



Enabling Grids for E-science

# WISDOM-II, status of preparation

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Information Society



- **Several laboratories have expressed an interest in proposing targets for a second computing challenge against neglected diseases.**
- **Several grid projects have expressed interest in contributing to the WISDOM initiative by providing computing resources.**
- **A rough estimation of the needed resources is about 500 CPU years and about 4 terabytes storage.**
- **Date: from October, 1st to December, 15<sup>th</sup>**

Organism	Target	Partner	Country	Status
<i>P. falciparum</i>	GST	U. of Pretoria	South-Africa	Ready
<i>P. falciparum</i>	DHFR	U. di Modena e Reggio Emilia	Italia	Under preparation
<i>P. vivax</i>	DHFR	U. of Los Andes	Venezuela	Under preparation
Plasmodium/ plant/mamal	Tubulin	CEA, Acamba project	France	Accepted

- **Other prospected targets**

- *P. falciparum*, DNA-polymerase – University of Glasgow, United Kingdom
- Leishmania, transketolase – University of Glasgow, United Kingdom
- Leishmania, MAP-Kinase1 - Bernhard Nocht Institute for Tropical Medicine, Germany

- **Known targets**

- DHFR from *P. falciparum*

- Known target of the Chloroquine drug
    - Chloroquine now inefficient against drug-resistance parasites due to DHFR mutations
    - Search for new drugs

- DHFR from *P. vivax*

- Plasmodium Vivax responsible for malaria in South America
      - *Malaria case in Corsica (France) during the summer*

- **New targets**

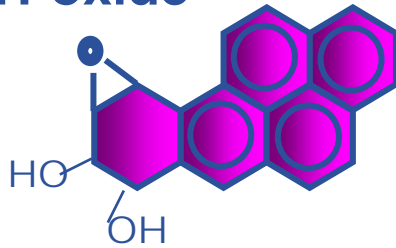
- Tubulin from *P. falciparum*

- Tubulin involved in cell replication, potential target for cancer treatment
    - Comparative docking of human and *P. falciparum*. tubulins

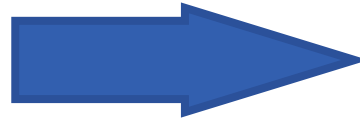
- GST from *P. falciparum*

- Protein involved in parasite detoxification
    - Search for inhibitors

PAH-oxide

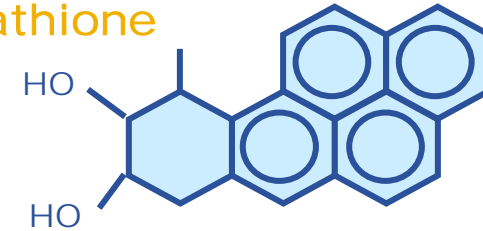


DNA Reactive



**GST**  
+ Glutathione

Glutathione



Inactive

- **Role:** Involved in detoxification phase in Plasmodium
- **Features:**
  - Co-crystallized structure available in PDB with GTX
  - Dimer
  - Binding site known
  - 4 inhibitors known
- **Problem:** present in almost all organisms (human...)

- **BioSolveIT make graciously available FlexX docking software for all the data challenge**
- **Difference with previous data challenges:**
  - More targets but less structures and parameters
  - FlexX is much faster than Autodock
  - Much higher virtual screening throughput expected
    - Present record from WISDOM-I: 11,6 docking computations per second
- **Room for additional deployment within the 500 CPU years requested**
  - Docking of new targets
  - Grid-enabled molecular dynamics
    - SCAI Fraunhofer
    - Reranking of WISDOM-I results (BioInfoGRID, University of Modena)

- **3,000 licenses will be available during the data challenge**
- **FLEXIm license server is maintained in SCAI Fraunhofer**
- **A second server will be installed in SCAI Fraunhofer**
- **Ports 23,200 and 23,201 required to be open on each Worker Node (ports already open for Globus)**
- **Tests on all grid nodes are required before the data challenge**

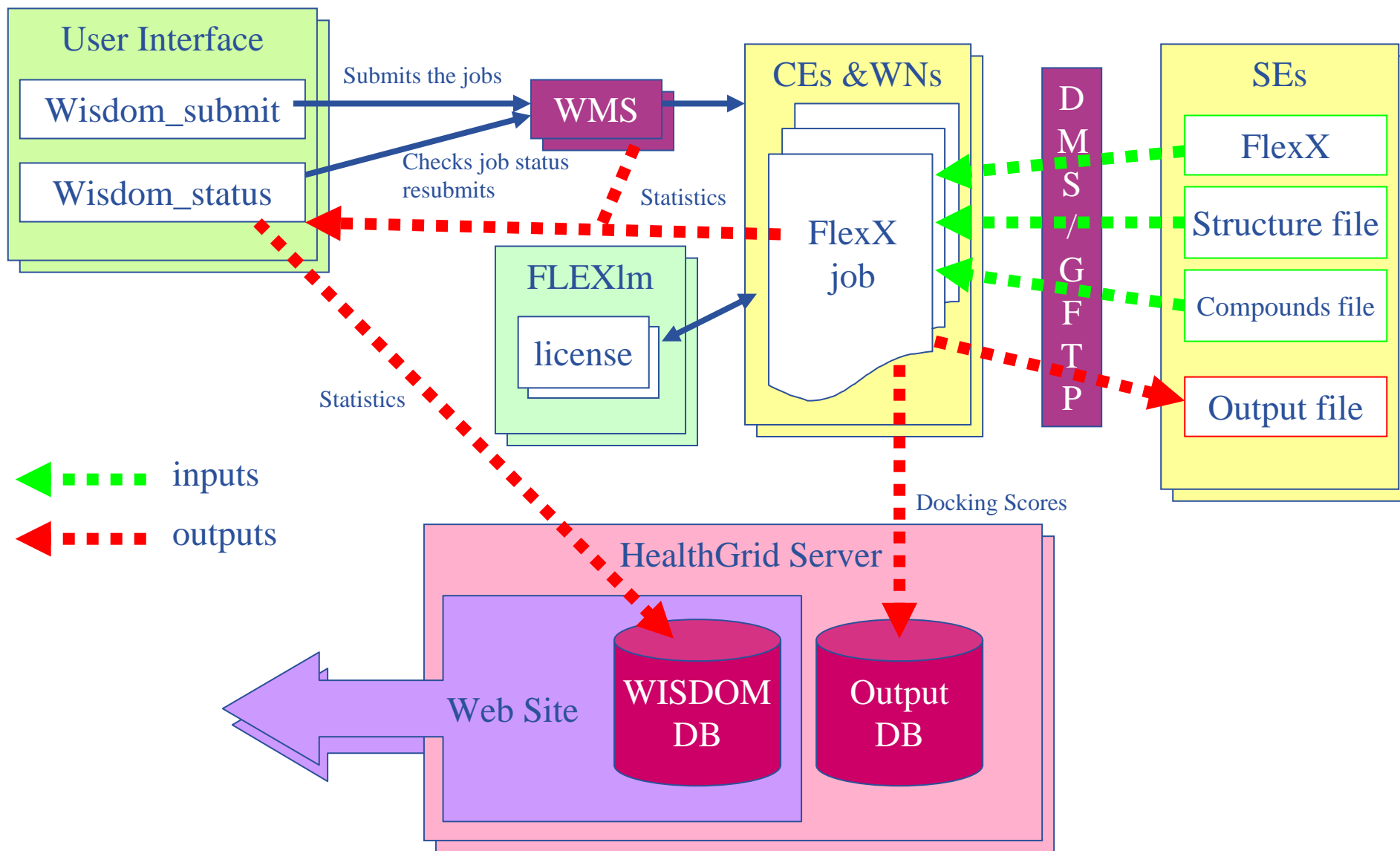
- **2 structures**
  - Chain A and B of the dimer
- **2 Flexx parameters**
  - Place particle: on/off
  - Max overlap volume: 2.5/5.0
  - No crystal water
- **4.3 million compounds from ZINC**
  - Random approach
- **FlexX software**
  - 30s by docking
- **4 different instances with 2400 jobs of 15h**



Infrastructure/ project	Experiment operator	Target to be deployed	CPUs contribution
EGEE	LPC, Embrace	All	Available: ~8000 CPUs Free CPUs: ~2000
BioInfoGRID	BioInfoGRID	All	?, included in Biomed
TWGrid	TWGrid	All	300, included in Biomed
Auvergrid	LPC	GST	500
EELA	UPV, ULA	DHFR <i>vivax</i>	500 (CIEMAT)
EUMedGRID	INFN ?	DHFR <i>falciparum</i>	?
EUChinaGRID	INFN ?	Tubulin	?

- **2 main scripts, running in parallel: wisdom\_submit, wisdom\_status**
- **No more input and output sandboxes in jobs in order to avoid RB overload or to prevent RB crash**
- **Job JDL and scripts are generated just before any submission in order to take CE/RB black list or job submission frequency modifications into account**
- **Dynamic insertions of docking scores and statistics in relational databases which allow real-time visualisation**

# Schema of the WISDOM docking production environment



- **October, 1: GST target on EGEE-biomed and Auvergrid**
- **October, 15: DHFR vivax on EGEE-biomed and EELA**
- **October, 15: DHFR falciparum on EGEE-biomed and EUMedGRID**
- **November, 1: Tubulin on EGEE-biomed and EUChinaGRID**
- **November, 1: MD (SCAI Fraunhofer)**
- **November, 15: MD (BioInfoGRID, University of Modena)**

# Credits

Academia Sinica

BioSolveIT

CNR-ITB

CNRS

CEA

Healthgrid

IN2P3

LPC

SCAI Fraunhofer

Università di Modena e Reggio Emilia

Université Blaise Pascal

University of Pretoria

University of Los Andes



Auvergrid

Accamba project

BioInfoGRID

Conseil Regional d'Auvergne

EGEE

Embrace

EUChinaGRID

EUMedGRID

European Union

Information and Media Technology

Share

TWGrid



With the sponsorship  
of università di Modena  
e Reggio Emilia

