

# ***Quantifying the Benefits of Exposure to Superstar Scientists***

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# ***Why focus on superstars?***

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- ***Pragmatic: superstar scientists leave trails that researchers can audit, “humdrum” scientists do not***
- ***Substantive: the “ortega hypothesis”***

# ***Two types of spillovers***

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- ***Spillovers to other scientists, through collaboration***
  - *“Superstar Extinction” with Jialan Wang, NBER WP #14577*
  
- ***Spillovers to Firms, through co-location***
  - *“Spillovers from Academia onto Industry: Evidence from Professional Transitions for the Superstars of Medicine” with Aruna Ranganathan and Bhaven Sampat*

# ***Project Contribution I: Better Data***

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- ***Superstar dataset, n=10,449***
- ***AAMC Roster, n=250K scientists over 30 years***
- ***USPTO Non-patent prior art match with PubMed***

# ***Article to Patent Match***

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## ➤ ***Start from a Patent...***

United States Patent  
Li, et al.

6,867,006  
March 15, 2005

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Antibodies to human chemotactic protein

### **Abstract**

A human chemotactic polypeptide, DNA (RNA) encoding it, and a procedure for producing such a polypeptide by recombinant techniques are disclosed. Also disclosed are methods of using the polypeptide for a number of purposes, including: stem cell mobilization, myeloprotection, neuronal protection, treating tumors, wound healing, treating parasitic infection, and regulating hematopoiesis. Also disclosed are polypeptide antagonists and diagnostic assays for identifying mutations in nucleic acid sequence encoding a polypeptide of the present invention and for detecting altered levels of the polypeptide of the present invention for detecting diseases are also disclosed.

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Inventors: **Li; Haodong** (Gaithersburg, MD), **Ruben; Steven M.** (Olney, MD), **Sutton, III; Granger** (Columbia, MD)

Assignee: **Human Genome Sciences, Inc.** (Rockville, MD)

Appl. No.: **10/141,965**

Filed: **May 10, 2002**

# ***Article to Patent Match [Cont'd]***

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- ***The usual approach to quantifying spillovers***
  - *Look at the other patents that cited by this patent*

## References Cited [\[Referenced By\]](#)

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	U.S. Patent Documents	
<a href="#">5179078</a>	January 1993	Rollins et al.
<a href="#">5237051</a>	August 1993	Garbers et al.
<a href="#">5350836</a>	September 1994	Kopchick et al.
<a href="#">5382658</a>	January 1995	Kronis et al.
<a href="#">5459128</a>	October 1995	Rollins et al.
<a href="#">5866373</a>	February 1999	Li et al.
<a href="#">5880263</a>	March 1999	Li et al.
<a href="#">6028169</a>	February 2000	Kreider et al.
<a href="#">6075124</a>	June 2000	Li et al.
<a href="#">6100389</a>	August 2000	Li et al.
<a href="#">6174995</a>	January 2001	Li et al.
<a href="#">6379926</a>	April 2002	Kreider et al.
<a href="#">6419917</a>	July 2002	Li et al.

# ***Article to Patent Match [Cont'd]***

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## ➤ ***Our (better, we think) approach***

- *Look at non-patent prior art cited by this patent*

### **Other References**

Beall, C.J., et al., "Conversion of Monocyte Chemoattractant Protein-1 into a Neutrophil Attractant by Substitution of Two Amino Acids," J. Biol. Chem. 267:3455-3459, American Society for Biochemistry and Molecular Biology, Inc. (1992). .

Berkhout, T.A., et al., "Cloning, in Vitro Expression, and Functional Characterization of a Novel Human CC Chemokine of the Monocyte Chemotactic Protein (MCP) Family (MCP-4) That Binds and Signals through the CC Chemokine Receptor 2B," J. Biol. Chem. 272:16404-16413, American Society for Biochemistry and Molecular Biology, Inc. (Jun. 1997). .

Bischoff, S.C., et al., "Monocyte Chemotactic Protein 1 Is a Potent Activator of Human Basophils," J. Exp. Med. 175: 1271-1275, Rockefeller University Press (1992). .

Bowie, J.U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," Science 247:1306-1310, American Association for the Advancement of Science (1990). .

# ***Article to Patent Match [Cont'd]***

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## ➤ ***Match the strings...***

### **Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions**

JAMES U. BOWIE,\* JOHN F. REIDHAAR-OLSON, WENDELL A. LIM,  
ROBERT T. SAUER

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An amino acid sequence encodes a message that determines the shape and function of a protein. This message is highly degenerate in that many different sequences can code for proteins with essentially the same structure and activity. Comparison of different sequences with similar messages can reveal key features of the code and improve understanding of how a protein folds and how it performs its function.

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specific positions in a cloned gene and uses selections or screens to identify functional sequences. This approach has been used to great advantage for proteins that can be expressed in bacteria or yeast, where the appropriate genetic manipulations are possible (3, 8-11). The end results of both methods are lists of active sequences that can be compared and analyzed to identify sequence features that are essential for folding or function. If a particular property of a side chain, such as charge or size, is important at a given position, only side chains that have the required property will be allowed. Conversely, if the chemical identity of the side chain is unimportant, then many different substitutions will be permitted.

- ***James Bowie (UCLA, was Sauer's postdoc) and Robert Sauer (MIT) are two of our superstars***
- ***This article is cited in 1,375 distinct patents...the most of any open science paper***

# ***Project Contribution II: Open Source Software Tools***

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- ***PubHarvester***  
*(<http://www.stellman-greene.com/PublicationHarvester/>)*
  
- ***SC/Gen***  
*(<http://stellman-greene.com/SCGen/>)*
  
- ***SciDist***  
*(<http://www.stellman-greene.com/ScientificDistance/>)*

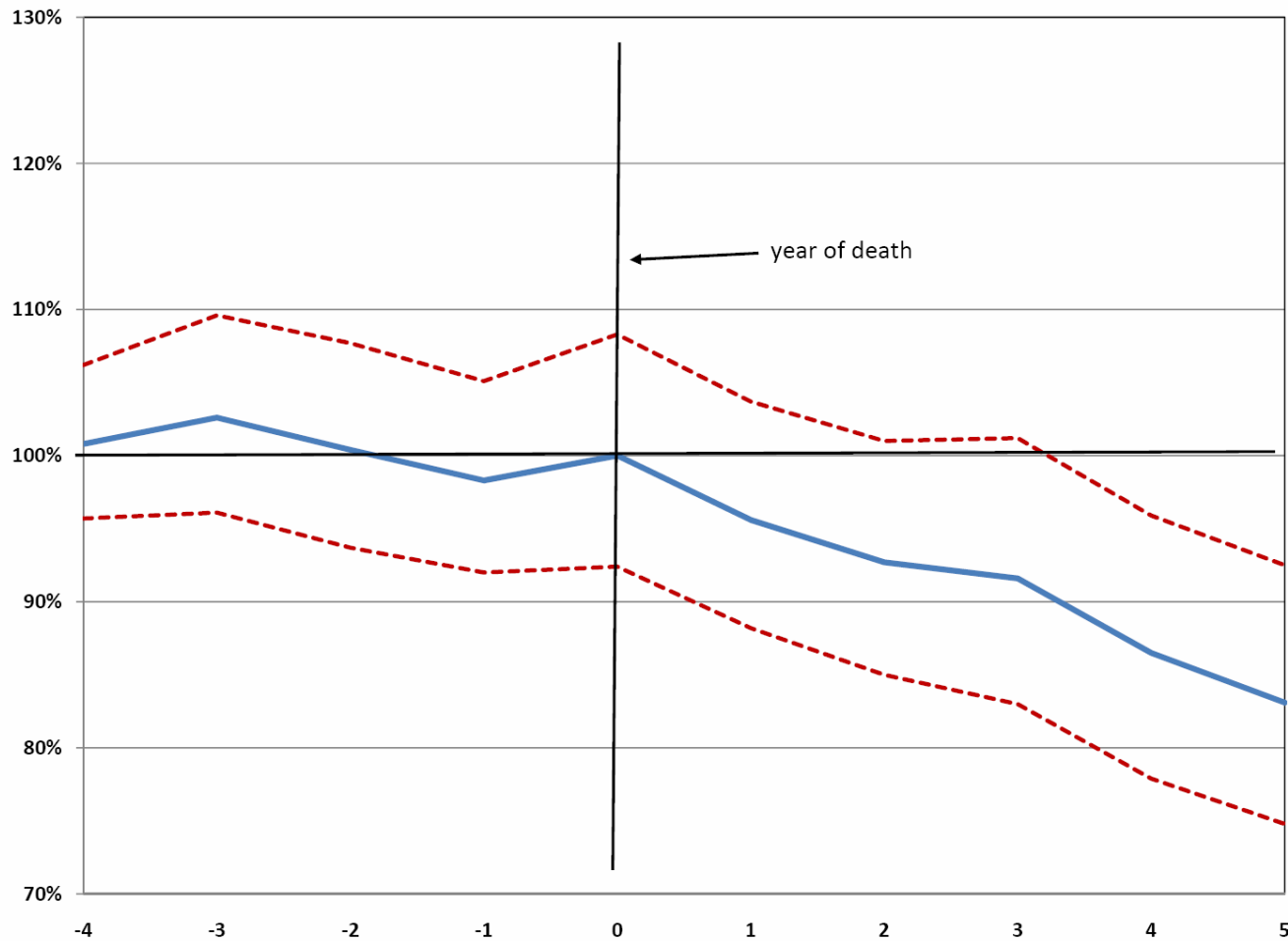
# ***Project Contribution III: Exploiting Natural Experiments***

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- ***Premature death (Project I)***
  
- ***Age of children (Project II)***

# *Superstar Extinction as Shock to Coauthor's Collaboration Network*

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# Age of Kids as Instrument for Superstar Mobility

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