Annexure IX

ASSESSMENT/EVALUATION REPORT OF UGC MAJOR RESEARCH PROJECT
Sponsored by
UNIVERSITY GRANT COMMISSION
BahadurshahJafar Marg, Delhi

A. DETAILS OF THE PROJECT

1. Title of the project	**Structure of Q-beta replicase in different ionic Strengths using single particle analysis**
2. Total duration of the project	**3 years**
3. Project status	**Completed**
4. Subject	**Bioinformatics**
5. File Number UGC reference number & date	**F.No. 41-665/2012(SR), Dated 23.07.12**
6. Grant approval	**Rs. 13, 37,542/-** ***(Thirteen Lakhs Thirty seven Thousand Five hundred Forty Two Only)***

B. Evaluation report of the Expert member

1.	Name of the principal investigator	**Dr. A. Murali**
2.	Designation	**Assistant Professor**
3.	Address , E-mail, phone	**Center for Bioinformatics, Pondicherry University, Pondicherry 605014** **E-mail: mayaluru@gmail.com**
4.	Whether work is focused on the title of the project	**Yes**
5.	Whether original work is done	**Yes**
6.	Whether significant contribution made the principal investigator	**Yes**
7.	Whether proposed work have relevance to the society/ scientific community	**Yes**
8.	What type of contribution found in the final report theoretical/ practical. If there are theoretical contribution given by the principal investigator, whether real application are given	**Experimental and Theoretical**
9.	Whether theoretical/ practical contribution and their results and finds are published	**Yes**
10.	Whether results and findings are significant	**Yes**
11.	Whether the significant publication are made by principal investigator in peer reviewed journal	**Yes**

12.	The number of publication made by the principal investigator in standard reputed journal	**Five (5)**
13.	Whether the contribution made by the principal investigator is sufficient	**Yes**
14.	The findings and results of the sanction major research projects are justifiable	**Yes**
15.	Whether completed project work meet the proposed objective	**Yes**
16.	Give your brief comments on the overall work of the project	Qbeta replicase subunits were modeled through *in silico* and validated by fitting them with their respective density maps obtained from TEM. Conformational changes by pH induced were analyzed for both T7RNAP and transcriptional inhibitor T7 lysozyme with molecular dynamics approach and their effect on the interaction was analyzed by molecular docking approach. Binding pattern of heparin was observed by docking heparin and few of its low molecular weight derivatives (LMW) [enoxaparin (PubChem CID: 772), bemiparin (PubChem CID: 25244225), fondaparinux (PubChem CID: 5282448) and idraparinux (PubChem CID: 3083445)] to T7RNAP. Enoxaparin has showed promising results to be a possible LMW alternative to heparin to be used as an inhibitor of T7RNAP. Possible mode of inhibition of T7RNAP by heparin has also been proposed. In addition, LGP2, a member of Retinoic acid Inducible Gene–I like receptors (RLR), one of the essential protein that induce antiviral response against many RNA viruses has also been modelled and docked with RNA.
17.	Any specific comments	All the objectives has been covered and 4 publications in reputed journals
18.	Indicate your overall assessment of the project poor/ good / excellent	**Excellent**

Date: 16.08.2019

16/08/2019

Place: Karaikudi

Signature

Name and Address of Expert

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Professor and Head
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