ICMJE DISCLOSURE FORM

Date: Apr. 24th, 2022
Your Name: Jiang-Tao Mou
Manuscript Title: Identification of genetic polymorphisms in unexplained recurrent spontaneous abortion based on whole exome sequencing
Manuscript number (if known): ________________________________

In the interest of transparency, we ask you to disclose all relationships/activities/interests listed below that are related to the content of your manuscript. “Related” means any relation with for-profit or not-for-profit third parties whose interests may be affected by the content of the manuscript. Disclosure represents a commitment to transparency and does not necessarily indicate a bias. If you are in doubt about whether to list a relationship/activity/interest, it is preferable that you do so.

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In item #1 below, report all support for the work reported in this manuscript without time limit. For all other items, the time frame for disclosure is the past 36 months.

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|------|-------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------|
| 1    | All support for the present manuscript (e.g., funding, provision of study materials, medical writing, article processing charges, etc.) | ___None<br>Time frame: Since the initial planning of the work<br>This study was funded by the Science and Technology Research Project of Chongqing Education Commission (KJQN202100427) and the Young and Middle-Aged Medical Talents Project of Chongqing Municipal Health Commission/Chongqing Science and Technology Bureau (2022GDRC001). |
| 2    | Grants or contracts from any entity (if not indicated in item #1 above). | ___V___None<br>Time frame: past 36 months |
| 3    | Royalties or licenses | ___V___None |
| 4    | Consulting fees | ___V___None |
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| 5 | Payment or honoraria for lectures, presentations, speakers bureaus, manuscript writing or educational events | √ None |
| 6 | Payment for expert testimony | √ None |
| 7 | Support for attending meetings and/or travel | √ None |
| 8 | Patents planned, issued or pending | √ None |
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| 10 | Leadership or fiduciary role in other board, society, committee or advocacy group, paid or unpaid | √ None |
| 11 | Stock or stock options | √ None |
| 12 | Receipt of equipment, materials, drugs, medical writing, gifts or other services | √ None |
| 13 | Other financial or non-financial interests | √ None |

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Date: Apr. 24th, 2022
Your Name: Shi-Xing Huang
Manuscript Title: Identification of genetic polymorphisms in unexplained recurrent spontaneous abortion based on whole exome sequencing
Manuscript number (if known): ____________________________________________

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| 3 | Royalties or licenses                                                                      | √ None                                                                             |
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Date: Apr. 24th, 2022
Your Name: Li-Li Yu
Manuscript Title: Identification of genetic polymorphisms in unexplained recurrent spontaneous abortion based on whole exome sequencing
Manuscript number (if known): ______________________________________________________________________

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Date: Apr. 24th, 2022
Your Name: Jing Xu
Manuscript Title: Identification of genetic polymorphisms in unexplained recurrent spontaneous abortion based on whole exome sequencing
Manuscript number (if known): 

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Date: Apr. 24th, 2022
Your Name: Qiao-Ling Deng
Manuscript Title: Identification of genetic polymorphisms in unexplained recurrent spontaneous abortion based on whole exome sequencing
Manuscript number (if known): ____________________________________________________________________

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Time frame: Since the initial planning of the work

Time frame: past 36 months
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Date: Apr. 24th, 2022
Your Name: Yi-Shan Xie
Manuscript Title: Identification of genetic polymorphisms in unexplained recurrent spontaneous abortion based on whole exome sequencing
Manuscript number (if known): ________________________________________________

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Date: Apr. 24th, 2022
Your Name: Kun Deng
Manuscript Title: Identification of genetic polymorphisms in unexplained recurrent spontaneous abortion based on whole exome sequencing
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