

# Generation of potential drugs *in silico*

Section for  
bioinformatics



Daslav Hranueli

# *Project team:*



**Ana Vukelić**  
**Antonio Starčević**  
**Janko Diminić**  
**Jurica Žučko**

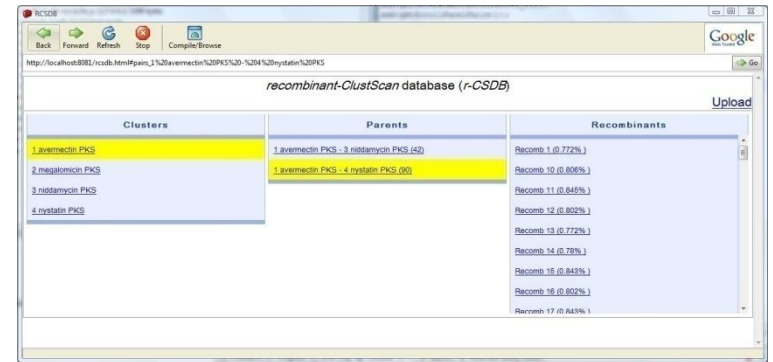





**Prof. John Cullum**  
**Students**



**School of Pharmacy**  
*University of London*  
**Dr. Paul F. Long**  
**Students**


# Programs, databases and Web portal developed:



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# *Scientific papers and patent application*

- **Published: 6 papers (4 in CC journals; 1 in 2009)**
- **In press: 2 (in CC journals)**
- **In preparation: 3 (planned for CC journals)**
- **Patent application submitted (PCT)**

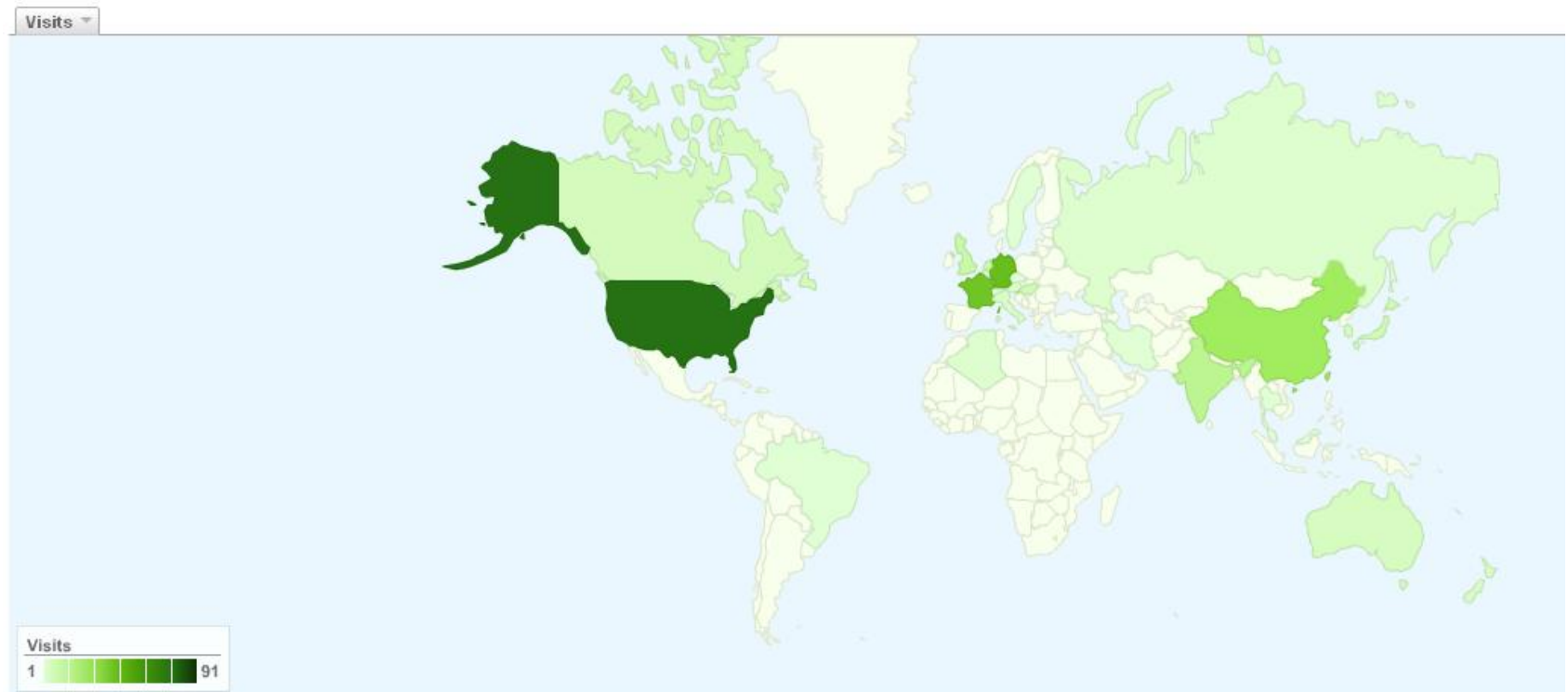
*Remains to be done:*

In collaboration with the: "Université des Sciences et Technologies de Lille"

**Development of *Norine* dedicated *ClustScan* and *CSDB***

# *Is it any good ?*

- Ten month after the publication of *ClustScan* paper (Starcevic *et al.*, *Nucleic Acids Res.*, 36, 6882-6892, 2008.) - 69 potential users have downloaded the program package
- 359 visitors from 29 countries have visited the Web portal

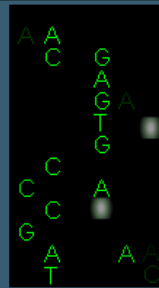


**359 visits came from 29 countries/territories**

Filtered for countries/territories excluding "Croatia"

# Is it any good ?

- 412 visitors have looked at *ClustScan* tutorial



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### News

Dec 2, 2008

[ClustScan paper published](#)

### Download

[Registration](#) - first you have to registrate in order to use ClustScan.

Requires minimally Java 5 installed on your local machine.

Download [Java JRE](#).

**Platforms Supported:** Windows Win2k/WinXP/Vista, Linux, OS X, Solaris nad AIX.

**Minimum:** 700 MHz Pentium or G4, 512 MB RAM

**Recommended:** 2.0 GHz or faster Core 2 Duo, 1024 or more MB RAM

Downloads:

- [ClustScan linux](#)
- [ClustScan windows](#)
- [ClustScan Mac OS](#)
- [ClustScan solaris motif](#)

# *Invitations:*

- **Book chapter:**

Frans J. de Bruijn (Ed.)

**Handbook of Molecular Microbial Ecology I:  
Metagenomics and Complementary Approaches**

- **Review article:**

Editor-in-Chief Satya P. Gupta, Professor

**CURRENT COMPUTER-AIDED DRUG DESIGN**

## *Future planning:*

- **Development of systems for the semi-automatic annotation of new microbial and human genomes**
  - [Development of *TAGS* (*T*ool for the *A*nalysis of *G*enome *S*equences)]
  - [Development of *GenTell* (*G*enome *I*n*T*elligence)]



# *Project team:*



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