



#### In silico docking against malaria: the WISDOM initiative

#### Presented by

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#### Bioinformatics Africa, 31 May 2007, Nairobi

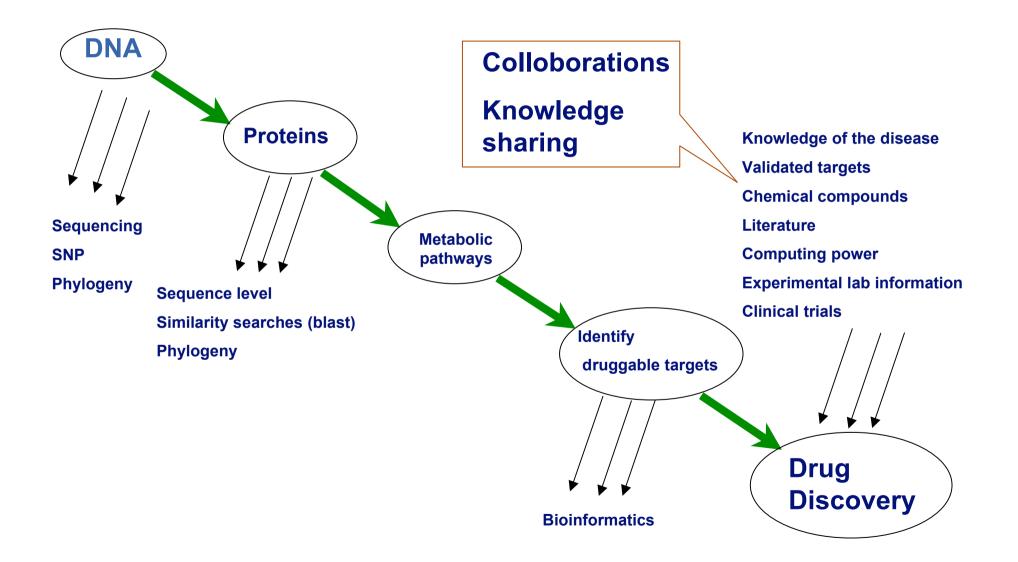




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http://www.itb.cnr.it/bioinfogrid

## **Bioinformatics and Drug discovery**



**BioinfoGRID** 





- Malaria
- Drug discovery and Screening
  - Computational Grids
- WISDOM, Wide In silico Docking on Grid
  - Resources used in Wisdom project
    - Results
    - Issues
    - Conclusions
    - Vision and long term vision

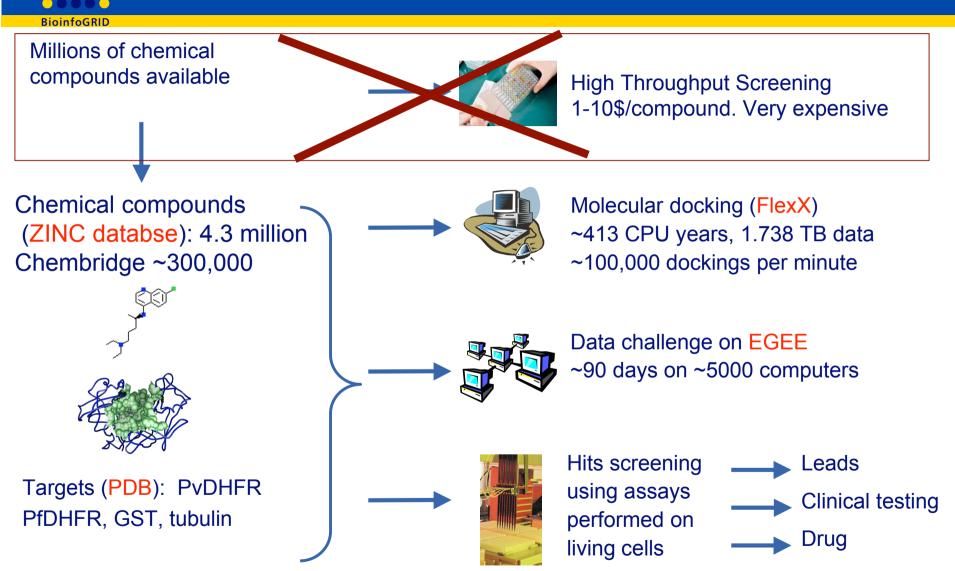


#### Introduction to the disease : malaria

~300 million people • A = Infective Stage 🛕 = Diagnostic Stage Human Liver Stages worldwide are affected Liver cell Infected liver cell REALTHIER PEOPL http://www.dpd.cdc.gov/dpdx Mosquito Stages P Ruptured 0 🛕 oocyst A Mosquito takes 1-1.5 million people a blood meal Exo-erythrocytic Cycle • njects sporozoites) Release of Oocyst sporozoites Ruptured schizont die every year Schizont С Sporogonic Cycle Human Blood Stages Widely spread Immature • trophozoite 10 Ookinete 0 (ring stage) Mosquito takes a blood meal (ingests gametocytes) Macrogametocyte в Caused by protozoan Erythrocytic Cycle • Mature 🙆 trophozoite Microgamete entering macrogamete ( parasites of the genus Rupture Plasmodium Exflagellated echizont microgametocyte Schizont 4 netocytes 🙆 Gametocytes P viva P. ovale P. malariae

#### **Complex life cycle with multiple stages**

### High Throughput Virtual Docking in WISDOM-II







• WISDOM project aims to build a collaboration platform for drug discovery using the Grid computing technology.

 This project intends to solve large-scale computation and data intensive scientific applications in the fields of drug discovery, Bioinformatics and Biology with the help of computational grids

♦ 4.3 million compound database with 3-D structure and physicochemical properties are screened against 4 different targets implicated in malaria to identify potential drug candidates.

➢ In WISDOM-I, on the biological side, three scaffolds have been identified against Plasmepsin and in vitro tests on the best compounds is under process on the best 30 compounds.

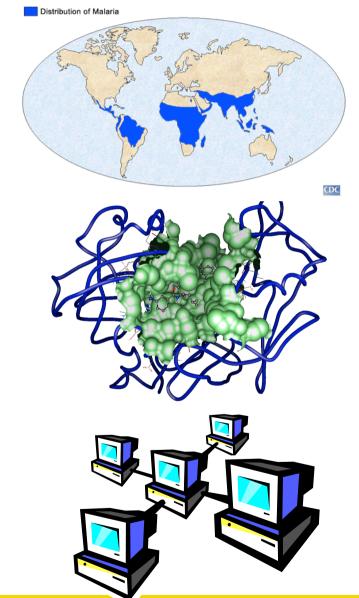
#### WISDOM : Wide In Silico Docking On Malaria

Biological goal

Proposition of new inhibitors for a different proteins produced by Plasmodium

- Biomedical informatics goal Deployment of *in silico* virtual docking on the grid
- Grid goal

Deployment of a CPU consuming application generating large data flows to test the grid operation and services => "data challenge"



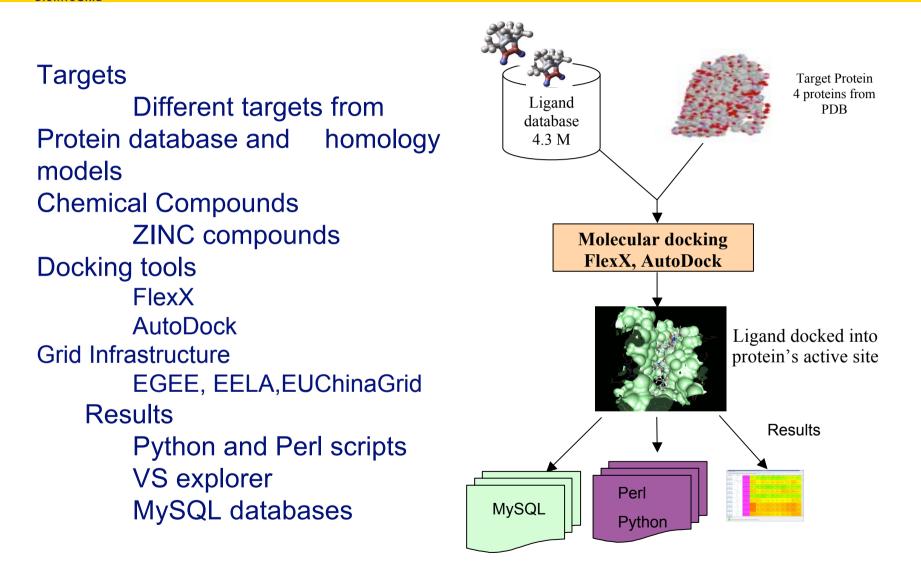


#### WISDOM-II - second large scale docking deployment

| Malaria target                             | Involved in                | Biology partners                                   |
|--|----------------------------|--|
| GST from <i>Plasmodium</i> falciparum      | Parasite<br>detoxification | U. of Pretoria,<br>South-Africa                    |
| DHFR from<br>Plasmodium vivax              | Parasite DNA<br>synthesis  | U. of Los Andes, Venezuela<br>U. of Modena, Italia |
| DHFR from Plasmodium<br>falciparum         | Parasite DNA<br>synthesis  | U. of Modena, Italia                               |
| Tubulin from<br>Plasmodium/plant/<br>mamal | Parasite cell replication  | CEA, Acamba<br>project, France                     |

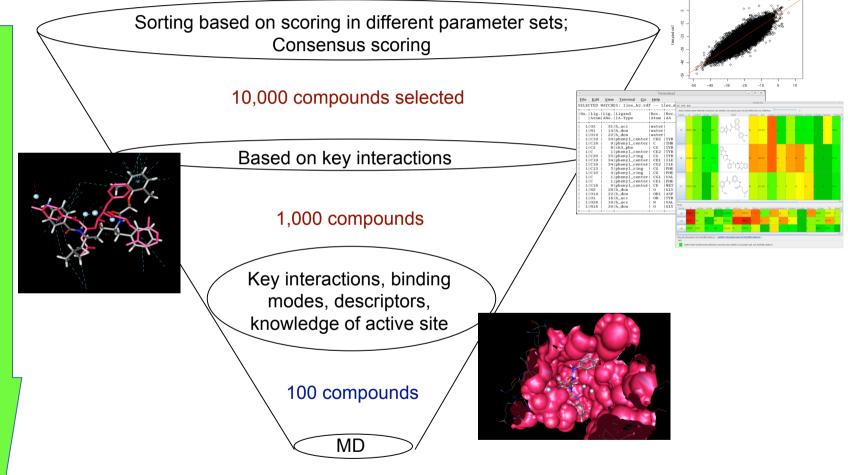


#### Materials and **Procedure** in WISDOM









30 compounds to be tested in experimental lab



 A grid is the combination of networked resources and the corresponding middleware, which provides services for the user

- Grids are unique tools for
  - Collecting and sharing information
  - Networking experts
  - Mobilizing resources routinely or in emergency

## The different kind of grids

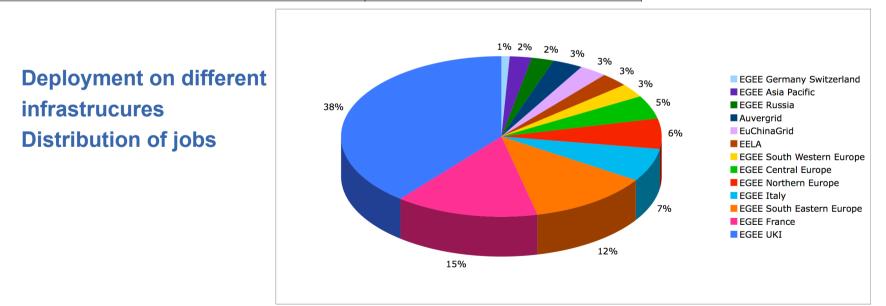
- Computing grid
  - Distributed processors
  - Services to submit jobs, to collect results
  - Impact: in silico search for new drugs or vaccines
- Data grid
  - Distributed data: databases, flat files
  - Services to collect, query, move and analyze the distributed data
  - Impact: collection and sharing of medical data
- Knowledge grid
  - Knowledge space using ontology to manipulate concepts and run complex in silico experiments
  - Impact: integration of "wet" laboratories in a collaboration space



## Instances on different infrastructures

**BioinfoGRID** 

| Target Structures                          | Number of instances deployed |
|--|------------------------------|
|  |                              |
| GST (A chain)                              | 4 on EGEE                    |
| GST (B chain)                              | 4 on EGEE                    |
| 2BL9 (P. vivax wild type DHFR)             | 3 on EGEE, 1 on EELA         |
| 2BLC (P. vivax double mutant DHFR)         | 3 on EGEE, 1 on Auvergrid    |
| Dm_vivax (P. vivax DHFR 2BLC minimized)    | 4 on EGEE                    |
| Wt_vivax (P. vivax DHFR 2BL9 minimized)    | 4 on EGEE                    |
| 1J3K (P. falciparum Quadruple mutant DHFR) | 4 on EGEE                    |
| 1J3I (P. falciparum Wild type DHFR)        | 3 on EGEE, 1 on EuChinaGrid  |
|  |                              |



## BioinfoGRID

## **Statistics of deployment**

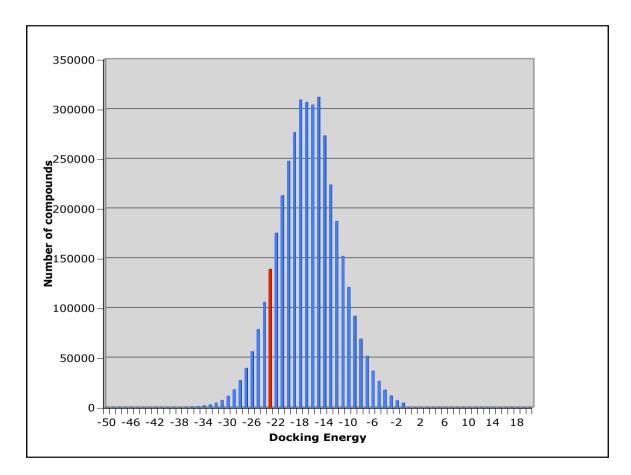
- First DC:
  - 80 CPU years
  - 1 TB
  - 1700 CPUs used in parallel
  - July 1st August 15th 2005
- 2nd DC
  - 100 CPU years
  - 800 GB
  - 1700 CPUs used used in parallel
  - April 1st May 15th 2006
- 3rd DC
  - 413 CPU years
  - 1.7 TB
  - Up to 5000 CPUs in parallel
  - 1st October 2006 31 January 2007

| Number of Jobs   | 77,504               |
|--|----------------------|
| Total Number of completed dockings                             | 156,407,400          |
| Estimated duration on 1 CPU                                    | (413 years)          |
| Duration of the experiment                                     | 76 days              |
| Average throughput   | 78,400 dockings/hour |
| Maximum number of loaded licences<br>(concurrent running jobs) | 5,000                |
| Number of used computing elements                              | 98                   |
| Average duration of a job                                      | 41 hours             |
| Average crunching factor                                       | 1,986                |
| Volume of output results                                       | 1,738 TB             |

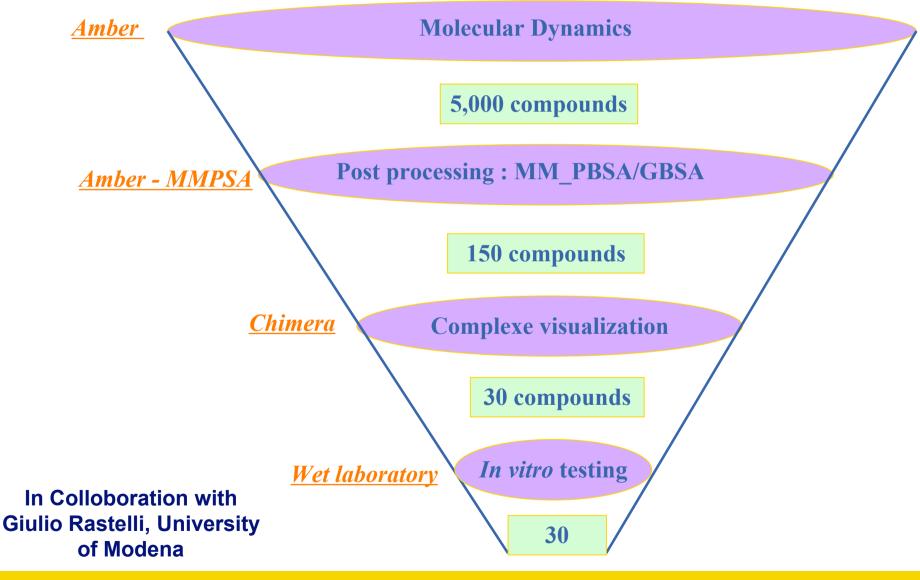


### **Biological results**

The repartition of docking energies of the ZINC database against GST A structure. (The red column represents a score of -24kj/Mol, the docking score of a co-crystallized ligand (GTX) of GST A chain)







#### Where grids can help medical development in Africa

- Contribute to the development and deployment of new drugs and vaccines
  - Improve collection of epidemiological data for research (modeling, molecular biology)
  - Improve the deployment of clinical trials on plagued areas
  - Speed-up drug discovery process (in silico virtual screening)
- Improve disease monitoring
  - Monitor drug delivery and vector control
  - Improve epidemics warning and monitoring system
- Improve the ability of African countries to undertake health innovation
  - Strengthen the integration of African life science research laboratories in the world community
  - Provide access to resources
  - Provide access to bioinformatics services



## **Grid added value**

- Grids offer unprecedented opportunities for resource sharing and collaboration
- Grids open exciting perspectives to handle the information flows
  needed to fight neglected diseases
  - Deployment of services for healthcare and research centers in endemic regions
  - Deployment of infrastructures (federation of databases) to collect biomedical data and improve disease monitoring
  - Cross-organizational collaboration space to share data and resources

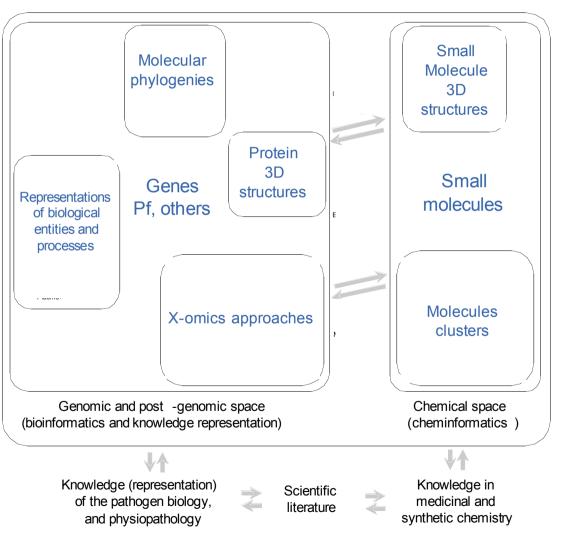
#### Challenges

- Infrastructure capacity building in Africa
- Grid technology must provide the services for data and knowledge management
- IT expertise and willingness to share information is needed from the participating healthcare centers

#### Beyond virtual screening, a chemogenomic space for malaria

#### Chemogenomic knowledge space

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Goals:

- comparison of protein sequences

high throughput
 reconstruction of molecular
 phylogeny

- representation of biological processes particularly metabolic pathways

- integration of genomic data, biological representations and functional profiling after drug treatments

- determination and prediction of protein structures

- virtual docking with drug candidate structures

#### Source: Birkholtz L.-M. et al., Malaria Journal, 2006

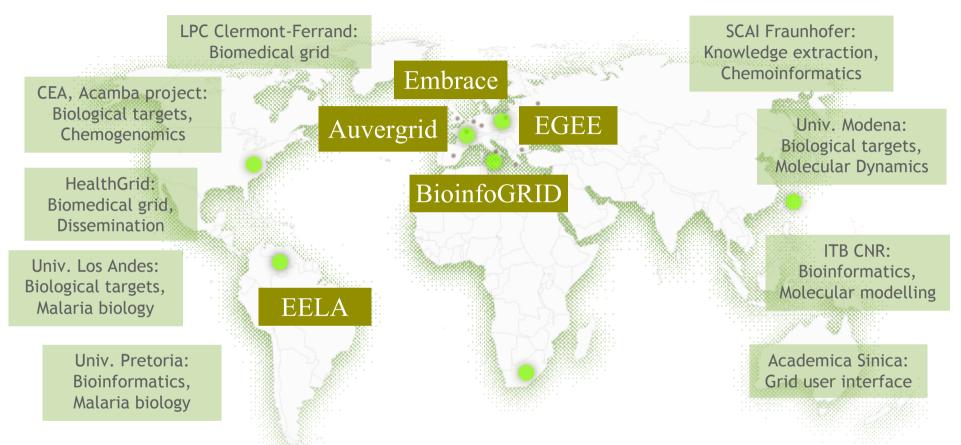
## Conclusion

# BioinfoGRID

- WISDOM proposes a new approach to drug discovery thanks to the grid
  - Rapid deployment of very large scale virtual screening
  - Collaborative environment for the sharing of data in the research community
- WISDOM fully exploits EGEE services and resources.
  - AMGA allows to store securely results and statistics immediately
  - Web Service Interface using WS-I profile guarantees interoperability
- First biochemical results demonstrate grid relevance to the drug discovery community
  - Grid is a superior tool to discover new drugs



#### Long term vision: a grid for malaria



#### Use the grid technology to foster research and development on malaria and other neglected diseases

Contacts also established with WHO, Microsoft, TATRC, Argonne, SDSC, SERONO, NOVARTIS, Sanofi-Aventis, Hospitals in subsaharian Africa,

## Perspectives on Malaria

- EGEE infrastructure open to host other CPU intensive applications relevant to research on Malaria i.e.
  - Search for drugs: virtual screening
  - Search for vaccines: data analysis
- Grids offer also unique opportunities for
  - Early detection
  - Epidemiological watch
  - Prevention
  - International collaboration
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## **Acknowledments**



**BioinfoGRID** 

#### wisdom.healthgrid.org