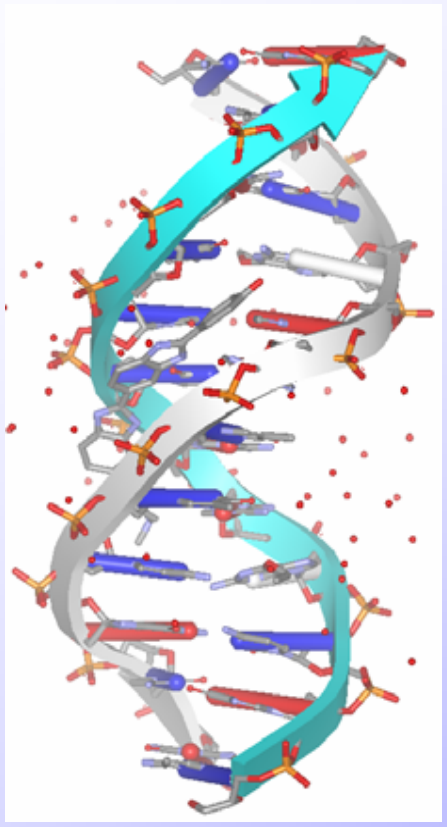
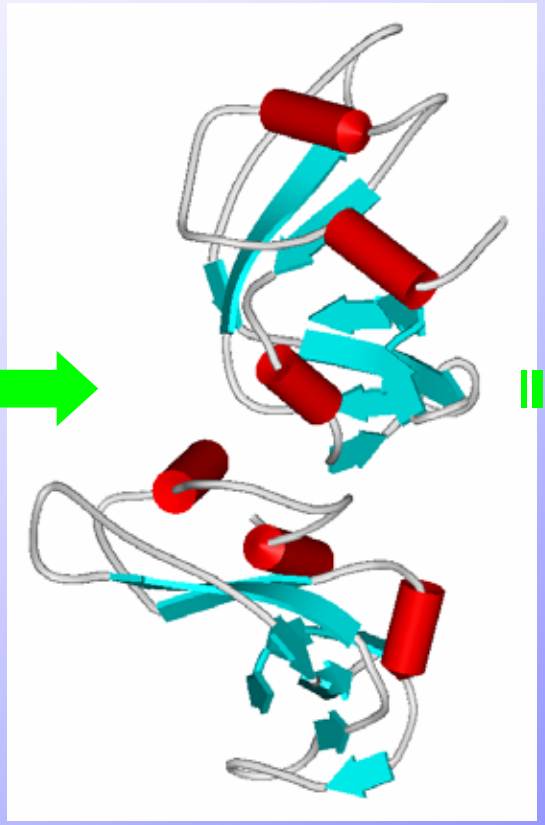
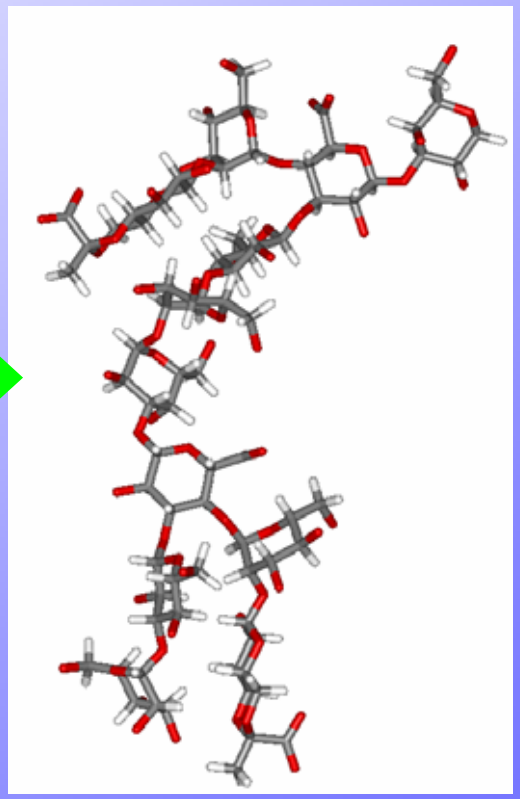
Glyco – MGrid

CyberInfraStructure for *e*-Glycomics

Biomacromolecules & Carbohydrates - Structural Motif







DNA (102D)

C G C A A A T T T G C G C G C
A A A T T T G C G

Protein (1W4Q)

LYS GLU THR ALA ALA ALA LYS PHE GLU
ARG GLN HIS MET ASP SER SER THR SER
ALA ALA SER SER SER ASN TYR CYS ASN

Carbohydrate (1CAP)

b-D-Manp-(1-6)+
|
a-D-Manp-(1-6)+
| |
b-D-Manp-(1-3)+ b-D-Manp-(1-4)-b-D-GlcpNAc

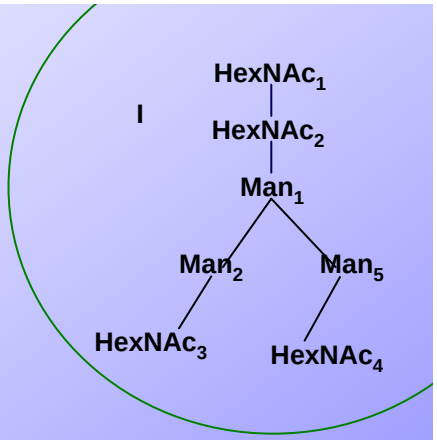
Gene – Genomics
Protein – Proteomics
Glycoconjugates – Glycomics

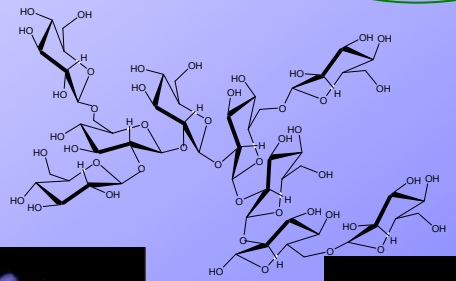
DNA
Protein

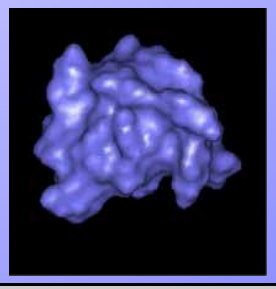
e-Glycomics

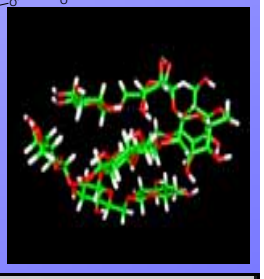
Sweet/
Sugar

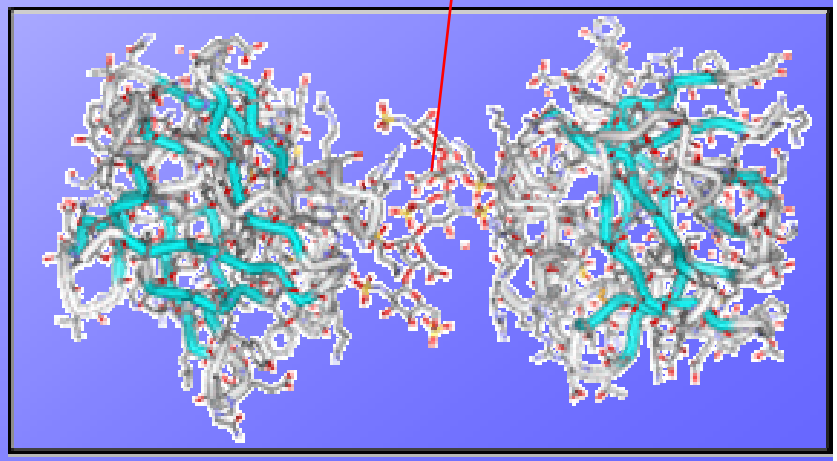
Carbohydrate











Emerging Technologies

AN MIT ENTERPRISE TECHNOLOGY REVIEW

Grid computing

Grid protocols link everything else - databases, simulation tools, and underutilized computing power. Computer grids function analogously to the electric grid. **Widely dispersed on-line resources become available to focus on the problem at hand.**

Glycomics

Glycomics is the effort to **understand and harness sugars that are naturally made** by the human body, in order to improve health by bolstering the immune system or by arresting disease processes. Sounds easy, but there is, **as of yet, no code that determines the structure of the sugars.**

CharmmGrid,
AmberGrid,
MGRID
GaussianGrid
GamessGrid

Molecular Simulations, Informatics, Theory & Analysis

Structure, DataBase, Informatics, Simulations

e-Glycomics & Glyco-MGrid

Web-Portal Molecular Grid

Novel Knowledge

Data Mining Prediction

***e*-GlycoScience** ***e*-GlycoScience**

Databases for Carbohydrates and Glyco-compounds in WWW

DataBase	DataBases			Simulations				
	1D Sequence	3D structure	User-Interface	Conformation Computing	Solvent Effect	Carbo-Parameter	Grid System	Sharing System
CarbBank	O	×	O	×	×	×	×	×
SUGABASE	O	×	O	×	×	×	×	×
SWEET	O	O	O	O	×	×	×	×
GlycoMaps Database	×	×	O	O	×	×	×	×
Glydict	×	×	×	O	×	×	×	×
CAZy	O	×	O	×	×	×	×	×
Glycoconjuate DataBank	O	O	O	×	×	×	×	×
GlycoSuite	O	×	O	×	×	×	×	×
Functional Glycomics	O	O	O	×	×	×	×	×
MD-Simulator	×	O	O	O	O	×	×	×
BioSimGrid	×	×	O	O	O	×	O	×
Glyco-MGrid System	O	O	O	O	O	O	O	O

CarbBank http://bssv01.lancs.ac.uk/gig/pages/gag/carbbank.htm SugarBase http://www.boc.chem.uu.nl/sugabase/sugabase.html
SWEET http://www.glycosciences.de/modeling/sweet2/doc/index.php GlycoMaps http://www.dkfz.de/spec/glycosciences.de/glycomaps/
MD-Simulator http://www.md-simulations.de/manager/ Glydict http://www.dkfz.de/spec/glydict/
CAZy http://afmb.cnrs-mrs.fr/CAZY/ Glycoconjugates DB http://akashia.sci.hokudai.ac.jp/
GlycoSuite https://tmat.proteomesystems.com/glycosuite/ Functional Glycomics http://www.functionalglycomics.org/static/consortium/
BioSimGrid http://www.biosimgrid.org/

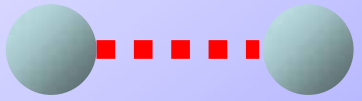
Molecular Simulations & Energy computation

Parameters are derived principally from experimental data, and some calculations. Sources include:

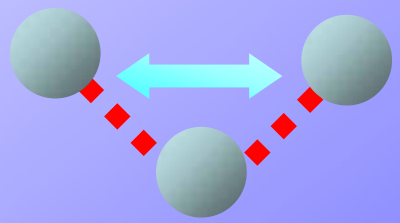
- IR spectra; bond stretching, angle bending, ...
- X-ray crystal structures; geometries and energetics
- solvent simulation to match physical properties (TIP3P)
- ab initio calculations; partial charges
- free energy perturbation with a known experimental result

$$E_{total} = \sum_{r} K_b (r - r_0)^2 + \sum_{\theta} K_\theta (\theta - \theta_0)^2 + \sum_{\phi} \left| K \right|_\phi - K_\phi \cos n\phi + K_\varpi (\omega - \omega_0)^2$$

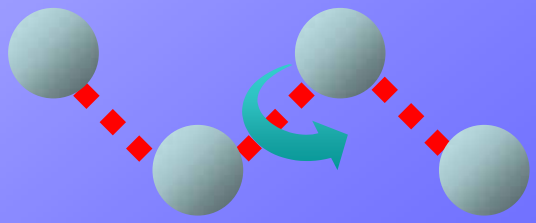
$$+ \sum [(\frac{A}{r_{ij}^{12}}) - (\frac{B}{r_{ij}^{6}})] sw(r_{ij}^2, r_{on}^2, r_{off}^2) + \sum (\frac{q_i q_j}{4\pi\varepsilon_0 r_{ij}})[1 - 2(\frac{r_{ij}}{r_{cut}})^2 + (\frac{r_{ij}}{r_{cut}})^4]$$



-bond-

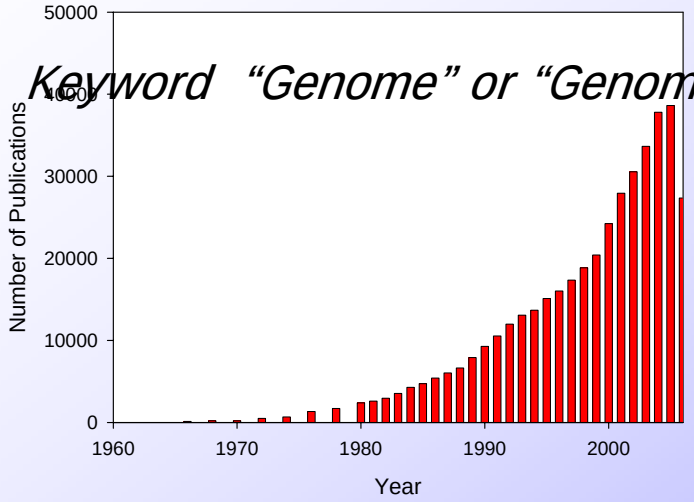


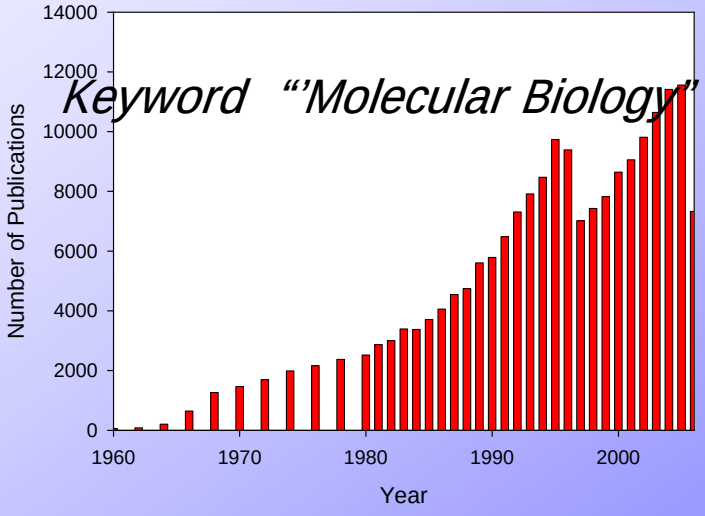
-angle-

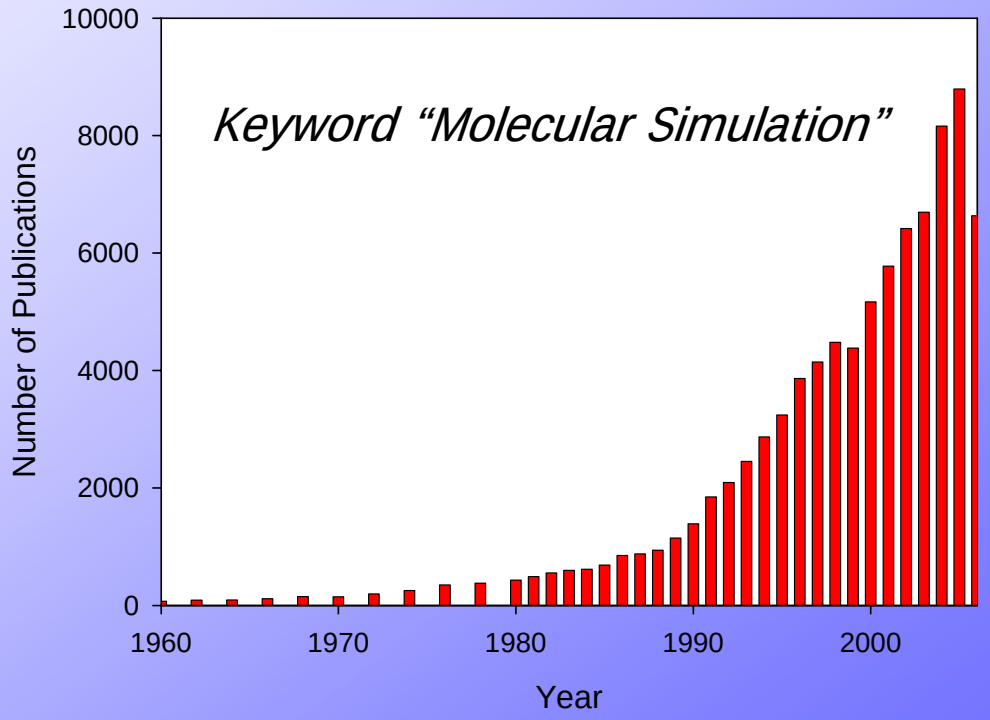


-dihedral-

Publication Increase during the last 45 years *- from SciFinder*







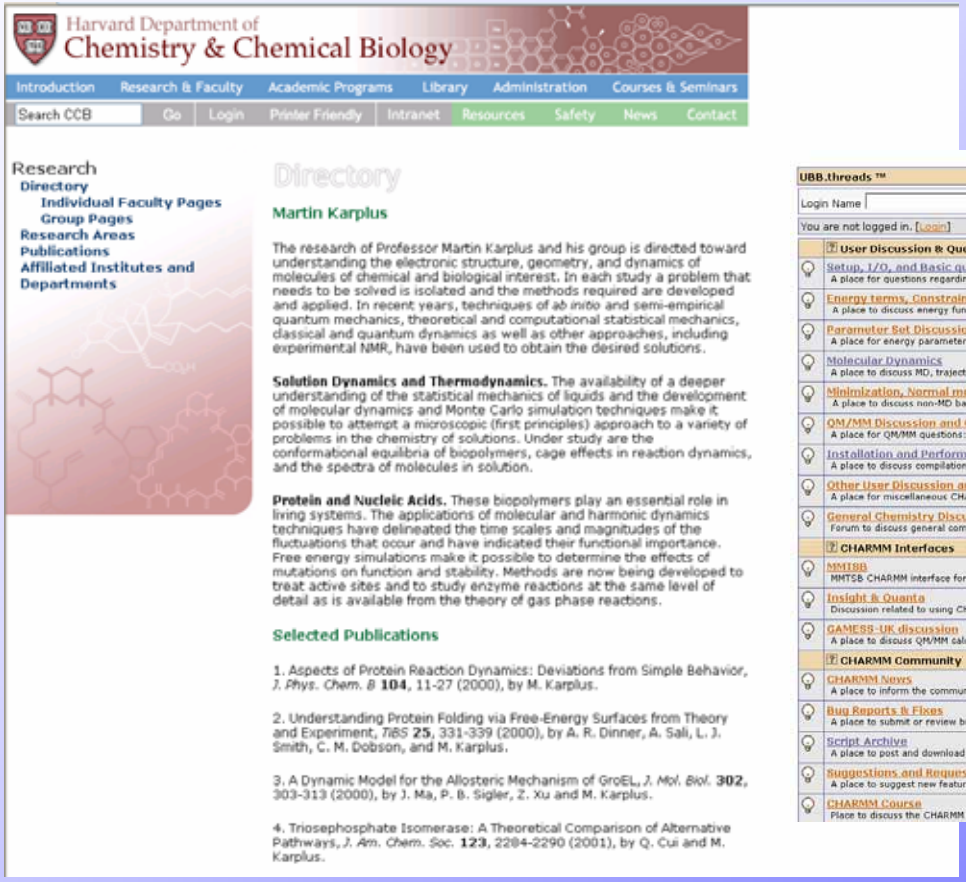
"Publish or perish" *refers to the pressure to publish work constantly in order to further or sustain one's career in academia. The competition for tenure-track faculty positions in academia puts increasing pressure on scholars to publish new work frequently.*

CHARMM

Chemistry at HARvard
Macromolecular Mechanics

Supporting Area

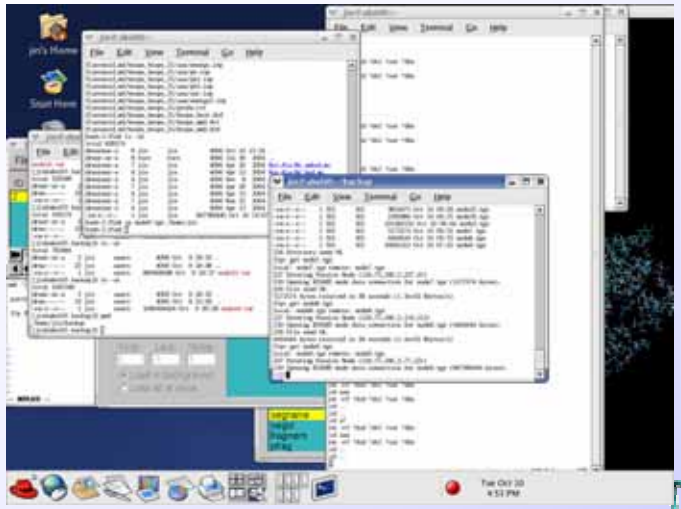
- Molecular Mechanics
- Molecular Dynamics
- Monte Carlo
- QM/MM
-Free Energy Calculation
- Coordinate Analysis



http://www.charmm.org

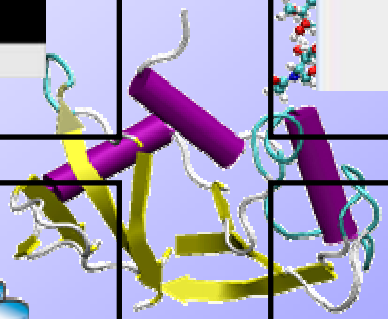
Molecular Simulations & e-Science

Shell Terminal

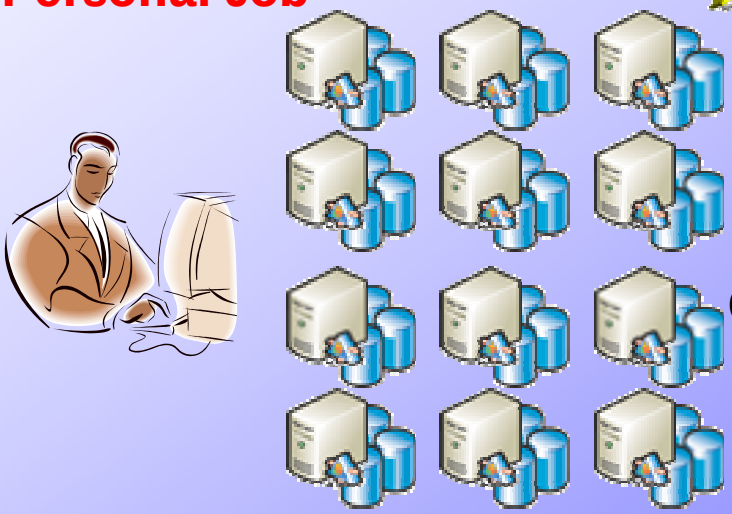


Web-Interface

Portal

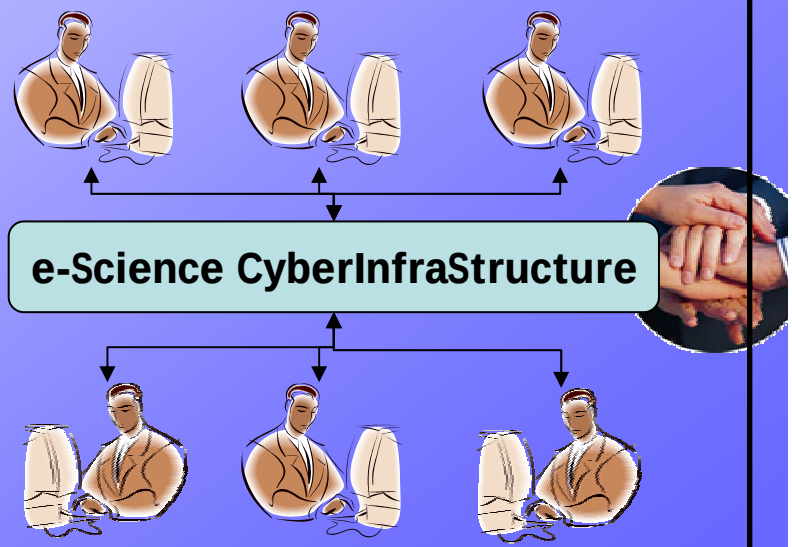


Personal Job

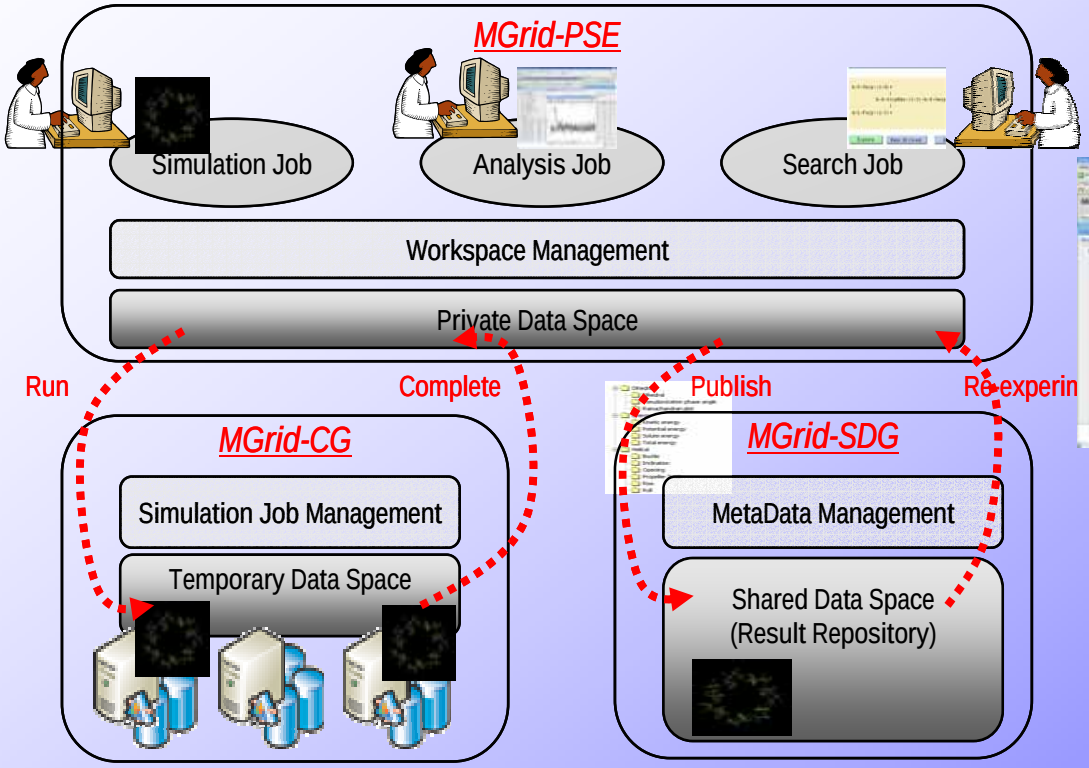


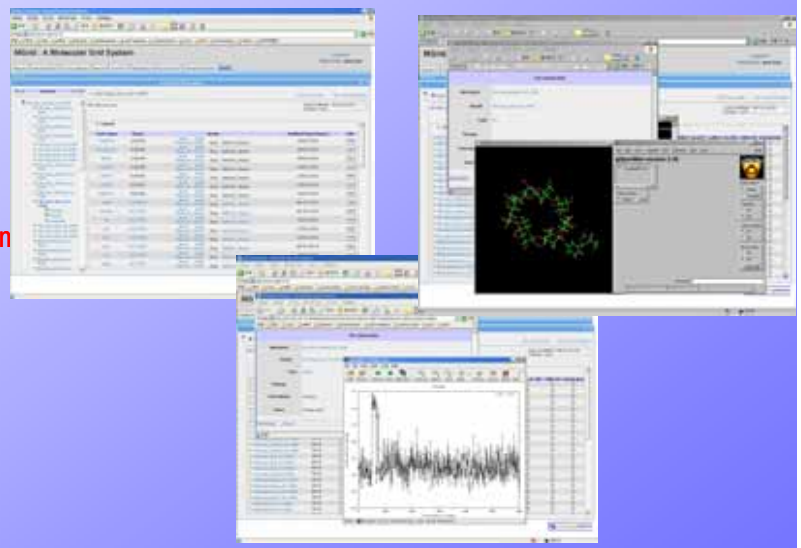
Collaboration

Multidisciplinary Work

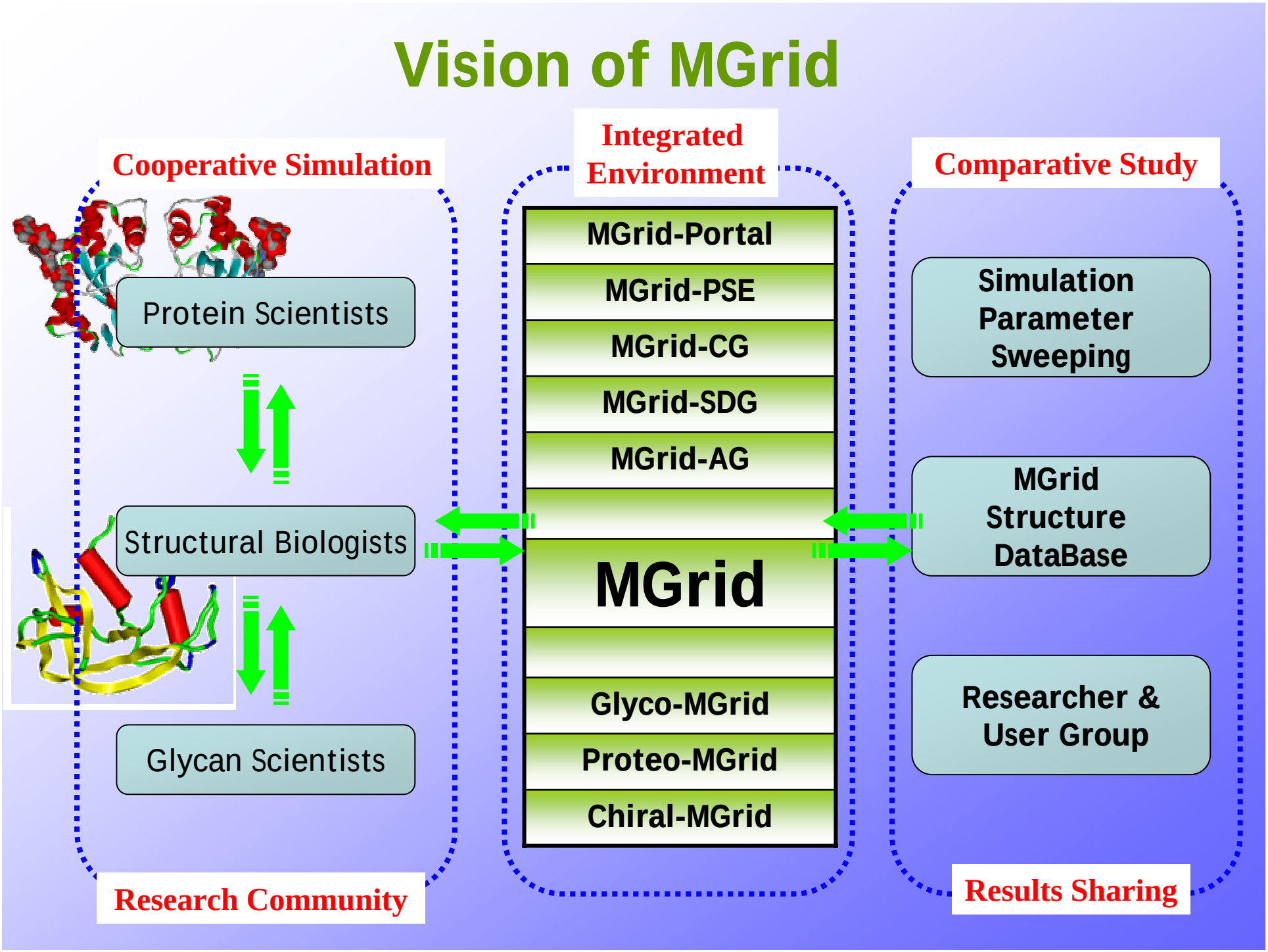


Architecture of MGrid

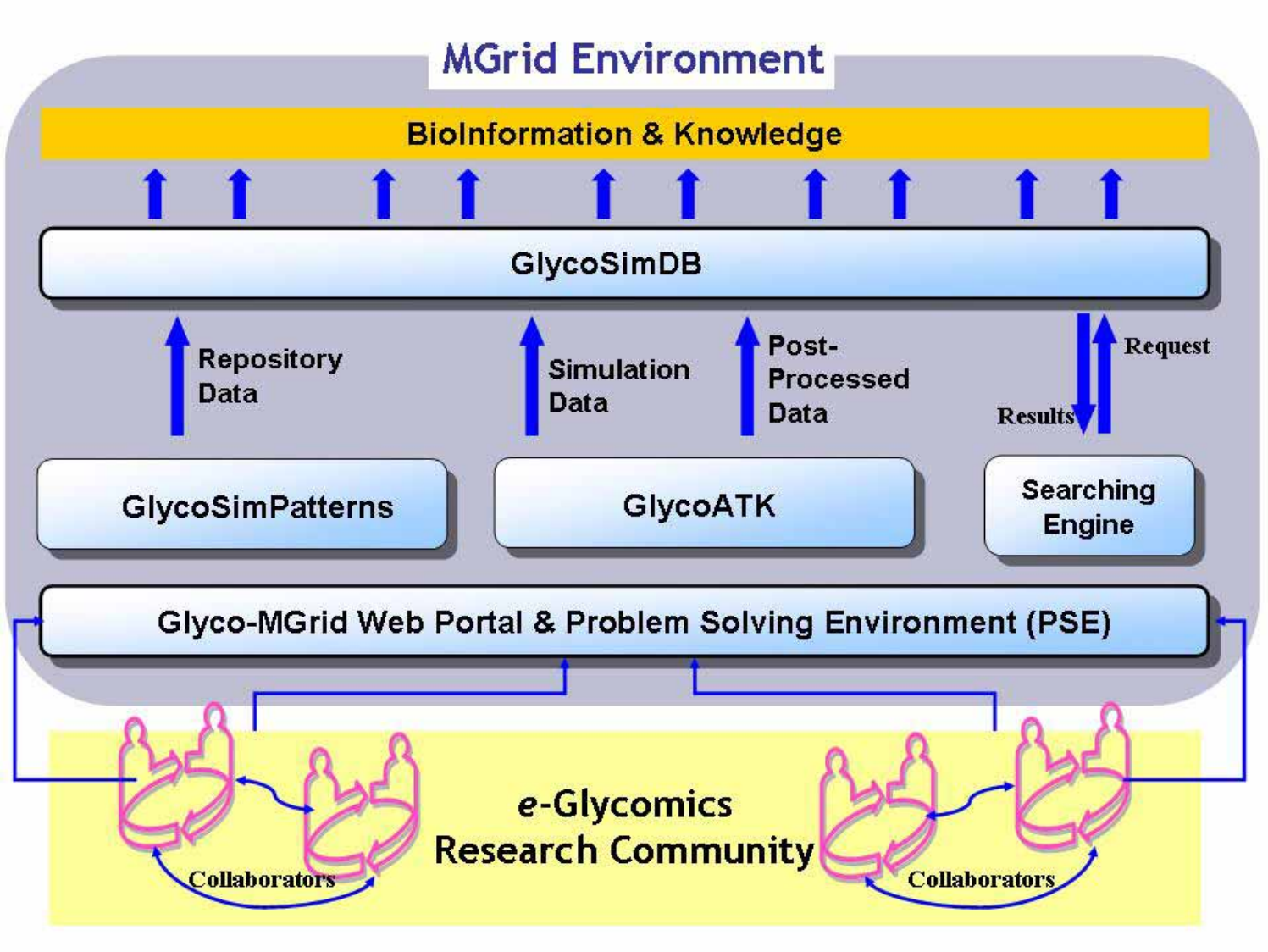




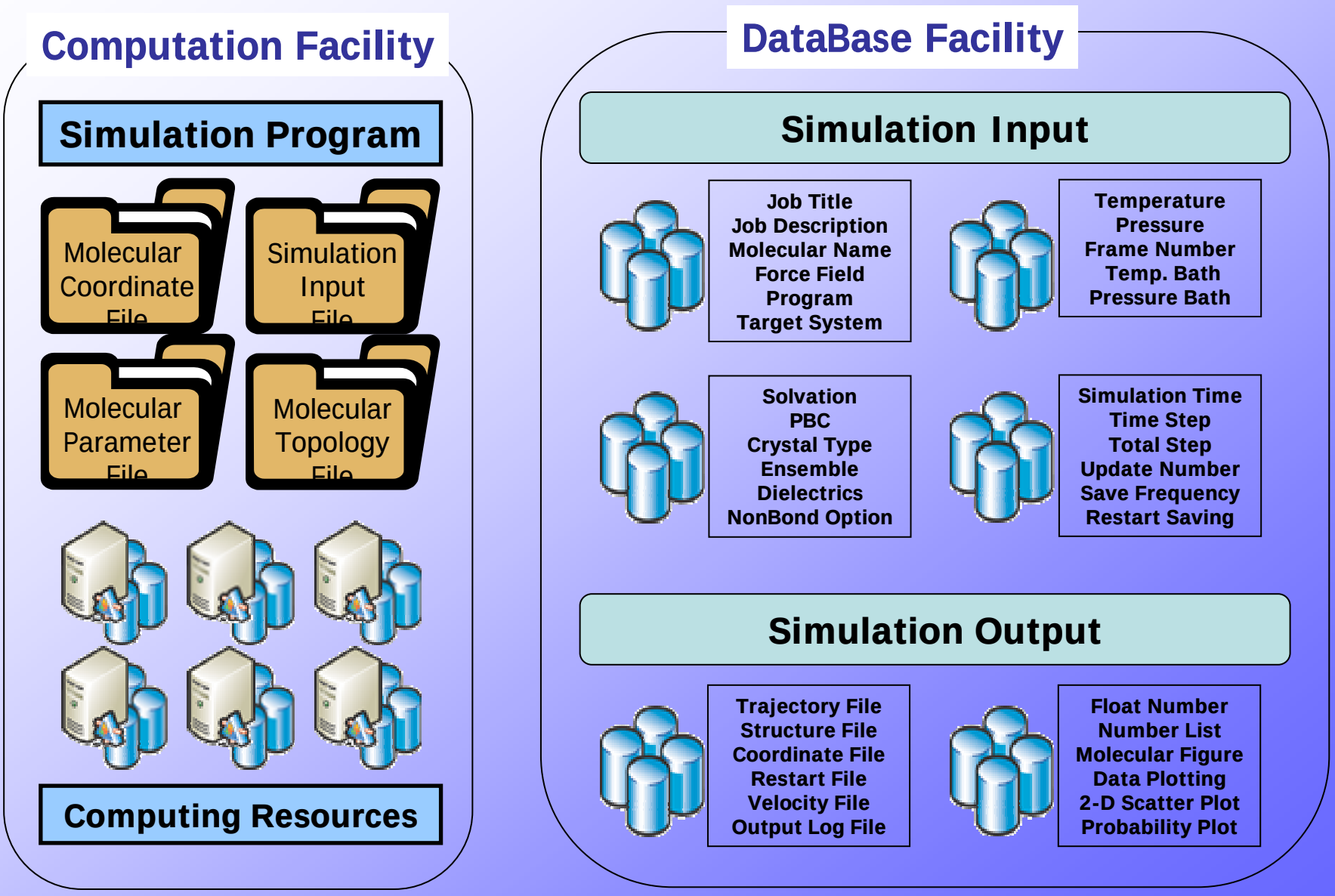
Vision of MGrid



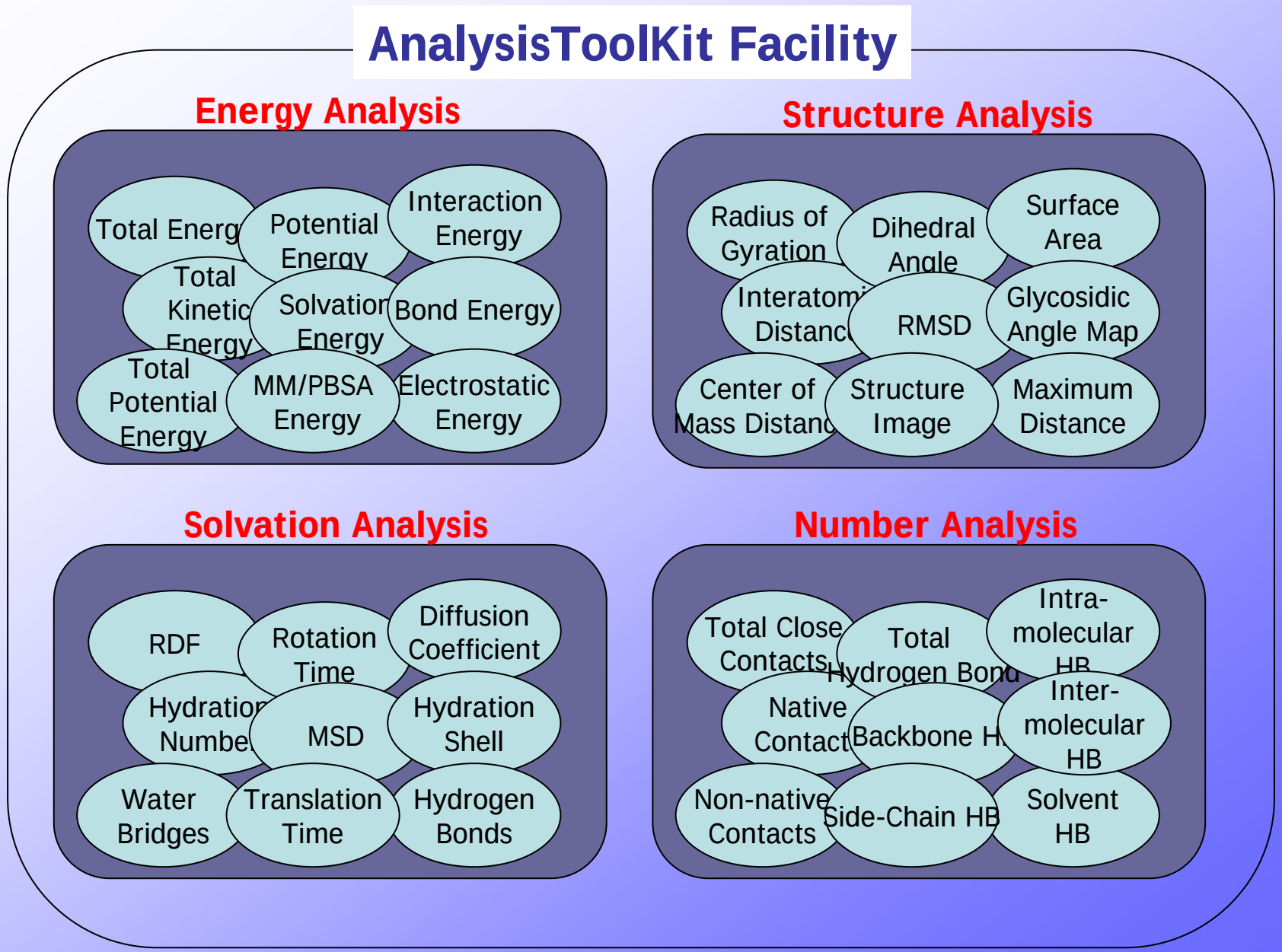
Architecture of Glyco-MGrid



Components of Glyco-MGrid

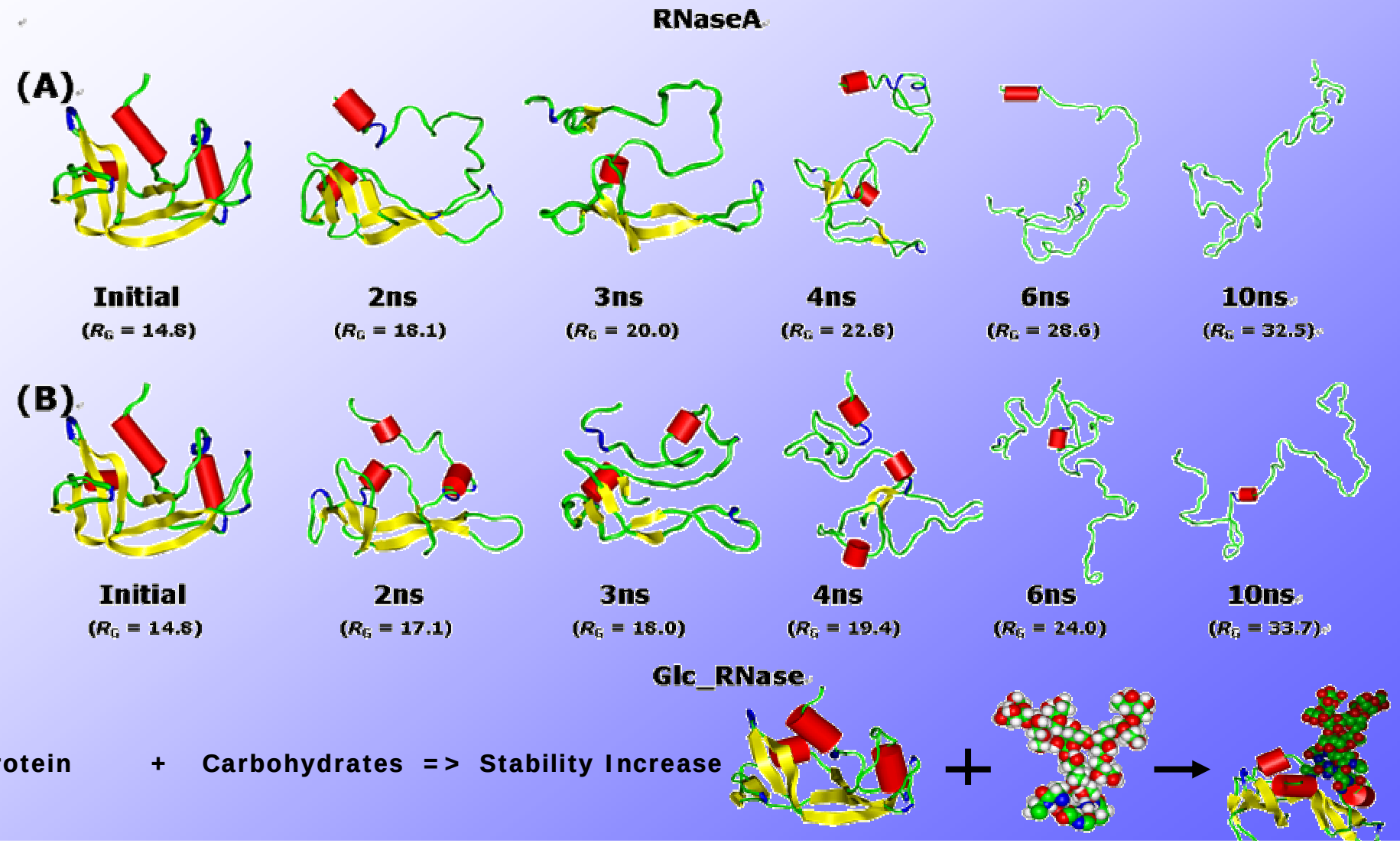


Components of Glyco-MGrid



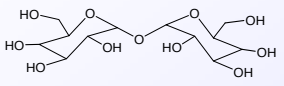
Research Example

Thermal Stability of Unglycosylated RNaseA and *N*-acetylglycosylated Glc_RNase

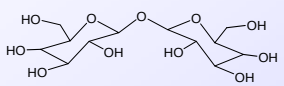


Research Example

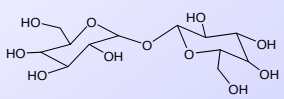
Conformation and Hydration of the Series of Sugars



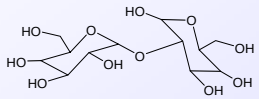
α-D-Glcp-1-1-α-D-Glcp
(**1**)



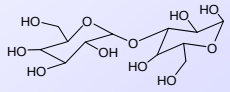
β-D-Glcp-1-1-β-D-Glcp
(**2**)



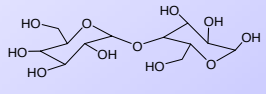
α-D-Glcp-1-1-β-D-Glcp
(**3**)



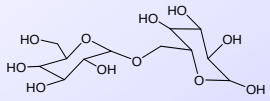
α-D-Glcp-1-2-α-D-Glcp
(**4**)



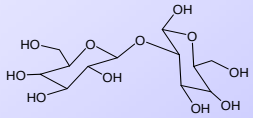
α-D-Glcp-1-3-α-D-Glcp
(**5**)



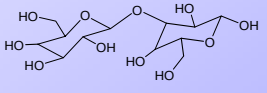
α-D-Glcp-1-4-α-D-Glcp
(**6**)



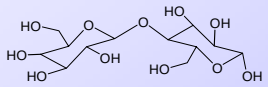
α-D-Glcp-1-6-α-D-Glcp
(**7**)



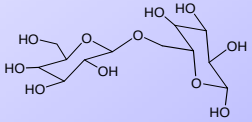
β-D-Glcp-1-2-β-D-Glcp
(**8**)



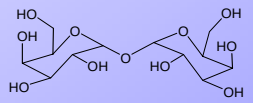
β-D-Glcp-1-3-β-D-Glcp
(**9**)



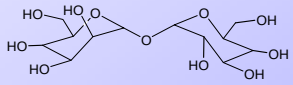
β-D-Glcp-1-4-β-D-Glcp
(**10**)



β-D-Glcp-1-6-β-D-Glcp
(**11**)

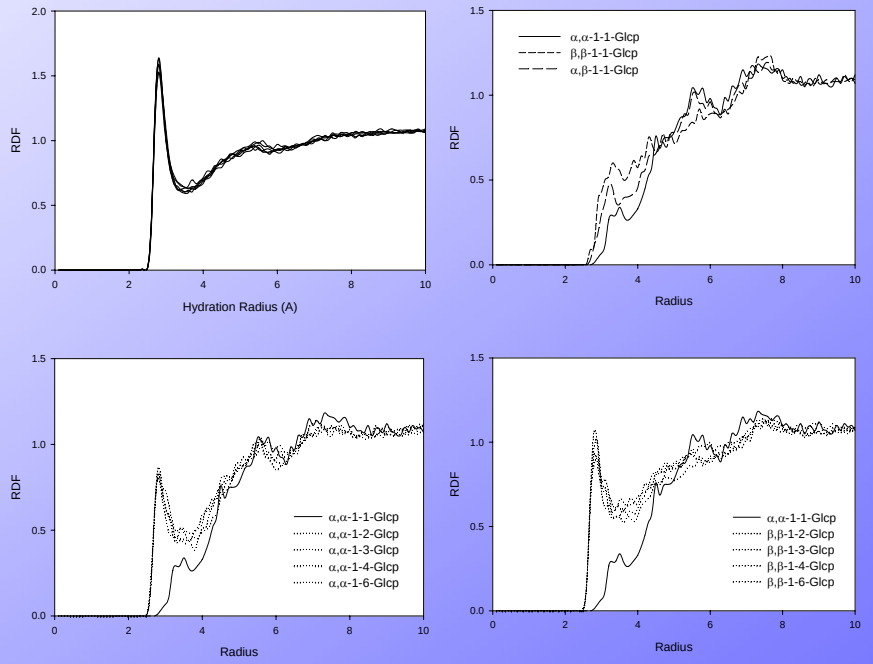


α-D-Galp-1-1-α-D-Galp
(**12**)



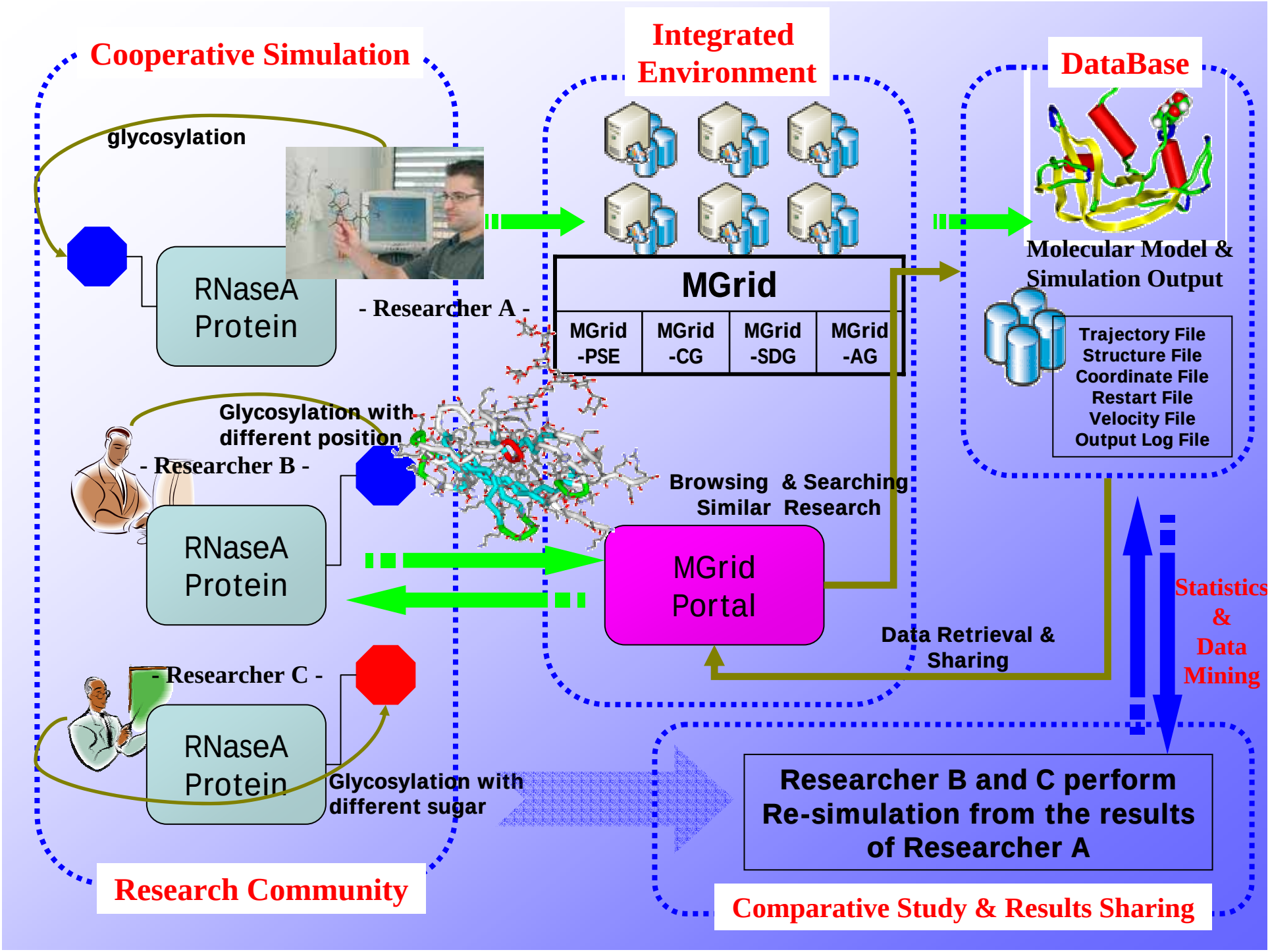
α-D-Manp-1-1-α-D-Manp
(**13**)

Schematic diagrams of the glycosidic linkage model of the sugars studied in this work.

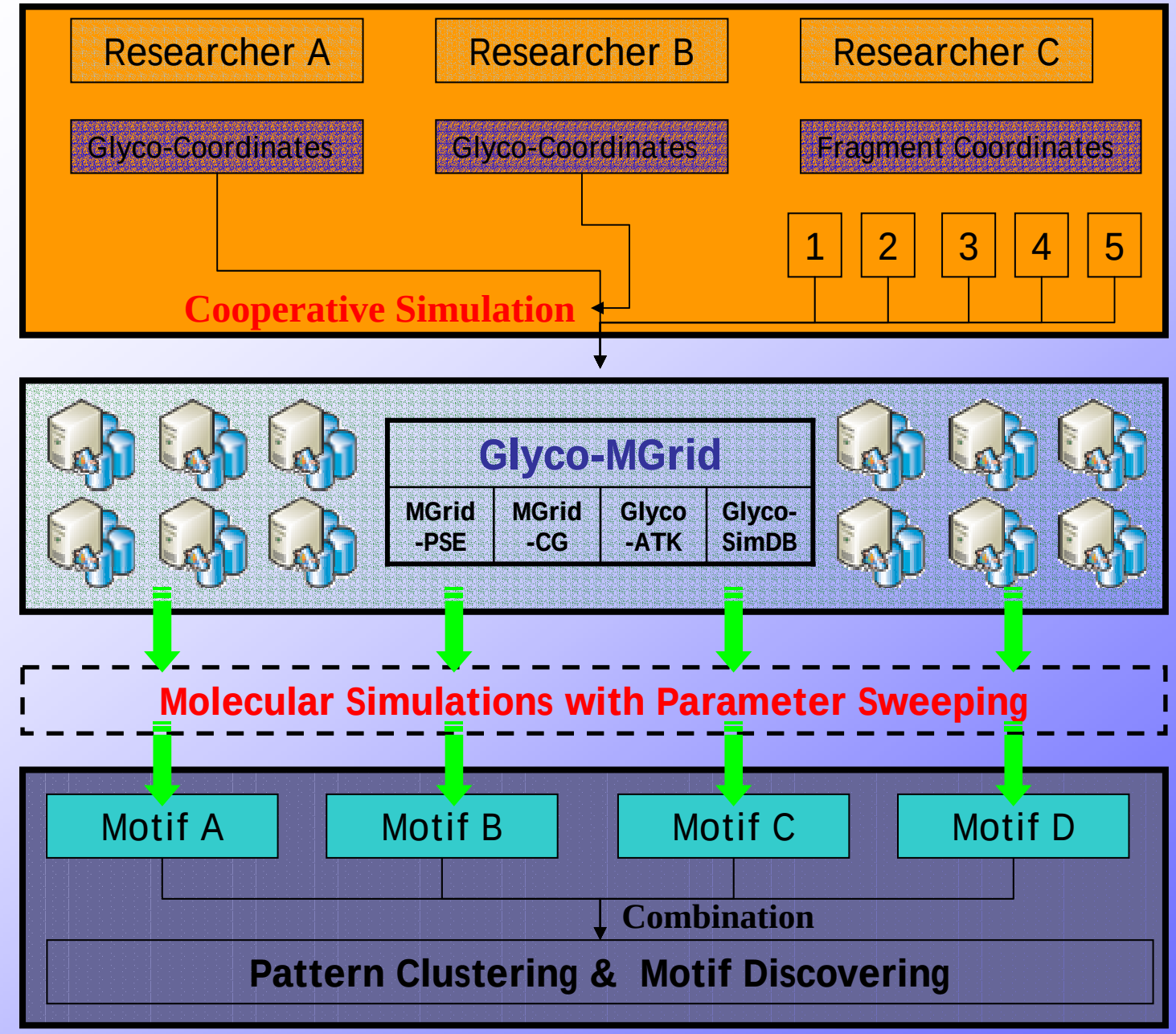


The radial distribution function (RDF) of water molecules around disaccharides. (A) RDF around all oxygen atoms of each disaccharides (B) RDF around glycosidic oxygen of **1**, **2**, and **3** (C) RDF around glycosidic oxygen of **1**, **4**, **5**, **6**, and **7** (D) RDF around glycosidic oxygen of **1**, **8**, **9**, **10**, and **11**. The RDF of water around whole trehalose is not dissimilar to other sugars. But, the RDF of water around glycosidic oxygen of trehalose is quite dissimilar to other linkage typed disaccharides. Only 1,1-linked trehalose showed anisotropic water distribution among the other 1,2-, 1,3-, 1,4- or 1,6-linked sugars.

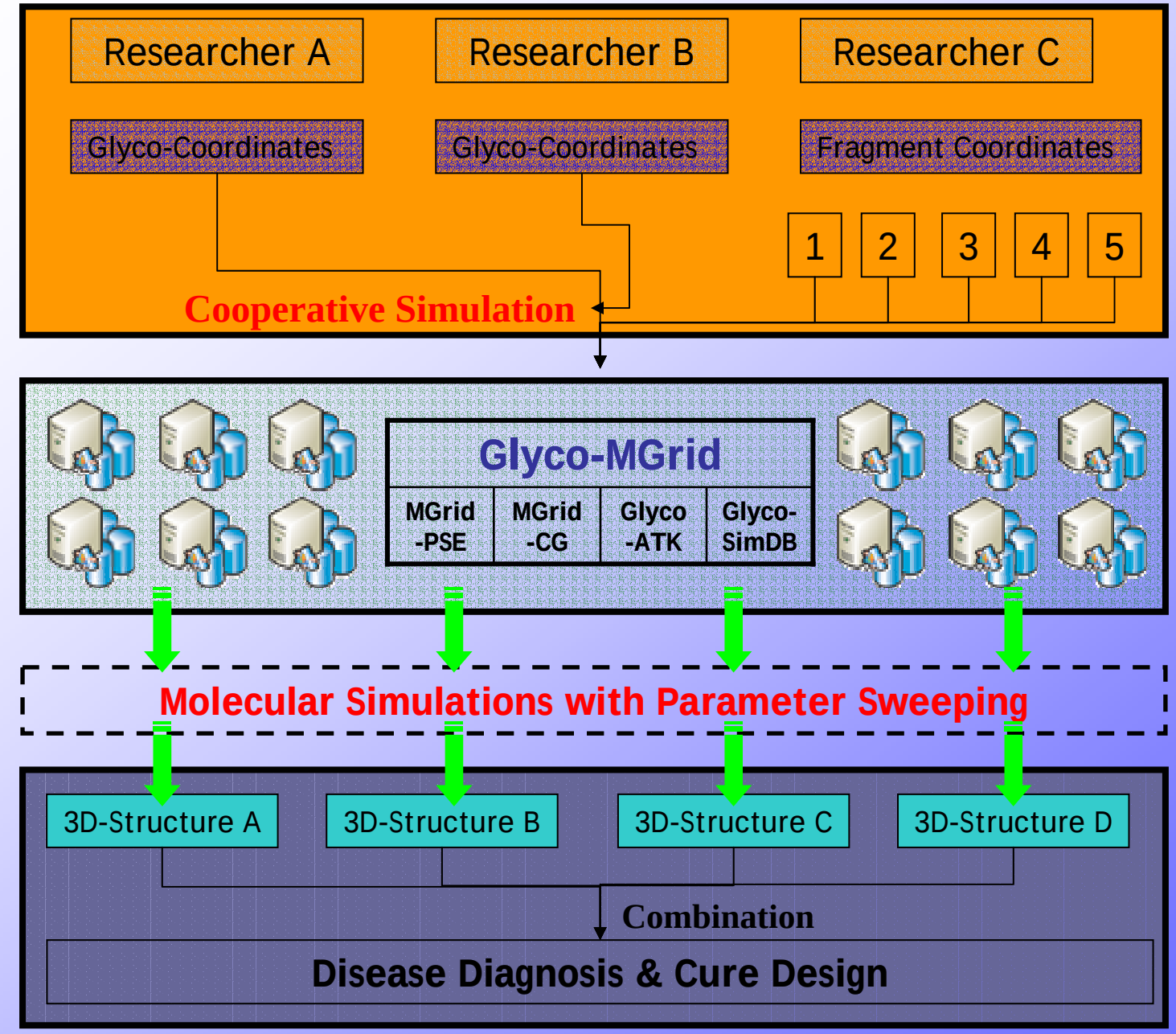
Youngjin Choi; Kum Won Cho; Karpjoo Jeong; Seunho Jung. Molecular dynamics simulations of trehalose as a 'dynamic reducer' for solvent water molecules in the hydration shell. Carbohydrate Research (2006) vol 341. 1020–1028


Cooperative Simulation
Integrated Environment
DataBase
glycosylation
RNaseA Protein
- Researcher A -
MGrid
MGrid -PSE
MGrid -CG
MGrid -SDG
MGrid -AG
Molecular Model & Simulation Output
Trajectory File
Structure File
Coordinate File
Restart File
Velocity File
Output Log File
Glycosylation with different position
- Researcher B -
RNaseA Protein
Browsing & Searching Similar Research
MGrid Portal
Data Retrieval & Sharing
Statistics & Data Mining
- Researcher C -
RNaseA Protein
Glycosylation with different sugar
Researcher B and C perform Re-simulation from the results of Researcher A
Research Community
Comparative Study & Results Sharing

Glyco-Structure Motif Searching Project Scenario



Disease-Related Glycan Modeling Project Scenario



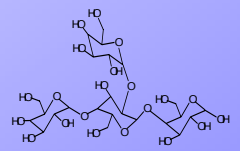
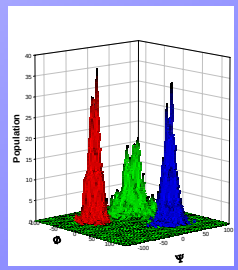
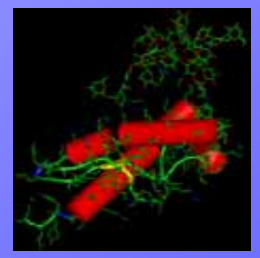
Research Community

Integrated Environment

Comparative & Statistical Study

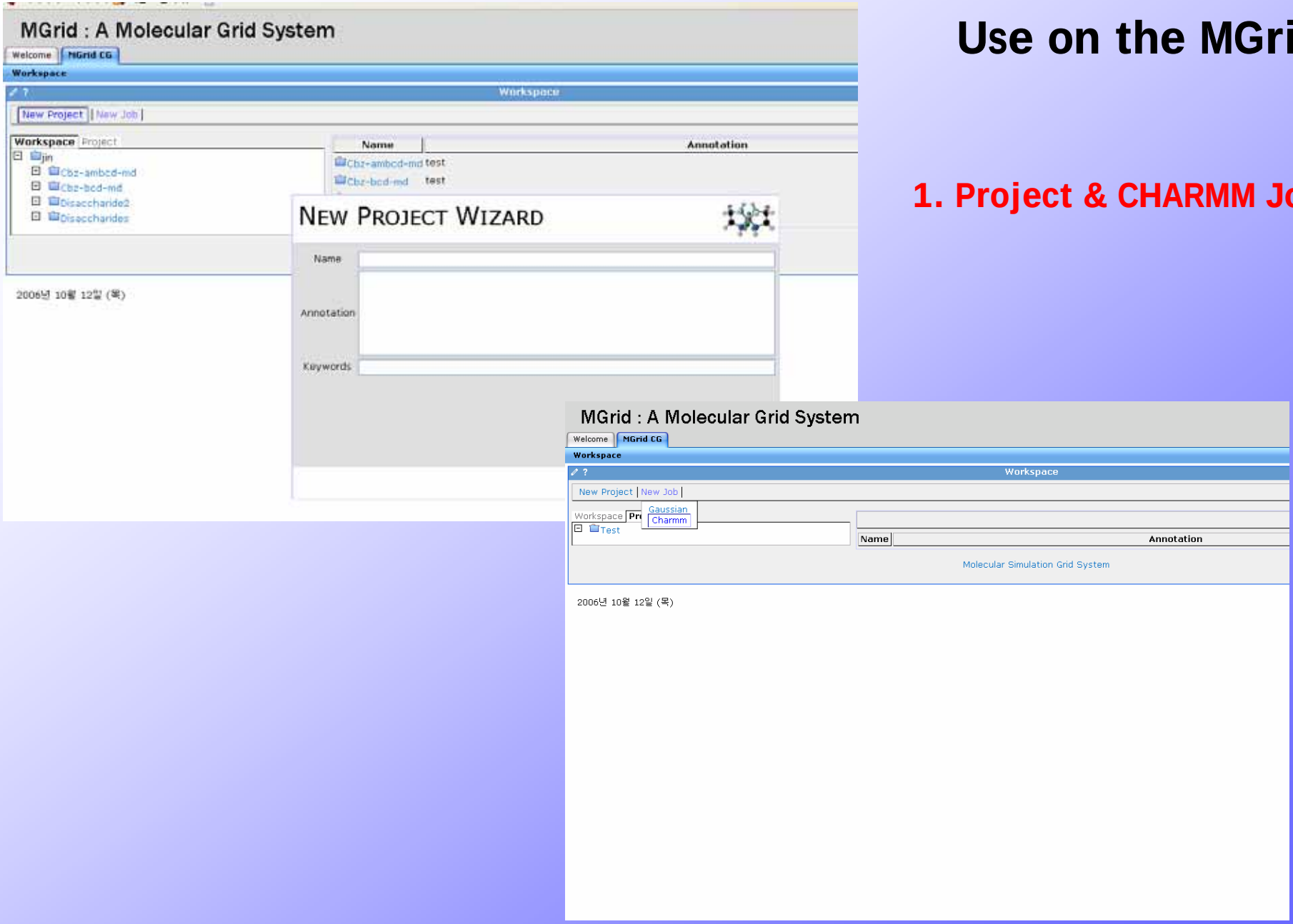
Results Sharing

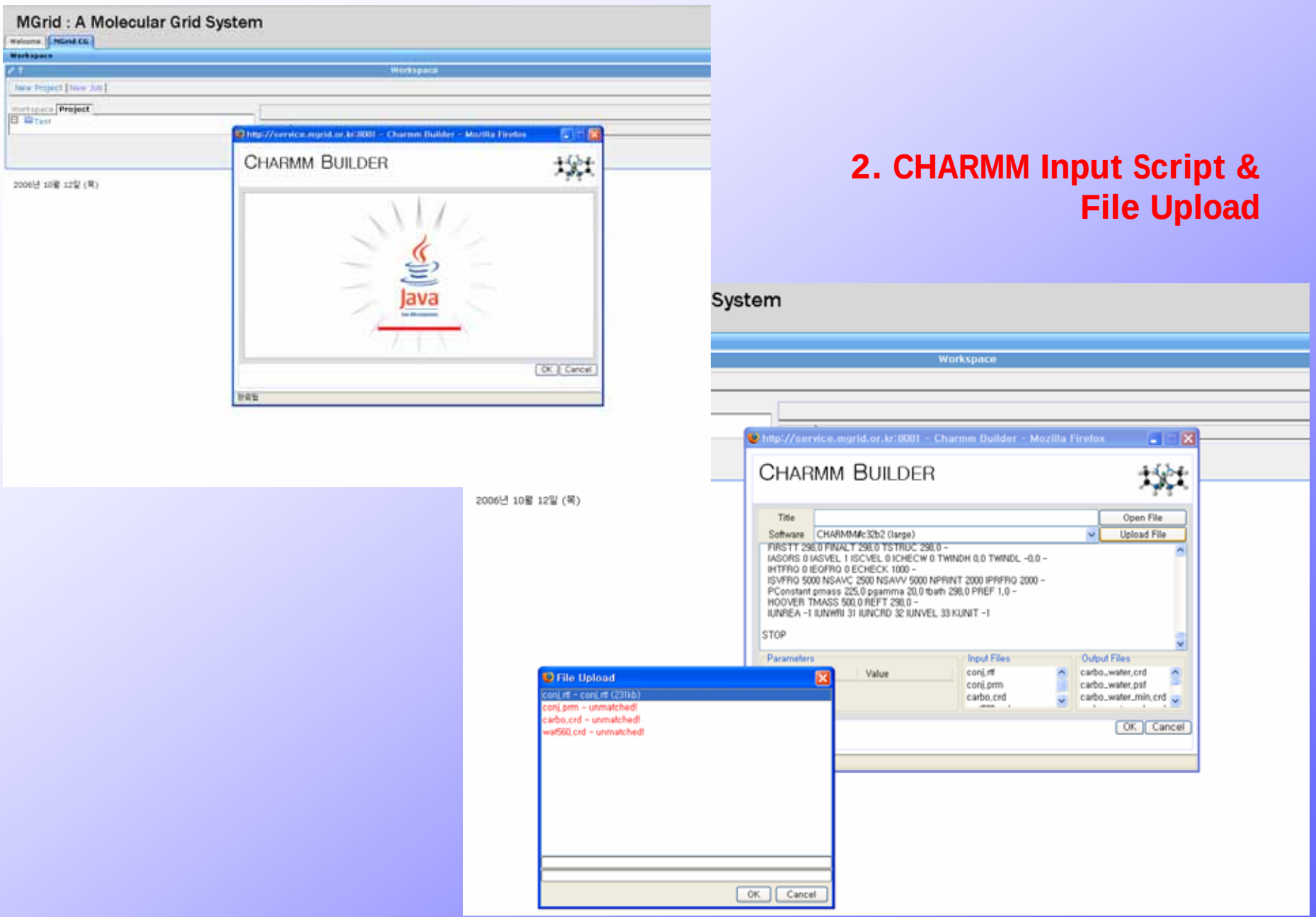
Current-Status of Glyco-MGrid Project

Glyco-compounds	Research Project	Job Details	Analyses
Glycan	Branching	Branching effect on the glycan conformation	
	Glycan Core	Calculation of biological core glycan structure	
Sugar compounds	Glycosidic Linkage	Glycosidic angle map of each glycosidic linkage	
Poly-saccharide	Microbial Carbohydrates	MC and MD conformational searching of bacterial carbohydrates	
	Cyclic Carbohydrates	Conformational characteristics of cyclic carbohydrates	
Glycoprotein	Unfolding	Unfolding simulations for the stability and conformations of glycosylated proteins	
	Folding	Folding simulations for the conformational effects of glycosylation	
	Function	MD simulations for the biological function of glycoproteins	

Use on the MGrid

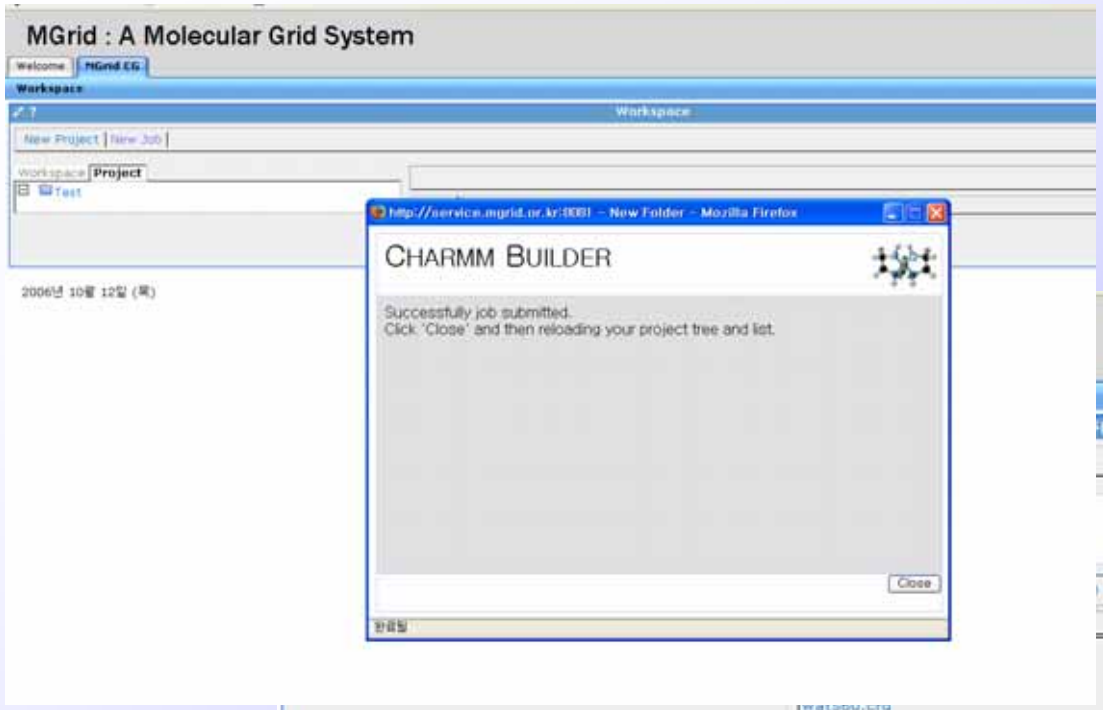
1. Project & CHARMM Job

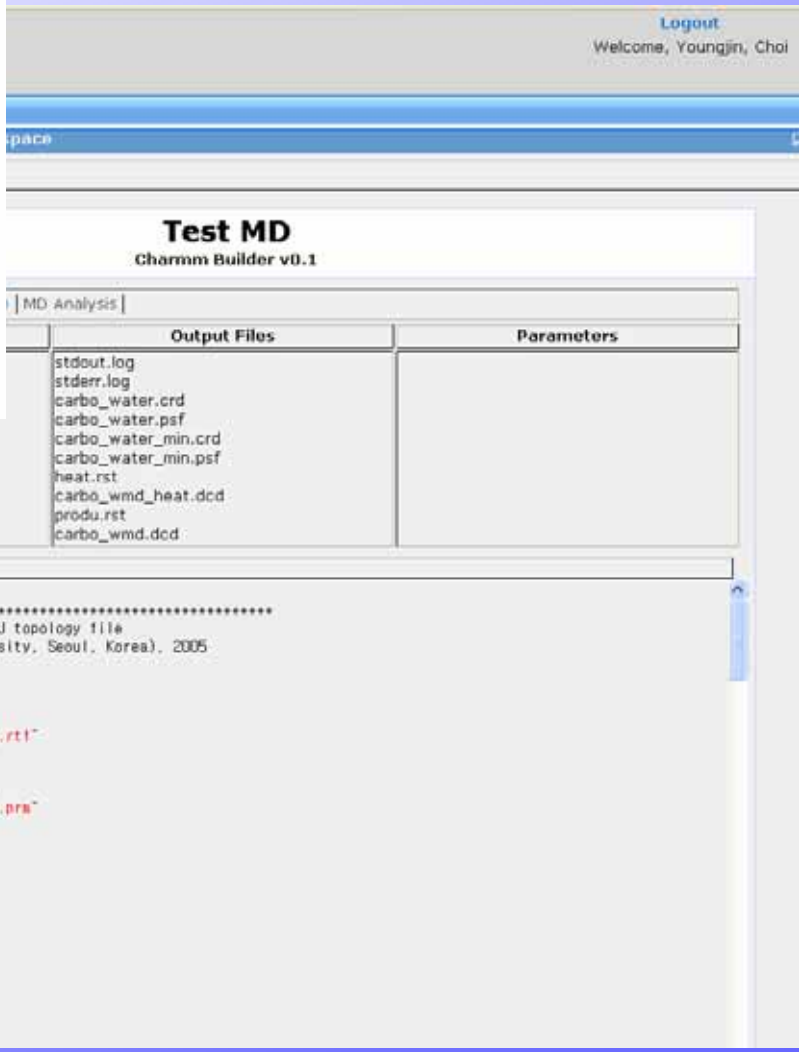




2. CHARMM Input Script & File Upload

3. CHARMM Job Running





4. Job Monitoring

파이어폭스 시작하기 최신 모질라 뉴스 Firefox Start

```
************************************************************************
* B-D-GALNAC-(1-2)-A-D-GALNAC CONJ TOPOLOGY FILE
* BY YOUNGJIN CHOI (KONKUK UNIVERSITY, SEOUL, KOREA), 2005
*  DATE:    10/11/ 6      9:20: 6      CREATED BY USER: kgrid001
*
 1650
    1    1 BDGA C1    -1.90618  -0.33720  -0.11626 CARB 1      0.00000
    2    1 BDGA H1    -1.78201  -0.65803  -1.16850 CARB 1      0.00000
    3    1 BDGA O1    -0.61511  -0.24352   0.49873 CARB 1      0.00000
    4    1 BDGA C5    -3.73286   1.04997  -0.75066 CARB 1      0.00000
    5    1 BDGA H5    -3.60339   0.65288  -1.77058 CARB 1      0.00000
    6    1 BDGA O5    -2.44842   0.98506  -0.12015 CARB 1      0.00000
    7    1 BDGA C2    -2.81678  -1.28416   0.67253 CARB 1      0.00000
    8    1 BDGA H2    -2.85895  -0.87748   1.69600 CARB 1      0.00000
    9    1 BDGA C3    -4.23898  -1.23903   0.13570 CARB 1      0.00000
   10    1 BDGA H3    -4.24870  -1.69411  -0.86863 CARB 1      0.00000
   11    1 BDGA O3    -5.09247  -1.97927   1.01161 CARB 1      0.00000
   12    1 BDGA HO3   -5.58328  -2.64647   0.47983 CARB 1      0.00000
   13    1 BDGA C4    -4.74113   0.18909   0.00565 CARB 1      0.00000
   14    1 BDGA H4    -5.68715   0.16295  -0.55113 CARB 1      0.00000
   15    1 BDGA O4    -4.98812   0.73973   1.29894 CARB 1      0.00000
   16    1 BDGA HO4   -5.30524   0.00689   1.85256 CARB 1      0.00000
   17    1 BDGA C6    -4.18738   2.49354  -0.84749 CARB 1      0.00000
   18    1 BDGA H61   -3.39991   3.10984  -1.31296 CARB 1      0.00000
   19    1 BDGA H62   -4.35751   2.91730   0.15655 CARB 1      0.00000
   20    1 BDGA O6    -5.37554   2.52950  -1.63009 CARB 1      0.00000
   21    1 BDGA HO6   -5.75734   3.44042  -1.65570 CARB 1      0.00000
   22    1 BDGA CAY   -2.04126  -4.95353   0.42375 CARB 1      0.00000
   23    1 BDGA HY1   -2.54297  -5.75209  -0.16131 CARB 1      0.00000
   24    1 BDGA HY2   -0.94220  -5.09458   0.36310 CARB 1      0.00000
   25    1 BDGA HY3   -2.34657  -5.03771   1.48852 CARB 1      0.00000
   26    1 BDGA CY    -2.39833  -3.62965  -0.11617 CARB 1      0.00000
   27    1 BDGA OY    -2.26073  -3.41044  -1.31824 CARB 1      0.00000
   28    1 BDGA N     -2.32389  -2.64058   0.77200 CARB 1      0.00000
   29    1 BDGA HN    -1.95845  -2.87291   1.67429 CARB 1      0.00000
   30    2 BDGA C1     3.94417  -1.69932   0.59315 CARB 2      0.00000
   31    2 BDGA H1     3.87497  -1.74811   1.69913 CARB 2      0.00000
   32    2 BDGA O1     4.69734  -2.76758   0.11356 CARB 2      0.00000
   33    2 BDGA HO1    5.13199  -2.46371  -0.70256 CARB 2      0.00000
   34    2 BDGA C5     1.71910  -0.85572   0.52414 CARB 2      0.00000
   35    2 BDGA H5     1.67792  -0.97075   1.61663 CARB 2      0.00000
   36    2 BDGA O5     2.63862  -1.84643   0.06137 CARB 2      0.00000
   37    2 BDGA C2     4.53387  -0.36287   0.13637 CARB 2      0.00000
   38    2 BDGA H2     4.46064  -0.34287  -0.96355 CARB 2      0.00000
   39    2 BDGA C3     3.63411   0.76134   0.62645 CARB 2      0.00000
   40    2 BDGA H3     3.65111   0.74571   1.72723 CARB 2      0.00000
   41    2 BDGA O3     4.11039   2.02698   0.16645 CARB 2      0.00000
   42    2 BDGA HO3    3.48782   2.71654   0.49083 CARB 2      0.00000
   43    2 BDGA C4     2.20157   0.54431   0.15196 CARB 2      0.00000
완료됨
```

파이어폭스 시작하기 최신 모질라 뉴스 Firefox Start

```
1
               Chemistry at HARvard Macromolecular Mechanics
                 (CHARMM) - Developmental Version 32b2   February 15, 2006
        Copyright(c) 1984-2001  President and Fellows of Harvard College
                              All Rights Reserved
      Current operating system: Linux-2.6.9-1.667smp(i686)@node11.konkuk.ac.
               Created on 10/11/ 6 at  9:13:36 by user: kgrid001

          Maximum number of ATOMS:     60120, and RESidues:       15030
          Current HEAP size:         10240000, and STACK size:   2000000

 RDTITL> ************************************************************************
 RDTITL> * B-D-GALNAC-(1-2)-A-D-GALNAC CONJ TOPOLOGY FILE
 RDTITL> * BY YOUNGJIN CHOI (KONKUK UNIVERSITY, SEOUL, KOREA), 2005
 RDTITL> *

 CHARMM>

 CHARMM>    bomb -1

 CHARMM>

 CHARMM>    open read unit 10 card name "conj.rtf"
 VOPEN> Attempting to open::conj.rtf::
 OPNLGU> Unit 10 opened for READONLY access to conj.rtf

 CHARMM>    read rtf unit 10  card
 MAINIO> Residue topology file being read from unit  10.
 TITLE> *>>>>>>> COMBINED CHARMM ALL-HYDROGEN TOPOLOGY FILE FOR <<<<<<<<<
 TITLE> *>>>>>>>>> CHARMM22 PROTEINS AND CHARMM27 LIPIDS <<<<<<<<<<
 TITLE> *FROM
 TITLE> *>>>>>>>>CHARMM22 ALL-HYDROGEN TOPOLOGY FILE FOR PROTEINS <<<<<<
 TITLE> *>>>>>>>>>>>>>>>>>>>> AUGUST 1999 <<<<<<<<<<<<<<<<<<<<<<<<<<<<<<
 TITLE> *>>>>>>> DIRECT COMMENTS TO ALEXANDER D. MACKERELL JR. <<<<<<<<<
 TITLE> *>>>>>> 410-706-7442 OR EMAIL: ALEX,MMIRIS.AB.UMD.EDU  <<<<<<<<<
 TITLE> *AND
 TITLE> *  wwwwwwwww CHARMM27 ALL-HYDROGEN LIPID TOPOLOGY FILE ///////
 TITLE> *  wwwwwwwwwwwwwwwwwwwwww DEVELOPMENTAL ////////////////////////
 TITLE> *               ALEXANDER D. MACKERELL JR.
 TITLE> *                        AUGUST 1999
 TITLE> * ALL COMMENTS TO ADM JR.  EMAIL: ALEX,MMIRIS.AB.UMD.EDU
 TITLE> *               TELEPHONE: 410-706-7442
 TITLE> *
 **** WARNING from RTFRDR **** The total charge of the residue, BETA,    0.2000000,
 does not equal the expected charge,    0.0000000.
          PRES C2         0.0
 There were   1 warning(s) from RTFRDR.

 CHARMM>    close unit 10
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5. Post-Processing of the Trajectory