



gLite grid enabled infrastructure

/O=dutchgrid

/O=users

/O=universiteit-utrecht

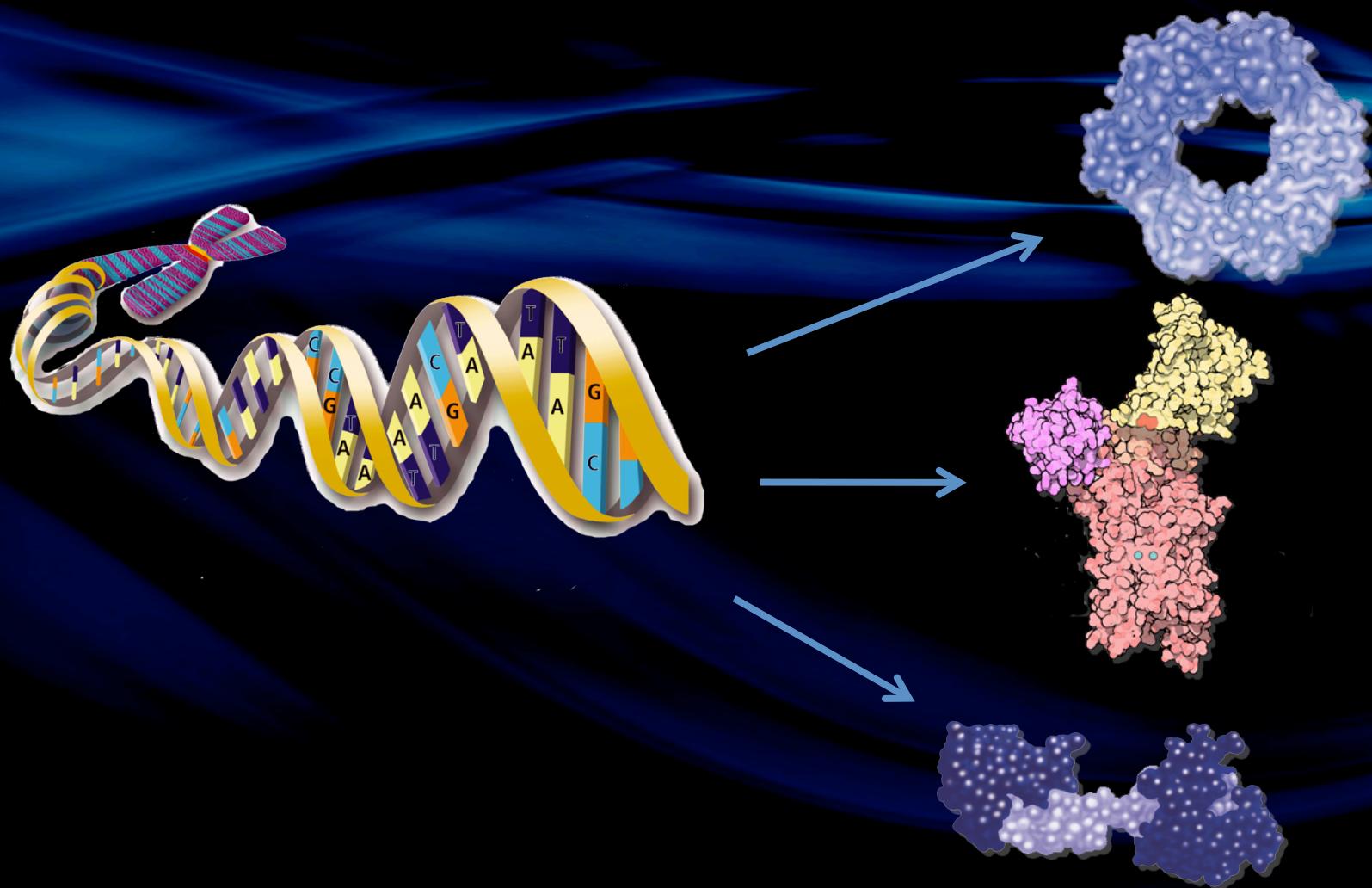
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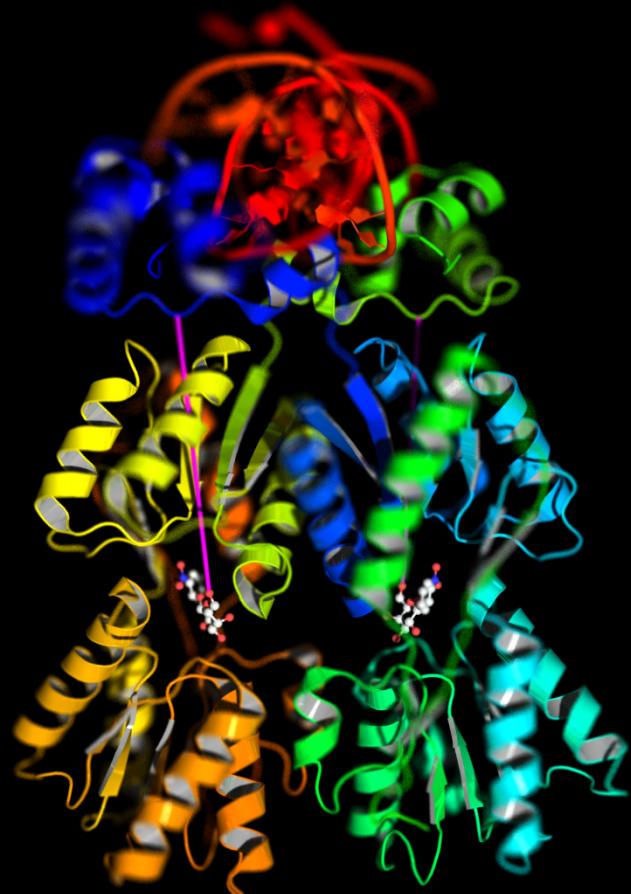
Outline

- Biological relevance of molecular machines
- Nuclear Magnetic Resonance
- enmr.eu virtual organization
- From Grid applications to web services
- enmr.eu VO status
- The future ... we-NMR

Biological background

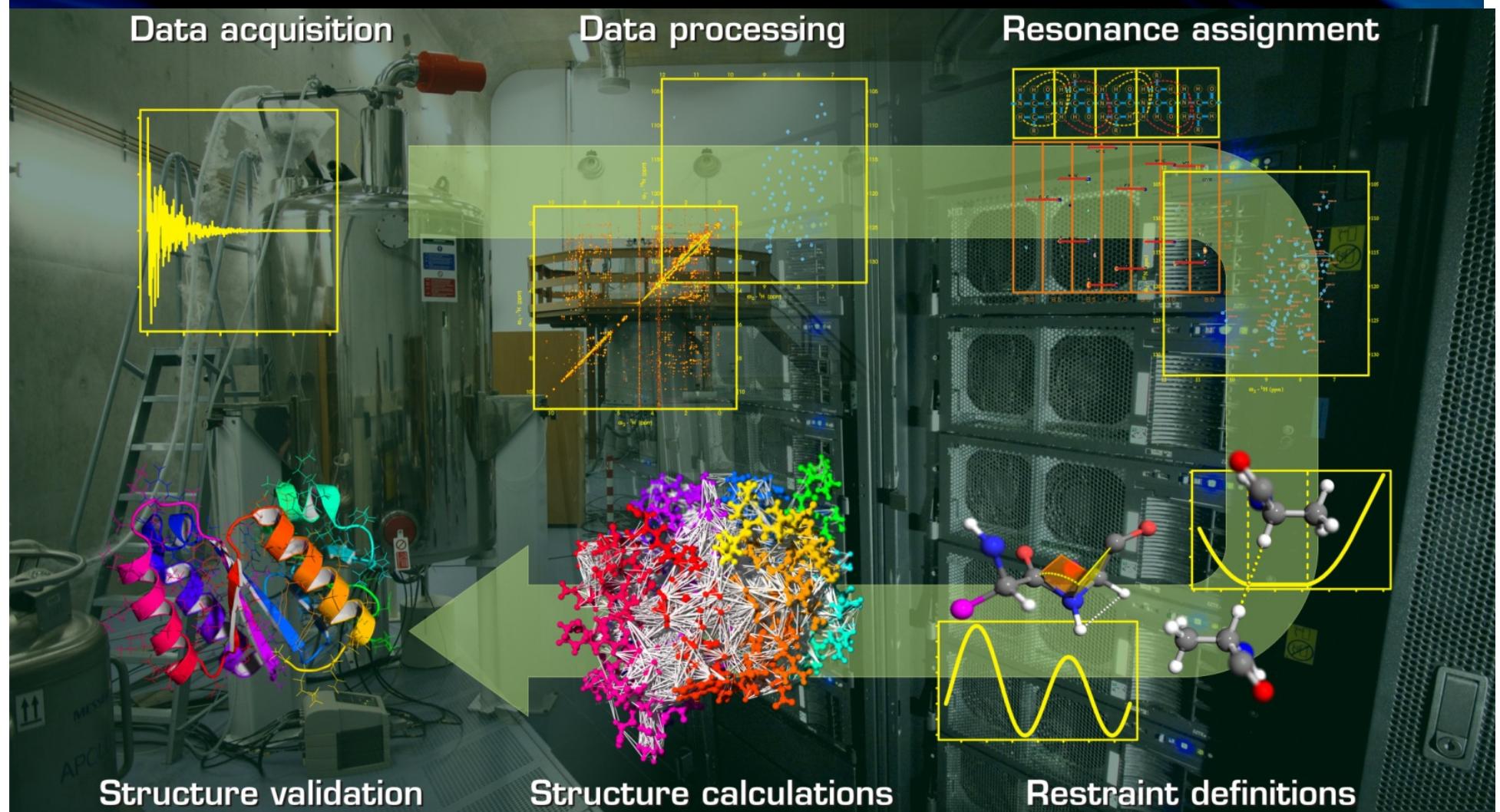


Structure of biomolecules. Why?

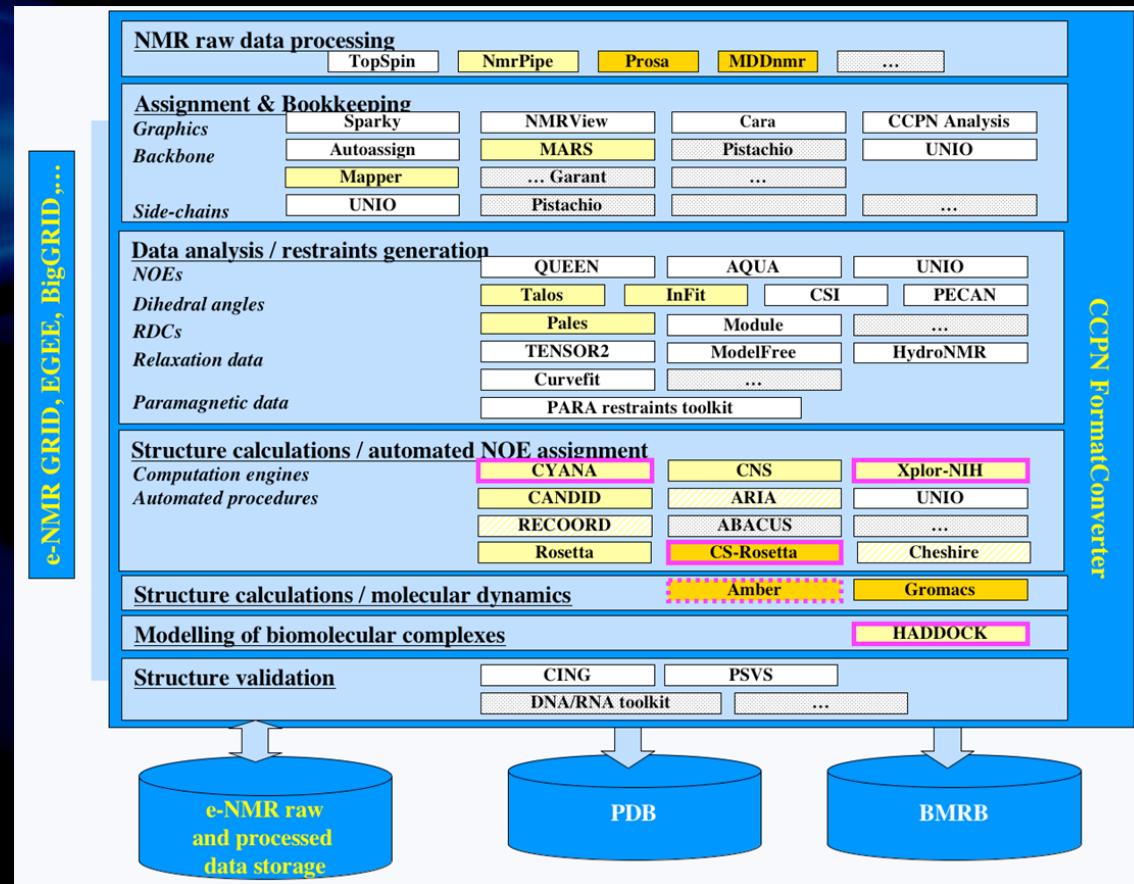


- Function and Mechanism of Action
- Design of Experiments
- Understand Effects of Mutations
- Drug Design

Nuclear Magnetic Resonance



Practical issues ...



- # programs
- Expertise
- CPU/storage space

e-NMR Objectives



- Integrated protocols of NMR applications
- Easy access to web interfaces
- Exploit GRID technology
- Lower the access level to GRID technology in life sciences

e-NMR : Integrated Infrastructure Initiative



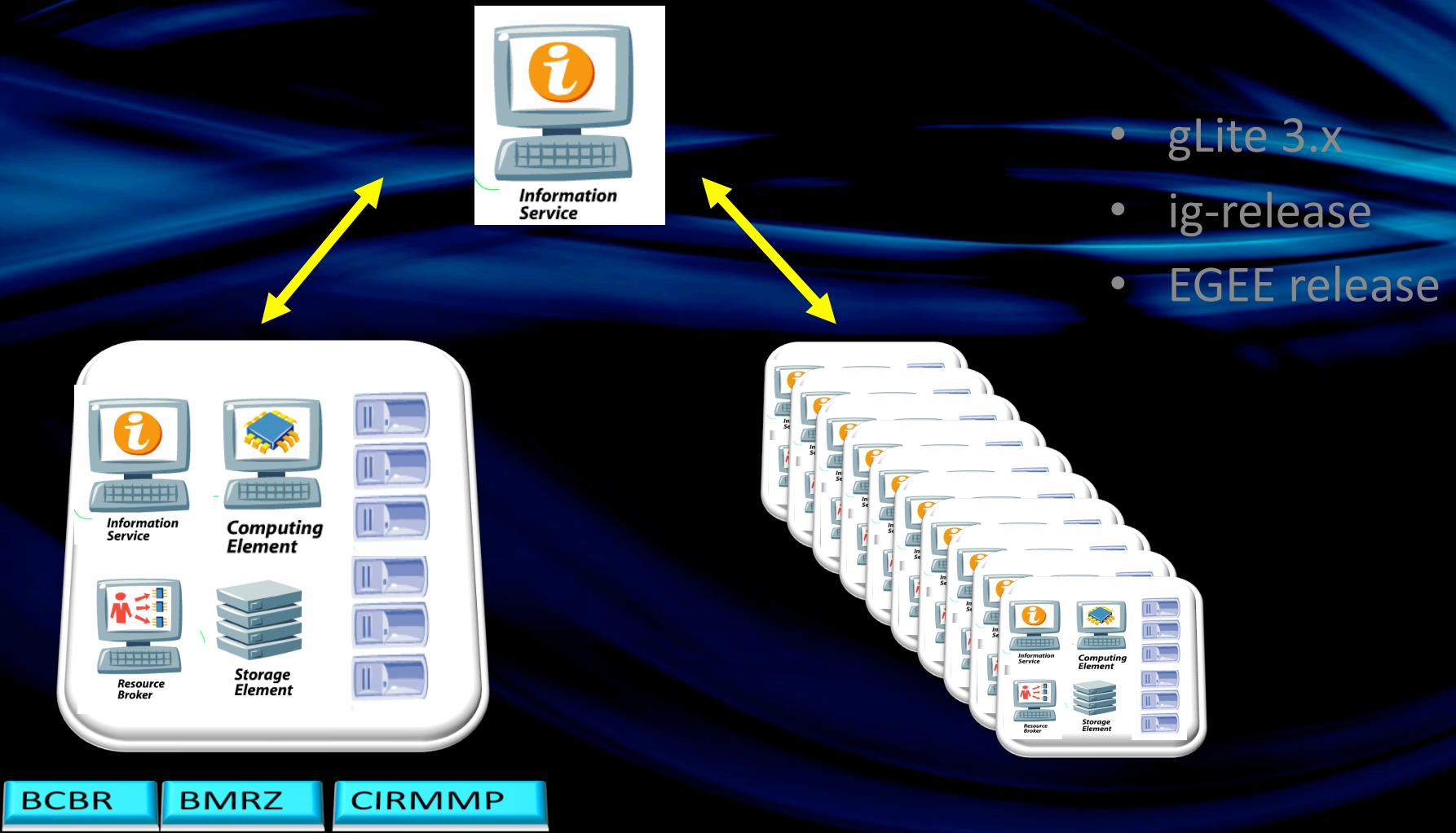
I3 initiatives

- EU-NMR
- EAST-NMR

Coordination action

- NMR-Life

enmr.eu VO grid architecture



e-NMR portal @ www.enmr.eu

e-NMR

NMR computational infrastructure

[Home](#) [HADDOCK](#) [Xplor-NIH](#) [CYANA](#) [CS-ROSETTA](#) [TALOS+](#) [MARS](#) [AutoAssign](#) [MDD](#) [RSS](#)
[FormatConverter](#) [3D-DART](#) [eNMR-Grid](#) [eNMR Wiki](#)

WELCOME TO THE E-NMR WEB PORTAL >>

e-NMR aims at deploying and unifying the NMR computational infrastructure in system biology, a project funded under the [7th framework program](#) of the European Union (Contract no. 213010 - e-NMR).

NMR plays an important role in life sciences (biomolecular NMR), and structural biology in particular, at both European and international levels. Our main objective is to optimize and extend the use of the NMR Research Infrastructures of [EU-NMR](#) through the implementation of an e-Infrastructure in order to provide the biomolecular NMR user community with a platform integrating and streamlining the computational approaches necessary for NMR data analysis and structural modelling (e-NMR).

HADDOCK BIOMOLECULAR DOCKING



[HADDOCK](#) (High Ambiguity Driven protein-protein DOCKing) is an information-driven flexible docking approach for the modeling of biomolecular complexes. HADDOCK distinguishes itself from ab-initio docking methods in the fact that it encodes information from identified or predicted protein interfaces in ambiguous interaction restraints (AIRs) to drive the docking process. [HADDOCK](#) can deal with a large class of modelling problems including protein-protein, protein-nucleic acids and protein-ligand complexes. | [GO TO SERVICE >>](#)

PROFILE >>



SERVICES

The e-NMR web portal is an easy gateway for you to use many of the powerful software packages ported by the e-NMR consortium to the GRID.

[LEARN MORE >>](#)

LINKS :

[NMR SPECTROSCOPY >>](#)
NMR Research Group, Bijvoet Center for Biomolecular Research, Utrecht University

HADDOCK web portal

HADDOCK

e-NMR (GRID-enabled) web portal

WELCOME TO THE E-NMR WEB PORTAL >>

This is the easy interface to the HADDOCK docking program. Please define the structure for each molecule you want to dock as well as the residues belonging to the interaction interface.

Docking is performed with default settings that work well for average complexes. If you do not have any special wishes for the system you want to have docked, this is the way to go.

Unfold the menus by clicking on the double arrows. Submit your job by providing your username and password and press submit.

You may supply a name for your docking run (one word)

Name

First molecule

Structure definition

Where is the structure provided?

Which chain of the structure must be used?

PDB structure to submit or: PDB code to download

Restraint definition

Data to drive the docking
Please supply residues as comma-separated lists of residue numbers

Active residues (directly involved in the interaction)

Passive residues (surrounding surface residues)

Define passive residues automatically around the active residues

What kind of molecule are you docking?

Second molecule

Username and password

Username

Password

e-NMR grid status

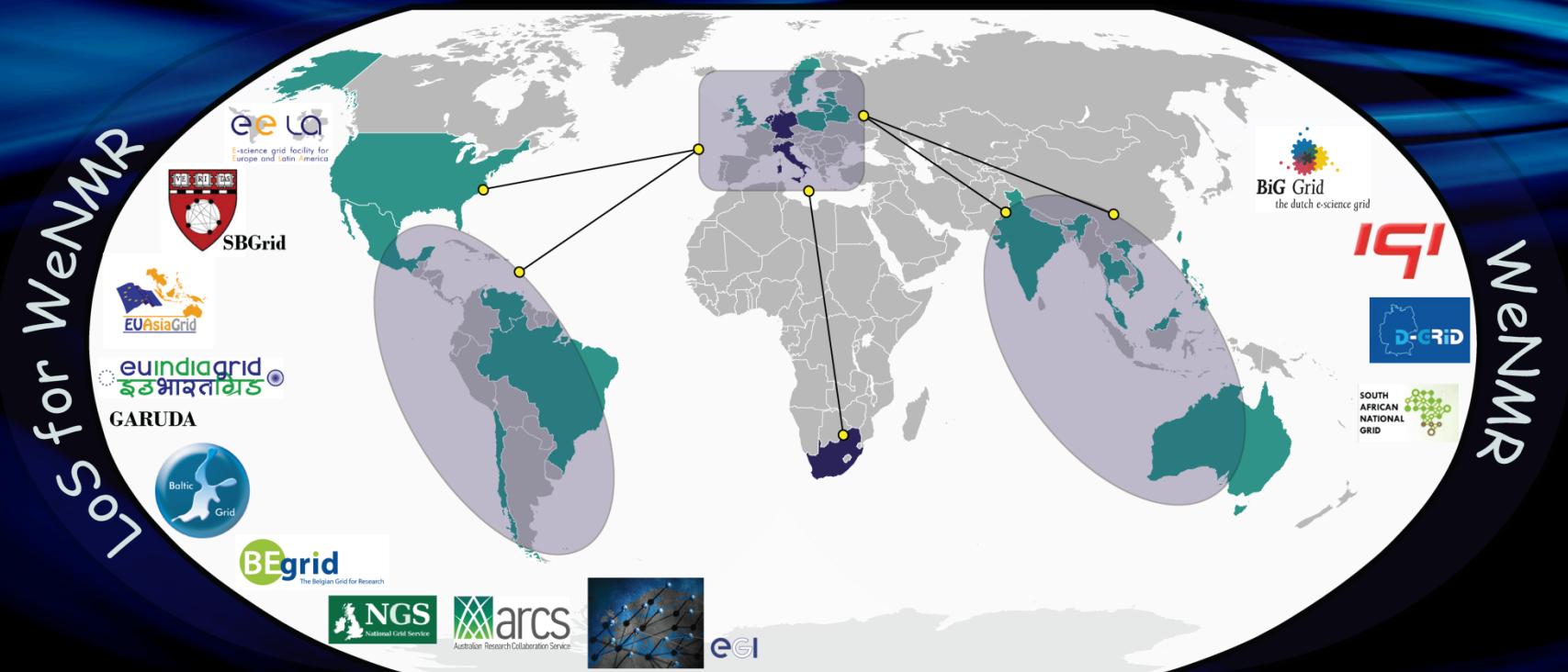
- 2nd largest VO in life sciences with 178 users registered (May 2010)
- 25% of life-science calculations done on the GRID
- 15 grid-sites in 5 countries with ~ 10K CPUs / 150 TB storage
- 9 web portals, ~ 20 applications ported to the grid
- ~ 200 CPU years over last year

Grid Status Report - May 2010																					
GSTAT		OK	INFO	NOTE	WARN	ERROR	CRIT	MAINT	OFF	SFT	.	OK	.	WARN	ERROR	CRIT	SchedDown				
Site List. sort by: siteName domain maxcpu status																					
No Site Reports GIIS Host bnode cernse gperf sanity serv serEntry version sclust totalCPU freeCPU runJob waitJob seAvail TB seUsed TB maxCPU avgCPU gice																					
1	BCBR	bdii1-enmr.chem.uu.nl	ok	note	ok	ok	ok	ok	GLITE-3_2_0	ScientificSL 5.4	44	0	16	37	1.81	0.10	44	43	±		
2	BMRZ-FRANKFURT	ce-enmr.chemie.uni-frankfurt.de	±	±	ok	ok	ok	ok	GLITE-3_1_0	ScientificSL 4.8	11	34	6	14	0.86	0.07	11	10	ok		
3	CIRMMP	ce-enmr.cerm.unifi.it	ok	note	ok	ok	ok	ok	GLITE-3_1_0	ScientificSL 4.5	8	12	0	0	0.48	0.03	8	7	ok		
4	CNR-ILC-PISA	grdice.ilc.cnr.it	±	±	ok	ok	ok	ok	GLITE-3_2_0	ScientificSL 5.4	2	2	2	0	0.23	0.18	2	1	ok		
5	HTC-BIGGRID	deimos.htc.biggrid.nl	±	±	ok	ok	ok	ok	GLITE-3_1_0	ScientificSL 4.6	412	1111	126	3	6.02	0.41	412	411	ok		
6	INFN-BARI	gridba2.ba.infn.it	±	±	±	error	error	±	na	na	na	na	na	na	na	na	757	264	sd		
7	INFN-CATANIA	grid005.ct.infn.it	±	±	ok	ok	ok	ok	GLITE-3_2_0	ScientificSL 4.5	440	76	358	444	5.44	34.07	440	217	ok		
8	INFN-LNL-2	t2-ce-03.lnl.infn.it	±	±	ok	ok	ok	ok	GLITE-3_1_0	ScientificSL 5.3	136	0	484	135	66.47	172.66	136	132	ok		
9	INFN-PADOVA	prod-bdii-02.pd.infn.it	ok	note	ok	ok	warn	ok	GLITE-3_1_0	ScientificSL 4.6	54	4	65	119	28.07	1.55	54	54	ok		
10	INFN-TRIESTE	grid001.ts.infn.it	±	±	ok	warn	error	ok	na	na	na	na	na	na	na	na	136	135	sd		
11	NIKHEF-ELPROD	siteinfo03.nikhef.nl	ok	ok	ok	ok	info	ok	GLITE-3_1_0	CentOS 5.4	1376	76	4898	0	0	3862.77	1376	1320	ok		
12	UKI-SCOTGRID-DURHAM	bdii.dur.scotgrid.ac.uk	±	±	ok	ok	ok	ok	GLITE-3_2_0	ScientificSL 5.3	168	0	664	185	26.85	7.30	168	167	ok		
13	ZA-NWU	ce-lnx1.nwu.ac.za	±	±	ok	warn	±	ok	GLITE-3_1_0	ScientificSL 4.7	24	16	0	0	na	na	24	23	±		
14	ZA-UCT-ICTS	za-uct-ce.uct.ac.za	±	±	ok	ok	±	ok	GLITE-3_1_0	ScientificSL 4.8	16	14	0	0	0.29	0.09	16	11	±		
15	ZA-UJ	glite-ce.grid.uj.ac.za	±	±	±	error	±	±	na	na	na	na	na	na	na	na	2	0	±		
											sites	countries	totalCPU	freeCPU	runJob	waitJob	seAvail TB	seUsed TB	maxCPU	avgCPU	
										Total	15	5	2691	1345	6619	937	0	4079.28	3586	2795	

VO users



The future ...



"Bridging the gap between European e-Science and Iberian America"

In brief

- e-NMR is a new GRID initiative in life sciences
- The e-NMR grid is operational at the various partner sites
- A variety of NMR applications have been successfully ported to the grid
- Several user-friendly web portals are operational
- Use-case examples and tutorials are available online
- Check the current status at www.enmr.eu

Acknowledgments



Antonino Rosato
Mirco Mazzuccato
Andrea Giachetti
Ivano Bertini
Dario Carotenuto
Alexandre Bonvin
Sjoerd de Vries
Gijs van der Schot
Marc van Dijk
Wim Vranken
Harald Schwabe
Henry Jonker
Peter Güntert
Victor Zhuravkin
Anurag Bagai
Johan van der Zwan
Rolf Boelens



Utrecht
University



gLite grid enabled infrastructure

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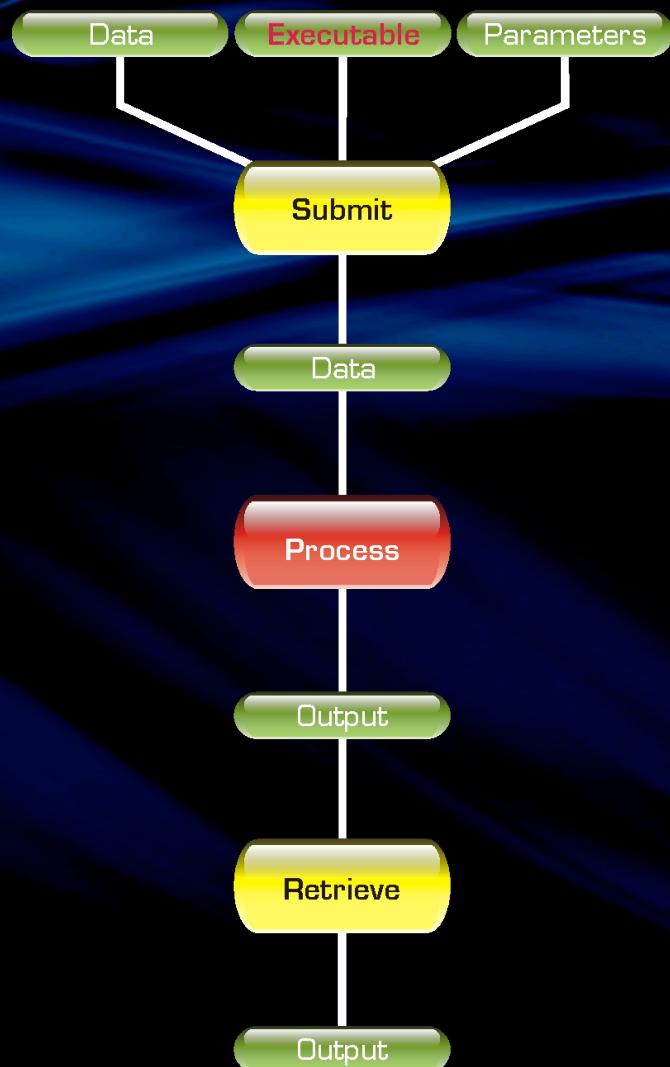
/O=users

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/OU=chem

/CN=Nuno Loureiro Ferreira

Running Applications on the GRID



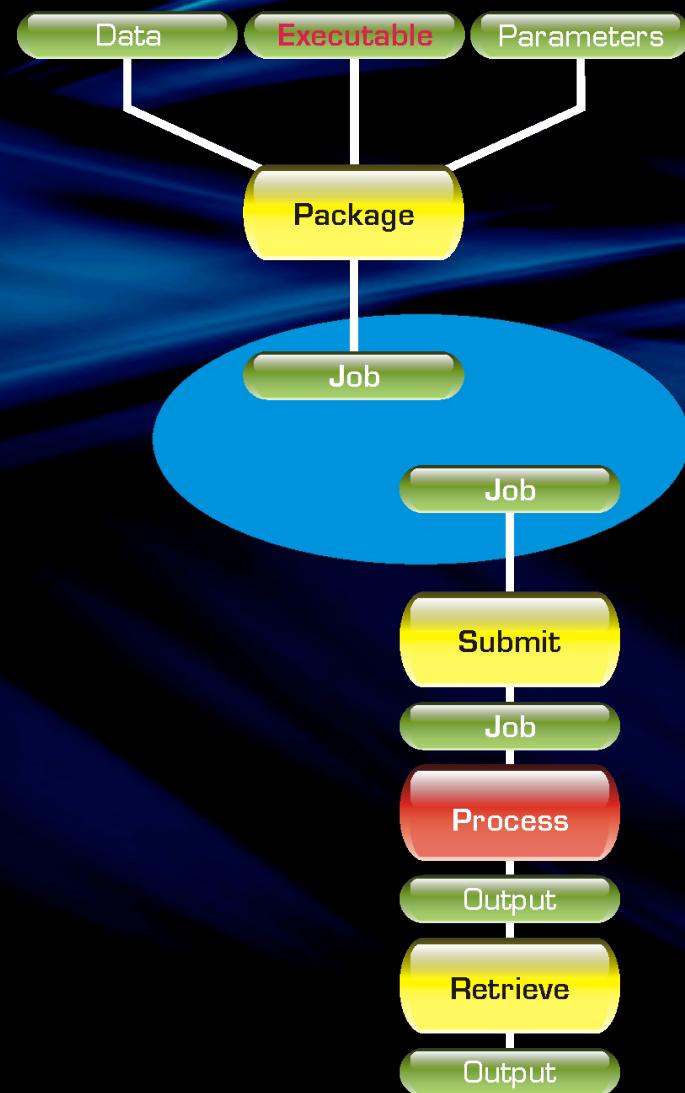
Job consisting of

- JDL
- Data
- Executable
- Program dependencies

Submission through WMS

Retrieval through WMS

Running Applications on the GRID

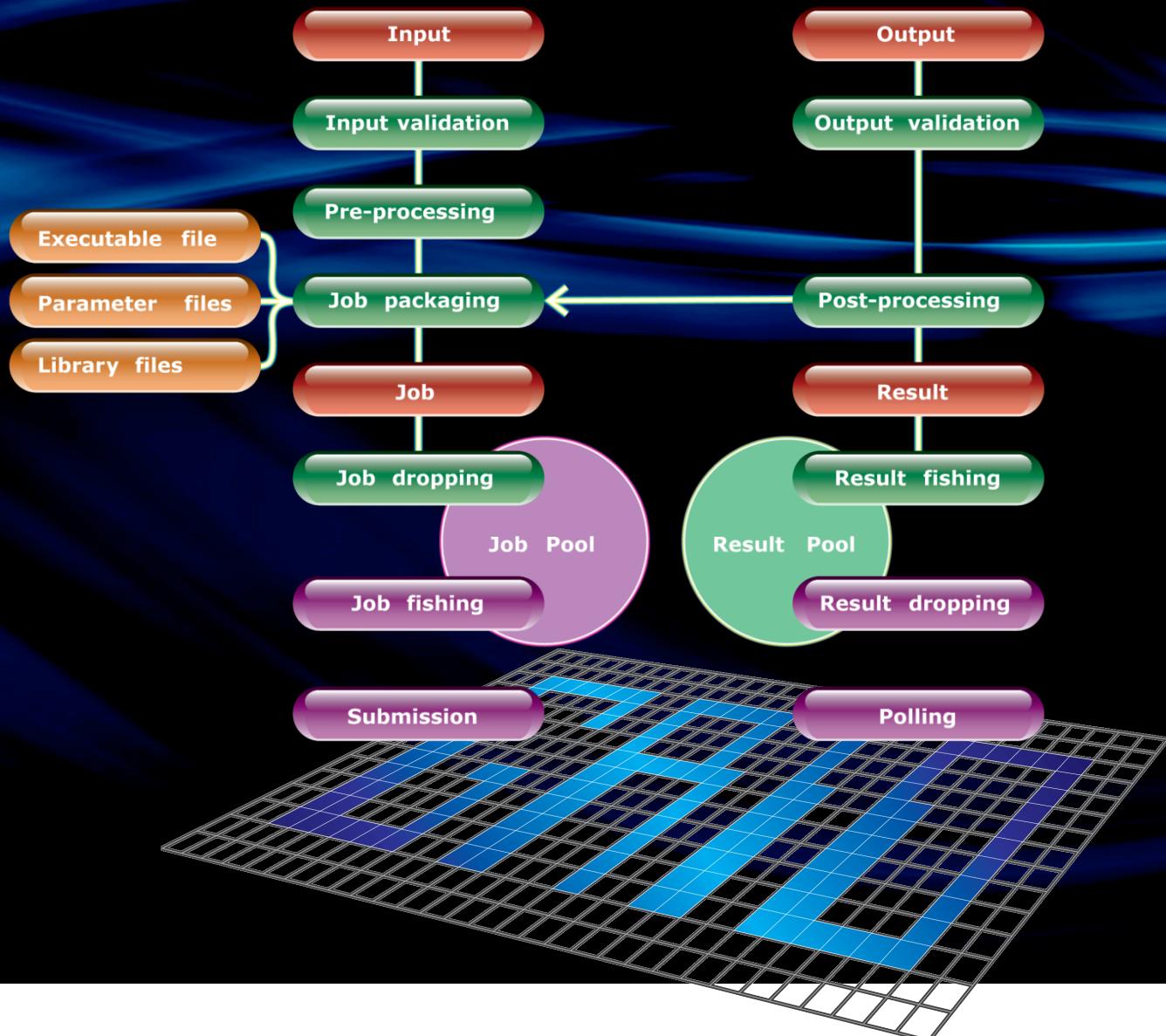


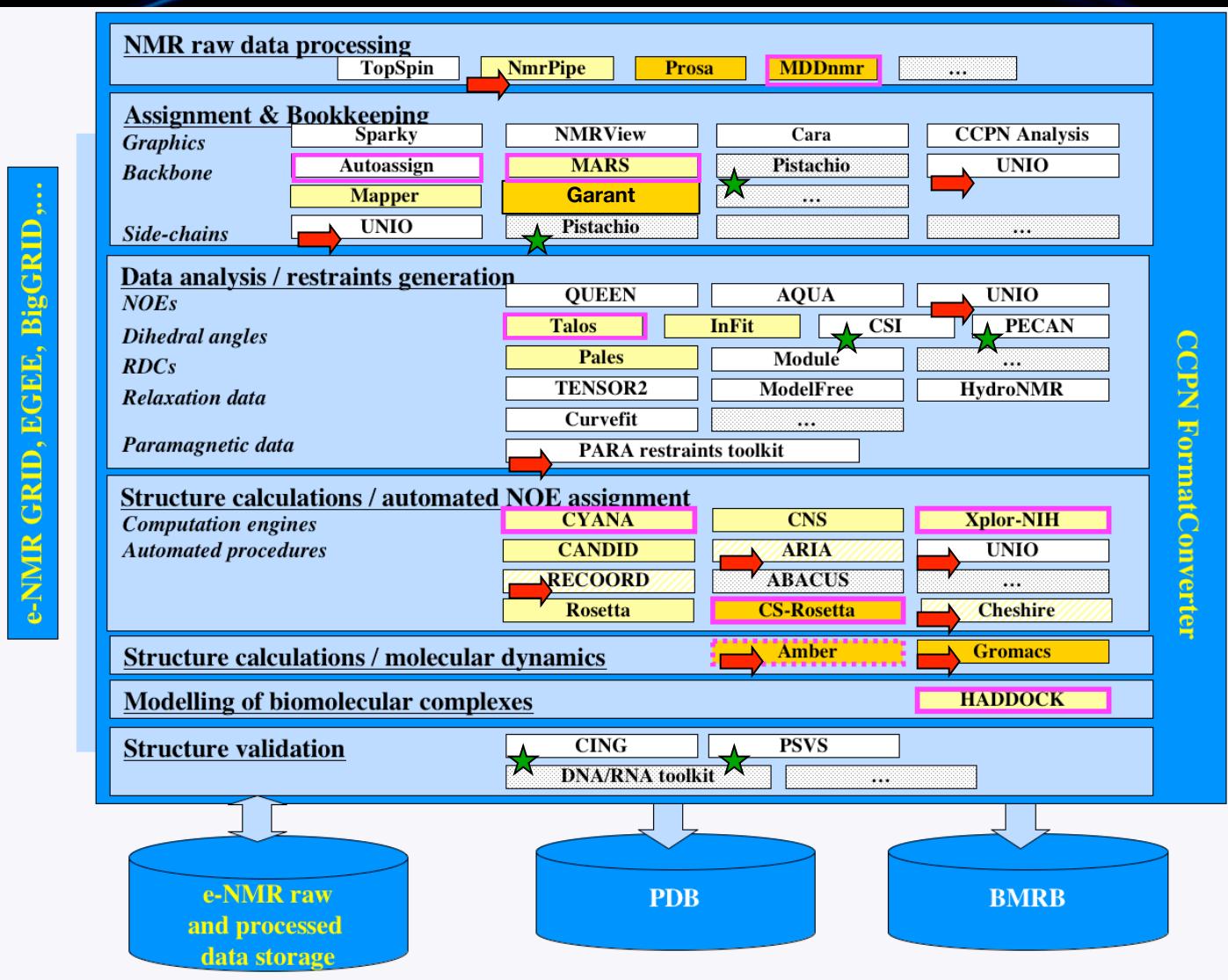
Jobs are packaged and deposited in a pool

Submission Daemon takes jobs from pool

Polling Daemon checks status for submitted jobs and retrieves data

From GRID application to Web service





- In progress
- GRID enabled
- GRID enabled (T3.4)
- web portal
- Portal development
- ★ Existing external web portals