

Bioinformatics Services for Systems Biomedicine

and

Computational molecular and systems approaches to identify disease-related SNPs

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LSCB bioinformatics Core facility

- Daily updated In-house repository of approx. 100 public domain databases (~10TByte)
- Data-integration and data handling
- Automatic pipelines for large scale data-analysis
- Network (re-)construction
- Large scale visualization tools for heterogeneous data
- Text-mining using large scale full-text corpora
- Setup and maintenance of Scientific Collaboration Web-portals
- IT-Infrastructure (2011): access to 1400 cores with 480 TeraByte of storage, expected to grow significantly over the next years

Setup of Scientific Collaboration Portals

TAMAHUD
Bioinformatics data analysis

SienaBiotech | University of Cambridge | TCP Innovations Limited | BioAlma | European Molecular Biology Laboratory

EMBL Bio-IT
The Portal for Computational Biology

Search...

FAQS WHO WE ARE CONTACTS NETWORK

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Resources

- Databases
 - Local Database Copies
 - SRS
- Linux Tools and Applications (BCR)
- Computing Resources
- R/Bioconductor Packages
- Image Processing and Analysis
- Group Services
- EMBL Centres
- Programming E-Books
- External Links

INTRODUCTION TO DATABASES

Bioinformatics and computational biology make extensive use of a wide range of publicly-available databases and data resources. This page provides links to a set of bioinformatics database resources, some of which are accessible only within EMBL, others of which are accessible also externally.

Local Databases - Programatic/Command-Line Access

Raw/Fast-File

Some/many public databases are relatively large (for example, GenBank 183.0, released in April 2011, contains 183,000 sequences); downloading and keeping such resources up-to-date takes considerable time and resources. However, through the effort required to obtain access this data is considerably reduced through the efforts of the Schneider Group. They have downloaded the data from a wide range of such databases, and make them available on the central shared EMBL file server in the /g/data directory. The Local Databases pages of this portal describe in more detail the resources available, and provide information on how you can access them.

Note that the files downloaded by the Schneider Group are the raw, often flat-file, versions of these databases - Local Databases - Programatic/Command-Line Access. We also provide complete alternative versions of the web servers that many of the "authors" of these databases provide to enable easier access to the data.

Sequence Retrieval System (SRS)

Chaetomium thermophilum Portal

About the Portal Features News The Project Members

Welcome to the Frontpage

The C. thermophilum portal hosts the joined project of the Structural and Computational Biology Research Unit of the EMBL-Heidelberg.

C. thermophilum is a thermophilic, filamentous ascomycete and can be isolated from composting plant material.

Resources

- BioCompendium
- Web server
- C. thermophilum sequence
- Literature
- Visualization modules
- Wiki and Blogs
- Document archive

Who's Online
We have 1 guest online

- Knowledge from biological databases
- Orthology Information
- Structural Features
- Pathway Information
- Gene Ontology
- P-P, P-C Interactions
- Chemistry Information
- Gene Expression Information (Previous)
- Gene Expression Analysis
- 254 CENIX primary hits analysis

BCR Linux software repository

Home About

search...

Categories

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- GRAPHICS
- HTS
- INTERNET
- LIBRARIES
- MS
- MULTIMEDIA
- NMR
- OFFICE
- PROGRAMMING
- SCIENCE
- SYSTEM
- TEXT
- UTILITIES
- X-RAY

Packages

ALL

List of all installed packages

Click column headers to sort the table. Click on a package name to display detailed information.

Package	Categories	Description	Updated
SONA	GRAPHICS, SCIENCE	Analysis, rebuilding, and visualization of DNA structures	2007-09-18
Acrobat Reader	GRAPHICS, INTERNET, OFFICE	THE reader for PDF files	2011-07-13
ActivePython	INTERNET, PROGRAMMING, SCIENCE, SYSTEM	The industry-standard Python distribution	2008-04-28
ActiveState TCL	GRAPHICS, INTERNET, MULTIMEDIA, PROGRAMMING, SCIENCE, SYSTEM	Industry-standard Tcl distribution.	2011-04-28
Adxv	SCIENCE, X-RAY	Display protein crystallography X-Ray diffraction data	2010-09-22
Amber	NMR, SCIENCE	A package of molecular simulation programs	2009-08-10
AmberTools	NMR, SCIENCE	Several packages to use independently or with Amber	2009-04-16
Amira	EM, SCIENCE, X-RAY	Visualize and manipulate biomedical data	2010-07-19
APBS	EM, SCIENCE, X-RAY	Numerical solution of the Poisson-Boltzmann equation	2011-07-23
ApE	NMR, SCIENCE	A Plasmid Editor	2010-07-07
Aria	SCIENCE	Automated NOE assignment and NMR structure calculation	2011-05-23
ARPiWARP	SCIENCE, X-RAY	Interpret and improve crystallographic electron density maps	2008-05-09
ATSAS	NMR, SCIENCE	Small-angle scattering data analysis from bio-macromolecules	2011-07-15
AUTO3DEM	EM, SCIENCE	Automated image reconstruction system	2008-07-07
AutoDock	NMR, SCIENCE	A suite of automated docking tools	2010-05-25
Azara	GRAPHICS, SCIENCE	A suite of programs to process and view NMR data	2008-01-08
BioPerl	PROGRAMMING, SCIENCE	A community effort for Perl code which is useful in biology	2011-07-15
Blender	MULTIMEDIA	Free open source 3D content creation suite	2009-07-27
blt	GRAPHICS, INTERNET, MULTIMEDIA, PROGRAMMING, SCIENCE, SYSTEM	BLT is an extension to the Tk toolkit	2007-08-08
Boost Libraries	PROGRAMMING, SYSTEM	Free peer-reviewed portable C++ source libraries	2011-03-01
Bowtie	HTS	an ultrafast, memory-efficient short read aligner	2011-05-06
boft	SCIENCE	A program for filtering 3D maps and applying B-factors	2008-03-11
boon	SCIENCE, X-RAY	Development of software for image and molecular	2011-04-28

Functional analysis of non-coding RNAs

Main Menu

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Resources

- BioCompendium
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Who's Online
We have 1 guest online

Systec: Functional analysis of non-coding RNAs in living cells

The secretory membrane transport ensures the delivery of proteins, lipids and carbohydrates to their proper cellular destinations, and, with this, cellular homeostasis and growth. An elaborate molecular machinery is involved to secure a tight spatial and temporal regulation of the secretory steps, and the basic principles as well as the core protein machinery have largely been elucidated over the last decades. However, this knowledge turned to be insufficient to explain the pathology of numerous human diseases associated with trafficking defects and to develop an effective pharmacological remedy. Therefore, potent high throughput technologies have been implemented with the aim to identify and functionally characterize all components of the secretory membrane trafficking. Indeed, hundreds of proteins were reported, whose role in the secretory processes were not anticipated before. Curiously, many of these proteins turned to be also involved in other cellular functions, thus, stimulating to investigate the secretory membrane trafficking as a crucial part of adaptive cellular responses. [More background](#)

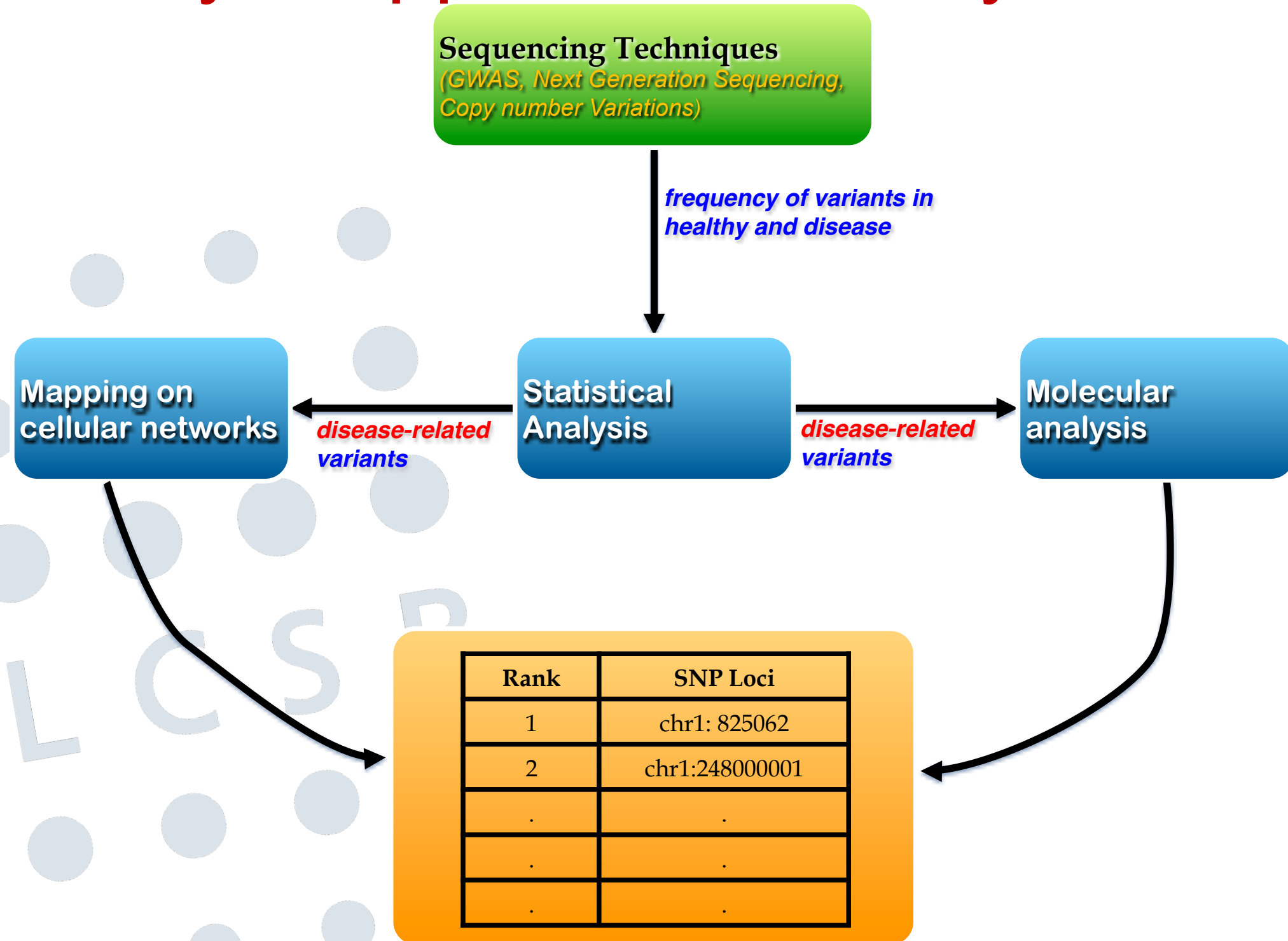
The project "Functional analysis of non-coding RNAs in living cells" has been structured to synergistically complement expertise, technologies and infrastructure that are already established in the VIROQUANT FORSYS center and BIOQUANT. The laboratories of Dr. H. Erbe (RNAi Screening Facility), Dr. L. Kaderali and Dr. V. Stokuvians are recently established research activities in the VIROQUANT/ BIOQUANT and the Excellence Cluster of CellNetworks at the University of Heidelberg and have already well-established collaborations and data exchange practices. The laboratories of Prof. R. Röhre (DKFZ) and Dr. R. Schneider (EMBL) already contribute to the VIROQUANT as described in (S.A. 3.5, 7.1), and have also started collaborations with the above listed partners. The newly integrated academia partner is the laboratory of Dr. A. Mokhr and two industrial partners Graftinity Pharmaceuticals GmbH and Zell-kontakt GmbH. The activities within the project are split into distinct workpackages (WPs) (see 7.1) and will be performed by the partners on a collaborative basis. [Work Packages](#)

Partners:

Setup of Scientific Collaboration Portals

- Access to project data
- Collaboration tools (Blog, wiki, document repository)
- Access to analysis pipelines
- Incorporated visualization tools
- Event calendars
- Projects:
 - TAMAHUD: Target and Markers for Huntington disease (FP6)
 - Systec: non-coding RNA's (BMBF)
 - EMBL Bio-IT portal (consolidation of EMBL Comp-Bio. resources)
 - C. thermophilum: EMBL Structure and Comp.Biol. project
 - Beta-JUDO: Beta-cell function in juvenile diabetes and obesity; FP7-HEALTH

Multilayer approach to study diseases



Projects:

1. COGIE - Complex Genetics of Idiopathic Epilepsies
2. EpiPGX - Epilepsy Pharmacogenomics

Predicting the effect of mutations in proteins

P23946: Chymase precursor
 ... **I**V**T**S**N**G**P**S**K**F**C**G**G**F**L**I**R**R**N**F**V**L**T**A**A****H** **C**A**G**R**S**I**T**V**T**L**G**A**H**N**I**T**E**E**E**D**T**W**Q**K**L**...

His66Arg
 ▼

Sequence alignment

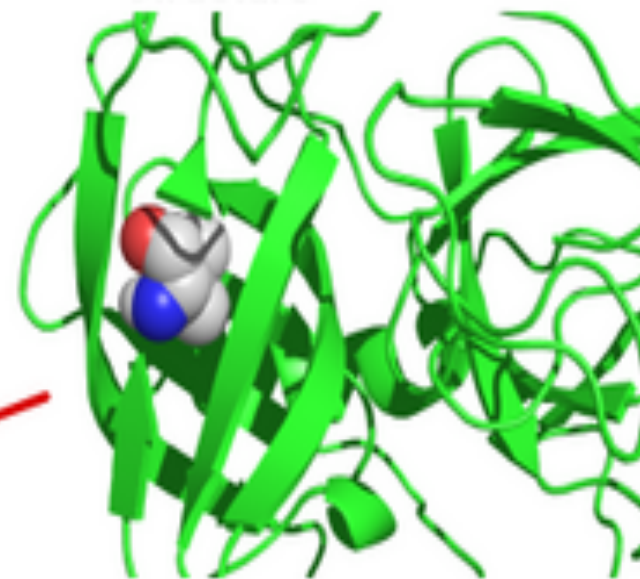
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L A S C G G F L I R R N F V L T A A H C A G R F I M V T L G A H N I Q K K
L A S C G G F L I R R N F V L T A A H C A G R F I M V T L G A H N I Q K K
L A S C G G F L I R R N F V L T A A H C A G R F I M V T L G A H N I Q K K
Q V A C G G F L I R R D F V L T A A H C A G R S V T V T L G A H N I Q K K
    
```

Feature annotation

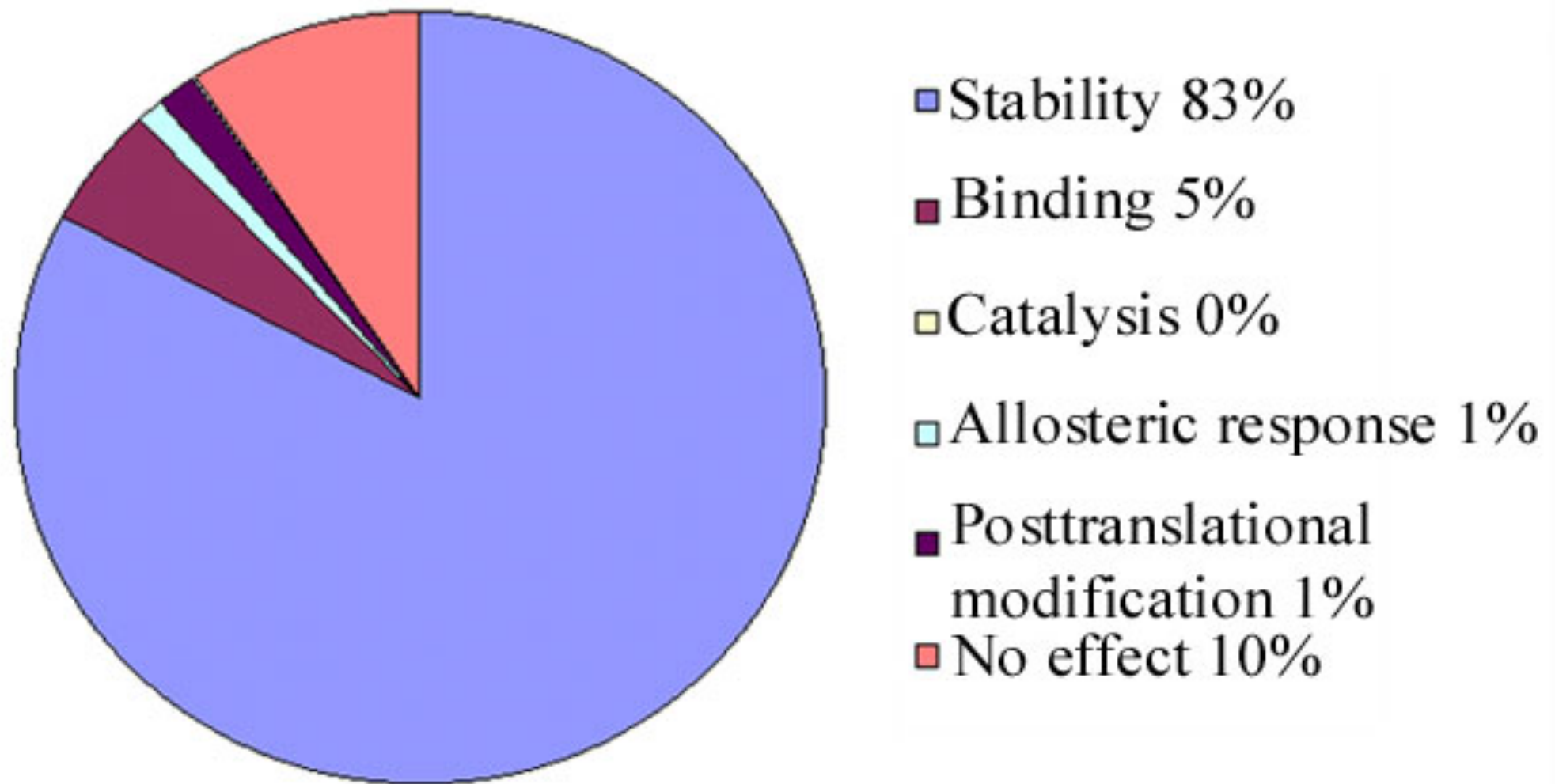
Key	Begin	End	Description
<u>ACT_SITE</u>	66	66	Charge relay system.
<u>ACT_SITE</u>	110	110	Charge relay system.
<u>ACT_SITE</u>	203	203	Charge relay system.

Structure



PREDICTION

Distribution of the Effects of Missense cSNPs on Protein Molecular Function for the *SNP-Disease*



SNP-disease

Higher level maps of GWAS genetic interactions

