# Prasun Kumar

## **Present Address**

Assistant Professor Department of Biological Sciences and Engineering Indian Institute of Technology Palakkad, Kerala E-mail: <u>pk@iitpkd.ac.in</u>, <u>prasun30@gmail.com</u>

#### **Professional Appointments**

| Oct 2024–<br>present   | Assistant Professor<br>Department of Biological<br>Sciences and Engineering<br>IIT, Palakkad             |
|------------------------|--|
| Dec 2023 –<br>Oct 2024 | Senior Bioinformatics Person<br>T-Therapeutics Ltd.<br>Cambridge, UK                                     |
| Jan 2017 –<br>Nov 2023 | Postdoctoral Research Associate<br>Department of Chemistry<br>University of Bristol<br>Bristol, UK       |
| Education              |  |
| Aug 2011–<br>Jun 2016  | Ph.D. in Computational Biology, Molecular Biophysics Unit, Indian Institute of Science, Bangalore, India |

Aug 2005– B.Tech. in Bioinformatics, SASTRA University, Thanjavur, India

#### **Publications**

May 2009

#### Research Publications in Journals

- An atlas of protein homo-oligomerization across domains of life. H. Schweke, T. Levin, M. Pacesa, C. A. Goverde, <u>P. Kumar</u>, et al, (2024) *Cell*, 187, 999-1010.
- CC+: A Searchable Database of Validated Coiled coils in PDB Structures and AlphaFold2 Models. <u>P. Kumar\*</u>, R. Petrenas, W.M. Dawson, H. Schweke, E.D. Levy and D. N. Woolfson\*, (2023) *Protein Science*, e4789.
- De novo design of discrete, stable 3<sub>10</sub>-helix peptide assemblies. <u>P. Kumar</u>\*, N.G. Paterson, J. Clayden and D. N. Woolfson\*, (2022) *Nature*, 607, 387–392.
- Socket2: A Program for Locating, Visualising, and Analysing Coiled-coil Interfaces in Protein Structures. <u>P. Kumar</u>\* and D. N. Woolfson\*, (2021) *Bioinformatics*, 37, 23, 4575–4577.
- RNAHelix: computational modeling of nucleic acid structures with Watson-Crick and non-canonical base pairs. D Bhattacharyya, S Halder, S Basu, D Mukherjee, <u>P. Kumar</u> and M.Bansal, (2017) *JI of Computer-Aided Molecular Design*, 1–17.
- 6. Identification of structural and functional analyses of PolyProline-II helices in globular proteins. **P. Kumar** and M.Bansal, (2016) *JI of Structural Biology*, 196, 3, 414–425.

- Dissecting π-helices: Sequence, Structure and Function. <u>P. Kumar</u> and M.Bansal, (2015) *FEBS Journal*, 282, 22, 4415–4432.
- Identification of local variations within secondary structures of proteins. <u>P. Kumar</u> and M.Bansal, (2015) *Acta Crystallographica Section D* 71, 5, 1077–1086.
- MolBridge: A program for identifying non-bonded interactions in small molecules and biomolecular structures. <u>P. Kumar</u>, S. Kailasam, S. Chakraborty and M. Bansal (2014) *J Appl Crystallogr* 47, 5, 1772–1776.
- 10. HELANAL-Plus: a web server for analysis of helix geometry in protein structures. <u>P.</u> <u>Kumar</u> and M.Bansal, (2012) *J Biomol Struct Dyn.*, 30,773–783.
- Identification, Activity and Disulfide connectivity of C-di-GMP Regulating proteins in M. tuberculosis. K. Gupta, <u>P. Kumar</u> and D. Chatterji, (2010) *PLoS ONE* 5, e15072.

### > Chapters in Books

- 1. Biomolecular Structures: Prediction, Identification and Analyses. <u>P. Kumar</u>, S. Halder and M. Bansal in Reference Module in Life Sciences, 2019, Vol 3, pp. 504–534.
- Defining α-helix geometry by Cα atom trace vs (φ-ψ) torsion angles: a comparative analysis. A. Shelar<sup>#</sup>, <u>P. Kumar<sup>#</sup></u> and M.Bansal in 'Biomolecular Forms and Functions' (Ed. M. Bansal and N.Srinivasan) IISc, Bangalore, 2013, pp.116–127.

#### \* corresponding author #both authors contributed equally Google Scholar Citations: 400 (as of October 2024)

#### **Technical Skills**

- Computational Skills
  - 1. Programming/Scripting: Perl, Python, Fortran77, R, C++
  - 2. Data analysis & Statistics: R, MATLAB, Python
  - 3. AI/ML based approach to design proteins
  - 4. Domain expertise: Protein design and engineering, Protein structure modeling, homology modeling, binding site analysis, function prediction, protein-protein interaction, sequence analysis
  - 5. Web development: HTML, CSS, CGI, JavaScript
  - 6. Software tools: AI based protein structure prediction tools like AlphaFold, Modeller, Rosetta, OpenBabel, NCBI tools and databases, CCP4 suite, Phenix
  - 7. Databases & OS: MySQL, Postgres, MongoDB, Linux, Mac
- Wet lab Skills
  - 1. Solid phase peptide synthesis
  - 2. HPLC
  - 3. Biophysical characterization: Circular Dichroism, Analytical Ultracentrifugation, SEC
  - 4. X-ray crystallography

#### Teaching & Mentoring Experience

- 2022 Mentored MSci student for his final year project.
- 2012 & 2013 Teaching Assistant for "Structural Bioinformatics" course in the Molecular Biophysics Unit department at Indian Institute of Science

#### Grants, Fellowships & Honors

- 2022 Travel award from "Generate: Biomedicine" for attending "8<sup>th</sup> Alpbach Workshop on Coiled-coil, Fibrous and Repeat Proteins", Alpbach, Austria
- 2015 Best Poster Prize for the poster titled "Intrinsic variations in the structures of spacer regions can critically influence the transcription" in MBU In-House symposium, IISc, Bangalore, India
- 2014 International Travel Support Grant from Department of Science and Technology, Government of India to attend Modeling of Biomolecular Systems Interactions, Dynamics, and Allostery: Bridging Experiments and Computations, Istanbul, Turkey
- 2013 Awarded Senior Research Fellowship (SRF) by the DBT-BINC
- 2011 Secured 97.8 percentile in the Graduate Aptitude Test in Engineering
- 2010 Awarded Junior Research Fellowship (JRF) by the DBT-BINC
- 2009 Secured AIR-9 in DBT-BINC examination
- 2008 Awarded Indian academy of science fellowship.
- 2005—2009 Dean's list, SASTRA University

#### Conferences & Symposia

#### Oral Presentations

- Socket2 and CC<sup>+</sup> 2022: Bioinformatics resources for assigning and analyzing coiled-coil structures and models. 8<sup>th</sup> Alpbach Workshop on Coiled-coil, Fibrous and Repeat Proteins, Alpbach, Austria (2022)
- 2. A de novo designed 3<sub>10</sub>-helical bundle. Focal Point organized by school of biochemistry, University of Bristol, Bristol, UK (2021)
- 3. Identification of local variations within secondary structures of proteins. MBU In-House symposium, IISc, Bangalore, India (2015)
- 4. Do not Call Me  $\alpha$ , I am  $\pi$ -helix. Humboldtkolleg on Interdisciplinary Science: Catalyst for Sustainable Progress, NIAS Auditorium, IISc Campus, Bangalore, India (2014)

#### Poster Presentations

- Constructing synthetic-peptide assemblies from de novo designed 3<sub>10</sub> helices. 8<sup>th</sup> Alpbach Workshop on Coiled-coil, Fibrous and Repeat Proteins, Alpbach, Austria (2022)
- 2. Peptides to proteins: Computational Design of a De Novo Three-helix Bundle. Synthetic Biology UK 2018, Bristol, UK (2018)
- 3. Do not Call Me  $\alpha$ , I am  $\pi$ -helix. EMBO Practical Course CEM3DIP 2016, Thiruvananthapuram, India (2016)
- 4. Identification of local variations within secondary structures of proteins. MBU In-House symposium, IISc, Bangalore, India (2015)
- Do not Call Me α, I am π-helix. Modeling of Biomolecular Systems Interactions, Dynamics, and Allostery: Bridging Experiments and Computations, Istanbul, Turkey (2014)

- 6. Intrinsic variations in the structures of spacer regions can critically influence the transcription. Modeling of Biomolecular Systems Interactions, Dynamics, and Allostery: Bridging Experiments and Computations, Istanbul, Turkey (2014)
- Amino acid distribution in 3<sub>10</sub>-helices and their significance for helix stabilization. International Conference on Biomolecular Forms and functions (ICBFF): A celebration of 50 years of the Ramachandran map", Bangalore, India (2013)
- 8. ASSIGN-A program for assigning regular secondary structure in the protein. 7th Asian Biophysics Association (ABA) Symposium, New Delhi, India (2011)
- 9. Albumin as a crosslinker in Hydrogels for sustained drug release A Mathematical analysis. XVI International conference of Society for Biomaterials and Artificial Organs, New Delhi, India (2006)

### Flash presentation

1. Constructing synthetic-peptide assemblies from de novo designed 3<sub>10</sub> helices. 8<sup>th</sup> Alpbach Workshop on Coiled-coil, Fibrous and Repeat Proteins, Alpbach, Austria (2022)

#### **Outreach & Administrative Services**

| 2019        | Data Scientist PI: Challenge proposal for Turing Data Study Group organized by Alan Turing Institute between 5 <sup>th</sup> August-11 <sup>th</sup> August                           |
|-------------|---|
| 2018 & 2019 | Organizer: ISAMBARD tutorial at CCPBioSim workshop, University of Bristol, Bristol, UK  |
| 2013        | Organizer: Molecular Biophysics Unit in-house symposium, Indian Institute of Science, Bangalore, India  |
| 2013        | Volunteer: 'International Conference on Biomolecular Forms and Functions<br>(ICBFF): A Celebration of 50 Years of Ramachandran Map', Indian Institute of<br>Science, Bangalore, India |
| 2012        | Volunteer: Indian National Science Academy Annual Meeting, Indian Institute of Science, Bangalore, India  |
| 2010        | Volunteer: 8 <sup>th</sup> Asia-Pacific Bioinformatics Conference, Indian Institute of Science, Bangalore, India  |

#### **Professional Activities**

- Reviewer for >20 manuscripts for journals: BMC Microbiology, Acta Crystallographica Section F, 3Biotech, Frontiers in Genetics, Archives of Microbiology, Computational Biology and Chemistry & Evolutionary Bioinformatics
- Review Editor for Computational Genomics section of Frontiers in Genetics and Protein Bioinformatics section of Frontiers in Bioinformatics

### Scientific Society Membership

2013–present Indian Biophysical Society 2018–present Biochemical Society