

Strains for PROTEIN EXPRESSION (Baseline Expression)

ER2507 (#E4121S)
F⁻ *ara-14 leuB6 fhuA2 Δ(argF-lac)U169 lacY1 glnV44 galK2 rpsL20*(Str^R) *xyl-5 mtl-5 Δ(malB) zjc::Tn5*(Kan^R) *Δ(mcrC-mrr)$_{HB101}$*

The *malE* gene is included in the *malB* deletion, so this strain does not make any MBP from the chromosome (simplifies interpretation of Western blots). Can be transformed with high efficiency, similar to RR1 and HB101. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11.

TB1 (#E4122S)
F⁻ *ara Δ(lac-proAB) [ϕ80dlac Δ(lacZ)M15] rpsL*(Str^R) *thi hsdR*

Provided with the pMAL Protein Fusion and Purification System. Gives good expression in many cases.

Strains for PROTEIN EXPRESSION (Protease-deficient Strains)

CAG597 (#E4123S)
F⁻ *lacZ(am) pho(am) tyrT[supC*(ts)*]] trp(am) rpsL*(Str^R) *rpoH(am)165 zhg::Tn10 mal(am)*

Defective in stress-induced proteases at high temperature. Difficult to transform–use electroporation. Suppresses amber mutations if grown at 30°C (not 37°C) and tyrosine is acceptable (7,15).

CAG626 (#E4124S)
F⁻ *lacZ(am) pho(am) lon trp(am) tyrT[supC(ts)] rpsL*(Str^R) *mal(am)*

Lacks Lon protease. Difficult to transform—use electroporation. Suppresses amber mutations if grown at 30°C (not 37°C) and tyrosine is acceptable (8,9).

CAG629 (#E4125S)
F⁻ *lacZ(am) pho(am) lon tyrT[supC(ts)] trp(am) rpsL*(Str^R) *rpoH(am)165 zhg::Tn10 mal(am)*

Like CAG597, but also lacks Lon protease. Best strain for expressing unstable proteins. Difficult to transform—use electroporation. Grows very poorly and is temperature sensitive. Suppresses amber mutations if grown at 30°C (not 37°C) and tyrosine is acceptable (8,9).

PR1031 (#E4126S) formerly **CAG748**
F⁻ *thr:Tn10*(Tet^R) *dnaJ259 leu fhuA2 lacZ90(oc) lacY glnU44 thi*

Lacks the DnaJ chaperone that can promote protein degradation (10,15). Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11.

ER2508 (#E4127S)
F⁻ *ara-14 leuB6 fhuA2 Δ(argF-lac)U169 lacY1 lon::miniTn10*(Tet^R) *glnV44 galK2 rpsL20*(Str^R) *xyl-5 mtl-5 Δ(malB) zjc::Tn5*(Kan^R) *Δ(mcrC-mrr)$_{HB101}$*

Like ER2507, but also lacks Lon protease. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11. Easier to transform than CAG626 (8,11).

KS1000 (#E4128S)
F′ *lacI^q lac$^+$ pro$^+$*/ *ara Δ(lac-pro) Δ(tsp)*≡ *Δ(prc)*::Kan^R *eda51::Tn10*(Tet^R) *gyrA*(Nal^R) *rpoB thi-1 argI(am)*

Defective in Prc, a periplasmic protease, which can cleave proteins that are overexpressed in the cytoplasm when the cells are lysed to make a crude extract. The original name for this protease is Tsp (tail specific protease) (12).

UT5600 (#E4129S)
F⁻ *ara-14 leuB6 secA6 lacY1 proC14 tsx-67 Δ(ompT-fepC)266 entA403 trpE38 rfbD1 rpsL109*(Str^R) *xyl-5 mtl-1 thi-1*

Deficient in OmpT, an outer membrane protease that cleaves between sequential basic amino acids. It can cleave proteins that are overexpressed in the cytoplasm when the cells are lysed to make a crude extract (13).

Strain for site-specific KUNKEL MUTAGENESIS

CJ236 (#E4141S)
FΔ(HindIII)::cat (Tra$^+$ Pil$^+$ Cam^R)*/ ung-1 relA1 dut-1 thi-1 spoT1 mcrA*

Used for making DNA containing uracil, primarily for site-specific mutagenesis (Kunkel method). Plasmid is pCJ105; this is pOX38 (F$^+$ with deletion of small Hind III fragment) with a chloramphenicol resistance cassette added (14).

Strains supplied as PLASMID HOSTS

ER2420 with pACYC177 (#E4151S)
F⁻ *ara-14 leu fhuA2 Δ(gpt-proA)62 lacY1 glnV44 galK2 rpsL20*(Str^R) *xyl-5 mtl-1 Δ(mcrC-mrr)$_{HB101}$*

We supply the cloning vector pACYC177 in this strain. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11. Strain is Amp^R and Kan^R (from plasmid) and Str^R (from chromosome).

ER2420 with pACYC184 (#E4152S)
F⁻ *ara-14 leu fhuA2 Δ(gpt-proA)62 lacY1 glnV44 galK2 rpsL20*(Str^R) *xyl-5 mtl-1 Δ(mcrC-mrr)$_{HB101}$*

We supply the cloning vector pACYC184 in this strain. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11. Strain is Tet^R and Cam^R (from plasmid) and Str^R (from chromosome).

ER2420 with pBeloBAC11 (#E4154S)
F⁻ *ara-14 leu fhuA2 Δ(gpt-proA)62 lacY1 glnV44 galK2 rpsL20*(Str^R) *xyl-5 mtl-1 Δ(mcrC-mrr)$_{HB101}$*

We supply the cloning vector pBeloBAC11 in this strain. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11. Strain is Cam^R (from plasmid) and Str^R (from chromosome).

POP2136 with pFOS1 (#E4153S)
F⁻ *glnV44 hsdR17 endA1 thi-1 aroB mal$^-$ cI857 lambdaPR tet^R*

We supply the fosmid vector pFOS1 in this strain. Suppresses many amber mutations when glutamine is acceptable but not the S_{100} or S_7 mutations of λ, e.g., λgt11. Strain is Amp^R (from plasmid) and Tet^R (from chromosome).

References

(1) Kelleher, J. and Raleigh, E.A. (1991) *J. Bacteriol.* 173, 5220–5223.
(2) Woodcock, D.M. et al. (1989) *Nucl. Acids Res.* 17, 3469–3478.
(3) Palmer, B.R. and Marinus, M.G. (1994) *Gene* 143, 1–12.
(4) Yanisch-Perron, C., Viera, J. and Messing, J. (1985) *Gene* 33, 103–119.
(5) Messing, J. (1979) *Recombinant DNA Technical Bulletin* (NIH) 2, 43–48.
(6) Gough, J. and Murray, N. (1983) *J. Mol. Biol.* 166, 1–19.
(7) Baker, T.A. et al. (1984) *Proc. Nat. Acad. Sci. USA* 81, 6779–6783.
(8) Grossman, A.D. et al. (1983) *Cell* 32, 151–159
(9) Chung, C.H. and Goldberg, A.L. (1981) *Proc. Nat. Acad. Sci. USA* 78, 4931–4935.
(10) Straus et al. (1988) *Genes Dev.* 2, 1851–1858.
(11) Kowit, J.D. and Goldberg, A.L. (1977) *J. Biol. Chem.* 252, 8350–8357.
(12) Silber, K.R. and Sauer R.T. (1994) *Mol. Gen. Genet.* 242, 237–240.
(13) Elish et al. (1988) *J. Gen. Microbiol.* 134, 1355–1364.
(14) Kunkel, T.A. et al. (1987). In R. Wu and L. Grossman (Eds.), *Methods in Enzymology* Vol. 154, (pp. 367–382). San Diego: Academic Press.
(15) Gross, C., personal communication.

Additional *E. coli* Strain Genotypes

These *E. coli* strains are not supplied by New England Biolabs. Sources are listed in blue type. A list of strains supplied free of charge by NEB can be found here.

Strain Sources
A = ATCC (http://www.atcc.org),
CGSC = *E. coli* Genetic Stock Center (http://cgsc.biology.yale.edu),
LTI = Invitrogen Life Technologies, N = Novagen, S = Stratagene

Strain (Source)	Ref	Genotype
71-18	2	F´ *lacI*^{q}Δ*(lacZ)M15 proA*$^+$*B*$^+$ /Δ*(lac-proAB) thi glnV*
BHB2688 (A)	3	F$^-$ *recA* λ^r *(*λ*E*$_{am}$*4 b2 red3 imm434 cIts Sam7)*
BHB2690 (A)	3	F$^-$ *recA* λ^r *(*λ*E*$_{am}$*15 b2 red3 imm434 cIts Sam7)*
BL21(DE3) (N)	17	F$^-$ *ompT gal [dcm] [lon] hsdS*$_B$ (r_B^- m_B^-; an *E. coli* B strain) with DE3, a λ prophage carrying the T7 RNA polymerase gene
BNN93 (A)	4, 5, 6	F$^-$ e14$^-$ (McrA$^-$) *hsdR* (r_K^- m_K^-) *glnV44 thr-1 leuB6 thi-1 lacY1 fhuA21 mcrB;* Some isolates circulating as C600 are actually BNN93
BNN102 (A)	4, 5, 6	BNN93 *hflA150*::Tn*10* (Tet^r); The strain known as C600hfl is better known as BNN102
C600 (CGSC)	5, 8	F$^-$ [e14$^-$ (McrA$^-$) or e14$^+$ (McrA$^+$)] *thr-1 leuB6 thi-1 lacY1 glnV44 rfbD1 fhuA21;* The original C600 is *Eco*K r$^+$m$^+$ McrBC$^+$; See BNN93†
C600hfl	4, 5, 6	BNN102 is sometimes called C600hfl
CES200 (A, CGSC)	1	F$^-$ *thr-1 ara-14* Δ*(gpt-proA)62 lacY1 tsx33 glnV44 galK2 hisG4 rfbD1 rpsL31* (Str^r) *kdgD51 xyl-5 mtl-1 argE3 leuB6 hsdR* (r_K^- m_K^+) *recB21 recC22 sbcB15 sbcC*
CSH18	9	F´ Δ*(lacZ)H125 proA*$^+$*B*$^+$/Δ*(lac-pro) glnV thi*
DB1316 (A, CGSC)	1, 6	F$^-$ *recD1014 mcrB1 hsdR2* (r_K^- m_K^+) *zjj202*::Tn*10* (Tet^r)
DH1 (LTI)	8	F$^-$ *glnV44 recA1 endA1 gyrA96* (Nal^r) *thi1 hsdR17* (r_K^- m_K^+) *relA1 spoT1? rfbD1?*
DH5αF´ (LTI)	6, 7	F´*/endA1 hsdR17* ($r_K^-m_K^+$) *glnV44 thi-1 recA1 gyrA* (Nal^r) *relA1* Δ*(lacIZYA-argF)U169 deoR* (ϕ80*dlac*Δ*(lacZ)M15*)
DL538	6, 10	NM621 *sbcC201*
DP50 (A)	3	F$^-$ *fhuA53 dapD8 lacY1 glnV44* Δ*(gal-uvrB)47 tyrT58 (=supF58) gyrA29* (Nal^r) Δ*(thyA)57 hsdS3* (r_K^- m_K^-)
ED8654 (CGSC)	11	F$^-$ e14$^-$ (McrA$^-$) *lac-3* or *lacY1 galK2 galT22 glnV44 supF58 metB1 hsdR514* (r_K^- m_K^+) *trpR55*
ED8767 (CGSC)	6, 11	F$^-$ e14$^-$ (McrA$^-$) *lac-3* or *lacY1 galK2 galT22 glnV44 supF58 metB1 mcrB1 hsdS3* (r_K^- m_K^-)
GM48 (A)	12	F$^-$ *thr leu thi lacY galK galT ara fhuA tsx dam dcm glnV44*

Strain (Source)	Ref	Genotype
GM2929 (CGSC)	12	F$^-$ *ara-14 leuB6 thi-1 fhuA31 lacY1 tsx-78 galK2 galT22 glnV44 hisG4 rpsL136* (Str^r) *xyl-5 mtl-1 dam13*::Tn*9* (Cam^r) *dcm-6 mcrB1 hsdR2* (r_K^- m_K^+) *mcrA recF143*
HB101 (A)	3, 13	F$^-$ Δ*(gpt-proA)62 leuB6 glnV44 ara-14 galK2 lacY1* Δ*(mcrC-mrr) rpsL20* (Str^r) *xyl-5 mtl-1 recA13*
JM83 (A)	2	F$^-$ *ara* Δ*(lac-proAB) rpsL* (Str^r)[ϕ*80* d*lac*Δ*(lacZ)M15*] *thi*
JM103 (A)	2	F´ *traD36 lacI*^{q}Δ*(lacZ)M15 proA*$^+$*B*$^+$*/ endA1 glnV sbcBC thi-1 rpsL* (Str^r) Δ*(lac-pro) (P1)* ($r_K^+m_K^+$ $r_{P1}^+m_{P1}^+$)
JM105 (A)	2	F´ *traD36 lacI*^{q}Δ*(lacZ)M15 proA*$^+$*B*$^+$*/thi rpsL* (Str^r) *endA sbcB15 sbcC? hsdR4* (r_K^- m_K^+) Δ*(lac-proAB)*
JM107 (A)	2	F´ *traD36 lacI*^{q}Δ*(lacZ)M15 proA*$^+$*B*$^+$/e14$^-$ (McrA$^-$) Δ*(lac-proAB) thi gyrA96* (Nal^r) *endA1 hsdR17* (r_K^- m_K^+) *relA1 glnV44*
JM110 (A)	2	F´ *traD36 lacI*^{q}Δ*(lacZ)M15 proA*$^+$*B*$^+$*/rpsL* (Str^r) *thr leu thi lacY galK galT ara fhuA dam dcm glnV44* Δ*(lac-proAB)*
K802 (A, CGSC)	3, 6, 8	See WA802
K803 (A, CGSC)	3, 6, 8	See WA803
LE392 (A, CGSC)	3	F$^-$ e14$^-$ (McrA$^-$) *hsdR514* (r_K^- m_K^+) *glnV44 supF58 lacY1 or* Δ*(lacIZY)6 galK2 galT22 metB1 trpR55*
MC1061 (A)	1, 7	F$^-$ *araD139* Δ*(ara-leu)7696 galE15 galK16* Δ*(lac)X74 rpsL* (Str^r) *hsdR2* (r_K^- m_K^+) *mcrA mcrB1*
MC4100 (A)	14	F$^-$ *araD139* Δ*(argF-lac)U169 rpsL150* (Str^r) *relA1 flbB5301 deoC1 ptsF25 rbsR*
MM294 (A)	8	F$^-$ *endA1 hsdR17* (r_K^- m_K^+) *glnV44 thi-1 relA1? rfbD1? spoT1?*
NM477	5, 6	C600 Δ*(hsdMS-mcrB)5* (r_K^- m_K^- McrBC$^-$)
NM554	5	MC1061 *recA13*
NM621	10	F$^-$ *hsdR* (r_K^- m_K^+) *mcrA mcrB glnV44 recD1009*
P2392 (S)	7	LE392*(P2)*
Q358 (A)	7	F$^-$ *hsdR* (r_K^- m_K^+) *glnV fhuA* (ϕ80^r)
Q359 (A)	7	Q358 *(P2)*
RR1 (A)	3	HB101 RecA$^+$
WA802 (A, CGSC)	3, 6, 8	F$^-$ e14$^-$ (McrA$^-$) *lacY1 or* Δ*(lac)6 glnV44 galK2 galT22 rfbD1 metB1 mcrB1 hsdR2* (r_K^- m_K^+)

Strain (Source)	Ref	Genotype
WA803 (A, CGSC)	3, 6, 8	F⁻ e14⁻ (McrA⁻) *lacY1 or Δ(lac)6 glnV44 galK2 galT22 rfbD1 metB1 mcrB1 hsdS3* (r_K^- m_K^-)
χ1776 (A, CGSC)	3	F⁻ *fhuA53 dapD8 minA1 glnV44 (=glnV44) Δ(gal-uvrB)40 minB2 rfb-2 gyrA25* (Nal^r) *thyA142 oms-2 metC65 oms-1 (tte-1) Δ(bioH-asd)29 cycB2 cycA1 hsdR2* (r_K^- m_K^+) *mcrB1?*
XL1-Blue (S)	15	F´ ::Tn*10 proA*$^+$ *B*$^+$ *lacI*^{q} *Δ(lacZ)M15/ recA1 endA1 gyrA96* (Nal^r) *thi hsdR17* (r_K^- m_K^+) *glnV44 relA1 lac*
Y1088 (A)	4	F⁻ *Δ(lac)U169 glnV supF hsdR* (r_K^- m_K^+) *metB trpR fhuA21 proC::Tn5* (pMC9; Tet^r Amp^r) NOTE: pMC9 is pBR322 with lacI^q inserted
Y1089†† (S)	4, 16	F⁻ *Δ(lac)U169 lon-100 araD139 strA hflA150::Tn10* (pMC9; Tet^r Amp^r)
Y1090†† (S)	4, 16	F⁻ *Δ(lac)U169 lon-100 araD139 rpsL*(Str^r) *supF mcrA trpC22::Tn10* (pMC9; Tet^r Amp^r)

† C600 lines obtained from different sources give different results. The original strain and that obtained from the *E. coli* Genetic Stock Center (Yale University) are McrA$^+$; derivatives traceable to the Brenner laboratory are McrA$^-$ (18).

†† No isolates of these strains tested showed pleiotropic phenotypes attributed to *lon* (i.e. were not mucoid, formed turbid λ plaques, grew well on rich media and did not filament). The strain is unlikely to be Lon-defective.

References

1. Wertman, K.F. et al. (1986) *Gene* 49, 253–262.
2. Yanisch–Perron, C., Viera, J. and Messing, J. (1985) *Gene* 33, 103–119.
3. Sambrook, J., Fritsch, E.F. and Maniatis, T. (1989). *Molecular Cloning: A Laboratory Manual*, (2nd ed.). Cold Spring Harbor: Cold Spring Harbor Laboratory Press.
4. Huynh,T.V. et al. (1985). In D.M. Glover (Ed.), *DNA Cloning* Vol. 1, (pp. 56–110). Oxford, England: IRL Press Limited.
5. Raleigh, E.A. et al. (1988) *Nucl. Acids Res.* 16, 1563–1575.
6. Woodcock, D.M. et al. (1989) *Nucl. Acids Res.* 17, 3469–3478.
7. Raleigh, E.A., Lech, K. and Brent, R. (1989). In F.M. Ausebel et al. (Eds.), *Current Protocols in Molecular Biology* (p. 1.4). New York: Publishing Associates and Wiley Interscience.
8. Berlyn, M.K.B. (1996). In F.C. Niedhardt et al. (Ed.), *Escherichia coli and Salmonella: cellular and molecular biology,* (2nd ed.), Vol. 2, (pp. 1715–1902). ASM Press.
9. Miller, J.H. (1972). *Experiments in Molecular Genetics.* Cold Spring Harbor: Cold Spring Harbor Laboratory Press.
10. Whittaker, P.A. et al. (1989) *Nucl. Acids Res.* 16, 6725–6736.
11. Murray, N.E. et al. (1977) *Mol. Gen. Genet.* 150, 53–61.
12. Palmer, B.R. and Marinus, M.G. (1994) *Gene* 143, 1–12.
13. Boyer, H.W, and Roulland–Dussoix, D. (1969) *J. Mol. Biol.* 41, 459.
14. Silhavy, T.J. et al. (1984) *Experiments with Gene Fusions* (pp. xi–xii) Cold Spring Harbor: Cold Spring Harbor Laboratory.
15. Bullock, W.O. et al. (1987) *BioTechniques* 5, 376–378.
16. Maurizi, M.R. et al. (1985) *J. Bacteriol.* 164, 1124–1135.
17. Studier, F.W. et al. (1990). In D.V. Goeddel (Ed.), *Methods in Enzymology* Vol. 185, (pp. 60–89). San Diego: Academic Press.
18. Alber, J., personal communication.