

## ESPS JOURNAL EDITOR-IN-CHIEF'S REVIEW REPORT

**Name of journal:** World Journal of Virology

**ESPS manuscript NO:** 16610

**Title:** Next-generation sequencing in clinical virology: Discovery of new viruses

**Journal Editor-in-Chief (Associate Editor):** Chun-Jung Chen

**Country:** Taiwan

**Editorial Director:** Xiu-Xia Song

**Date sent for review:** 2015-04-30 16:28

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ACADEMIC CONTENT EVALUATION	LANGUAGE QUALITY EVALUATION	CONCLUSION
<input type="checkbox"/> Grade A: Excellent	<input checked="" type="checkbox"/> Grade A: Priority publishing	<input checked="" type="checkbox"/> Accept
<input type="checkbox"/> Grade B: Very good	<input type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> High priority for publication
<input checked="" type="checkbox"/> Grade C: Good	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Revision
<input type="checkbox"/> Grade D: Fair		
<input type="checkbox"/> Grade E: Poor	<input type="checkbox"/> Grade D: Rejected	<input type="checkbox"/> Rejection

### JOURNAL EDITOR-IN-CHIEF (ASSOCIATE EDITOR) COMMENTS TO AUTHORS

The development and evolution of methods of nucleic acid sequencing have great impact on biological sciences, including microorganism identification. Those PCR- and microarray-based methods rely on a fragment of known sequence thereby are not applicable to unknown, novel targets. To override the limitation, the next generation sequencing provides a platform working in sequence-independent manner. Due to the complicated nature, unknown novel viruses might be emerged as threatening and lethal pathogens to human health. This manuscript briefly described the evolution of DNA sequencing platform and highlighted the application of next generation sequencing on novel virus identification. The summarized information is helpful to the readers. Other reviewers also put high credit on it. It is suitable for publication.