

A Structural and Functional Bioinformatics Study of QTY-designed Retinylidene Proteins

Siqi Pan¹ and Shuguang Zhang²

¹Shanghai World Foreign Language Academy, 400 Baihua Road, Shanghai 200233, China

²Lab of Molecular Architecture, Media Lab, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA

Corresponding author:

Shuguang Zhang²

Email address: Shuguang@MIT.EDU

ABSTRACT

This is the abstract!

Keywords: Keyword1; Keyword2; Keyword3

INTRODUCTION

Intro

- * Families of opsins - vertebrate vs. bacterial
- * General features of vertebrate opsin; structure and function
- * Activation mechanism of rhodopsin
- * Expression, function of each opsin
- * General features of bacterial opsin; structure, function, applications
- * Why solubilize
- * History of solubilizing studies of rhodopsin and bacteriorhodopsin
- * Intro to AlphaFold
- * Existing QTY studies
- * Intro to GROMACS
- * Existing rhodopsin bioinformatics studies

RESULTS AND DISCUSSION

Results

- * discuss the QTY code
- * describe and explain Table1
- * describe and explain Fig1
- * describe and explain Fig2 ; I need more discussion here
- * describe and explain Fig3
- * discuss AlphaFold3 predictions
- * describe, explain, discuss MD results (Fig3 and Fig4) ; I need more discussion here
- * future scopes and potential applications
- * conclusion

METHODS

Methods

- * protein sequences UniProt
- * AlphaFold3 server
- * superimposition (PDB, AlphaFold, PyMOL)
- * Structure visualization (PyMOL, ChimeraX)
- * MD simulation (GROMACS, etc.; detailed params; analysis techniques)

42 **SUPPLEMENTARY MATERIAL**

43 Can be found at...

44 **DATA AVAILABILITY STATEMENT**

45 Can be found at...

46 **AUTHOR CONTRIBUTIONS**

47 A.O., A.T. and A.F. conceived the presented idea; A.O. wrote the main manuscript; All authors have read and agreed to
48 the published version of the manuscript.

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51 any Author Accepted Manuscript version arising from this submission.

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54 **COMPETING INTERESTS**

55 The authors declare no conflict of interest.

56 **ETHICS STATEMENT**

57 No ethics issues...

58 **REFERENCES**