

**Interferon gamma induces prostaglandin G/H synthase-2 through an autocrine loop via the epidermal growth factor receptor in human bronchial epithelial cells.**

K Asano, ... , M Klagsbrun, J M Drazen

*J Clin Invest.* 1998;101(11):2611-2611. <https://doi.org/10.1172/JCI119233C1>.

**Correction**

Original citation: *J. Clin. Invest.* 1997;99(6):1057–1063. doi:10.1172/JCI119233. Citation for this correction: *J. Clin. Invest.* 1998;101(11):2611. doi:10.1172/JCI119233C1. An incorrect version of Table 1 was printed with the article. A revised version of the table appears below; corrections are in bold.

**Find the latest version:**

<https://jci.me/119233C1/pdf>



In, K.H., K. Asano, D. Beier, J. Grobholz, P.W. Finn, E.K. Silverman, E.S. Silverman, T. Collins, A.R. Fischer, T.P. Keith, K. Serino, S.W. Kim, G.T. De Sanctis, C. Yandava, A. Pillari, P. Rubin, J. Kemp, E. Israel, W. Busse, D. Ledford, J.J. Murray, A. Segal, D. Tinkleman, and J.M. Drazen.

*The Journal of Clinical Investigation*. Volume 99, No. 5, March 1997.

Page 1131.

An incorrect version of Table I was printed with the article. A revised version of the table appears below; corrections are in bold.

*Table I. PCR Primers Used in Mutation Identification and Sequencing 5-lipoxygenase*

Region of interest	Sense primer (5' to 3')	Antisense primer (5' to 3')
Negative regulatory region*		
(-1557 to -1844)	AAA GAA CAG CGT TGG TGG AT	CAA ATT CAT TGT GTT GCA TGT G
(-292 to -727)	ACC ACT GGC GAT CTC TGG	CTC CTC AGC GAG GTG TCT G
Positive regulatory region*		
(-854 to -931)	TTA GCC GAG ATC AAT ACA CGC	GGG TGT GGA GAA GGT TTC G
Transcription factor binding region*		
(-88 to -212)	AGG AAC AGA CAC CTC GCT GAG GAG AGA C	GAG CAG CGA GCG CCG GGA GCC TCG GC
Exon 1	CGC CAT GCC CTC CTA CAC	CCA CGC TCG AAG TCG TTG TA
Exon 2	TCT CCT TCC CAG GTG GAT	GCT CAC CGC GTC C
Exon 3	CTT TCT TTA CAG CAA AGT TG	tac acA CTC ACC CAT ATT G
Exon 4	TCT CAT GCT CAG ATG GAT G	ACT TAC GCT TTG GA
Exon 5	TGG AGA ACC TGT TCA TCA ACC	TCA CCA GAA ATA GTG TTG CTG A
Exon 6	CCT GGT AGA GGG GGT CAT GAA TC	ACC TCC TGC TCC AAG CTG AGC T
Exon 7	TGC CTC CTG CAG CAA GGG	GCC TAC CTG GAT
Exon 8	CCA ATG TAT CAG CTC AAC	gct atc CTG TAC CTT GAA
Exon 9	CCC TCC CCA GCT GCT GGT	ACC CAC CTT GTC AAA GCG GCC
Exon 10	CAC TCC AGG CCA ACG CCA CA	CCA CAC CAG GAG CCC GTC GT
Exon 11	CCC CTG AGC CAG GTT CAC G	cca cga aCC CTA CCT GAG GA
Exon 12	TTC CAC CCT AGG CTT CCC	GCC TAC CTG GCC GAA GTT
Exon 13	GTG CTC CTG GAT CCC CAA T	CTC GTT TTC CTG GAA CTG GC
Exon 14	CTG GGC CCT CAG CTG TTC	CAC ATG GAA CAA GAC CCA TT

\*Position is reference to the ATG translation start site as +1.

