

## Kanchan Anand

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**Current Position:** Research Fellow in the Structural and Computational Biology Unit at the European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany

**Education:** Ph.D. in Macromolecular Crystallography (structure determination and analysis of coronavirus main proteinases) from the Friedrich-Schiller University of Jena in Germany

**Non-scientific Interests:** Family, music, cooking

I was born and raised in India and moved to Germany to pursue my Ph.D. in the group of Professor Hilgenfeld at the University of Jena (currently at University of Luebeck, Germany). During my doctorate thesis, I solved the structure of coronavirus main proteinase, a structure much awaited at the time of the SARS epidemic in 2003. After receiving my Ph.D, I joined Sanofi Aventis in Frankfurt, Germany, where I crystallized and solved the structure of Thrombin Activable Fibrinolysis Inhibitor (TAFI), a highly unstable metalloprotease that stabilizes blood clots. This work promoted the understanding of the instability of the mature enzyme and also helps to predict its ligands.

In order to continue my research interest in virology, I moved to a structural biology group at EMBL-Heidelberg with an EMBO long-term fellowship. Presently, I am working on structure determination and analysis of HIV Cyclin T1-Tat-TAR-Cdk9 complex. I am currently supported by a Marie Curie individual fellowship.

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**Read Dr. Anand's article entitled:** The Crystal Structure of Thrombin-activable Fibrinolysis Inhibitor (TAFI) Provides the Structural Basis for Its Intrinsic Activity and the Short Half-life of TAFIa

<http://www.jbc.org/cgi/content/full/283/43/29416>