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Invitation to review a manuscript for Clinical Epigenetics - CLEP-D-15-00065

From: **Clinical Epigenetics Editorial Office** (em@editorialmanager.com)
Sent: Thu 8/27/15 9:54 PM
To: Shicheng Guo (shicheng.guo@hotmail.com)

CLEP-D-15-00065
The differential expression of mRNAs and long noncoding RNAs between ectopic and eutopic endometrium provides new insights into adenomyosis
Clinical Epigenetics

Dear Dr. Guo,

I would like to invite you to review the manuscript above which has been submitted to Clinical Epigenetics. Further details including the full abstract can be found at the end of this email.

If you are able to review this submission please click on this link:

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We ask reviewers to return their report within 14 days of agreeing to review, however if you need more time please do let us know as we may be able to arrange an alternative deadline.

You are requested to submit your review online by using the Editorial Manager system which can be found at:

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Your username is: shicheng.guo@hotmail.com
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In order to keep delays to a minimum, please accept or decline this invitation online within the next three days. If you are unable to review the manuscript, we would be most grateful if you could suggest alternative reviewers.

Thank you for your time, and I look forward to hearing from you.

Best wishes,

Trygve Tollefsbol, Ph.D., D.O.
Clinical Epigenetics
http://www.clinicalepigeneticsjournal.com/

CLEP-D-15-00065
Research
The differential expression of mRNAs and long noncoding RNAs between ectopic and eutopic endometrium provides new insights into adenomyosis
Clinical Epigenetics

Abstract: Abstract
Background: Adenomyosis, defined as ectopic endometrial tissue within the myometrium, can often be misdiagnosed as multiple uterine leiomyomata or endometrial thickening. We therefore performed a combined mRNA and long noncoding (lnc)RNA microarray and bioinformatic analysis of eutopic and ectopic endometrium in women with adenomyosis to better understand its pathogenesis and help in the development of a semi-invasive diagnostic test.
Results: A total of 586 mRNAs were increased and 305 mRNAs decreased in ectopic endometrium of adenomyosis compared with eutopic endometrium, while 388 lncRNA transcripts were up-regulated and 188 down-regulated in ectopic compared with paired eutopic endometrial tissue.
Conclusion: mRNA and lncRNA expression was comparable in eutopic and ectopic endometria. Bioinformatic analysis suggested a series of metabolic and molecular abnormalities in adenomyosis, which have many similarities with endometriosis. Furthermore, our study constitutes the first known report of lncRNA expression patterns in human adenomyosis ectopic and eutopic endometrial tissue.