

Manish Datt

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Experience

2015-2021: Assistant Professor at Division of Biological & Life Sciences, School of Arts & Sciences, Ahmedabad University, Gujarat, India.

2017-2017: Visiting Assistant Professor at Olin College of Engineering, Needham, MA, US

2012-2015: Research Scientist at Structural and Computational Biology group at International Center for Genetic Engineering and Biotechnology, India.

2010-2012: Postdoctoral Scholar at Center for Proteomics and Bioinformatics at Case Western Reserve University, Cleveland, OH, USA.

Education

2004-2010: Ph.D. in **Bioinformatics** from Institute of Microbial Technology, India.

2002-2004: M.Sc. in **Biotechnology** from Panjab University, India.

1998-2001: B.Sc. in **Biochemistry** from University of Delhi, India.

Summary of Qualifications

I have broad training in life sciences, bioinformatics, and computational biophysics. Extensive experience in simulating dynamics of macromolecules and their complexes using all-atom molecular mechanic force-fields. My doctoral research involved simulation of protein-DNA complexes to study intermolecular recognition mechanisms. Also, comprehensive analysis of methods for protein-DNA docking was performed during PhD. I have strong expertise in protein structure analyses and modeling interaction of proteins with other biomolecules. During postdoctoral research molecular modeling and docking studies on different pharmaceutically important proteins was performed. I have successfully completed a project on Hidden Markov Model based genome annotation for identification of potential drug targets in fungal pathogens. In addition, developed an algorithmic workflow for annotation of disease-associated mutations in human aminoacyl-tRNA synthetases. Recently, I have delineated allosteric interactions in the malarial tyrosyl-tRNA synthetase via molecular dynamics simulations. I am proficient in programming and high performance computing under different platforms. I am an active member of the team engaged in the development of project-based learning courses for interdisciplinary learning and education. I have designed and delivered Bioinformatics related courses for both undergraduate and postgraduate students.

Teaching

Academic activities: I teach courses in bioinformatics, computational structural biology, and enzymology to undergraduate and postgraduate students at the life science division. Also, I teach bioinformatics to B. Tech students at the engineering school. I have successfully supervised three MSc and three MTech theses and am currently mentoring one Master's student.

Project-Based Learning: I am actively involved in designing new courses and in the development and implementation of Ahmedabad University's proprietary pedagogy – ENABLE (ENGagement and Application Based Learning and Education). The new courses are being designed such that students can learn basic science irrespective of their academic backgrounds.

Conference/ Workshops

2021 – Great Lakes Bioinformatics conference (GLBIO2021). Virtual Event.

2019 – Regional Young Investigator Meeting at IIT Jodhpur.

2018 – International Conference on Computational Biology (InCoB) at JNU, New Delhi.

2016 – National conference on **Chemistry of Light and Medicine** at IIT Gandhinagar.

2015 – International conference on Mathematical and Computational Biology at IIT Roorkee.

2014 – International conference on Mathematical and Computational Biology at IIT Kanpur.

2013 – Workshop on Proteomics methods at ICGEB, New Delhi, India.

2010 – Great Lakes Bioinformatics conference (GLBIO 2010) at Ohio State University, Columbus OH, USA

2009 – International conference on DNA-Protein Transactions and 12th transcription Assembly at IMTECH, Chandigarh, India.

2009 – International conference on Open Source for Computer-Aided Drug Design (OSCADD-2009) at IMTECH, Chandigarh, India.

2008 – Bioinformatics workshop at Himachal Pradesh University, Shimla, India.

2007 – Workshop on Developing Applications for GARUDA (DAG 07) at Jawaharlal Nehru University, Delhi, India.

2007 – CHARMM workshop at University of Hyderabad, Hyderabad, India.

2006 – Discovery Studio Workshop at University of Pune, Pune, India.

2006 – Structure based design using InsightII at IMTECH, Chandigarh, India.

Publications

- 1) Interplay of substrate polymorphism and conformational plasticity in *Plasmodium* tyrosyl-tRNA synthetase.
Datt M*
Computational Biology and Chemistry, 2021. <https://doi.org/10.1016/j.compbiolchem.2021.107582>
- 2) Gupta M, Wani A, Ahsan AU, Ali M, Chibber P, Singh S, Digra SK, **Datt M**, Bharate SB, Vishwakarma RA, Singh G, Kumar A.
Safranal inhibits NLRP3 inflammasome activation by preventing ASC oligomerization. Toxicol Appl Pharmacol. 2021 May 18;423:115582. doi: 10.1016/j.taap.2021.115582. PMID: 34019860
- 3) Doshi K, Pandya N, **Datt M***.
In silico assessment of natural products and approved drugs as potential inhibitory scaffolds targeting aminoacyl-tRNA synthetases from *Plasmodium*.
3 Biotech. 2020 Nov;10(11):470. doi: 10.1007/s13205-020-02460-6. Epub 2020 Oct 12.
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- 6) **Datt M**.
Geometric analysis of the conformational features of protein structures.
Book chapter in BIOMAT conference proceedings, 2015.
- 7) Shukla S, Kanwal R, Shankar E, **Datt M**, Chance MR, Fu P, MacLennan GT, Gupta S.
Apigenin blocks IKK α activation and suppresses prostate cancer progression. Oncotarget. 2015 Oct 13;6(31):31216-32.
- 8) Chahar P, Kaushik M, Gill SS, Gakhar SK, Gopalan N, **Datt M**, Sharma A, Gill R.
Genome-Wide Collation of the Plasmodium falciparum WDR Protein Superfamily Reveals Malarial Parasite-Specific Features.
PLoS One. 2015 Jun 4;10(6):e0128507
- 9) **Datt M** and Sharma A.
Evolutionary and structural annotation for disease-associated mutation in human aminoacyl-tRNA synthetases
BMC Genomics. 2014 Dec 4;15:1063

- 10) **Datt M** and Sharma A.
Novel and unique domains in aminoacyl-tRNA synthetases from human fungal pathogens *Aspergillus niger*, *Candida albicans* and *Cryptococcus neoformans*
BMC Genomics. 2014 Dec 5;15:1069
- 11) **Datt M** and Sharma A.
Conformational landscape of the ATP recognition loop in aminoacyl-tRNA synthetases.
J Struct Funct Genomics. 2014 Jun;15(2):45-61
- 12) Aneja R, **Datt M**, Yadav S, Sahni G.
Multiple Exosites Distributed across the Three Domains of Streptokinase Co-Operate to Generate High Catalytic Rates in the Streptokinase-Plasmin Activator Complex.
Biochemistry. 2013 Dec 10;52(49):8957-68.
- 13) Mbonye UR, Gokulrangan G, **Datt M**, Dobrowolski C, Cooper M, Chance MR, Karn J.
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- 17) Kiselar JG, **Datt M**, Chance MR, Weiss MA.
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- 18) Yadav S, Aneja R, Kumar P, **Datt M**, Sinha S, Sahni G.
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J Biol Chem. 2011 Feb 25;286(8):6458-69.
- 19) Kaur H, **Datt M**, Ekka MK, Mittal M, Singh AK, Kumaran S.
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specificity of the virulence-associated response regulator from *Mycobacterium tuberculosis*.
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- 22) Aneja R, **Datt M**, Singh B, Kumar S, Sahni G.
Identification of a new exosite involved in catalytic turnover by the streptokinase-plasmin
activator complex during human plasminogen activation.
J Biol Chem. 2009 Nov 20;284(47):32642-50.
- 23) Yadav S, **Datt M**, Singh B, Sahni G.
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site-specific mutagenesis.
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enzyme activity.
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mesophile protein through structure-guided 'protein surface grafting'.
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References

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