Anat Zvi
Curriculum Vitae

Education

1986 - 1989	Ben Gurion University, Beer Sheva, Israel, Faculty of Chemistry. B. Sc. Degree in Biophysical Chemistry, January 1990.
1990 - 1992	M. Sc. student at the Feinberg Graduate School of the Weizmann Institute of Science, Rehovot, Israel, Faculty of Chemistry, Department of Structural Biology. Subject of my thesis: *2D-NMR Studies of the Solution Conformation of an HIV Peptide and Its Interactions with a Virus Neutralizing Antibody.* Supervisor: Prof. Jacob Anglister. M. Sc. Degree in Chemistry, May 1992.
1992 -1998	Ph. D. student at the Feinberg Graduate School of the Weizmann Institute of Science, under the Supervision of Prof. Jacob Anglister. Topic of Research: *NMR Studies of an HIV-1 Peptide in Complex with an Anti-gp120 Neutralizing Antibody: Structure and Interactions*. Ph. D. Degree in Chemistry, December 1998.

Employment (2000-present)

Researcher in Bioinformatics at the Department of Biochemistry & Molecular Genetics,
Israel Institute for Biological Research (IIBR), Ness Ziona, Israel.
Current position: Equivalent to Associate Professor, Head of the Bioinformatics Facility at IIBR.

Research activities

- Research of HIV antigen-antibody complexes by high-resolution NMR.
- Establishment and heading of a bioinformatics infrastructure for large scale analysis of microbial genomes.
- Support of various research activities in different aspects of bioinformatics, immunoinformatics, functional genomics, proteomics and various applications of next generation sequencing.
- Analyses of whole microbial genomes, identifying genes of interest for vaccine design, diagnostics and various aspects of pathogenesis.
- Development and application of novel computational strategies for mapping hotspots of T-cell epitopes in microbial genomes and

identification of determinants involved in the cellular-based immune and protective response.

- Analyses of Next-generation sequencing data of B-cell receptor libraries, employing computational tools for investigation of population structure and differential repertoire profiling.

Applications: Genome-based rational reductive strategy aimed at identification of novel *Bacillus anthracis* vaccine candidates (Reverse Vaccinology). Application of computational strategies toward characterization of virulence factors as well as vaccine candidates in *Yersinia pestis*. Data mining, bioinformatic and immunoinformatic analyses of *Francisella tularensis* Schu S4 genome in search for novel vaccine candidates. Whole-genome immunoinformatic analysis of *Mycobacterium tuberculosis* towards large scale identification of immunodominant CTL epitopes. Whole-genome immunoinformatic analysis of *Francisella tularensis* in search for CTL and Th epitopes. Whole-genome immunoinformatic analysis of *Yersinia pestis* in search for CTL epitopes. Bioinformatic analysis of large-scale B-cell immunoglobulin repertoire sequencing data generated from rhesus-vaccinated with ricin.