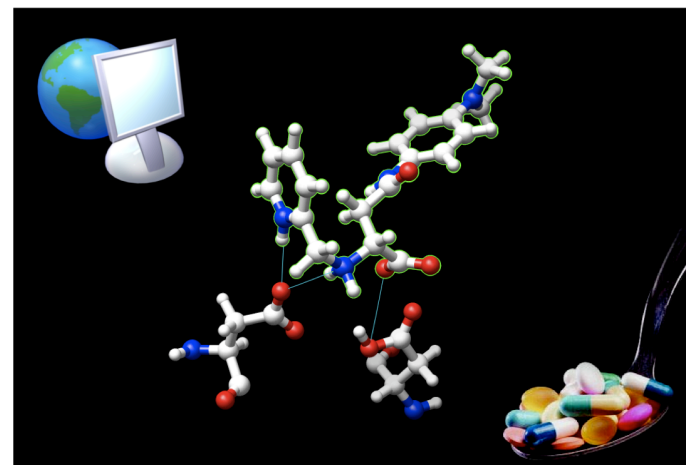


WISDOM EXPERIENCE - CURRENT STATUS -

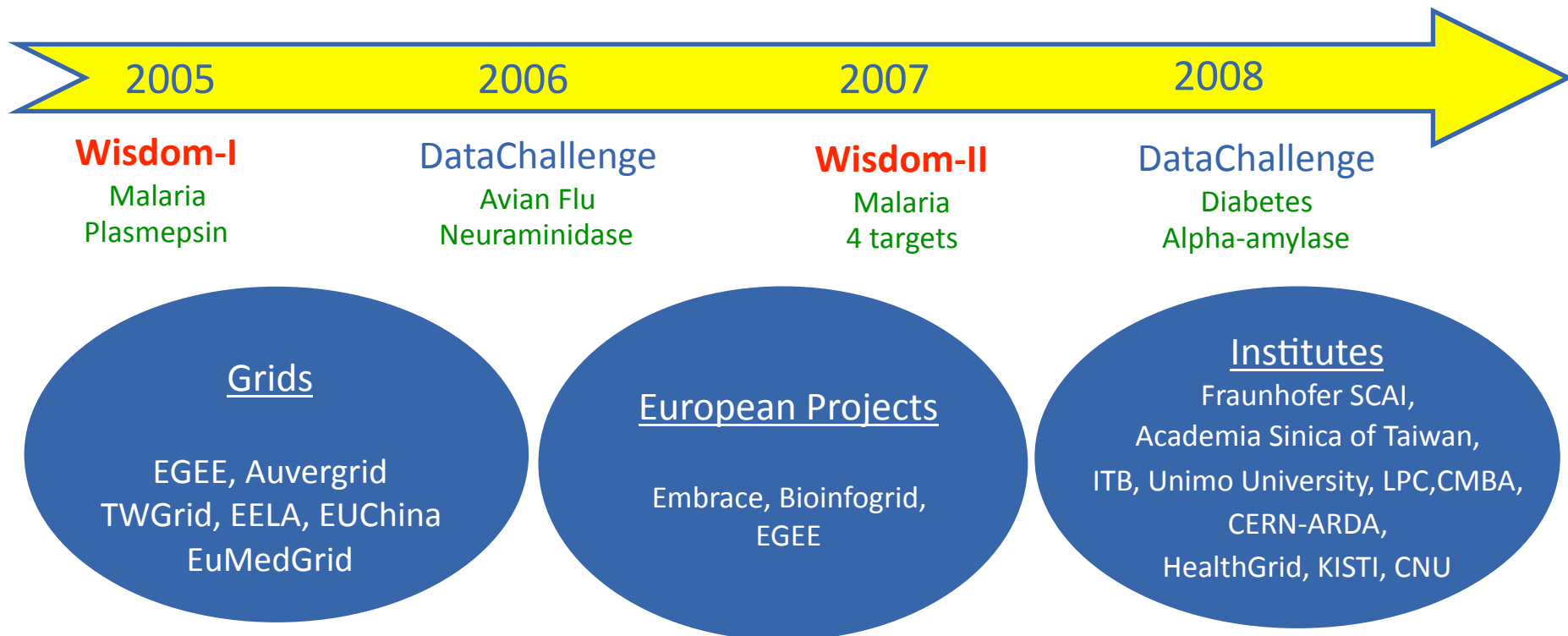
Ana Lucia DA COSTA
CNRS-IN2P3

EGEE Conference
ISTANBUL
September 25th 2008

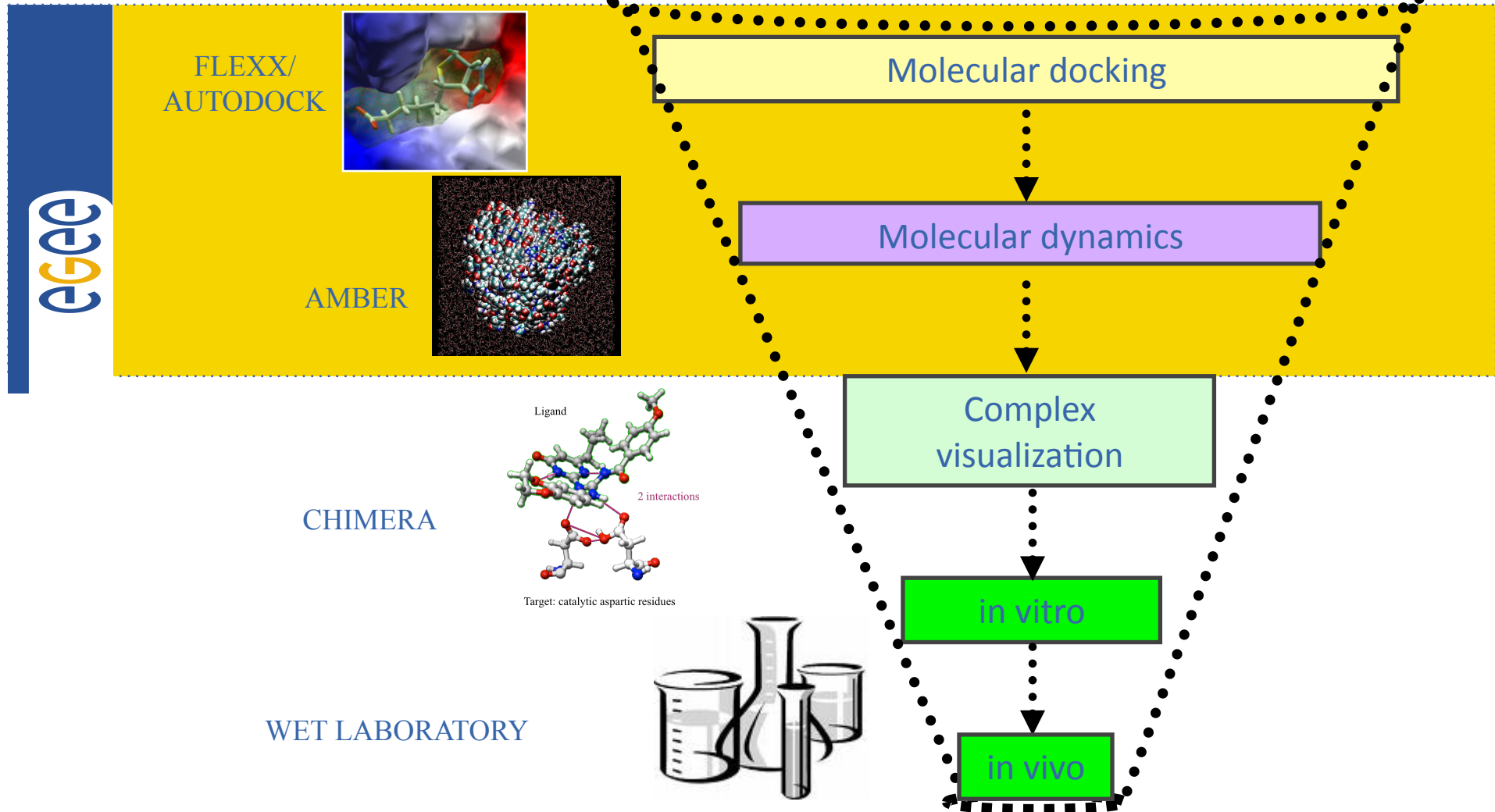


- 1. INTRODUCTION**
- 2. Virtual screening status**
 - 1. Wisdom 1: Plasmepsin**
 - 2. Wisdom 2: GST, PfDHFR**
- 3. New project: Pancreatic Alpha Amylase**
- 4. Evolution of Wisdom Production Environment**
- 5. CONCLUSION / PERSPECTIVES**

WISDOM (World-wide In Silico Docking On Malaria) initiative aims to demonstrate the relevance and the impact of the grid approach to address drug discovery for neglected and emerging diseases.



Drug discovery workflow



Biological results: targets

MALARIA TARGETS

IMPLICATED IN

PARTNERS INVOLVED IN



Plasmeprin from
Plasmodium falciparum

Hemoglobin
degradation

SCAI, Germany,
CNRS, France

CNU,
Sth Korea

GST from *Plasmodium falciparum*

Parasite
detoxification

Univ. of Pretoria,
South-Africa

Univ. of Pretoria,
South-Africa

DHFR from *Plasmodium falciparum*

Parasite DNA
synthesis

Univ. of Modena,
Italia

Univ. of Mahidol,
Thailand

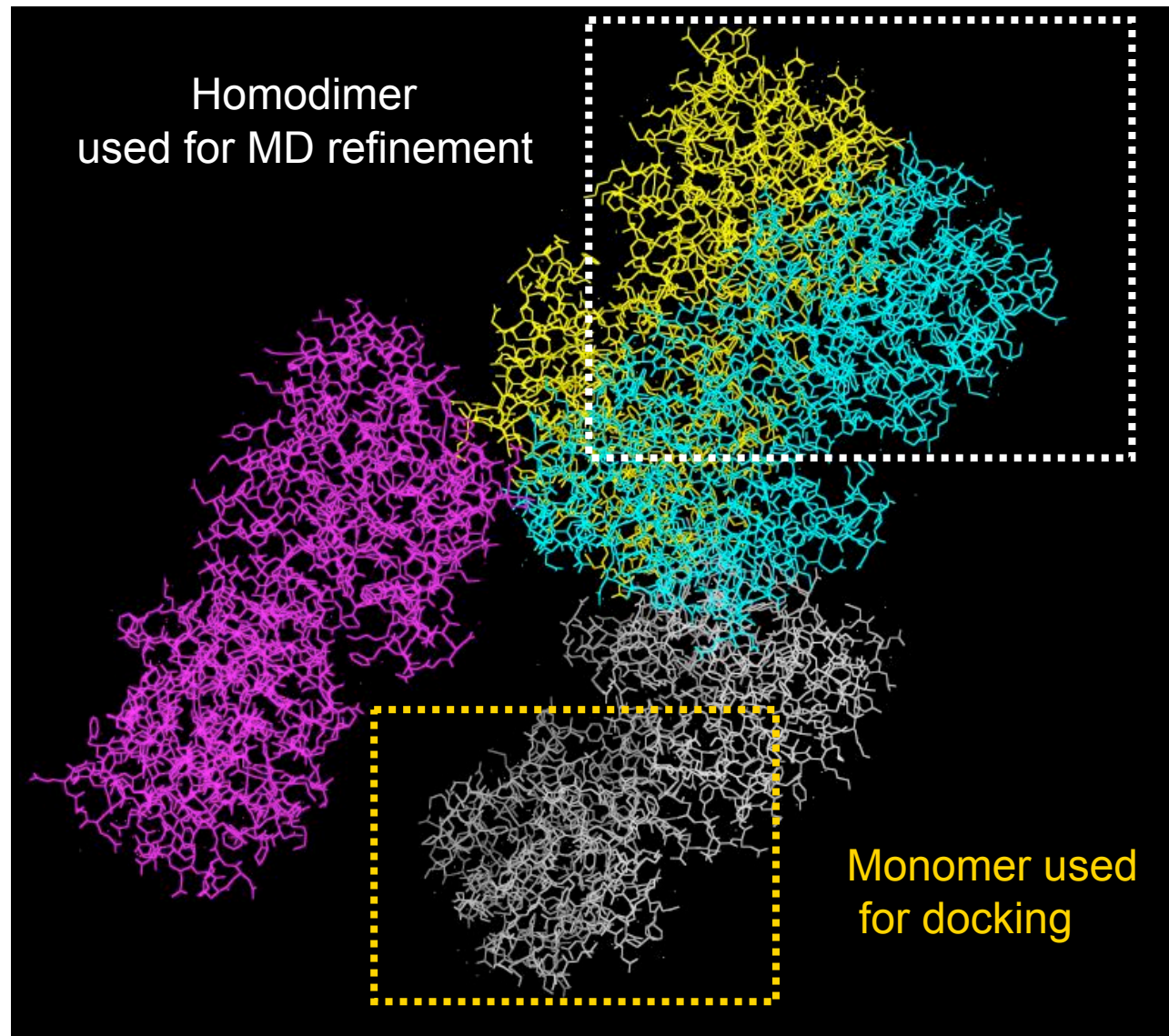
- ***In vitro* results : 30 Compounds tested**
 - > New experiments performed decreasing reaction time
 - 3 compounds with $IC_{50} < \text{Pepstatin A}$ (reference inhibitor)
 - 2 thiourea compounds (known scaffold)
 - 1 guanidino compound (new scaffold)
 - 4 compounds have good IC_{50} values $< 10 \text{ nM}$
 - 4 compounds with no inhibition activity
 - Others $> 10 \text{ nM}$
- ***In vivo* results : 10 Compounds tested**
 - 5 compounds $IC_{50} > 8.3 \mu\text{M}$
 - 4 compounds $IC_{50} > 25 \mu\text{M}$
 - 1 Thiourea compound with lowest $IC_{50} = 5,2 \mu\text{M}$

Low selectivity between red blood cells and parasite cells

- Re-ranking of compounds according to their free energy of binding calculated using MM-PBSA and MM-GBSA
- Analysis of interaction focusing on H-Bond between ligands and Asp54, Ile14 and Ile164 (key residues in wr9 interactions)
- Visualization of best scoring compounds (~200)
 - Evaluation of mobility after MD
 - Evaluation of binding orientation, comparison with WR99210
- Selection of the **16 best scored compounds for in vitro testing** based on:
 - Good interactions with the target
 - Reasonable chemical structure

Credit Gianluca Degliesposti

WISDOM-2-> GST



METHOD 1:

- Checking clashes with second subunit of the functional biological dimer minimized for 5000 best scored compounds.
- These 5000 compounds were refined by MD procedure and checked afterwards.
- Post MD analysis will include the following:
 - Check of clashes of compounds using Chimera
 - Do an interaction analysis, focussing on the key amino-acids, looking for the H-bonding with the ligand.
- Compile a list of 100 top performing ligands

METHOD 2:

- Extract the best 15000 molecules based on their docking score (FlexX) as well as their binding modes.
- Try to extract scaffold structures that can be linked to inhibition / activity using libMCS from Chemaxon.
- Clustering these molecules based on their molecular fingerprints.
- Extracting the centroids from these clusters
- Selection of the **25 best compounds for in vitro testing** based on:
 - Good interactions with the target
 - Leadlike and druglike structures

- **32 compounds under testing** + compounds all other the virtual screening workflow to validate - > Total : 60 cpds
- Reference: S-hexyl glutathione is a known inhibitor inhibiting GST about 40% at 500 uM -> bench mark for testing the compounds.
- A primary screen was done on the 60 compounds:
 - 1mM of the glutathione substrate
 - 500 uM, 250uM and 100 uM compound concentrations.
- 6 compounds were currently highlighted
-> Further kinetic studies
- Problems with solubility were encountered.

New project → α -Amylase



PARTNERS INVOLVED IN

TARGET

Human Pancreatic
Alpha-amylase

IMPLICATED IN

Break down
Dietary starch



KISTI, Sth Korea
CNRS, France



CNU,
Sth Korea

- **Drug Target**

- Control of HPA activity can be used as a means of controlling blood glucose levels
- Inhibitors of alpha-amylase : treatment of diabetes or obesity

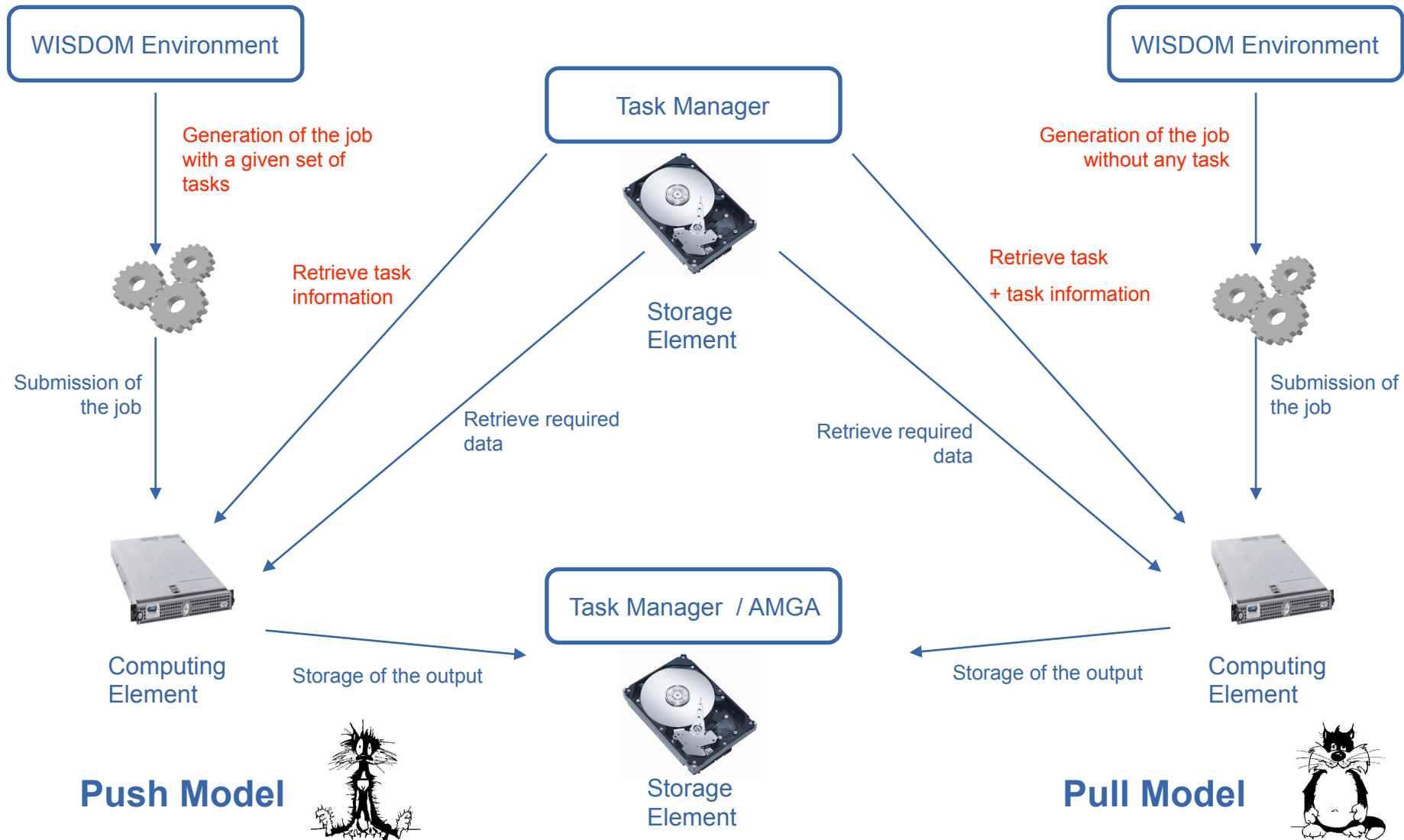
- **Improvement in database preparation:**

- Use of Chembridge Database to ease the commercial availability in comparison with ZINC
- A.D.M.E.T filtering of database (FAF drugs tool with 200 rules)

After 3 years of development, the WISDOM environment has reached its final stage. A new environment is designed to improve its:

- **Flexibility:** Environment is suitable for short deadline jobs submissions and large-scale computing-intensive deployments.
- **Efficiency:** As soon as a task is submitted idle agents can pick it up and start running it almost instantly.
- **Versatility:** Environment can be used in multiple area like bioinformatics, physics...

Evolution of Wisdom Prod. E



Evolution of Wisdom Prod. E



Statistics of the last large-scale deployment (credits to Kisti):

Number of tasks submitted	Corresponding CPU time	Real processing time on the Grid	Agents running concurrently	Average task retrieval time
300,000	40 years	2,5 days	7,000	2 seconds

- > Crunching factor of 6000 that shows a distribution efficiency of 85%.

Credit J. Salzemann

- **Biochemical aspect:** successful results validated the combination of EGEE Grid and *in silico* drug discovery
 - > suggesting that the overall WISDOM approach used to select the candidates is able to discover potential inhibitors.
- **Grid aspect:** new WISDOM production environment allowed good grid performances
 - > performances similar to those obtained on clusters with grid scalability
 - > grid workload management overhead is reduced.

- **Current WISDOM developments target non-grid experts:**
 - “**Bioinformatics platform**” for simple and transparent use of grid services through the WISDOM environment.
= >> **DEMO 10**
 - “**DrugScreeener-G**”: integrated environment for grid-based virtual screening under the WISDOM environment (Kisti)
= >> **POSTER 10**
- **Future WISDOM deployments on:**
 - DEISA (MD)
 - OSG (docking)
 - ALABAMA SUPERCOMPUTER CENTER (docking)

Acknowledgments



In particular:

V. Breton

V. Kasam

J. Salzemann

V. Bloch

N. Jacq

M. Botha

M. Hofmann

M. Zimmermann

A. Maas

M. Reichstadt

G. Fettahi

L. Milanesi

S. Hwang

S. Ahn

N. Kim

S. Lee

G. Degliesposti

G. Rastelli

For biochemical results

– Chonnam National Univ.

Hee-Kyoung KANG

Young-Min KIM

Doman Kim

– CNRS-UMR 5539

Nadia Saidani

Eric Marechal

THANKS FOR
YOUR ATTENTION

