

Drug discovery on the grid: the WISDOM initiative... and beyond

V. Breton

CNRS-IN2P3, LPC Clermont-Ferrand

Credit: A. Da Costa, V. Kasam

- **Goals**
- **Materials and methods**
- **Results**
- **Issues encountered**
- **Perspectives**

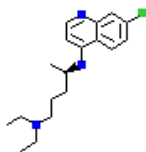
- **WISDOM stands for World-wide In Silico Docking On Malaria**
- **Main objective: use grids to foster R&D on neglected diseases**
- **Driving idea: grid-enabled drug discovery should enable non for profit public – private partnership at reduced cost**

Millions of potential drugs to test against interesting proteins!

Compounds:

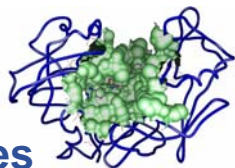
ZINC: 4.3M

Chembridge: 500 000



Targets:

PDB: 3D structures



High Throughput Screening
~10\$/compound, several hours

Too costly for neglected disease!



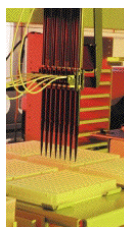
Molecular docking (**FlexX**, **Autodock**)
~1 to 15 minutes



Data challenge on **EGEE**
~ 2 to 30 days on ~5000 computers

Cheap and fast!

Selection of the best hits



Hits screening using assays performed on living cells



Leads
Clinical testing
Drug

Enabling Grids for E-science

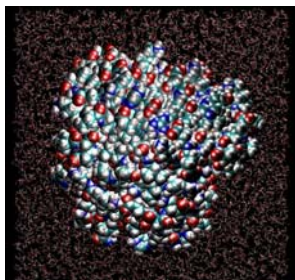
FLEXX
AUTODOCK



Millions

Molecular docking

AMBER

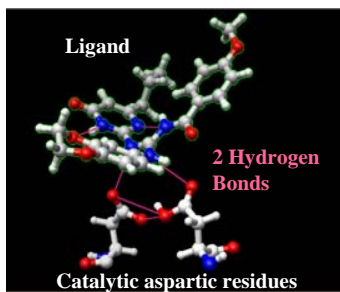


5000

Molecular dynamics

Re-ranking
MMPBSA-GBSA

CHIMERA



180

Complex
visualization

WET LABORATORY



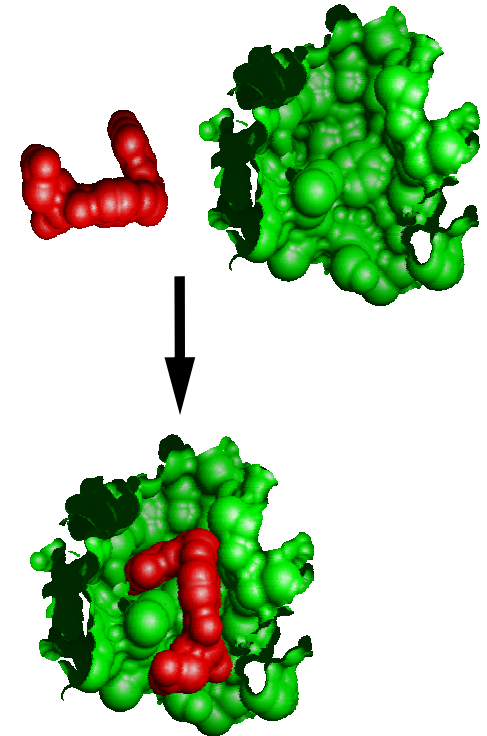
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In vitro
tests

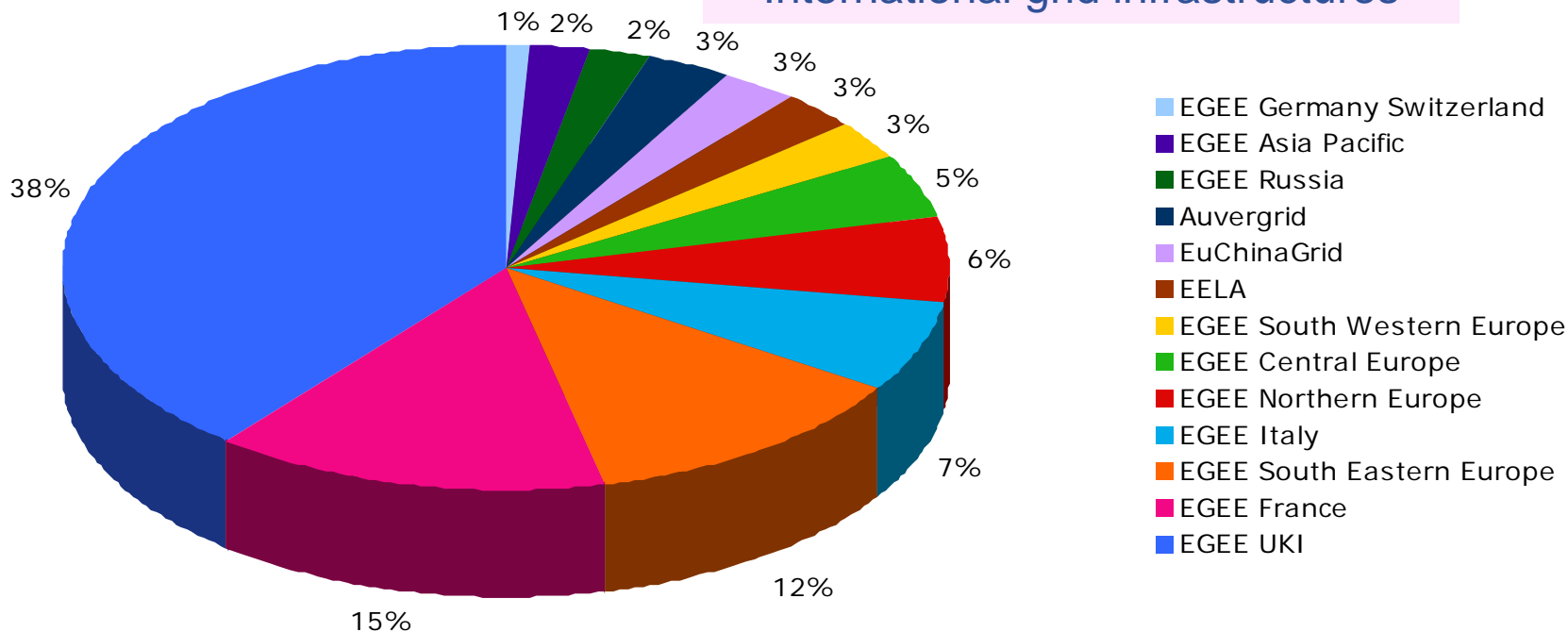
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In vivo
tests

- **Targets : structures publicly available on Protein Data Base**
 - Re-refinement of the structures on the Grid (Embrace - EGEE)
- **Docking software packages**
 - Open source: Autodock
 - Licensed: FlexX
- **Public database of drug-like ligands**
 - Chembridge (~ 500.000 compounds)
 - Zinc (> 4 Millions)



Significant contributions from several International grid infrastructures

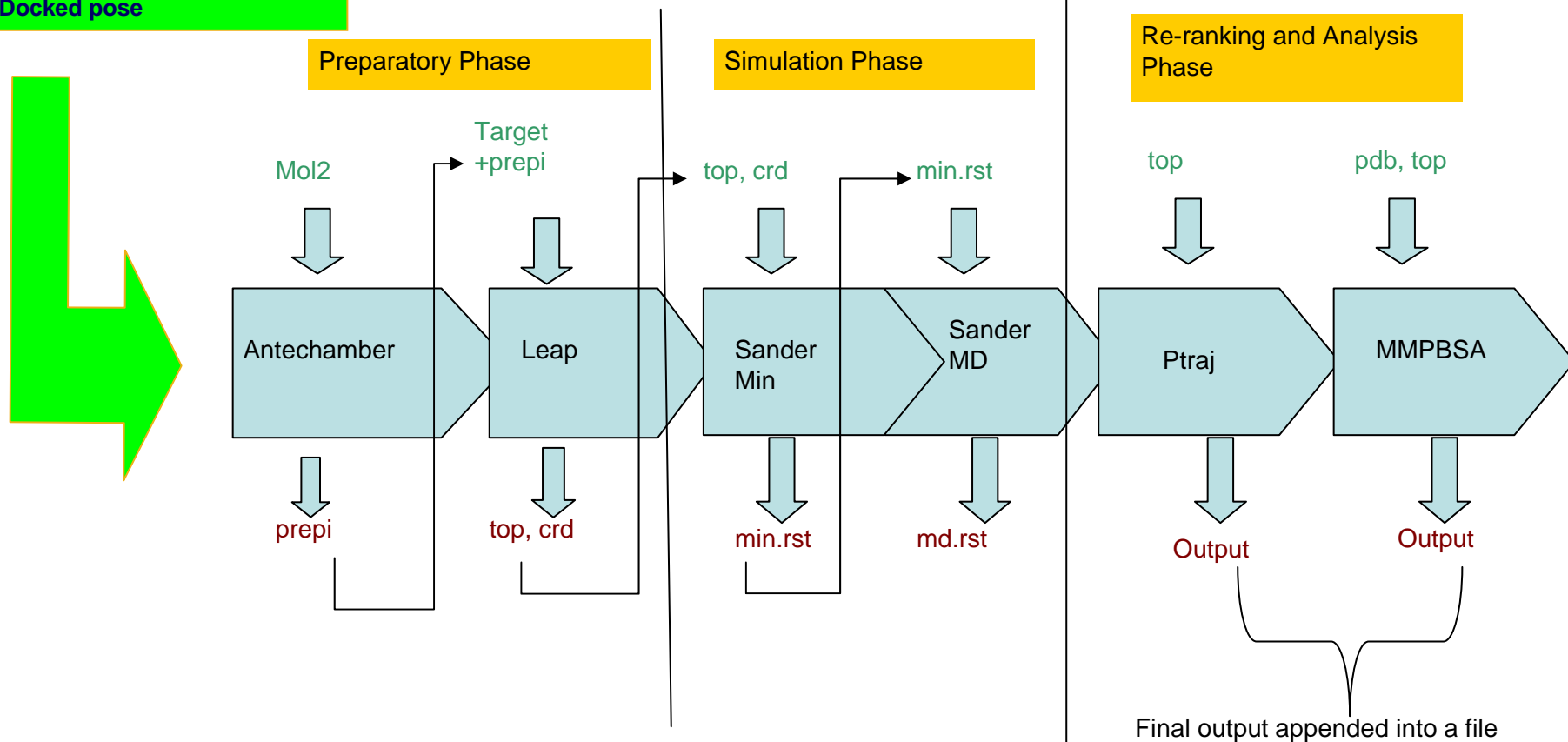


Over 420 CPU years in 10 weeks to dock 4 malaria targets in 2006
A record throughput of 100.000 docked compounds per hour

Best hits from docking step based on:

- Docking energy
- Docked pose

For one complete simulation, all necessary steps are embedded in one single script.



□ A. Ferrari, G. Degliesposti, M. Sgobba, G. Rastelli. Validation of an automated procedure for the prediction of relative free energies of binding on a set of aldose reductase inhibitors. *Bioorganic & Medicinal Chemistry*. 2007. In Press.

25, 000 compounds:

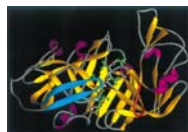
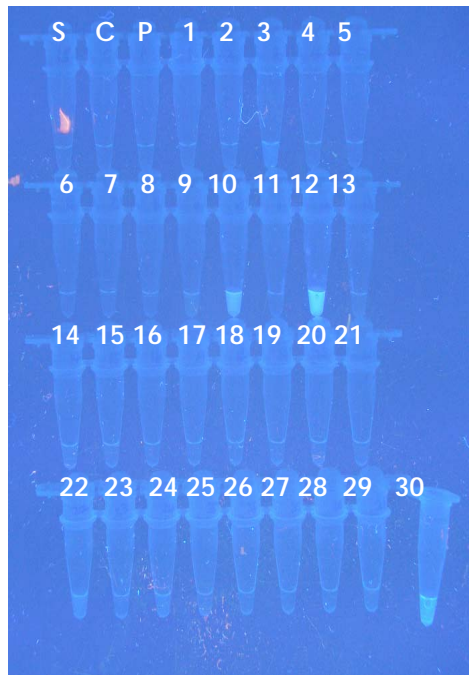
- Plasmepsin: 5000 compounds
- Pf-DHFR: 15,000 compounds
- Pf-GST: 5000 compounds

Number of Jobs	500
Total Number of compounds simulated	25000
Estimated duration on 1 CPU	347 days
Duration on the grid	25 days
Maximum number of concurrent running jobs	90
Number of computing elements used	1
Average duration of a job	16.6 hours

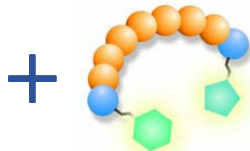
Dates	Target (s)	CPU consumed EGEE AuverGrid	Data produced	Specific features	Status
Summer 2005	Malaria: plasmepines	80 years	1TB	First data challenge	In vitro tests In vivo tests
Spring 2006	Avian flu: Neuraminidase N1	100 years*	800 GB	<45 days needed for preparation	In vitro tests
Winter 2006	Malaria: GST, DHFR, Tubulin	400 years	1,6TB	> 100.000 dockings / hr	Under analysis
Fall 2007	Avian flu: Neuraminidase N1	Estimated 100 CPU years*	Estimated 800 GB*	Joint deployment on CNGrid	First stage under analysis
Spring 2008	Diabetes: amylase	Estimated 120 CPU years	Estimated 800 GB	New production environment	Under way
Spring 2008	Malaria: DHPS	To be estimated	To be estimated	Joint deployment on desktop grid	In preparation

Inhibitor only

30 min reaction



Plasmepsin



FRET substrate



30 compounds

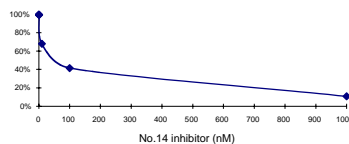
Compound	IC ₅₀ FRET (nM) ^a
1	154.91
2	146.03
3	209.90
4	101.32
5	174.97
6	91.32
7	86.61
8	98.72
9	248.84
10	241.51
11	107.80
12	127.31
13	155.54
14	72.17
15	123.93

16	85.48
17	73.65
18	82.59
19	74.56
20	72.24
21	71.24
22	163.50
23	99.56
24	115.62
25	88.23
26	94.42
27	75.62
28	100.40
29	114.84
30	246.37

• All 30 compounds show inhibition activity for nM concentration

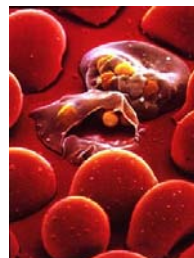
• 6 compounds have IC₅₀ under 80 nM

Fluorescence measurement
→ IC₅₀



- Impact on *Plasmodium falciparum* growth

Compound	IC ₅₀ (M)
1	>8,3E-06
2	>>2,5E-05
3	>8,3E-06
4	>8,3E-06
5	4,63E-06
6	>8,3E-06
7	>>2,5E-05
8	3,76E-06
9	>8,3E-06
10	>>2,5E-05



P. falciparum
infected
red blood
cells

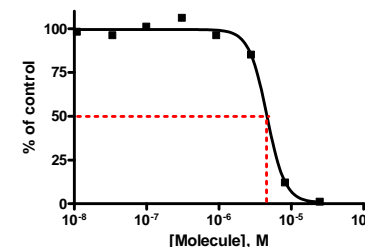
+



10 compounds

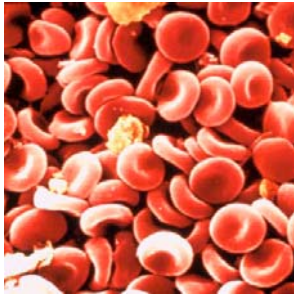


Radioactivity
incorporation
in parasite
-> IC₅₀



2 compounds show IC₅₀ in micromolar range

- Cytotoxicity on Human Cell model



Human cells

+

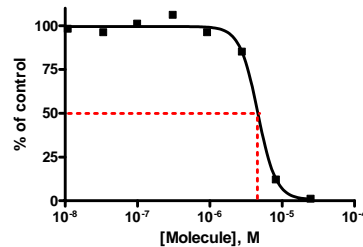


10 compounds

Results not yet known

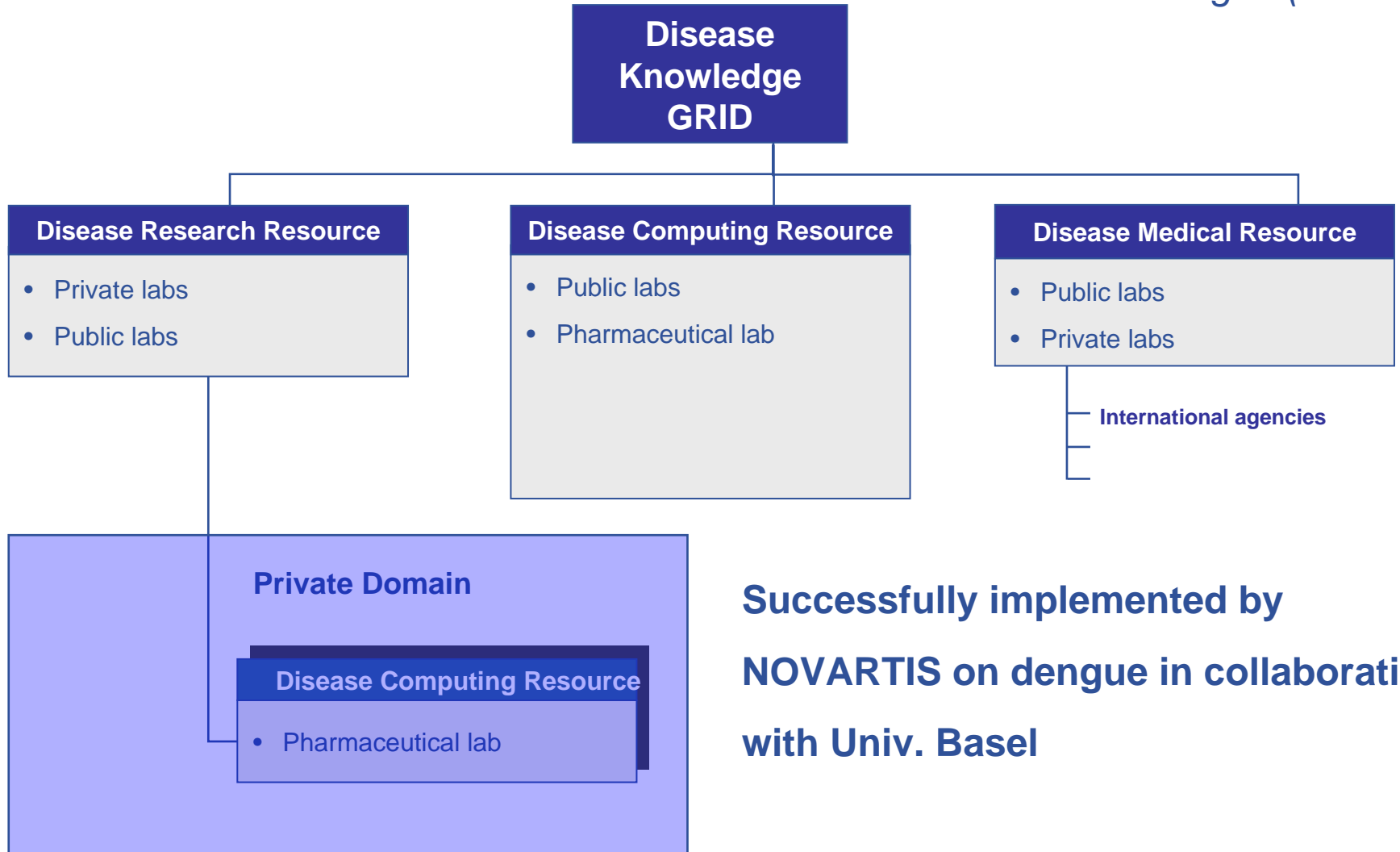


**Radioactivity
incorporation
on Human Cells
→ IC50**



- **Most docking and Molecular Dynamics software packages are distributed under commercial licenses**
- **Solutions found on a case by case basis**
- **FlexX: licenses made freely available by BioSolveIT**
 - License server deployed at Fraunhofer Institute
 - One token per grid node running FlexX
 - Up to 5000 concurrent tokens used
- **Amber: gentleman agreement**
 - Users: Amber available only to grid users from institutes owning an Amber license
 - Resources
 - § First step: Amber deployed only on clusters owning an Amber license
 - § Second step: Amber freely deployed on the grid

Credit: R. Ziegler (Novartis)



**Successfully implemented by
NOVARTIS on dengue in collaboration
with Univ. Basel**

- **Molecules selected *in silico* belong to public databases**
 - Molecules patented for their antimalarial activity
- **Who claims IP?**
 - Many actors: computing centres, WISDOM collaboration partners, wet labs
 - Agreed statement
 - § all information including analysis of potential hits are made publicly available. If a group takes screening information and synthesizes the physical compound and tests it extensively in the wet-lab, it might establish IP on their side and can establish claims on the physical compound and its behavior in biological assays as long as they cite the source for their initial analysis correctly.

- **Docking one biological target on 1 million drug-like compounds requires between 2 and 30 CPU years depending on the software**
- **Requests received from research groups around the globe for docking targets related to numerous diseases**
 - AIDS, Avian Flu, Diabetes, Malaria, Schistosomiasis, Tuberculosis
- **Need for more resources**
- **Interoperability -> Access to multiple grids**
 - Interoperability of desktop grids and EGEE for molecular docking (EDGES)
 - Implementation of open standards to access EGEE and DEISA for molecular dynamics (OMII-Europe)

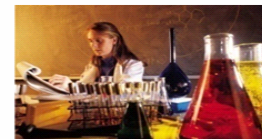
Open
Standards
allow same
client for all
steps



GridSphere Portal

JSR168

X.509 PKI



WISDOM
scientist

client-side

FleXX
AutoDock
job
submission

2

JSDL

SAML

SAML

1

SAML

VOMS

Trust

6

JSDL

SAML

AMBER
job
submission

proprietary
AuthZ
mechanism

3

OGSA-BES
CREAM-BES

XACML

SAML

gLite

FleXX

4

AutoDock



Compound list
(potential drugs)



SRM

OGSA-DMI

5

Gap: proprietary Data
Transfer/Access mechanisms
so far adopted only

proprietary
AuthZ
mechanism

7

OGSA-BES
UNICORE-BES

XACML

SAML

UNICORE

AMBER

8



Distributed
European
Infrastructure for
Supercomputing
Applications

Final
Compound list

9

Standards implemented by OMII-Europe I

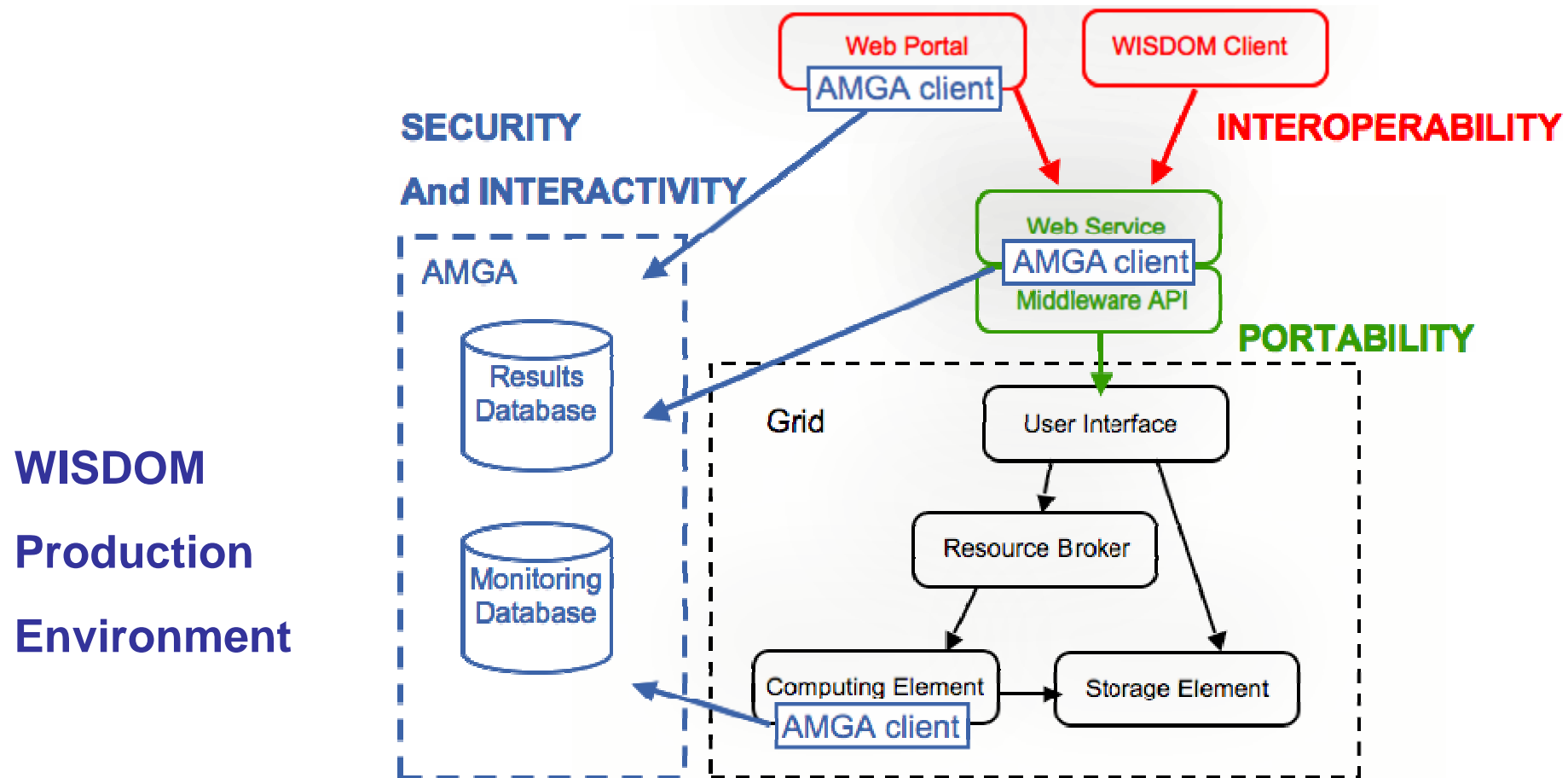
Scientific Software

Standards implemented by OMII-Europe II
(if funded)

n

Steps in
the process

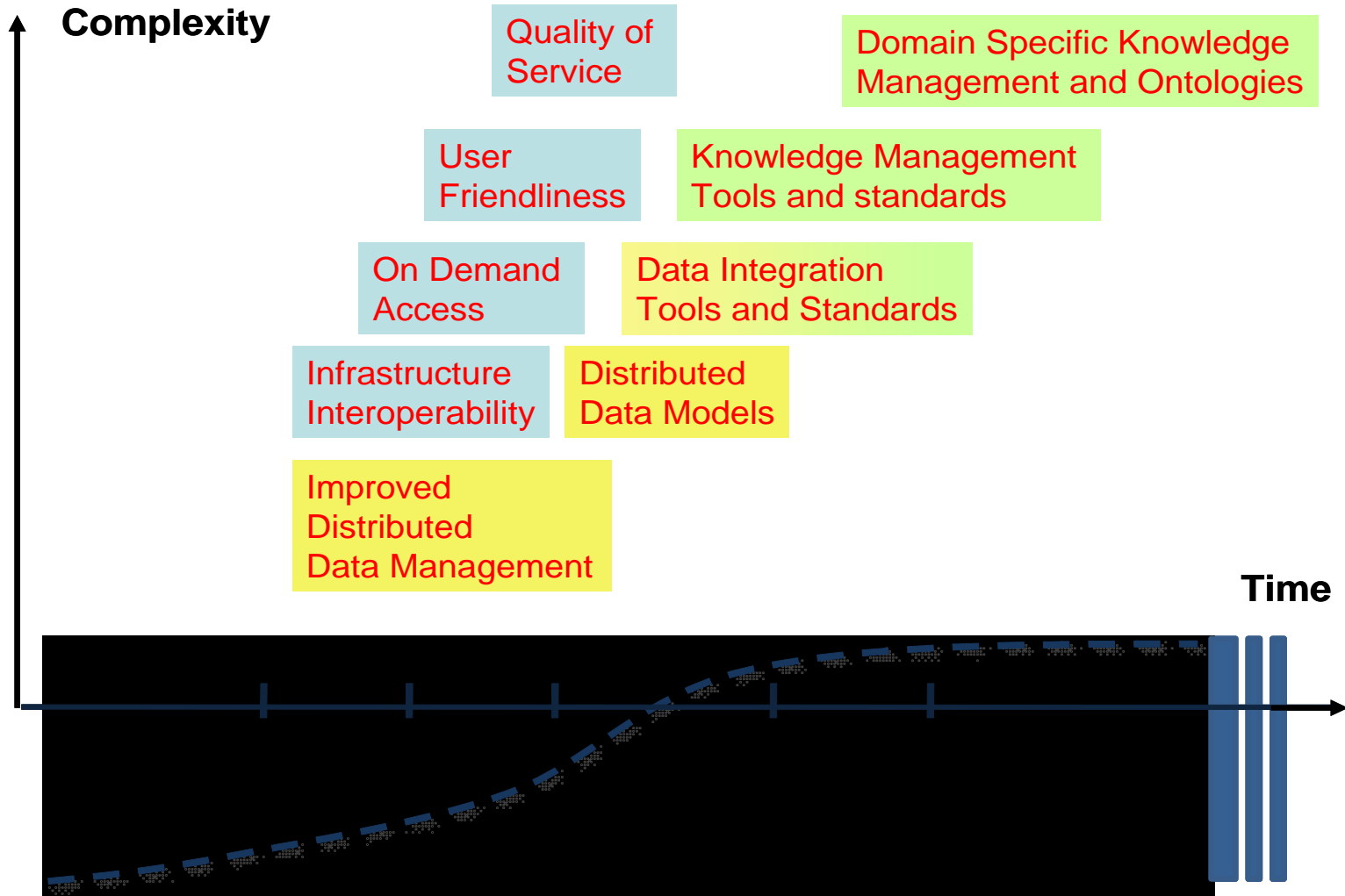
- All biomedical data (input, output) are stored in a metadata catalogue with fine grain access control



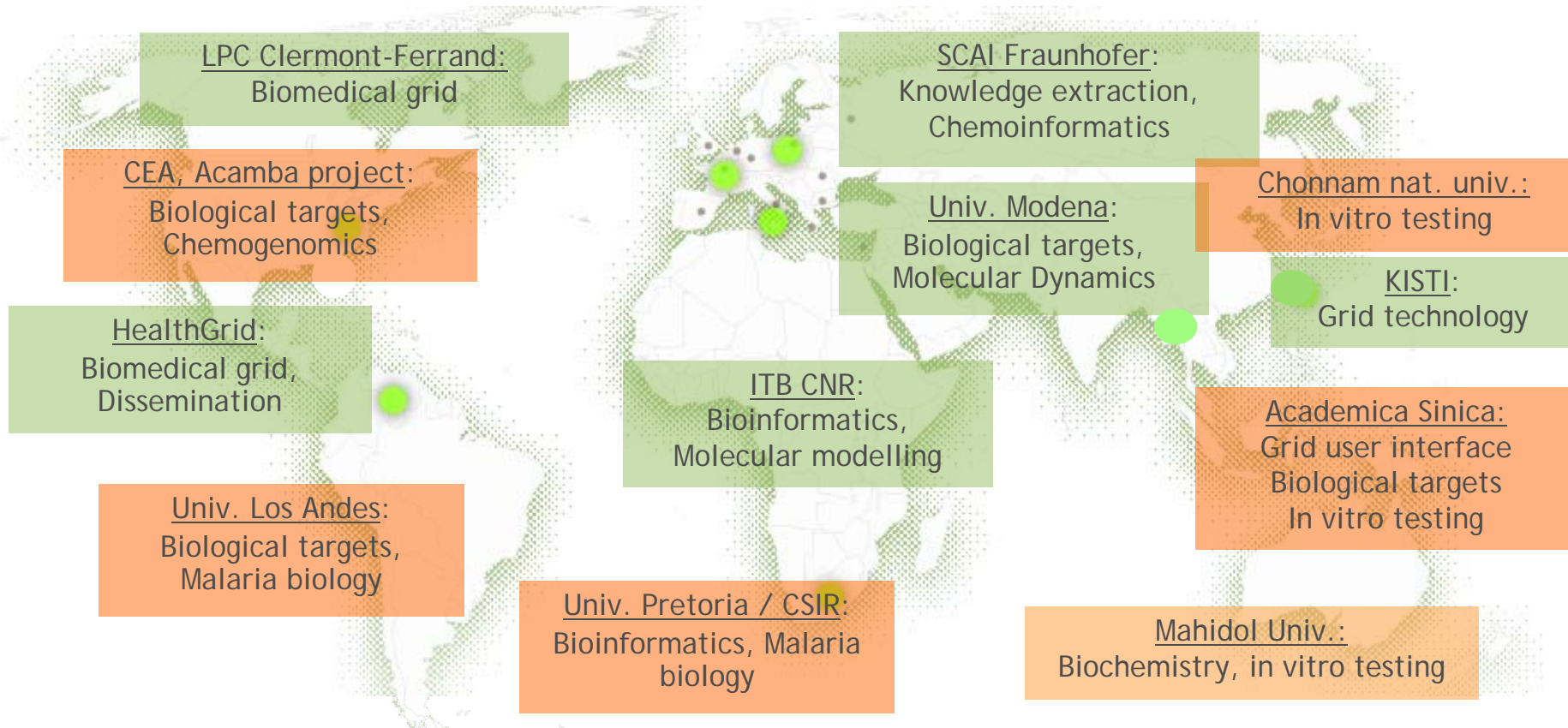
- **Innovative Medicines Initiative (European Commission)**
 - Goal: revitalize the biopharmaceutical research and development (R&D) environment for Europe
- **Strategic Research Agenda**
 - Identification of bottlenecks in the pharmaceutical R&D process
 - Recommendations to improve competitiveness
- **Key action: improve knowledge management**
 - Develop enhanced knowledge representation models and **data exchange standards** for complex systems,
 - Build a core reference database of validated experimental data extracted from the literature,
 - **Design standards for** and build an expert tool to allow the federation of local databases in a secured environment.

- Capacity to search, query, extract, integrate and share data in a scientifically and semantically consistent manner across heterogeneous sources (public and proprietary) ranging from chemical structures and “omics” to clinical trial data,
- Capacity to integrate and share scientific tools (e.g., modelling, simulation) as modules in a generic framework and apply them to relevant dynamic data sets,
- Expressive data representation and exchange standards,
- Dynamic and customizable configuration of applications,
- Encapsulation of validated physiological models, when applicable,
- Flexible, secure (covering all aspects of data protection encountered in a biomedical context), and scalable IT infrastructure.

- Develop a strategy to identify the areas of interest to all stakeholders,
- **Provide mechanisms** for data federation across heterogeneous data sources,
- Provide a flexible and secure collaborative environment serving all stakeholders,
- **Provide standards** and mechanisms for consistent data integration and data sharing,
- **Provide standards** and mechanisms for consistent integration of complex scientific tools and computational models,
- **Insure interoperability** of computing services across organizations,
- Develop broad and generic research projects for bridging gaps in current technologies.



- **In silico drug discovery routinely deployed on grid infrastructures**
 - Number of issues already addressed
- **Next step: improve knowledge management to enable pharmaceutical R&D environment**



Academia Sinica, Taiwan

Hung-Chun LEE, Simon C. LIN (Grid Computing Center)
Ying-Ta WU, Chon-Chen LEE (Genomic Research Center)

HealthGrid

Nicolas SPALINGER, Nicolas JACQ,

SCAI-Fraunhofer Institute, Germany

Martin HOFMANN, Vinod KASAM

Modena University, Italy

Giulio RASTELLI, Gianluca DEGLIESPOSTI

Chonnam National University, Korea

Doman KIM, Young-Min KIM (Neuraminidases), Hee-Kyoung KANG
(Plasmeprin)

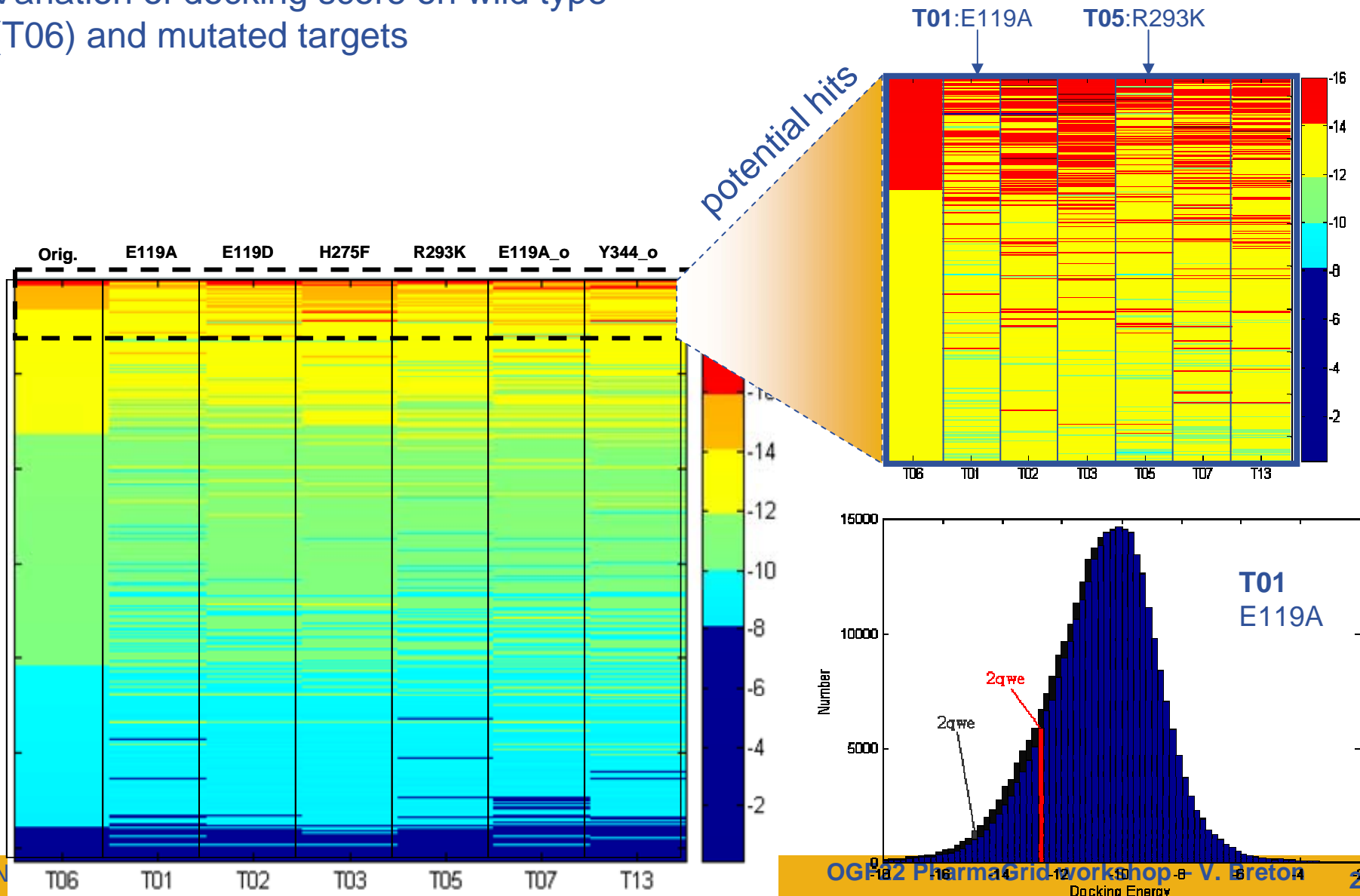
ITB-CNR

Luciano MILANESI, Pasqualina D'URSI, Gabrielle TROMBETTI

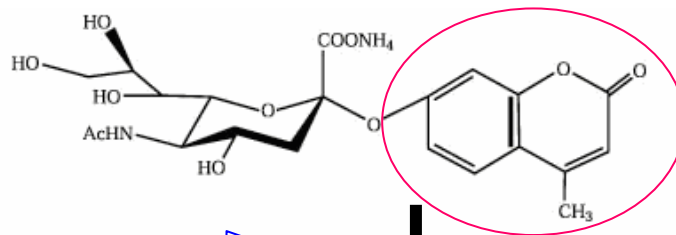
CNRS-IN2P3-LPC, Clermont-Fd, France

Jean SALZEMANN, Ana DA COSTA,
Vincent BLOCH, Yannick LEGRE

Variation of docking score on wild type (T06) and mutated targets



4-Methylumbelliferyl-*N*-acetyl- α -*D*-neuraminic acid ammonium salt
[4MU-NANA]; Substrate



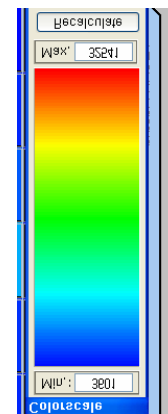
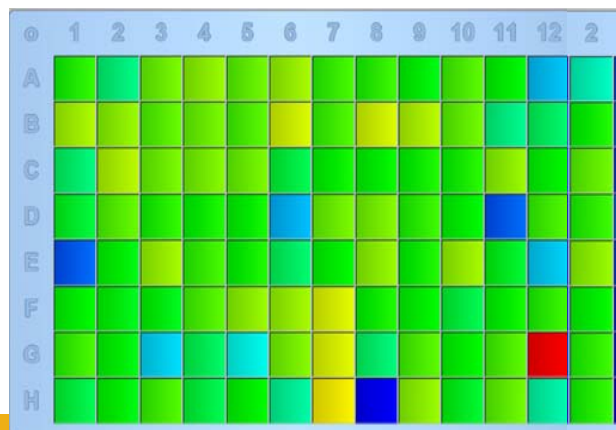
First screening
(200 nmol)

Recombinant Neuraminidase

Second screening
(2 nmol)

Kinetic study

Spectrofluorometric detector RF-551
362 nm excitation and 448 nm emission wavelengths

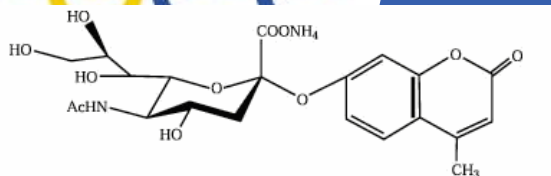


Red

Blue

Inhibition

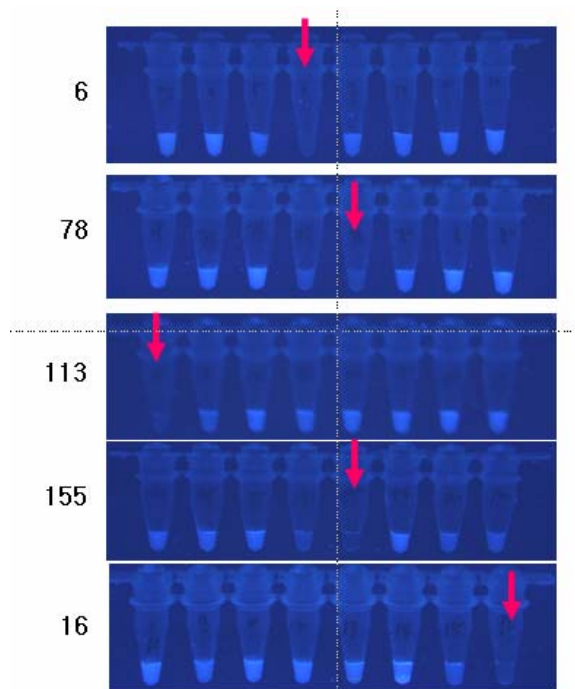
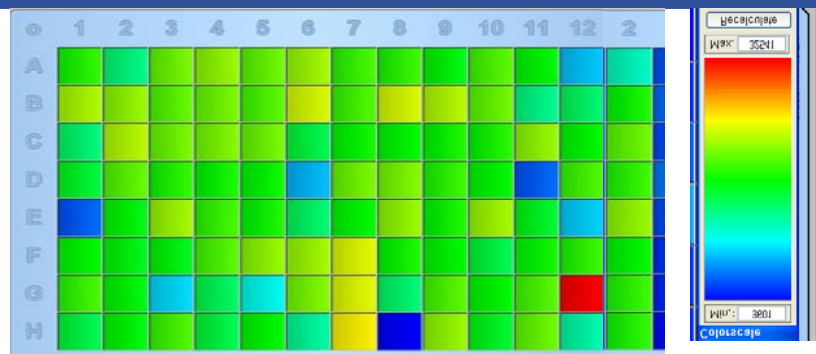
Results on 308 compounds tested in vitro



4MU-NANA
: 20 μ M/RM

Neuraminidase
: 10 mU/reaction

Measure at excitation 362 nm and
emission at 448 nm



On UV

Rank	Compounds	Relative activity of Neu1
1	113	67
2	16	72
3	6	73
4	155	74
5	78	78
63	⋮ Tamiflu ⋮	⋮ 100 ⋮