GeneQuery™ Human ECM Degradation qPCR Array Kit (GQH-ECM)
Catalog #GK105

Product Description
ScienCell's GeneQuery™ Human ECM Degradation qPCR Array Kit (GQH-ECM) profiles 88 key genes involved in extracellular matrix (ECM) degradation. The ECM comprises molecules secreted by cells that provide structural and biochemical support. Its roles include supporting intercellular communication, growth factor storage, and regulating cell migration and motility. Degradation of the ECM thus influences growth factor release, chemotaxis, cell migration, and cellular adhesion. Enzymes classically involved in ECM degradation include serine proteases, threonine proteases, and matrix metalloproteinases. Brief examples of how included genes may be categorized are shown below:

- **ECM components:** ACAN, COL18A1, COL4A1, FGG, LAMA5, NTN4
- **Proteases:** ADAM10, ADAMTS1, BMP2, CAPN9, CTSG, MMP2, MMP9
- **Protease inhibitors:** A2M, CAST, SERPINH1, TIMP1, TIMP2
- **ECM proteoglycans:** BGN, DCN, LTBP2, LUM, PCOLCE
- **Cell adhesion receptors and glycoproteins:** CD44, CEACAM8, FN1, HSPG2, SPARC

GeneQuery™ qPCR array kits are qPCR ready in a 96-well plate format, with each well containing one primer set that recognizes and efficiently amplifies a specific target gene's cDNA. The carefully designed primers ensure that: (i) the optimal annealing temperature in qPCR analysis is 65°C (with 2 mM Mg^{2+} and no DMSO); (ii) the primer set recognizes all known transcript variants of the target gene, unless otherwise noted; and (iii) only one gene is amplified. Each primer set has been validated by qPCR with melt curve analysis and gel electrophoresis.

GeneQuery™ qPCR Array Kit Controls
Each GeneQuery™ plate contains eight controls (Figure 1):
- Five target housekeeping genes (β-actin, GAPDH, LDHA, NONO, and PPIH), which enable normalization of data.
- The Genomic DNA (gDNA) Control (GDC), which detects gDNA contamination in cDNA samples. This primer set targets a non-transcribed region of the genome.
- Positive PCR Control (PPC), which tests whether samples contain inhibitors or other factors that may negatively affect gene expression results. The PPC consists of a predispensed synthetic DNA template and a primer set that can amplify it. The sequence of the DNA template is not present in the human genome and thus tests the efficiency of the polymerase chain reaction itself.
- The No Template Control (NTC), which can be used to monitor DNA contamination introduced during workflow (e.g. from such sources as reagents, tips, and the lab bench).

Kit Components

Component	Quantity	Storage
GeneQuery™ array plate with lyophilized primers	1	4°C or -20°C
Optical PCR plate seal	1	RT
Nuclease-free H_2O	2 mL	4°C

Additional Materials Required (Materials Not Included in Kit)

Component	Recommended
Reverse transcriptase	MultiScribe Reverse Transcriptase (Life Tech, Cat. #4311235)
cDNA template	Customers' samples
qPCR master mix	FastStart Essential DNA Green Master (Roche, Cat. #06402712001)

Quality Control

All primer sets are validated by qPCR with melt curve analysis and analyzed by gel electrophoresis. Single band amplification is confirmed for each set of primers.

Product Use

GQH-ANG is for research use only. It is not approved for human or animal use or for application in clinical or *in vitro* diagnostic procedures.

Shipping and Storage

This product is shipped at ambient temperature. Upon receipt, the plate should be stored at 4°C and is good for up to 12 months. For long-term storage (>1 year), store at -20°C in a manual defrost freezer.

Procedures

Note: The primers in each well are lyophilized.

1. Prior to use, allow plates to warm to room temperature.
2. Briefly centrifuge at 1,500x g for 1 minute before slowly peeling off the seal.
3. Prepare 20 μl PCR reactions for one well as shown in Table 1.

Table 1

cDNA template	0.2 – 250 ng
2x qPCR master mix	10 μl
Nuclease-free H_2O	variable
Total volume	*20 μl*

*Important: **Only** use polymerases with hot-start capability to prevent possible primer-dimer formation. **Only** use nuclease-free reagents in PCR amplification.*

4. Add the mixture of 2x qPCR master mix, cDNA template, and nuclease-free H_2O to each well containing the lyophilized primers. Seal the plate with the provided optical PCR plate seal.

   Important: In NTC control well, do NOT add cDNA template. Add 2x qPCR master mix and nuclease-free H2O only.

5. Briefly centrifuge the plates at 1,500x g for 1 minute at room temperature. For maximum reliability, replicates are strongly recommended (minimum of 3).

6. For PCR program setup, please refer to the instructions of the master mix of the user's choice. We recommend a typical 3-step qPCR protocol for a 200nt amplicon:

Three-step cycling protocol

Step	Temperature	Time	Number of cycles
Initial denaturation	95°C	10 min	1
Denaturation	95°C	20 sec	40
Annealing	65°C	20 sec	
Extension	72°C	20 sec	
Data acquisition	Plate read		
Recommended	*Melting curve analysis*		1
Hold	4°C	Indefinite	1

7. (Optional) Load the PCR products on 1.5% agarose gel and perform electrophoresis to confirm the single band amplification in each well.

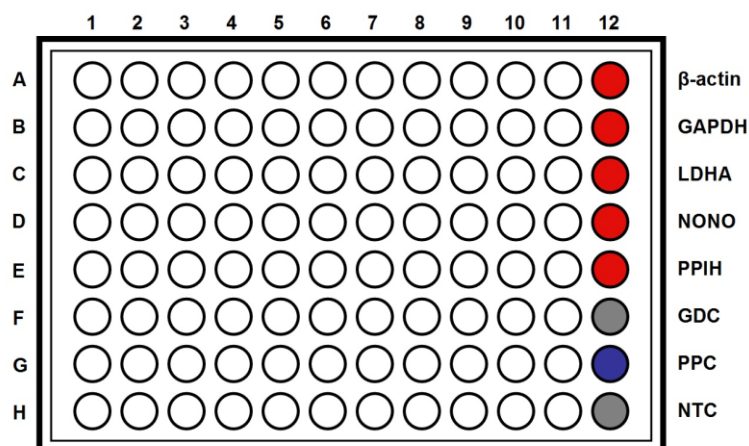Figure 1. Layout of GeneQuery™ qPCR array kit controls.

Table 2. Interpretation of control results:

Controls	Results	Interpretation	Suggestions
Housekeeping gene controls	Variability of a housekeeping gene's Cq value	The expression of the housekeeping gene is variable in samples; cycling program is incorrect	Choose a constantly expressed target, or analyze expression levels of multiple housekeeping genes; use correct cycling program and make sure that all cycle parameters have been correctly entered
gDNA Control (GDC)	Cq ≥ 35	No gDNA detected	N/A
	Cq < 35	The sample is contaminated with gDNA	Perform DNase digestion during RNA purification step
Positive PCR Control (PPC)	Cq > 30; or The Cq variations > 2 between qPCR Arrays.	Poor PCR performance; possible PCR inhibitor in reactions; cycling program incorrect	Eliminate inhibitor by purifying samples; use correct cycling program and make sure that all cycle parameters have been correctly entered
No Template Control (NTC)	Positive	DNA contamination in workflow	Eliminate sources of DNA contamination (reagents, plastics, etc.)

Figure 2. A typical amplification curve showing the amplification of a qPCR product.
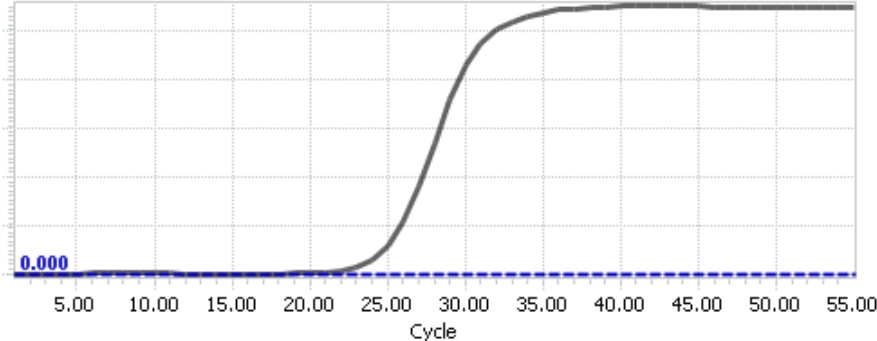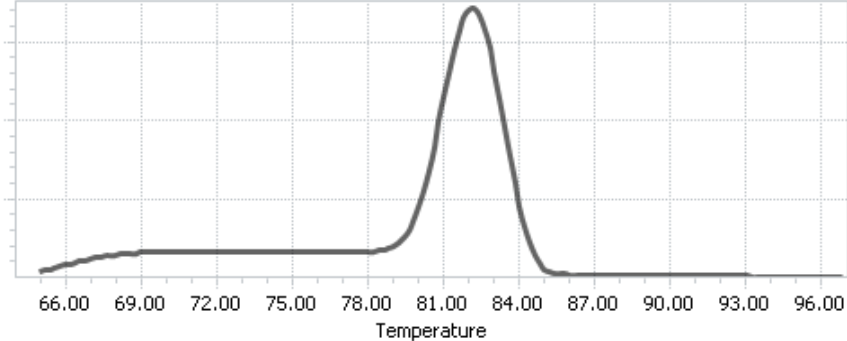

Figure 3. A typical melting peak of a qPCR product.

Quantification Method: Comparative ΔΔCq (Quantification Cycle Value) Method

1. **Note:** Please refer to your qPCR instrument's data analysis software for data analysis. The method provided here serves as guidance for quick manual calculations.

   You can use one or more housekeeping genes as a reference to normalize samples.

   Important: We highly recommend using all 5 housekeeping genes included in this kit, β-actin, GAPDH, LDHA, NONO, and PPIH.

2. For a single housekeeping gene, ΔCq (ref) is the quantification cycle number change for that housekeeping gene (HKG) between an experimental sample and control sample.

   $$\Delta Cq \text{ (ref)} = Cq \text{ (HKG, experimental sample)} - Cq \text{ (HKG, control sample)}$$

   When using multiple housekeeping genes as a reference, we recommend normalizing using the geometric mean [1] of the expression level change, which is the same as normalizing using the arithmetic mean of ΔCq of the selected housekeeping genes.

   $$\Delta Cq \text{ (ref)} = \text{average } (\Delta Cq \text{ (HKG1)}, \Delta Cq \text{ (HKG2)},......., \Delta Cq \text{ (HKG n)}) \text{ (n is the number of housekeeping genes selected)}$$

   If using all 5 housekeeping genes included in this kit, β-actin, GAPDH, LDHA, NONO, and PPIH, use the following formula:

   $$\Delta Cq \text{ (ref)} = (\Delta Cq(\beta\text{-actin}) + \Delta Cq(GAPDH) + \Delta Cq(LDHA) + \Delta Cq(NONO) + \Delta Cq(PPIH)) /5$$

   Note: ΔCq (HKG) = Cq (HKG, experimental sample) - Cq (HKG, control sample), and ΔCq (HKG) value can be positive, 0, or negative.

3. For any of your genes of interest (GOI),

   $$\Delta Cq \text{ (GOI)} = Cq \text{ (GOI, experimental sample)} - Cq \text{ (GOI, control sample)}$$

   $$\Delta\Delta Cq = \Delta Cq \text{ (GOI)} - \Delta Cq \text{ (ref)}$$

   Normalized GOI expression level fold change $= 2^{-\Delta\Delta Cq}$

References

[1] Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A, Speleman F. (2002) "Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes." *Genome Biol.* 3(7): 1-12.

Example: Comparative ΔΔCq (Quantification Cycle Value) Method

Table 3. Cq (Quantification Cycle) values of 2 genes-of-interest and 5 housekeeping genes obtained for experimental and control samples.

	Genes of Interest		Housekeeping Genes				
Samples	GOI1	GOI2	*β-actin*	*GAPDH*	*LDHA*	*NONO*	*PPIH*
Experimental	21.61	22.19	17.16	17.84	20.12	19.64	26.40
Control	33.13	26.47	18.20	18.48	20.57	19.50	26.55

ΔCq (ref) = (ΔCq(β-actin)+ΔCq(GAPDH)+ΔCq(LDHA)+ΔCq(NONO)+ΔCq(PPIH)) /5

$\qquad$ = ((17.16-18.20)+(17.84-18.48)+(20.12-20.57)+(19.64-19.50)+(26.40-26.55))/5

$\qquad$ = -0.43

ΔCq (GOI1) = 21.61 - 33.13

$\qquad$ = -11.52

ΔCq (GOI2) = 22.19 - 26.47

$\qquad$ = -4.28

$\Delta\Delta$Cq (GOI1) = ΔCq (GOI1) - ΔCq (ref)

$\qquad$ = -11.52 - (-0.43)

$\qquad$ = -11.09

$\Delta\Delta$Cq (GOI2) = ΔCq (GOI2) - ΔCq (ref)

$\qquad$ = -4.28 - (-0.43)

$\qquad$ = -3.85

Normalized GOI1 expression level fold change = $2^{-\Delta\Delta Cq\ (GOI1)}$

$\qquad\qquad = 2^{11.09}$

$\qquad\qquad = 2180$

Normalized GOI2 expression level fold change = $2^{-\Delta\Delta Cq\ (GOI2)}$

$\qquad\qquad = 2^{3.85}$

$\qquad\qquad = 14.4$

Conclusion: Upon treatment, expression level of GOI1 increased 2,180 fold, and expression level of GOI2 increased 14.4 fold.

GeneQuery™ Human ECM Degradation qPCR Array Plate Layout* (*8 controls* in Bold and Italic)

	1	2	3	4	5	6	7	8	9	10	11	12
A	A2M	ADAMTS4	CAPN1	CEACAM8	COL4A1	CTSG	FGB	LAMA2	LOX	MMP3	PLG	*β-actin*
B	ACAN	ADAMTS5	CAPN10	COL11A1	COL4A3	CTSS	FGG	LAMA3	LTBP2	MMP7	PSEN1	*GAPDH*
C	ADAM10	BGN	CAPN2	COL14A1	COL4A5	CTSV	FN1	LAMA5	LUM	MMP8	SERPINH1	*LDHA*
D	ADAM12	BMP1	CAPN3	COL18A1	COL5A1	DCN	HSPG2	LAMB1	MMP1	MMP9	SPARC	*NONO*
E	ADAM15	BMP10	CAPN9	COL1A1	COL5A2	DMD	HTRA1	LAMB2	MMP12	NCSTN	SPP1	*PPIH*
F	ADAM17	BMP2	CASP3	COL1A2	COL6A1	DMP1	KLK12	LAMB3	MMP13	NID1	TIMP1	*GDC*
G	ADAM8	BMP4	CAST	COL2A1	COL6A3	FBN1	KLK7	LAMC1	MMP14	NTN4	TIMP2	*PPC*
H	ADAMTS1	BMP7	CD44	COL3A1	COL7A1	FGA	LAMA1	LAMC2	MMP2	PCOLCE	VCAN	*NTC*

* gene selection may be updated based on new research and development

Appendix. Plate type choice chart.

Plate type A

Brand	Model	kit catalog #
ABI / Life Tech	ABI 5700	GK105-A
	ABI 7000	GK105-A
	ABI 7300	GK105-A
	ABI 7500	GK105-A
	ABI 7700	GK105-A
	ABI 7900 HT	GK105-A
	QuantStudio	GK105-A
	ViiA 7	GK105-A
Bio-Rad	Chromo4	GK105-A
	iCycler	GK105-A
	iQ5	GK105-A
	MyiQ	GK105-A
	MyiQ2	GK105-A
Eppendorf / Life Tech	Matercycler ep realplex 2	GK105-A
	Matercycler ep realplex 4	GK105-A
Stratagene	MX3000P	GK105-A
	MX3005P	GK105-A

Plate type B

Brand	Model	kit catalog #
ABI / Life Tech	ABI 7500 Fast	GK105-B
	ABI 7900 HT Fast	GK105-B
	QuantStudio Fast	GK105-B
	StepOnePlus	GK105-B
	ViiA 7 Fast	GK105-B
Bio-Rad	CFX Connect	GK105-B
	CFX96	GK105-B
	DNA Engine Opticon 2	GK105-B
Stratagene	MX4000	GK105-B

Plate type C

Brand	Model	kit catalog #
Roche	Lightcycler 96	GK105-C
	Lightcycler 480 (96-well)	GK105-C