**Brian E. Saunders**

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**SUMMARY**

* **Over 15 years of experience with biological sequence analysis and biological databases**
* **Extensive experience in relational database design and management**
* **Highly motivated, rigorous and detail-oriented bioinformatics programmer**
* **Recognized as an outstanding, efficient, dependable, self-starter with strong work ethic**
* **Proven strong leadership and project management, consistently achieving objectives**
* **Excellent communication combined with strong analytical and problem solving skills**

**PROFESSIONAL EXPERIENCE**

**Project Leader and Bioinformatics Analyst, UCSD Signaling Gateway 2006 – 2014**

**University of California, San Diego (UCSD) - San Diego Supercomputer Center**

Headed UCSD Signaling Gateway Molecule Page Project (<http://www.signaling-gateway.org>).

Duties: Sequence analysis, public database mining, supervision and coordination of a multi-disciplinary team, relational database design, curation, and management.

* Designed, implemented and optimized automated data annotation pipeline
* Annotated over 4,000 cell signaling genes in the Signaling Gateway [Molecule Pages](http://www.signaling-gateway.org/molecule/) database
* Mined annotations from over a dozen public biological databases (Genbank, ENSEMBL, EntrezGene, UniProt, GO, PRINTS, PFAM, InterPro, BIND, Homologene, etc.)
* Developed algorithms for tracking any given gene across multiple varied databases, with different formats and nomenclatures
* Integrated the results of sequence analysis software (e.g. BLAST) with public biological database cross-references
* Developed and maintained a complex Perl pipeline for automated mirroring, extracting and parsing of external database information
* Designed and curated a complex Oracle schema with nearly a hundred tables with hundreds of thousands of data rows for storing the Signaling Gateway Molecule Page data
* Developed and optimized automatic database loading scripts for Oracle relational database
* Served an instrumental role in the peer-reviewed electronic publication of over 700 Molecule Pages in the Nature Publishing Group
* Drastically improved the speed of returning Molecule Page query results through optimization of highly complex SQL queries and Oracle database tables

**Bioinformatics Analyst, Alliance for Cellular Signaling 2001 – 2006  
University of California, San Diego (UCSD) - San Diego Supercomputer Center**  
Duties: Provided bioinformatics customer support to the Alliance for Cellular Signaling (AfCS), a multi-team effort from different leading universities and research centers.

* Worked with multi-disciplinary teams of laboratory scientists and computer programmers to design tools for experimental data analysis
* Developed sequence analysis pipelines to annotate Agilent microarray chips
* Developed a clustering algorithm that was crucial in identifying novel signaling proteins
* Developed Perl scripts for automated PCR primer and plasmid design for signaling genes
* Developed scripts for restriction digestion analysis
* Designed annotation mechanisms, clustering analysis, and custom relational database schema for yeast 2-hybrid experimental data

**Programmer Analyst, Biology Workbench 1999 – 2001**  
**University of California, San Diego (UCSD) - San Diego Supercomputer Center**  
Development, operation, and maintenance of an integrated web-based software tool for biologists (<http://workbench.sdsc.edu>).

* Developed a user-friendly, powerful web-based software for sequence analysis with easy-to-use, point-and-click interface
* Integrated dozens of sequence analysis tools and biological databases, utilizing CGI/Perl scripts
* Managed account system with over 100,000 users

**SKILLS**

* **Programming languages: Perl, HTML, SQL, XML, C, R, Shell**
* **Operating systems: UNIX, Windows, Linux, Mac**
* **Servers and Interfaces: Perl DBI , CGI/Perl, CVS, TOAD, Oracle, Apache**
* **Bioinformatics tools: BLAST, ClustalW, MAFFT, MUSCLE, HMMPFAM, FingerPRINTScan, PRIMER3, InterProScan, Bowtie2, BWA, SAMtools suite, Picard, FastQC**
* **Public databases: Genbank, Entrez Gene, UniProt, UniGene, Homologene, GO, ENSEMBL, PFAM, InterPro, PRINTS, BIND, IntACT**

**EDUCATION**

**Ph.D. Chemical Engineering, University of Wisconsin-Madison Dec 1996**

**B.S. Chemical Engineering, Purdue University May 1990**

**PUBLICATIONS**

Dinasarapu AR, Saunders B, Ozerlat I, Azam K, Subramaniam S. Signaling gateway molecule pages--a data model perspective. Bioinformatics. 2011 Jun 15;27(12):1736-8.

Saunders B, Lyon S, Day M, Riley B, Chenette E, Subramaniam S, Vadivelu I. The Molecule Pages database. **Nucleic Acids Res.** 2008 Jan;36(Database issue):D700-6.

Zavzavadjian JR et al. The alliance for cellular signaling plasmid collection: a flexible resource for protein localization studies and signaling pathway analysis. **Mol Cell Proteomics**. 2007 Mar;6(3):413-24.

Lee JA et al. Components of the antigen processing and presentation pathway revealed by gene expression microarray analysis following B cell antigen receptor (BCR) stimulation. **BMC Bioinformatics**. 2006 May 2; 7:237.

Cotter D, Maer A, Guda C, Saunders B, Subramaniam S. LMPD: LIPID MAPS proteome database. **Nucleic Acids Res.** 2006 Jan 1;34(Database issue):D507-10.

Maer A, Saunders B, Unwin R, Subramaniam S. Chapter 9: Biology Workbenches in **Databasing the Brain: From Data to Knowledge (Neuroinformatics)** (eds Koslow S & Subramaniam S) 153-165 (Wiley, Hobken, NJ, 2005).

Zhu X et al. Analysis of the major patterns of B cell gene expression changes in response to short-term stimulation with 33 single ligands. **J Immunol**. 2004 Dec 15;173(12):7141-9.

Li J, Ning Y, Hedley W, Saunders B, Chen Y, Tindill N, Hannay T, Subramaniam S. The Molecule Pages Database. **Nature**. 2002 Dec 12;420(6916):716-7.