Product Manual

Myotonic Dystrophy GLDM PCRProber™ Kit

Non-radioactive Myotonic Dystrophy Genotyping by PCR* Analysis

CTG Repeat Detection

Kit for amplification and non-radioactive detection of Myotonic Dystrophy CTG trinucleotide repeats region amplified PCR product.

Catalog No. 40-2026-32 5 blots (50 reactions)
Store at -20°C
For research use only. Not for use in diagnostic procedures for clinical purposes

***Important information**

Storage instructions
Kit components require different storage conditions.
Immediately upon receipt store components as labeled.
Caution: DO NOT FREEZE COMPONENTS LABELED TO BE STORED AT 4°C.

190 Saw Mill River Road | Hawthorne, NY 10532-1515 | tel: 914-769-1192 | fax: 914-769-1193 | www.genelink.com

Material supplied

Myotonic Dystrophy GLDM PCRProber™ Kit

Catalog No.: 40-2026-32 5 blots (50 reactions)

Kit for amplification and non-radioactive detection of Myotonic Dystrophy CTG trinucleotide repeats region amplified PCR product.

Individual components of the kit can be ordered using the appropriate catalog number.

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GLDM PCRProber™ Kit components
Sufficient for 50 x 50 µl reaction

Product	Size	Description	Storage	Catalog No.
GLDM PCR Component A	1.5 ml	GLDM PCR premix with primers	-20 °C.	40-2026-32A
GLDM PCR Component B	200 µl	GLDM PCR Component B	-20 °C.	40-2026-32B
GLDM PCR Component C	800 µl	GLDM PCR Component C	-20 °C.	40-2026-32C
Sequencing loading buffer	1 ml	Seq loading buffer	-20 °C.	40-5027-00

Hybridization and Detection kit components
Sufficient for processing five 16 x 16 cm blots

Product	Size	Description	Storage	Catalog No.
GLDM PCRProber™	12 µl	Alkaline Phosphatase labeled probe	Store at 4°C.	40-2026-31
Hybwash Stock A	250 ml	Hybridization Wash Concentrate	Store at 15-25°C. (Room Temperature)	40-5020-25
Hybwash Stock B	60 ml	Hybridization Wash Concentrate	Store at 15-25°C. (Room Temperature)	40-5021-60
Lumisol ™ III hybridization buffer	80 ml	Hybridization Buffer	Store at 4 °C.	40-5024-80
10 x AP detection buffer	60 ml	Alkaline Phosphatase Buffer	Store at 15-25°C. (Room Temperature)	40-5031-60
CDP-star ready to use AP Substrate spray	10 ml	Alkaline Phosphatase Chemiluminescent Substrate	Store at 4 °C.	40-5010-10

Myotonic Dystrophy Genotyping

Background

Myotonic dystrophy (**Dystrophia Myotonica, DM**) is the most common form of adult onset muscular dystrophy. It is an autosomal dominant disorder with a prevalence of about 1 in 8000. The incidence varies from 1 in 475 in a region of Quebec to about 1 in 25,000 in European populations and is extremely rare in African populations. Clinical expression is highly variable and is related to age of onset. Onset of this disorder commonly occurs during young adulthood. However, it can occur at any age and is extremely variable in degree of severity. Myotonic dystrophy affects skeletal muscle and smooth muscle, as well as the eye, heart, endocrine system, and central nervous system. People with the mildest form of DM often go undiagnosed and usually cataracts and minimal muscle involvement are the only visible sign of the condition. The classical form of DM usually develops in early adult life and is characterized by progressive muscle stiffness and weakness.

Congenital DM (CDM) is the most severe form of the disease and is almost always inherited from affected mothers. It presents in newborn babies who suffer from respiratory distress, hypotonia, motor and mental retardation and facial diplegia. Diagnosis can be difficult if the family history is not known because muscle wasting may not be apparent and cataracts and myotonia are absent. CDM patients who survive the neonatal period eventually learn to walk but 60-70% are mentally retarded. By the age of 10 they develop myotonia and in adulthood they develop the additional complications associated with adult onset disease.

Identification of the mutation in DM

The myotonic dystrophy gene locus and the underlying mutation were identified in 1992 (1-3). An expressed sequence called cDNA25 was shown to detect a two-allele *Eco*RI polymorphism (8.6kb and 9.8kb) on Southern blots of normal individuals. It also detects a larger variable fragment in DM patients, which can be up to 5kb longer than the larger, normal allele. When this fragment is transmitted from an affected parent, it often increases in size, correlating well with the severity of the disease in the affected child. The variable band can also show somatic heterogeneity in lymphocyte DNA that is seen as a diffuse smear on a Southern blot. The *Eco*RI polymorphism is due to the insertion or deletion of consecutive Alu repeats 5 kb distal to the unstable region – the 8.6kb allele contains two Alu repeats and the 9.8kb normal allele and the enlarged DM alleles are associated with five Alu repeats. The discovery of unstable DNA at the DM locus provided an explanation for the phenomenon of anticipation seen in DM. Sequence analysis of genomic clones spanning the expanded region revealed that the mutation causing the instability is a trinucleotide repeat (CTG) which is highly polymorphic in the normal population and which increases dramatically in length in DM patients.

Number of CTG repeats	Clinical Condition	Symptoms
5-27 repeats	unaffected	
50-100 repeats	mild:	cataracts, slight muscle problems later on in life
100-1000 repeats	classical:	myotonia, muscle wasting, premature balding, gonadal atrophy, cardiac conduction defects
1000-4000	congenital:	hypotonia, mental retardation, facial diplegia

There are no definite repeat size boundaries for the three clinical groups and there are overlaps between the groups. A trimodal distribution is observed in European populations, with $(CTG)_5$ being the most frequently occurring allele, alleles of 11,12,13 and 14 make up the second mode and the final mode represents alleles of 19 and above.

Meiotic instability

The meiotic instability of the DM mutation has been shown to be dependent on the size of the parental repeat. For $(CTG)_n$ repeats of <0.5kb a positive correlation between the size of the repeat and inter-generational enlargement was found equally in male and female meioses but with CTG sequences of more than 0.5 kb observed that intergenerational variation was greater through female meioses (4). The tendency for a repeat to undergo contraction was observed almost exclusively in male meioses. It was found that the length of the CTG repeat expansion in DM patients was greater in DNA isolated from muscle than in lymphocyte DNA (5). Rare cases have been reported where expansion of the CTG repeats is not seen in individuals where the clinical symptoms are unequivocal and this may due to a deletion or point mutation as seen in some of the other triplet repeat disorders such as fragile X syndrome.

The underlying mutations of DM are expansions of the CTG repeats located in the 3' untranslated region (UTR) of the myotonic dystrophy protein kinase (*DMPK*) gene on chromosome 19q. Severity of the disease is correlated with the length of the repeat expansion. Normal individuals have from 5 to 30 repeat copies; mildly affected persons have at least 50 repeats, while more severely affected patients have expansion of the repeat-containing segment up to several kilobase pairs.

Expansion is frequently observed in parent-to-child transmission, but extreme expansions are not transmitted through the male line. This explains: 1.) the occurrence of the severe congenital form is almost exclusively in the offspring of affected women; 2.) anticipation is commonly observed in affected families, that is, the disease demonstrates earlier onset and greater severity in each successive generation. The overall risk of having a congenitally affected child for any carrier woman is about 10%. If the woman has clinical signs of the condition, the risk of congenital myotonic dystrophy in offspring is 40% and this rises to 50% in subsequent pregnancies if an affected child has previously has been born.

Genotyping

Molecular diagnosis of myotonic dystrophy involves a combination of direct PCR analysis and Southern blotting tests to determine the CTG-repeat number within the DMPK gene. PCR can identify CTG expansions between 5-200 CTG repeats.

With larger expansions, Southern blot analysis of restriction fragments can be used for an accurate measure of the repeat size. Genomic DNA is digested with Bam HI or Pst I. The DNA blot is then hybridized with either GLDM1 or GLDM2 CTG repeat specific DNA probe.

Table 1: Trinucleotide Repeats in Human Genetic Disease

Disease	Repeat[a]	Normal Length[b]	Intermediate Length (Premulation)[a,b]	Full Disease Length[b]
Fragile XA (FRAXA)	$(CGG)_n$	6-52	59-230	230-2,000
Fragile XE (FRAXE)	$(CCG)_n$	4-39	? (31-61)	200-900
Fragile XF(FRAXF)	$(CGG)_n$	7-40	?	306-1,008
FRA16A	$(CCG)_n$	16-49	?	1,000-1,900
Jacobsen Syndrome (FRA11B)	$(CGC)_n$	11	80	100-1,000
Kennedy Syndrome (SMBA)	$(CAG)_n$	14-32	?	40-55
Myotonic Dstrophy (DM)	$(CTG)_n$	5-37	50-80	80-1,000; congenital, 2,000-3,000
Huntington disease (HD)	$(CAG)_n$	10-34	36-39	40-121
Spincerebellar ataxia 1 (SCA1)	$(CAG)_n$	6-39	…	40-81 (Pure)
Spincerebellar ataxia 2 (SCA2)	$(CAG)_n$	14-31	…	34-59 (Pure)
Spincerebellar ataxia 3 (SCA3)/Machado Joseph disease (MJD)	$(CAG)_n$	13-44	?	60-84
Spincerebellar ataxia 6 (SCA6)	$(CAG)_n$	4-18	?	21-28
Spincerebellar ataxia 7 (SCA7)	$(CAG)_n$	7-17	?	38-130
Haw River syndrome (HRS; also DRPLA))	$(CAG)_n$	7-25	?	49-75
Friedreich ataxia (FRDA)	$(GAA)_n$	6-29	? (>34-40)	200-900

[a] Typically, repeats tracts contain sequence interruptions. See Pearson and Sinden (1998*a*) for a discussion of the sequence interruptions.
[b] No. of triplet repeats.
[c] A question mark (?) indicates potential mutagenic intermediate length, and an ellipsis (…) indicates none. Not all disease are associated with a permutation length repeats tract or permutation disease condition.-

Molecular Analysis

The direct analysis of CTG repeats in the *DMPK* gene (chromosomal locus 19q13) is clinically available. An increased number of CTG repeats is identified in essentially 100% of patients with DM. The number of CTG repeats ranges from 5 to 37 in normal alleles. GTG repeat lengths in the range from about 38 to 49 are considered "premutations." Persons with CTG expansions in the premutation range have not been reported as having developed symptoms, but their children are at risk of inheriting a larger repeat size. Persons with CTG repeat length greater than 50 are frequently symptomatic.

Myotonic Dystrophy genotyping can be done by direct PCR amplification of the CTG trinucleotide repeats region or by Southern analysis. In most cases both methods are used to complement the results. Congenital mutations usually cannot be identified by PCR and southern analysis is the preferred method to distinguish full mutations.

The size of the CTG repeats can be determined by PCR analysis and sizing preferably on a sequencing gel. The PCR products can be either labeled with ^{35}S or ^{32}P followed by autoradiography. Another attractive alternate is to run a cold PCR reaction followed by blotting and hybridization with an alkaline phosphatase conjugated probe for non-radioactive detection

Southern blot analysis for Myotonic Dystrophy mutation detection involves the cleavage of DNA with either Bam HI or Pst Ienzyme This method detects the size of CTG repeats region by hybridization of probe GLDM1 or GLDM2 to DNA that has been digested with the appropriate restriction enzyme and blotted onto a membrane. The CTG repeat in the normal range yields a ~1377 bp with Bam HI and a ~1136 bp with Pst I digested DNA.

References

1. Fu YH, Pizzuti A, Fenwick RG Jr, King J, Rajnarayan S, Dunne PW, Dubel J, Nasser GA, Ashizawa T, de Jong P, et al. (1992) An unstable triplet repeat in a gene related to myotonic muscular dystrophy. Science 255: 1256-1258.
2. Aslanidis et al. (1992) Cloning of the essential myotonic dystrophy region and mapping of the putative defect. Nature 355: 548-551.
3. Brook et al. (1992) Molecular basis of myotonic dystrophy: expansion of a trinucleotide (CTG) repeat at the 3-prime end of a transcript encoding a protein kinase family member. Cell 68: 799-808.
4. Lavedan et al. (1993) Myotonic dystrophy: size- and sex-dependent dynamics of CTG meiotic instability, and somatic mosaicism. Am. J. Hum. Genet. 52: 875-883.
5. Anvret et al. ((1993) Larger expansions of the CTG repeat in muscle compared to lymphocytes from patients with myotonic dystrophy. Human Molecular Genetics 2:1397-1400.
6. Mathieu J, Allard P, Potvin L, Prevost C, Begin P (1999) A 10-year study of mortality in a cohort of patients with myotonic dystrophy. *Neurology* 52:1658-62
7. Redman JB, Fenwick RG Jr, Fu YH, Pizzuti A, Caskey CT (1993) Relationship between parental trinucleotide GCT repeat length and severity of myotonic dystrophy in offspring. *JAMA* 269:1960-5

Procedure

Procedure: CTG Repeats Analysis by PCR

The procedure outlined below can be finished in less than 24hrs.

Day 1 afternoon start PCR and leave it to proceed overnight. Prepare a 6% polyacrylamide-7 M urea gel (15-well, 0.75mm, 16x16cm^2) and leave it overnight. Day 2 proceed with the rest of the procedure.

PCR Premix Preparation

Thaw individual components. *Promptly store at -20^{o}C after use*. Prepare ***fresh*** before use enough PCR premix for the number of reactions to be performed. Prepare 10% more for pipeting allowance. Prepare 49μl final volume reactions. Example for the preparation of one 49μl premix volume is given below. Follow the same ratio for preparing other final volumes.

DM PCR premix	
GLDM PCR Component A [Cat No. 40-2026-32A]	**29μl**
GLDM PCR Component B [Cat No. 40-2026-32B]	**4μl**
GLDM PCR Component C[Cat No. 40-2026-32C]	**16μl**
Total Volume. Mix gently	**49μl**

'Hot start' PCR

Program two PCR thermal cycler files as follows

A. 'Hot start' 5' denaturation at 94^{o}C, hold at 60^{o}C

B. DM CTG amplification PCR file

94^{o}C 30 sec, 61^{o}C 60 sec., 72^{o}C 2 min., 30 cycles. One Cycle 72^{o}C 7 min Hold at 4^{o}C

Use 44 μl of the PCR premix for each reaction, add 50-100 ng DNA and start 'Hot start' denaturation for five minutes at 94^{o}C.

While waiting for the five minute denaturation add Taq polymerase to the left over PCR premix. Add 2.5 units Taq polymerase per 10 μl of the left over PCR premix. *Label this tube as Enzyme Mix*

While the PCR is on hold at 60^{o}C (after the initial 5' denaturation at 94^{o}C) add 5 μl of the enzyme mix to each tube. After adding to all the tubes start the PCR file for cycling.

Precipitate PCR products by ethanol precipitation. Dissolve the pellets in 5μl of sterile H_2O and then add 5 μl of seq. Loading buffer.

Electrophoresis & Electroblotting

Prepare a 6% polyacrylamide-7 M urea gel (15-well, 0.75mm, 16x16cm^2). Pre-electrophorese for 10 minutes at 25 Watts constant (~ 500 volts or 45 mAmps constant).

Heat the samples at 75^{o}C for 5 min. Chill on ice. Load 5 μl to the gel. Run the gel constantly at 25 Watts constant (~ 500 volts or 45 mAmps constant) till xylene cyanol dye runs out, electrophorese 10 minutes more after that. (total electrophoresis time ~1hr.).

While gel is running, prepare for electroblotting. Soak positively charged nylon membrane in water for nearly 5 minutes, then keep soaked in 1 X TBE. Setup transfer following the electrotransfer apparatus manufacturers directions. Electro-transfer at 400 mA for 1 hr. in 1xTBE.

Hybridization & Detection

Prepare for hybridization and detection while electroblotting.

Reagent Preparation

Hybwash I:

Add 35ml of Hybwash stock A, 312 ml of sterile deionized water, mix and then add 3.5 ml of Hybwash stock B.

Hybwash II

Add 7.5ml of Hybwash stock A, 340 ml of sterile deionized water, mix and then add 3.5 ml of Hybwash stock B.

1 x Detection buffer

To make 100ml of 1x Detection buffer, add 10 ml of 10x Detection buffer and 90 ml of sterile deionized water.

Procedure

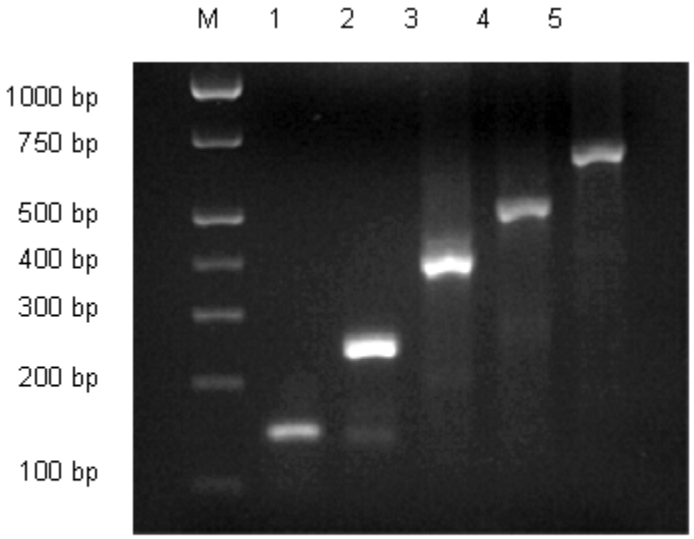
1. After electrotransfer, wash the blot in 50 ml Hybwash I at 55^{o}C for 5 min.
2. Prehybridize (roller bottle or bag) in 7.5 ml of pre-warmed Lumisol III at 55^{o}C for 30 min.
3. Replace with 7.5ml fresh Lumisol III, (pre-warmed at 55^{o}C) containing 2 μl of GLDM PCRProber™ . Hybridize at 55^{o}C for 30 min. DO NOT EXCEED 30 minutes.
4. Wash the blot in 75 ml of pre-warmed Hybwash I for 7 minutes at 55^{o}C Repeat 3 times. Total of four washes.
5. Wash the blot in 150 ml pre-warmed Hybwash II for 5 min at 55^{o}C. Repeat once. Total of two washes.
6. Wash the blot in 25 ml1x Detection Buffer at room temperature for 5minutes. Repeat 3 times. Total of four washes.
7. Transfer blot to a plastic sheet, (sheet protector cut from two sides to open up) and drain off excess buffer. Wipe off edges with paper towel. Blot should not be allowed to dry.
8. Spray CDP-star ready-to-use substrate evenly to cover the blot. DO NOT OVER SPRAY. Cover the blot with plastic sheet and wipe entire surface of the covered blot to expel any excess substrate and air bubbles. Expose the film at room temperature for 1 hr. or for shorter or longer time as required.
9. Luminescence continues for at least 24 hours and signal intensity remains almost constant during the first few hours. Multiple exposures can be taken to achieve the desired signal strength.

For re-hybridization the membrane can be stripped of the probe by washing in 50 ml of Hybwash II sol. at 65^{o}C for 30 min. with gentle agitation.

Results and Interpretation

- Amplified fragment of ~144bp contains 12 CTG repeats.
- Run control samples to compare results.

Number of CTG repeats	Clinical Condition	Comments
5-27 repeats	unaffected	
50-100 repeats	mild:	
100-1000 repeats	classical:	Perform Southern blot analysis
1000-4000	congenital:	Perform Southern blot analysis



Lane M is molecular weight markers. Lanes 1-5 represents PCR products from DM genomic clones that contain 12, 45, 93, 129 and 182 CTG repeats respectively.

Frequently Asked Questions/Troubleshooting

1. General Comment. Initially the addition of more steps in the detection protocol as compared to radioactive detection may seem annoying, but is worth the patience. All the steps have to be optimized. Following the protocol exactly works, especially running denaturing gel is important. Our kit is optimized to give results. A few initial rounds of optimization may be required. Once the investigator is experienced with all the manipulations, getting good results should be routine.

2. High Background. The background problem may be due to various reasons and has to be optimized in each lab. Here at Gene Link we use Boehringer Mannheim products, the membrane is nylon positively charged catalog number 1209 272. Other positively charged membranes work but do not give consistently low background. The main reason for background is inadequate blocking and/or the membrane itself is curled, folded or has scratches and creases that trap the probe. We advise using glass trays or bottles for all washing and hybridization procedures. Plastic inherently has small surface variations and can scratch the membrane. We would also advise increasing the washing and stringency and exposure to x-ray film for one hour initially. Wash again if you observe too much background and no real signal in an hour. Expose for longer time if the one hour exposure gives nearly no background. We get good signal in a 2 hr. exposure.

Again, to summarize, the background problem varies from lab to lab and has to be optimized. Once optimized, you will consistently get excellent signal in 1-2 hr. exposure.

3. Reliable Detection. The system will be able to detect reliably the CTG repeats up to 200 repeats. Detection beyond this is dependent on the PCR conditions and gel systems but is NOT reliable. Any DNA sample which does not give a reliable CTG repeat analysis on this system clearly indicates either a failure of the PCR reaction or a DNA with extensive CTG repeats. A particular DNA sample not yielding a PCR product on duplicate analysis clearly indicates the possibility of long CTG repeats. In cases like these we suggest that southern analysis should be done using the GLDMDig2 GeneProber™ gene detection system to clearly determine the genotype. Southern analysis is also strongly advised when both the alleles are not reliably genotyped

Appendix: **Protocols**

Genomic DNA Purification

Genomic DNA is usually extracted from blood. A simple procedure is given below that purifies ~10 µg DNA from 300 µl blood using a 30 minute procedure.

Omni-Pure™ Genomic DNA Purification System Catalog Number: 40-4010-01
Rapid DNA Purification Protocol for 300 µl Whole Blood

A. Initial Preparation

1. Label two sets of 1.5 ml tubes per sample.
2. Add 900 µl GD-1 solution (RBC Lysis Solution) to one tube for each sample.
3. Add 300 µl Isopropanol (2-propanol) to one tube for each sample. Cap the tubes.

B. Cell Lysis

1. To the tube containing 900 µl GD-1 solution (RBC Lysis Solution) using a filter tip pipet transfer 300 µl whole blood. Cap and gently mix by inversion. Incubate for 1-3 minutes at room temperature. Mix by inversion a few times during this incubation period. Incubate longer for fresh blood cells as they are intact and not lysed already.
2. Centrifuge at 3 K rpm for 20 seconds to pellet the white blood cells. A reddish white pellet should be clearly visible. Decant and discard supernatant leaving behind the last few droplets. Do not totally remove the supernatant.
3. Completely resuspend the white blood cell pellet by vigorously vortexing the tube. Ensure that the pellet is completely resuspended.
4. To the resuspended cells add 300 µl GD-2 solution (Cell Lysis Solution). Mix by gentle vortexing. You will notice release of DNA by the thickening of the liquid in the sample. Samples may be stored at this stage for processing later. It has been shown that the samples are stable in Cell Lysis Solution for at least 2 years at room temperature.

C. Protein Precipitation

1. Add 100 µl GD-3 solution (Protein Precipitation Solution) to the sample in cell lysis solution.
2. Vortex vigorously for 20 seconds. Small particles of brown color will appear and be visible at this stage.
3. Centrifuge at 5 K rpm for 1 minute to pellet the precipitated proteins. A clearly visible brown pellet containing proteins should be collected at the bottom of the tube.

D. DNA Precipitation

1. Decant the supernatant containing the DNA to a new appropriately labeled tube (see initial preparation above) containing 300 µl 100% Isopropanol (2-propanol).
2. Mix the sample by inversion until a visible white floating DNA strand-particle is identified. mixing by inversion 30-40 times is usually sufficient.
3. Centrifuge at 6 K rpm for 1 minute to collect the DNA as a pellet. A white DNA pellet should be clearly visible.
4. Decant supernatant and place tube inverted on a clean Kimwipe™ tissue paper to drain the remaining supernatant.
5. To remove residual salts, add 300 µl of 70% ethanol. Vortex gently.
6. Centrifuge at 6 K rpm for 1 minute to collect the DNA as a pellet. Gently take out the tubes so that the pellet is not dislodged. While holding the tube, rotate tube so that you can watch the pellet. Now carefully decant the ethanol, keeping an eye on the pellet so that it does not flow away.
7. Place tube inverted on a clean Kimwipe™ tissue paper to drain the remaining ethanol.
8. Air dry the DNA pellet. Do not use vacuum.

E. DNA Reconstitution & Use

1. Add 100 µl of GD-4 solution (DNA Reconstitution Solution). Vortex gently. Incubate at 60°C for 5 minutes to facilitate dissolution or keep overnight at room temperature.
2. Store DNA at 4 °C. For long-term storage, place sample at –20 °C or –80 °C.
3. Average yield of 10 µg is expected from 300 µl blood DNA. The range is between 5 µg to 15 µg.
4. The 100 µl of purified DNA obtained will have an average concentration of ~ 100 ng/µl.
5. For PCR amplification use 1-2 µl.
6. Use 100 µl for restriction digestion followed by Southern blot analysis.
7. It is convenient to perform multiple 300 µl blood DNA purification instead of scaling up the procedure.

Gel Electrophoresis of DNA

Gel electrophoresis of PCR products is the standard method for analyzing reaction quality and yield. PCR products can range up to 10 kb in length, but the majority of amplifications are at 1 kb and below. Agarose electrophoresis is the classical method to analyze amplification products from 150 bp to greater than 10 kb. Polyacrylamide gel electrophoresis should be used for resolution of short fragments in the range of 100 bp to 500 bp when discrimination of as small as a 10 bp difference is required.
PAGE gels for PCR products can be formulated with the amount of cross-linker chosen to give pore sizes optimal for the size of DNA fragment desired. Gels are most often stained in ethidium bromide, even though the fluorescence of this stain is quenched by polyacrylamide, which decreases sensitivity 2-5 fold. This decrease in sensitivity generally does not present a problem, because most PCR reactions yield product levels in the microgram range, and ethidium will detect as little as 1/10 of this amount. Polyacrylamide gels can be stained by silver staining for more sensitive detection.

Agarose Gel Electrophoresis of DNA

Agarose gels are typically run at 20 to 150V. The upper voltage limit is the amount of heat produced. At room temperature about 5 Watts is correct for a minigel (Volts x Amps = Watts). At low voltages migration is linearly proportional to voltage, but long DNA molecules migrate relatively faster in stronger fields. Migration is inversely proportional to the log of the fragment length; a log function also governs migration rate and gel concentration (0.5 to 2% for most purposes). Furthermore, supercoiled / circular DNA molecules migrate at different rates from linear molecules; single-stranded DNA and RNA migrate at similar rates, but usually faster than double-stranded DNA of the same length. Salt in the samples increases conductivity and, hence, migration rate.
The buffers used for most neutral agarose gels (the gel itself and the solution in which it lies) is 1 x TAE or 1 x TBE. Agarose powder is added to the buffer at room temperature, heated in a microwave and boiled slowly until the powder has dissolved. Cast the gel on a horizontal surface once the agarose has been cooled to ca. 60° C (just cool enough to hold) and add 0.1 µg of ethidium bromide solution for each ml of gel volume. At times, during removal of the comb, it is possible to tear the bottom of the sample wells gels, which results in sample leakage upon loading. This can be avoided by removing the comb after the gel has been placed in the running buffer.

• Use TAE buffer for most molecular biology agarose gel electrophoresis.

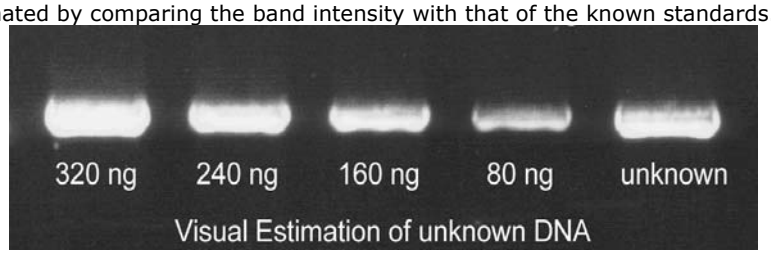
Recipe

1 X TAE Buffer
Agarose Gel Electrophoresis Buffer
40 mM Tris-Acetate pH 7.8
1 mM EDTA

1 X TBE
Agarose and Polyacrylamide Gel Electrophoresis Buffer
0.089 M Tris
0.089 M Boric Acid
0.002 M EDTA

Spectrophotometric Determination of DNA Concentration & Estimation by Agarose Gel Electrophoresis

Measuring the optical density (OD) or absorbance at 260 nm (A_{260}) in a UV spectrophotometer is a relatively accurate method for calculating the concentration of DNA in an aqueous solution if a standard curve is meticulously prepared. An A_{260} of 1, using a 1 cm path length, corresponds to a DNA concentration of 50 µg/ml for double stranded DNA, 40 µg/ml for RNA and 33 µg/ml for oligonucleotides. However, this method is not suitable for determining concentrations of dilute solutions of DNA, as the sensitivity of this method is not very high. For reliable readings, the concentration of double stranded DNA must be greater than 1 µg/ml. A simple, inexpensive method for the estimation of nanogram quantities of DNA is described in the following section. We recommend the use of agarose gel electrophoresis for routine approximate determination of DNA concentration.
The amount of DNA in a sample may be estimated by running the sample alongside standards containing known amounts of the same-sized DNA fragment. In the presence of ethidium bromide staining, the amount of sample DNA can be visually estimated by comparing the band intensity with that of the known standards.



An unknown amount of a 4 kb DNA fragment (unknown) was run alongside known quantities (indicated in nanograms) of the same DNA fragment. As estimated by visual comparison with the known standards, the unknown sample contained 240-320 ng of DNA.

Ethidium bromide is a carcinogen. Follow Health and Safety Procedures established by your institution.
Follow proper Hazardous Material Disposal procedures established by your institution.

•Use 0.1 µg of ethidium bromide solution for each ml of gel volume.

Polymerase Chain Reaction

PCR Components and Analysis
PCR buffer conditions vary and it is imperative to optimize buffer conditions for each amplification reaction. At Gene Link most amplification reactions have been optimized to work with the following standard buffer condition, unless otherwise indicated.

dNTP Concentration
Standard dNTP concentration of 0.2 mM of each base is used. See section on PCR additives when dNTP concentration is changed.

$MgCl_2$ Concentration
The concentration of Mg^{++} will vary from 1-5 mM, depending upon primers and substrate. Since Mg^{2+} ions form complexes with dNTPs, primers and DNA templates, the optimal concentration of $MgCl_2$ has to be selected for each experiment. Low Mg^{2+} ions result in a low yield of PCR product, and high concentrations increase the yield of non-specific products and promote mis-incorporation. Lower Mg^{2+} concentrations are desirable when fidelity of DNA synthesis is critical. The recommended range of $MgCl_2$ concentration is 1-4 mM, under the standard reaction conditions specified. At Gene Link, using the standard PCR buffer with KCl, a final dNTP concentration of 0.2 mM, a $MgCl_2$ concentration of 1.5 is used in most cases. If the DNA samples contain EDTA or other chelators, the $MgCl_2$ concentration in the reaction mixture should be raised proportionally. Given below is an $MgCl_2$ concentration calculation and addition table using a stock solution of 25 mM $MgCl_2$.

Recipe

Standard Gene Link PCR Buffer Composition	
10 X PCR buffer	**1 X PCR buffer**
100 mM Tris-HCl pH 8.3	10 mM
500 mM KCl	50 mM
15 mM $MgCl_2$	1.5 mM
0.01% Gelatin	0.001%

Recipe

2.0 mM dNTP Stock Solution Preparation*	
Component	**Volume**
100 mM dGTP	100 µl
100 mM dATP	100 µl
100 mM dTTP	100 µl
100 mM dCTP	100 µl
Water	4.6 ml
Total Volume	5 ml
*Aliquot and freeze	

$MgCl_2$ Concentration & Addition Table								
Final concentration of $MgCl_2$ in 50 µl reaction mix, (mM)	1.0	1.25	1.5	1.75	2.0	2.5	3.0	4.0
Volume of 25 mM $MgCl_2$, µl	2	2.5	3	3.5	4	5	6	8

Primer Concentration

The final concentration of primers in a PCR reaction is usually 0.5 to 1 µM (micromolar). This is equivalent to 0.5 to 1 pmol/µl. For a 100 µl reaction you would add 50 to 100 pmols. At Gene Link we use 0.5 pmol/µl in the final PCR.

Always use filter barrier pipette tips to prevent cross contamination

Genemer™ Reconstitution
Stock Primer Mix: Dissolve the supplied 10 nmols of lyophilized Genemer™ in 100 µl sterile TE. The 10 nmols of primers when dissolved in 100 µl will give a solution of 100 µM i.e. 100 pmols/µl.

Recipe

TE Buffer pH 7.5 Composition
1 X TE Buffer pH 7.5
10 mM Tris-HCl pH 7.5
1 mM EDTA

Primer Mix: Prepare a 10 pmols/µl Primer Mix solution by a ten fold dilution of the stock primer mix.
Example: Add 180 µl sterile TE to a new tube, to this tube add 20 µl of primer stock solution. Label this tube as Primer Mix 10 pmols/µl.

Amplification Thermal Cycling
Hot Start: It is essential to have a 'Hot Start' profile for amplification of any fragment from a complex template like human genomic DNA. Taq polymerase has low activity at room temperature and it is essential to minimize any mis-priming in the first cycle of amplification. A typical hot start profile is given below. Various enzyme preparations are available which are activated by heat in the first cycle. A simple hot start protocol is given below that can be used with regular Taq polymerase. See the section on PCR additives for amplification of products from high GC content templates.

• Program your thermal cycler instrument with an amplification profile prior to beginning the amplification protocol. Consult your appropriate instrument manufacturer's manual.

Recipe

Typical PCR Premix (/ 50µl)	
Component	**Volume**
10 x PCR Buffer	5 µl

Hot Start		
Step	**Time & Temperature**	**Cycles**
Initial Denaturation	95 °C for 5 minutes	1
Annealing	60 °C Hold Infinity	Hold
Comments: Add Taq premix while on hold.		

Amplification File

The initial denaturation step at 94 °C for 30 seconds is sufficient for all templates. The number of cycles is usually set to 30 and is sufficient to amplify 1-10 µg of product depending on the initial concentration of template. A higher number of cycles from 35-45 cycles may be used, but internal priming on the product and over amplification of unwanted bands often result from over-cycling. Generally, it is better to focus on optimizing reaction conditions than to go beyond 35 cycles.

Typical Amplification File			
Step	**Temperature**	**Time**	**Cycles**
Denaturation	94 °C	30 sec.	30
Annealing	*	30 sec.	
Elongation	72 °C	30 sec.	
Fill in Extension	72 °C	7 minutes	1
Hold	4 °C	Infinity	Hold
Based on the Tm of the primers. Usually varies from 50 °C to 65 °C			

PCR Premix Preparation (PP)		
Component	**1 X 50 µl Rxn.**	**10 X 50 µl Rxns.**
Sterile Water	32 µl	320 µl
10 X PCR Buffer	4.5 µl	45 µl
2.0 mM dNTP	5 µl	50 µl
10 pmol/µl Primer Mix	2.5 µl	25 µl
Taq Enzyme Mix (EM)	5 µl	50 µl
Template DNA (~500 ng)	1-2 µl	Add 1-2 µl DNA to each tube
Total Volume	50 µl	
Keep on ice during set up. After adding template start PCR File		

2.0 mM dNTP mix (each)	5 µl
Primer Mix (10 pmol/µl each) or 2.5µl of 10 pmol/µl of individual primer (final 25 pmol of each primer/50µl)	2.5 µl
H_2O	37.5 µl
Total Volume	50 µl

Recipe

PCR reaction (/50µl)	
Component	**Volume**
PCR premix	45 µl
100ng/µl diluted DNA	1 µl
Hot start and then add	
Taq premix	5 µl

Recipe

Taq Premix EM (/50µl)	
Component	**Volume**
PCR Premix	6 µl
Taq polymerase (5 u/µl)	0.25µl
Add 5 µl/50 µl rxn after initial denaturation.	
Use 2.5 units of Taq for 100 µl reactions. Taq is usually supplied at a concentration of 5 units/µl	

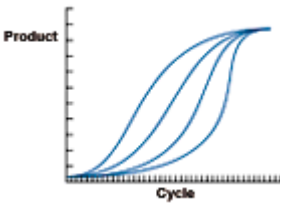
- The PCR premix preparation protocol is written considering that more than one amplification reaction will be performed at the same time. If only one reaction is planned then there is no need to prepare the Taq Enzyme Mix (EM).

Recipe

Gene Link PCR Buffer
1 X PCR Buffer
10 mM Tris-HCl pH 8.3
50 mM KCl
1.5 mM $MgCl_2$
0.001% Gelatin

Yield and Kinetics

The target will be amplified by up to 10^6 fold in a successful reaction, but the amplification will usually plateau at 1-10 µg. Thus, 1 pg of target sequence in the reaction is a good place to begin.



PCR reactions produce product in a nonlinear pattern. Amplification follows a typical exponential curve until some saturation point is reached. Generally products will not be further amplified once 1-5 µg has been generated. Saturation by one product of a reaction does not always prevent further amplification of other generally unwanted products. Over-cycling may decrease the quality of an otherwise good reaction. When first optimizing a reaction, it is advisable to take samples every 5 or 10 cycles to determine the number of cycles actually needed.

PCR Additives

DNA polymerases need to elongate rapidly and accurately to function effectively *in vivo* and *in vitro*, yet certain DNA regions appear to interfere with their progress. One common problem is pause sites, at which DNA polymerase molecules cease elongation for varying lengths of time. Many strong DNA polymerase pauses are at the beginnings of regions of strong secondary structure such as template hairpins (1). Taq polymerase used in PCR suffers the same fate and GC-rich DNA sequences often require laborious work to optimize the amplification assay. The GC-rich sequences possess high thermal and structural stability, presumably because the high duplex melting temperature that permits stable secondary structures to form, thus preventing completion of a faithful replication (2).

Nucleotide analog 7-deaza dGTP is effective in reducing the secondary structure associated with GC rich region by reducing the duplex stability (4). Betaine, DMSO and formamide reduces the Tm and the complex secondary structure, thus the duplex stability (1-5). Tetramethyl ammonium chloride (TMAC) actually increases the specificity of hybridization and increases the Tm. The use of TMAC is recommended in PCR conditions using degenerate primers.

These PCR additives and enhancing agents have been used to increase the yield, specificity and consistency of PCR reactions. These additives may have beneficial effects on some amplification and it is impossible to predict which agents will be useful in a particular context and therefore they must be empirically tested for each combination of template and primers.

PCR Additives		
Additive	**Purpose & Function**	**Concentration**
7-deaza-2'-deoxyguanosine; 7-deaza dGTP	GC rich region amplification. Reduce the stability of duplex DNA	Totally replace dGTP with 7-deaza dGTP; or use 7-deaza dGTP: dGTP at 3:1
Betaine (N,N,N-trimethylglycine = [carboxymethyl]trimethylammonium)	Reduces Tm facilitating GC rich region amplification. Reduces duplex stability	Use 3.5M to 0.1M betaine. Be sure to use Betaine or Betaine (mono)hydrate and **not** Betaine HCl.
BSA (bovine serum albumin)	BSA has proven particularly useful when attempting to amplify ancient DNA or templates, which contain PCR inhibitors such as melanin.	BSA concentration of 0.01 µg/µl to 0.1 µg/ µl can be used.
DMSO (dimethyl sulfoxide)	DMSO is thought to reduce secondary structure and is particularly useful for GC rich templates.	DMSO at 2-10% may be necessary for amplification of some templates, however 10% DMSO can reduce *Taq* polymerase activity by up to 50% so it should not be used routinely.
Formamide	Reduces secondary structure and is particularly useful for GC rich templates.	Formamide is generally used at 1-5%. Do not exceed 10%.
Non-ionic detergents e.g. Triton X-100, Tween 20 or Nonidet P-40 (NP-40)	Non-ionic detergents stabilise *Taq* polymerase and may also supress the formation of secondary structure.	0.1-1% Triton X-100, Tween 20 or NP-40 may increase yield but may also increase non-specific amplification. As little as 0.01% SDS contamination of the template DNA (left-over from the extraction procedure) can inhibit PCR by reducing *Taq* polymerase activity to as low as 10%, however, inclusion of 0.5% Tween-20 or -40 will effectively neutralize this effect.
TMAC (tetramethylammonium chloride)	TMAC is used to reduce potential DNA-RNA mismatch and improve the stringency of hybridization reactions. It increases Tm and minimizes mis-pairing.	TMAC is generally used at a final concentration of 15-100 mM to eliminate non-specific priming.

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Purification of PCR Product

Various purification methods are available for the purification of PCR products. The selection of a particular method over another is based on the downstream application and the initial robustness of the amplification. Usually no further purification is required for most cloning experiments if a single fragment is amplified, whereas for sequencing applications the amplified product should be purified from the primers and any other minor amplification products.

The preferred method of purification of an amplified fragment is the excision of the fragment band after agarose gel electrophoresis. This method yields the purification of a single fragment; as such care should be taken to excise a gel piece containing a single electrophoretically resolved fragment. The Omni-Clean™ Purification System available from Gene Link can be used for this purpose. Catalog No. 40-4110-10 for bead based system; 40-4120-10 for spin column based system and 40-4130-10 for DNA concentration. Please refer to product insert for detailed protocol or visit **www.genelink.com**.

A. **Purification of DNA from gel slices using glass beads. Provides purified single fragment.**
[Omni-Clean™ Gel DNA Beads Purification System; Catalog No. 40-4110-10]

Protocol

1. By weight, determine the volume of the excised DNA fragment.
2. Add 3 volumes of NaI solution and heat to 55 °C. Visually determine the dissolution of gel pieces.
3. Add 1 µl of glass bead suspension per µg of DNA and vortex.
4. Centrifuge at 2K rpm for 20 seconds to pellet glass bead/DNA complex. Discard supernatant.
5. Re-suspend pellet in 400 µl Omni-Clean™ wash buffer. Centrifuge at 2K rpm for 20 seconds and discard wash buffer.
6. Pipet out any remaining buffer in the tube.
7. Add 25 µl water or TE; re-suspend pellet and centrifuge at 2K rpm for 20 seconds.
8. The supernatant contains the purified DNA. Using a pipet, collect the supernatant and transfer to a new appropriately labeled tube.

B. **Purification of DNA from gel slices using spin column. Provides purified single fragment.**
[Omni-Clean™ Gel DNA Spin Column Purification System; Catalog No. 40-4120-50]

Protocol

1. By weight, determine the volume of the excised DNA fragment.
2. Add 3 volumes of NaI solution and heat to 55 °C. Visually determine the dissolution of gel pieces.
3. Add the above solution to the spin column assembled on a collection tube.
4. Let the solution flow by gravity or centrifuge at 2K rpm for 20 seconds. Discard flow through collected in the collection tube.
5. Add 400 µl Omni-Clean™ wash buffer to the spin column. Centrifuge at 2K rpm for 2 minutes and discard wash buffer collected in the collection tube.
6. Replace the collection tube with a new appropriately labeled 1.5ml tube.
7. Add 25 µl water or TE to the spin column. Let sit for 3 minutes.
8. Centrifuge at 2K rpm for 2 minutes.
9. The collection tube contains the purified DNA.

C. **Purification of DNA from solution using glass beads. Provides removal of salts, primers and dNTP.**
[Omni-Clean™ DNA Beads Concentration System; Catalog No. 40-4130-10]

Protocol

1. Determine volume of DNA solution and add 3 volumes of NaI solution.
2. Add 1 µl of glass bead suspension per µg of DNA.
3. Centrifuge at 2K rpm for 20 seconds to pellet glass bead/DNA complex. Discard supernatant.
4. Re-suspend pellet in 400 µl Omni-Clean™ wash buffer.
5. Centrifuge at 2K rpm for 20 seconds and discard wash buffer.
6. Pipet out any remaining buffer in the tube.
7. Add 25 µl water or TE; re-suspend pellet and centrifuge at 2K rpm for 20 seconds.
8. The supernatant contains the purified DNA. Using a pipet, collect the supernatant and transfer to a new appropriately labeled tube.

D. **Purification of DNA from solution using spin column. Provides removal of salts, primers and dNTP.**
[Omni-Clean™ DNA Spin Column Concentration System; Catalog No. 40-4140-10]

Protocol

1. Determine volume of DNA solution and add 3 volumes of NaI solution.
2. Add the above solution to the spin column assembled on a collection tube.
3. Let the solution flow by gravity or centrifuge at 2K rpm for 20 seconds. Discard flow through collected in the collection tube.
4. Add 400 µl Omni-Clean™ wash buffer to the spin column. Centrifuge at 2K rpm for 2 minutes and discard wash buffer collected in the collection tube.
5. Replace the collection tube with a new appropriately labeled 1.5ml tube.
6. Add 25 µl water or TE to the spin column. Let sit for 3 minutes.
7. Centrifuge at 2K rpm for 2 minutes.
8. The collection tube contains the purified DNA.

PEG Precipitation

Primers and salts are efficiently removed by a simple PEG precipitation. This method is recommended for downstream DNA sequencing application. This method is generally used for plasmid DNA.

Protocol

1. To 50 µl of amplified PCR reaction add 6.0 µl of 5 M NaCl and 40 µl of 13% (w/v) PEG 8000. Incubate the mixture on ice for 20-30 minutes.
2. Collect the DNA precipitate by centrifugation at maximum speed for 15 minutes at 4 °C in a microfuge. Carefully remove the supernatant by gentle aspiration.
   The pellet of DNA is translucent and generally invisible at this stage.
3. Rinse the pellet with 500 µl of 70% ethanol.
   The precipitate changes to a milky-white color and becomes visible.
4. Carefully pour off the 70% ethanol. Rinse the DNA pellet once more with 70% ethanol. Store the tube in an inverted position at room temperature until the last visible traces of ethanol have evaporated.
5. Dissolve the DNA in 20 µl of H_20.
6. Run an aliquot on an agarose gel to confirm the presence of the correct amplified product. The purified DNA is sequence grade and can be used directly for sequencing.

Gel Filtration

Primers and salts are efficiently removed by gel filtration using Sephadex G-50. This method is recommended for downstream DNA sequencing application.

Protocol

1. Hydrate Sephadex G-50 ahead of time in sterile water or TE (10mM Tris pH 8, 1 mM EDTA). Take out from fridge if already stored hydrated. Bring to room temperature.
2. Assemble a spin column on a collection tube.
3. Add 700 µl of hydrated Sephadex G-50 to each spin column, initiate flow using rubber bulb or any other method.
4. Allow flowing by gravity till there is no more fluid left above the Sephadex G-50 bed. Discard flow through from the collection tube.
5. Spin the spin column placed inside the collection tube for 2 minutes at 3 K rpm.
6. Change collection tube to new 1.5 ml tube appropriately labeled with sample name.
7. Apply up to 50 µl sample gently to the G-50 bed of the column.
8. Spin for 2 minutes at 3 K rpm.
9. Purified sample is collected in the collection tube. The eluent collected in the 1.5 ml tube is free of salts and primers shorter than 35-40mer.

References

1. Kovarova, M; and Draber, P; (2000) New Specificity and yield enhancer for polymerase chain reactions (2000) Nucl. Acids. Res. 28: e70.
2. Henke, W., Herdel, K., Jung, K., Schnorr, D. and Stefan A. Loening, S. (1997) Betaine improves the PCR amplification of GC-rich DNA sequences. Nucl. Acids Res. 25: 3957-3958.
3. Daniel S. Mytelka, D.S., and Chamberlin, M.J.,(1996) Analysis and suppression of DNA polymerasepauses associated with a trinucleotide consensus. Nuc. Acids Res.,. 24:2774–278.
4. Keith, J. M., Cochran, D.A.E., Lala, G.H., Adams, P., Bryant, D.and Mitchelson, K.R. (2004) Unlocking hidden genomic sequence. Nucl. Acids Res. 32: e35.
5. Owczarzy, R., Dunietz, I., Behlke, M.A., Klotz, I.M. and Joseph A. Walder. (2003) Thermodynamic treatment of oligonucleotide duplex–simplex equilibria. PNAS, 100:14840-14845.

Myotonic Dystrophy Product Ordering Information

Product	Size	Catalog No.
Myotonic Dystrophy Genemer™ Primer pair Primers for amplification of CTG triple repeat spanning region. The quantity supplied is sufficient for 400 regular 50 µl PCR reactions.	10 nmols	40-2026-10
Myotonic Dystrophy GeneProber™ GLDM1 Probe unlabeled Myotonic dystrophy CTG triple repeat spanning region unlabeled probe for radioactive labeling and Southern blot detection of Bam HI digested DNA.	500 ng	40-2026-40
Myotonic Dystrophy GeneProber™ GLDM2 Probe unlabeled Myotonic dystrophy CTG triple repeat spanning region unlabeled probe for radioactive labeling and Southern blot detection of Pst I digested DNA.	500 ng	40-2026-39
Myotonic Dystrophy GeneProber™ GLDMDig1 Probe Digoxigenin labeled Myotonic Dystrophy CTG triple repeat spanning region digoxigenin labeled probe for non-radioactive Southern blot detection.	110 µL	40-2026-41
Myotonic Dystrophy PCRProber ™ AP labeled probe Alkaline phosphatase labeled probe	12 µL	40-2026-31
Myotonic Dystrophy PCRProber ™ Kit for chemiluminescent detection Kit for performing PCR amplification and chemiluminescent based detection.	5 blots [50 rxns]	40-2026-32
GLDM Genemer™ Kit for Radioactive Detection Kit for amplification and radioactive detection of Myotonic Dystrophy CTG triple repeat region amplified PCR products using ^{35}S or ^{32}P. 100 Reactions.	1 Kit [100 rxns]	40-2026-20
GLDM GScan Kit for fluorescent detection Kit for performing fluorescent PCR amplification based detection. Various dye kits. XX=FM for 6-Fam; HX for Hex; TT for Tet; C3 for Cy3 and C5 for Cy5.	1 Kit [100 rxns]	40-2026-15XX

Genemer™ GScan Control DNA Cloned fragment of the mutation region of a particular gene. These control DNA's are ideal genotyping templates for optimizing and performing control amplification with unknown DNA. The size of the triple repeats has been determined by sequencing and gel electrophoresis. The stability of size repeats upon cloning and amplification has NOT been determined. Thus, the size should be considered approximate and there is no claim for each fragment to contain the exact number of triple repeats. These control DNA's are sold with the express condition that these NOT be used for exact triple repeat size determination of DNA of unknown genotype. The control DNA should be used for determining the performance of specific Genemer™ and PCRProber™ Gene Link products.

GLDM 12 ~CTG repeat Genemer™ Control DNA	500 ng	40-2026-01
GLDM 45 ~CTG repeat Genemer™ Control DNA	500 ng	40-2026-02
GLDM 93 ~CTG repeat Genemer™ Control DNA	500 ng	40-2026-03
GLDM 129 ~CTG repeat Genemer™ Control DNA	500 ng	40-2026-04
GLDM 194 ~CTG repeat Genemer™ Control DNA	500 ng	40-2026-05

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Genemer™ Product Ordering Information

Genemer™ Primer pair for gene or mutation specific amplification. Special optimized conditions may be required for certain amplifications

Product	Size	Catalog No.
Fragile X (spanning CGG triple repeat region) Genemer™; 10 nmols	10 nmols	40-2004-10
Huntington Disease (spanning CAG triple repeat region) Genemer™; 10 nmols	10 nmols	40-2025-10
Myotonic Dystrophy (spanning CTG triple repeat region) Genemer™; 10 nmols	10 nmols	40-2026-10
Friedreich's Ataxia (spanning GAA triple repeat region) Genemer™; 10 nmols	10 nmols	40-2027-10
Factor V Genemer™; 10 nmols	10 nmols	40-2035-10
Factor VIII (Hemophilia) Genemer™ Pack Genemer™; 10 nmols	10 nmols	40-2036-10
STS (Steroid Sulfatase) Genemer™; 10 nmols	10 nmols	40-2023-10
HGH (Human Growth Hormone) Genemer™; 10 nmols	10 nmols	40-2024-10
Sickle Cell Genemer™; 10 nmols	10 nmols	40-2001-10
RhD (Rh D gene exon 10 specific) Genemer™; 10 nmols	10 nmols	40-2002-10
Rh EeCc (Rh Ee and Cc exon 7 specific) Genemer™; 10 nmols	10 nmols	40-2003-10
Gaucher (various mutations) Genemer™; 10 nmols	10 nmols	40-2047-XX
Cystic Fibrosis (various mutations) Genemer™; 10 nmols	10 nmols	40-2029-XX
SRY (sex determining region on Y) Genemer™; 10 nmols	10 nmols	40-2020-10
X alphoid repeat Genemer™; 10 nmols	10 nmols	40-2021-10
Y alphoid repeat Genemer™; 10 nmols	10 nmols	40-2022-10

Genemer™ Control DNA Product Ordering Information

Genemer™ control DNA is a cloned fragment of the mutation region of a particular gene. These control DNA are an ideal genotyping template for optimizing and performing control amplification with unknown DNA.

Product	Size	Catalog No.
Sickle Cell Genemer control DNA (HbA, S and C available)	500 ng	40-2001-0X
GLFX CGG Genemer Control DNA; Fragile X (16, 29, 40, 60 & 90 CGG repeats available)	500 ng	40-2004-0X
GLHD CAG Genemer Control DNA; Huntington Disease (18, 34, 44, 89 & 134 CAG repeats available)	500 ng	40-2025-0X
GLDM CTG Genemer Control DNA; Myotonic Dystrophy (12, 45, 93, 129 & 194 CTG repeats available)	500 ng	40-2026-0X

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Related Products Ordering Information

Taq Polymerase & Master Mix		
Product	**Catalog No.**	**Unit Size**
Taq DNA Polymerase; 400 units; 5 µ/µL; 80 µL	40-5200-40	400 units
Taq PCR Kit; 200 x 50 µL reactions	40-5211-01	200 reactions
Taq PCR Kit with controls; 200 reactions	40-5212-01	200 reactions
PCR Master Mix (2X); 100 x 50 µL reactions (2 tubes x 1.3 mL)	40-5213-01	100 reactions
PCR Master Mix (2X); 200 x 50 µL reactions (4 tubes x 1.3 mL)	40-5213-02	200 reactions

Related Products Ordering Information

PCR Additives & Reagents		
Product	**Catalog No.**	**Unit Size**
Taq DNA Polymerase 300 units; 5 µ/µL; 60 µL	40-5200-30	300 units
PCR Buffer Standard (10 X); 1.6 mL	40-3060-16	1.6 mL
PCR Buffer Mg Free (10 X) ; 1.6 mL	40-3061-16	1.6 mL
Taq Polymerase Dilution Buffer; 1 mL	40-3070-10	1 mL
dNTP 2mM (10X) ; 1.1 mL	40-3021-11	1.1 mL
$MgCl_2$; 25 mM; 1.6 mL	40-3022-16	1.6 mL
Omni-Marker™ Universal Unlabeled; 100 µL	40-3005-01	100 µL
Primer and Template Mix; 500 bp; 40 reactions; 100 µL	40-2026-60PT	100 µL
Nuclease Free Water; 1.6 mL	40-3001-16	1.6 mL
DMSO; 1 mL	40-3031-10	1 mL
TMAC (Tetramethyl ammonium chloride) 100 mM; ; 1 mL	40-3053-10	1 mL
KCl 300 mM; 1 mL	40-3059-10	1 mL
Betaine; 5M; 1 mL	40-3032-10	1 mL

Omni-Marker™		
Product	**Catalog No.**	**Unit Size***
Omni-Marker™ Universal unlabeled; 100 µL	40-3005-01	100 µL
Omni- Marker™ Universal unlabeled; 500 µL	40-3005-05	500 µL
Omni-Marker™ Universal unlabeled; 1 mL	40-3005-10	1 mL
Omni- Marker™ Low unlabeled;100 µL	40-3006-01	100 µL
Omni-Marker™ Low unlabeled; 500 µL	40-3006-05	500 µL
Omni- Marker™ Low unlabeled; 1 mL	40-3006-10	1 mL
Omni-Marker™ GScan-2 Tamra labeled 50 bp - 600 bp; 100 µL	40-3062-01	100 µL
Omni-Marker™ GScan-2 Tamra labeled 50 bp - 600 bp; 500 µL	40-3062-05	500 µL

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Southern Blot Buffers& Reagents

Product	Catalog No.	Unit Size
Agarose Tablets, 0.5 gm each 100 Tablets	40-3011-10	100 tablets
Agarose LE Molecular Biology Grade; 100 g	40-3010-10	100 g
Agarose LE Molecular Biology Grade; 500 g	40-3010-50	500 g
Hybwash A, Hybridization Wash Solution; 200 mL	40-5020-20	200 mL
Hybwash B, Hybridization Wash Solution; 100 mL	40-5021-10	100 mL
TAE Buffer; 50X Concentrate; 100 mL	40-3007-01	100 mL
TAE Buffer; 50X Concentrate; 1000 mL	40-3007-10	1000 mL
TBE Buffer; 5X Concentrate; 1000 mL	40-3008-10	1000 mL
10x Washing buffer; 200 mL	40-5025-20	200 mL
10% Blocking solution; 100 mL	40-5026-10	100 mL
Seq. Loading buffer; 1 mL	40-5027-00	1 mL
10x AP Detection buffer; 100 mL	40-5031-10	100 mL
Lumisol™ I Hybridization Solution; contains formamide; 200 mL	40-5022-20	200 mL
Lumisol™ II Hybridization Solution; for non-toxic hybridizations; 200 mL	40-5023-20	200 mL
Lumisol™ III Hybridization Solution; for oligo probes; 200 mL	40-5024-20	200 mL

Loading Buffers

Product	Catalog No.	Size
Gel Loading Buffer 5X BPB/XC non-denaturing; 1 mL	40-3002-10	1 mL
Gel Loading Buffer 5X BPB/XC non-denaturing; 15 mL	40-3002-15	15 mL
Gel Loading Buffer 10X BPB/XC non-denaturing; 1 mL	40-3003-10	1 mL
Gel Loading Buffer 10X BPB/XC non-denaturing; 15 mL	40-3003-15	15 mL
Gel Loading Buffer 5X Orange G/XC non-denaturing; 1 mL	40-3004-10	1 mL
Gel Loading Buffer 5X Orange G/XC non-denaturing; 15 mL	40-3004-15	15 mL
Gel Loading Buffer 2X BPB/XC Denaturing for Sequencing; 1 mL	40-5027-10	1 mL
Gel Loading Buffer 2X BPB/XC Denaturing for Sequencing; 15 mL	40-5027-15	15 mL
DNA SDS Gel Loading Buffer 5X BPB/XC DNA binding protein denaturing buffer; 1 mL	40-5028-10	1 mL
DNA SDS Gel Loading Buffer 5X BPB/XC DNA binding protein denaturing buffer; 15 mL	40-5028-15	15 mL
RNA Gel Loading Buffer 2X BPB/XC with ethidium bromide; 1 mL	40-5029-10	1 mL
RNA Gel Loading Buffer 2X BPB/XC with ethidium bromide; 15 mL	40-5029-15	15 mL
RNA Gel Loading Buffer 2X BPB/XC without ethidium bromide; 1 mL	40-5030-10	1 mL
RNA Gel Loading Buffer 2X BPB/XC without ethidium bromide; 15 mL	40-5030-15	15 mL

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Notes: