High Throughput Genomic and Proteomic Sample Preparation Using Corning® Filtr*EX*™ 96 and 384 Well Filter Plates

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Abstract

The industrialization of genomics and proteomics demands the miniaturization of filtration devices to a more automation-compatible format. In response to this need, Corning has developed the Filtr*EX* 96 and 384 well filter plate platforms. These products are based on unique patented technology that allows individual filter disks to be integrally sealed in a microplate format. The objective of the current study was to demonstrate the utility of these filter plates in high throughput genomic and proteomic sample preparation methods using standard vacuum and centrifugation techniques. High throughput methods were developed for plasmid, PCR fragment and sequencing reaction clean up as well as protein size separation and desalting/concentration. The results clearly demonstrate that these products can be used to perform rapid, low cost, high quality purification of both DNA and protein and that they are compatible with standard laboratory equipment and automation.

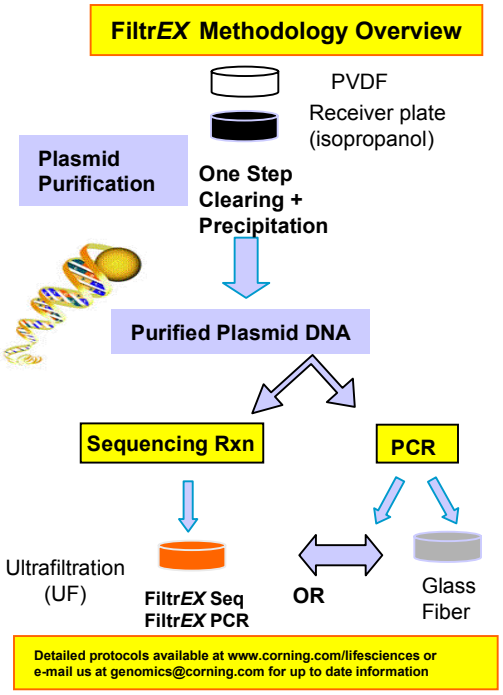

Figure 1. Filtr*EX* 96 well filter plate design
Proprietary nozzle design and individually integrally sealed filter disks prevents filtrate cross contamination. Rigid design and wide skirt allows for robotic handling and bar coding. **US Patent 6,391,241**

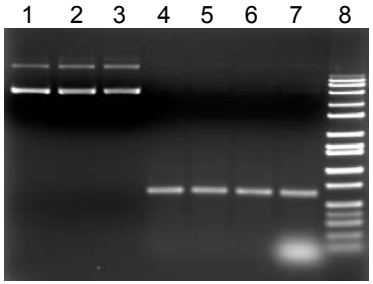

Figure 2. Plasmid and PCR samples purified using Filtr*EX* 96 well glass fiber plate.
Lanes 1, 2 and 3 contain plasmid DNA.
Lanes 4, 5 and 6 contain purified PCR reactions.
Lane 7 contains the unpurified PCR reaction.

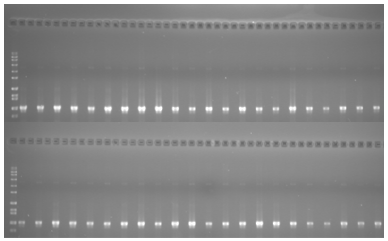

Figure 3. Absence of cross-talk in Filtr*EX* 384 well filter plate
DNA and control buffer samples were purified in alternating wells of a Filtr*EX* 384 PVDF filter plate. Samples were eluted into a receiver plate and amplified by PCR. Note the absence of contaminating product in control wells.

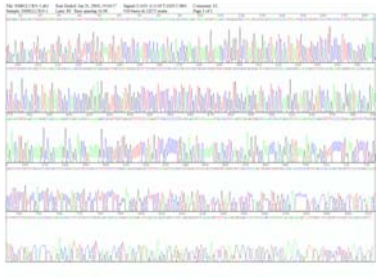

Figure 4. Filtr*EX* Seq UF cleanup of Big Dye® sequencing reaction.
ABI Version 3.1, 4 µl undiluted
Q20 Phred = 829

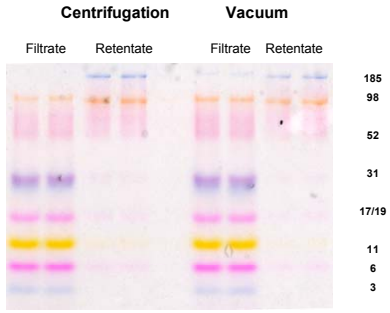

Figure 5. Protein Size Exclusion Using 100 K MWCO UF membrane in a 96 well plate format.
Protein ladder was filtered through a 100 K molecular weight cut off (MWCO) membrane and the filtrates and retentates were collected. Note exclusion of 185 kD protein.

ABI 3730: Big Dye (version 1.0)				Phred	
Clone	Process	Big Dye - µl	Resusp. vol.	Q20	Classification
Filtr*EX* Seq 1	10 min / 2,000 x g	2	40 µl	815	good
Filtr*EX* Seq 2	10 min / 2,000 x g	2	40 µl	735	good
Filtr*EX* Seq 3	10 min / 2,000 x g	2	40 µl	828	good
Filtr*EX* Seq 4	10 min / 2,000 x g	2	30 µl	845	good
Filtr*EX* Seq 5	10 min / 2,000 x g	2	30 µl	823	good
Filtr*EX* Seq 6	10 min / 2,000 x g	2	30 µl	829	good
Sephadex 1	2 x Wash + 5 min / 2,000 x g	2	NA	816	good
Sephadex 2	2 x Wash + 5 min / 2,000 x g	2	NA	823	good
Sephadex 3	2 x Wash + 5 min / 2,000 x g	2	NA	783	good
ABI 3700: Big Dye (version 3.1)				**Phred**	
Clone	Process	Big Dye - µl	Resusp. vol.	Q20	Classification
Filtr*EX* Seq 1	10 min / 3,000 x g	1	30 µl	819	good
Filtr*EX* Seq 2	10 min / 3,000 x g	2	30 µl	739	good
Filtr*EX* Seq 3	10 min / 3,000 x g	4	30 µl	747	good
Sephadex 1	2 x Wash + 5 min / 990 x g	1	NA	704	good
Sephadex 2	2 x Wash + 5 min / 990 x g	2	NA	786	good
Sephadex 3	2 x Wash + 5 min / 990 x g	4	NA	806	good

Table 1. Sequence data from Filtr*EX* Seq 96 vs. Sephadex G-50 cleanup.
Big Dye sequencing reactions were purified by Filtr*EX* Seq 96 (UF) or Sephadex G-50. The results are equivalent to Sephadex G-50 cleanup. Sequence was generated by Lark, Inc.(top panel) and GATC Biotech, AG (bottom panel)

Conclusions

- Filtr*EX* 96 & 384 well filter plates incorporate design features that ensure well integrity and prevent sample cross contamination
- The filter plates are compatible with both vacuum and centrifugation protocols.
- The rigid skirted design meets SBS standards and ensures bar code and automation compatibility.
- Filtr*EX* Seq plates offer a simpler alternative to gel filtration methods for dye terminator removal.
- The availability of different media types allows the user to perform a wide variety of common genomic and proteomic sample prep methods in an easy to use, standardized format.