Curriculum vitae

Vishram L. Terse, Ph.D.

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Employment History

2021 – · · · ·   🔖 **Bioinformatics Scientist I,** MedGenome Labs Ltd.

Education

2013 – 2020   🔖 **Ph.D., NCBS, Bengaluru (India)** Biology (computational).
Thesis title: *Understanding protein folding and domain swapping using structure based model MD simulations.* PI: Dr. Shachi Gosavi

2011 – 2013   🔖 **M.Sc. IIT Bombay, Mumbai (India).** Biotechnology.
Thesis title: *Functional annotation of putative glycosyltrasferases from Mycobacterium tuberculosis (computational project).* Guide: Prof. P. V. Balaji.

2008 – 2011   🔖 **B.Sc. KET's V. G. Vaze college, Mumbai (India)** Biotechnology.

Skills

🔖 MD simulations (coarse grained and atomistic) using GROMACS and their analysis.

🔖 Analysis of simulation trajectories using contact maps to understand how proteins fold.

🔖 Identifying structural features and functional regions of proteins using a theoretical construct called folding motif.

🔖 Setting up bioinformatics pipeline for ligand screening using AutoDock.

🔖 Programming languages: perl, shell, C, python, MATLAB , R and SQL.

🔖 Familiar with pbs for cluster job submission.

🔖 Experienced in Unix based environments (Fedora/CentOS/Ubuntu).

🔖 Text editors : vim and VS Code, Version control : Git/GitHub.

🔖 Visualization softwares: vmd and pymol

🔖 Image editors : Adobe illustrator and GIMP

Research Publications

Journal Articles

1. Das, A., Yadav, A., Gupta, M., R, P., **Terse**, **V. L.**, Vishvakarma, V., … Maiti, S. (2021). Rational design of protein-specific folding modifiers. *Journal of the American Chemical Society*, *143*(44), 18766–18776. PMID: 34724378. 🔗 doi:10.1021/jacs.1c09611

2   **Terse**, **V. L.**, & Gosavi, S. (2021). The molecular mechanism of domain swapping of the c-terminal domain of the sars-coronavirus main protease. *Biophysical Journal, 120*(3), 504–516. 🔗 doi:10.1016/j.bpj.2020.11.2277

3   Mascarenhas, N. M., **Terse**, **V. L.**, & Gosavi, S. (2018). Intrinsic disorder in a well-folded globular protein. *The Journal of Physical Chemistry B, 122*(6), 1876–1884. PMID: 29304275. 🔗 doi:10.1021/acs.jpcb.7b12546

4   **Terse**, **V. L.**, & Gosavi, S. (2018). The sensitivity of computational protein folding to contact map perturbations: The case of ubiquitin folding and function. *The Journal of Physical Chemistry B, 122*(49), 11497–11507. 🔗 doi:10.1021/acs.jpcb.8b07409

Projects

Ph.D. projects

- Intrinsic disorder in well-folded globular proteins.
- The sensitivity of computational protein folding to contact map perturbations: The case of ubiquitin folding and function.
- Investigating the cause of domain swapping in the C-terminal domain of main protease ($M^{pro}C$) from SARS-CoV.
- Understanding the domain swapping mechanism in mutant protein G and its application in designing a novel domain swapped dimer (unpublished).

Summer internships

2009-2011   3 consecutive summer internships under POBE programme at JNCASR, Bangalore which include lectures, lab training and two cell biology related projects.

Conferences

2019   Attended and presented poster at EMBO protein-protein interaction workshop and EMBO IDP conference.

2014, 2016   Attended and presented poster at International protein folding conference

2014 - 2019   Member of Protein Journal club at NCBS. Its activities include presenting and discussing recent papers related to protein structure, function, folding and design.

2011   Represented Mumbai University at Inter University Research Festival, Avishkar.

2011   Attended Graduate Student's Meet organised by ACTREC.

Organisational/Managerial skills

2019   Volunteer at the EMBO protein protein interaction workshop.

2012   **Generations 2011, BSBE, IIT Bombay.**, Contributed to the organization of National level Biotechnology Festival organized by Symbiotek, Bioschool Association, IIT Bombay.

2009-2010   Was a member of centre for talent search to train students for national talent search exam.