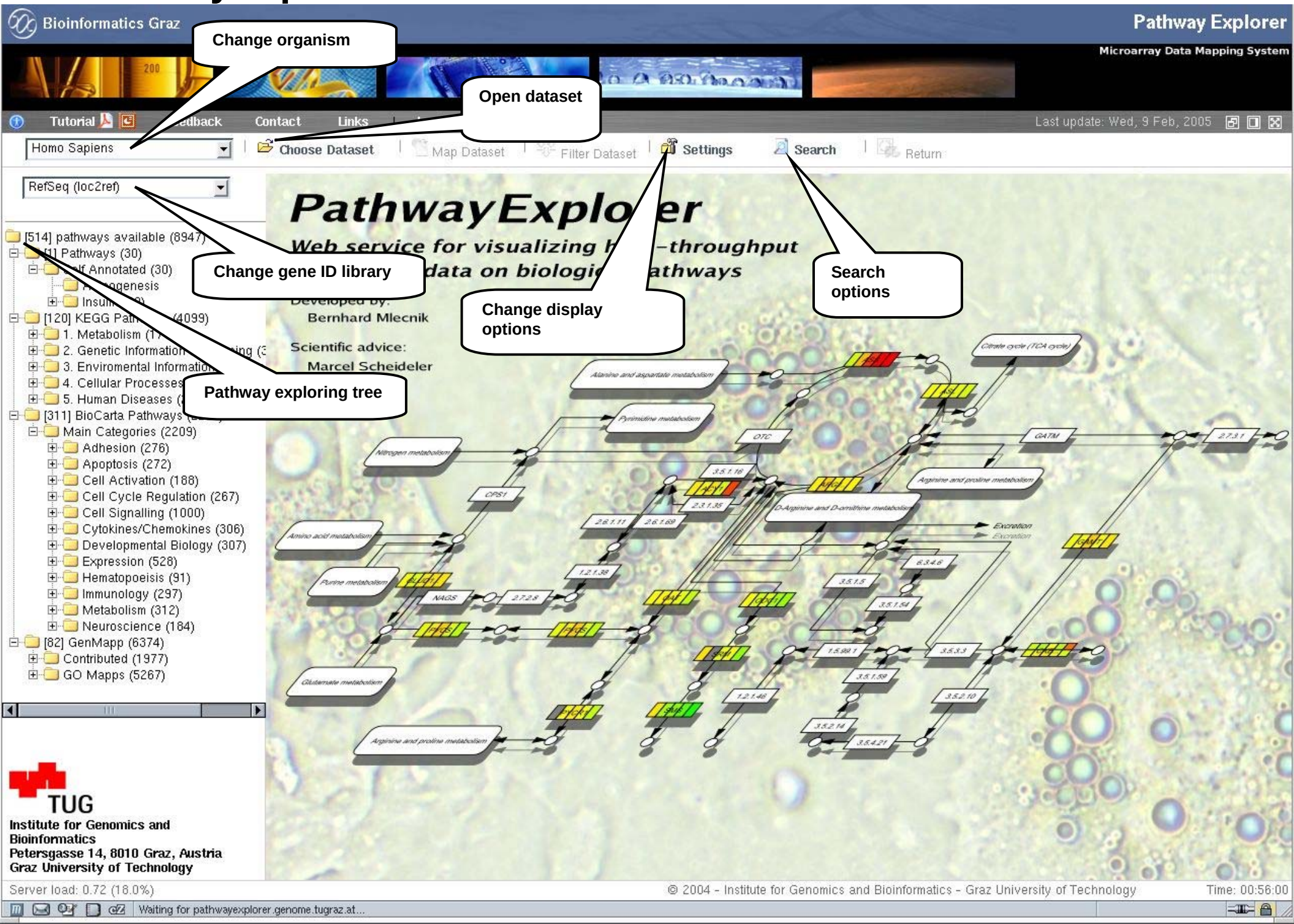
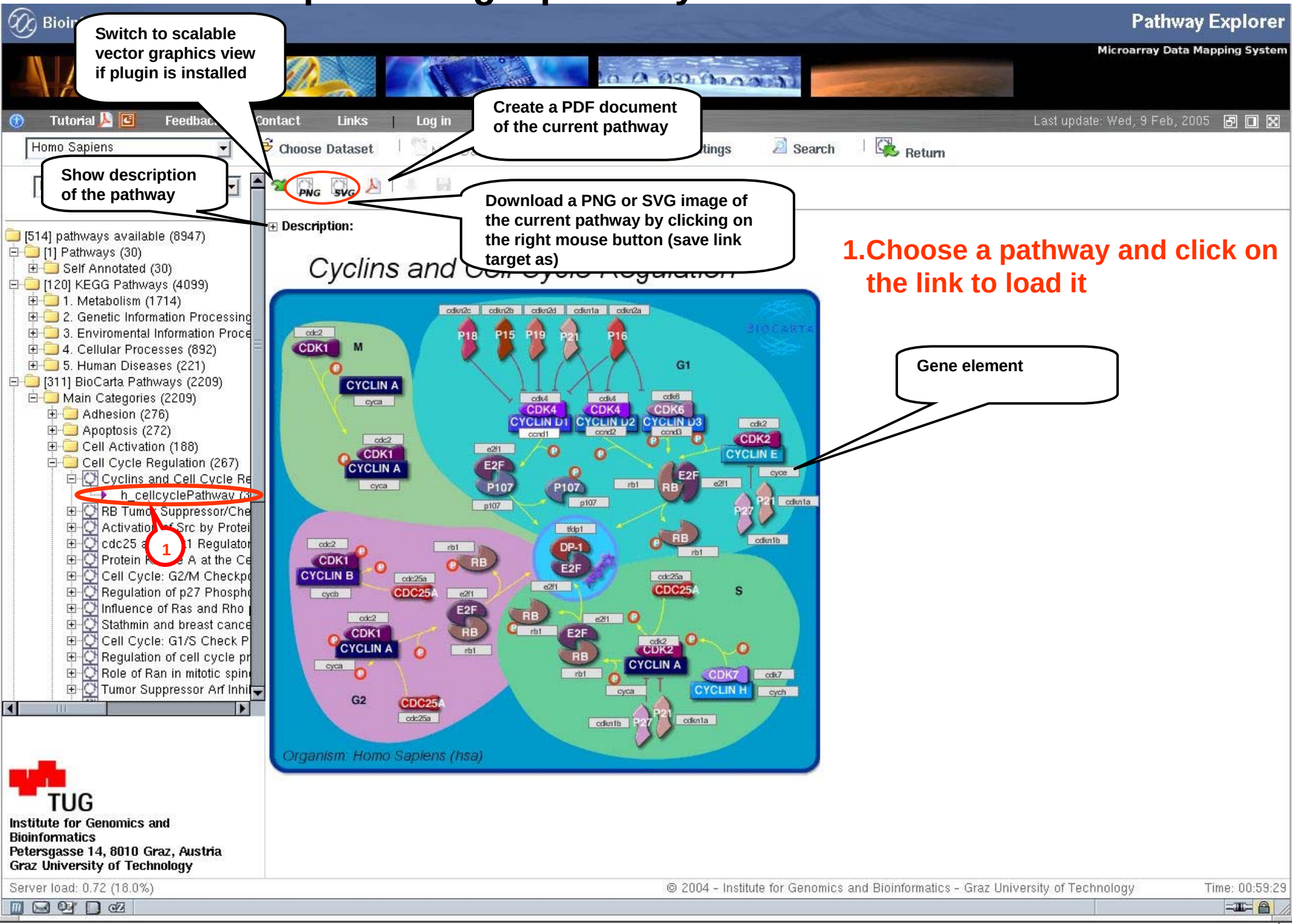
PathwayExplorer Tutorial

Contents

1. PathwayExplorer overview



2. Select and open a single pathway



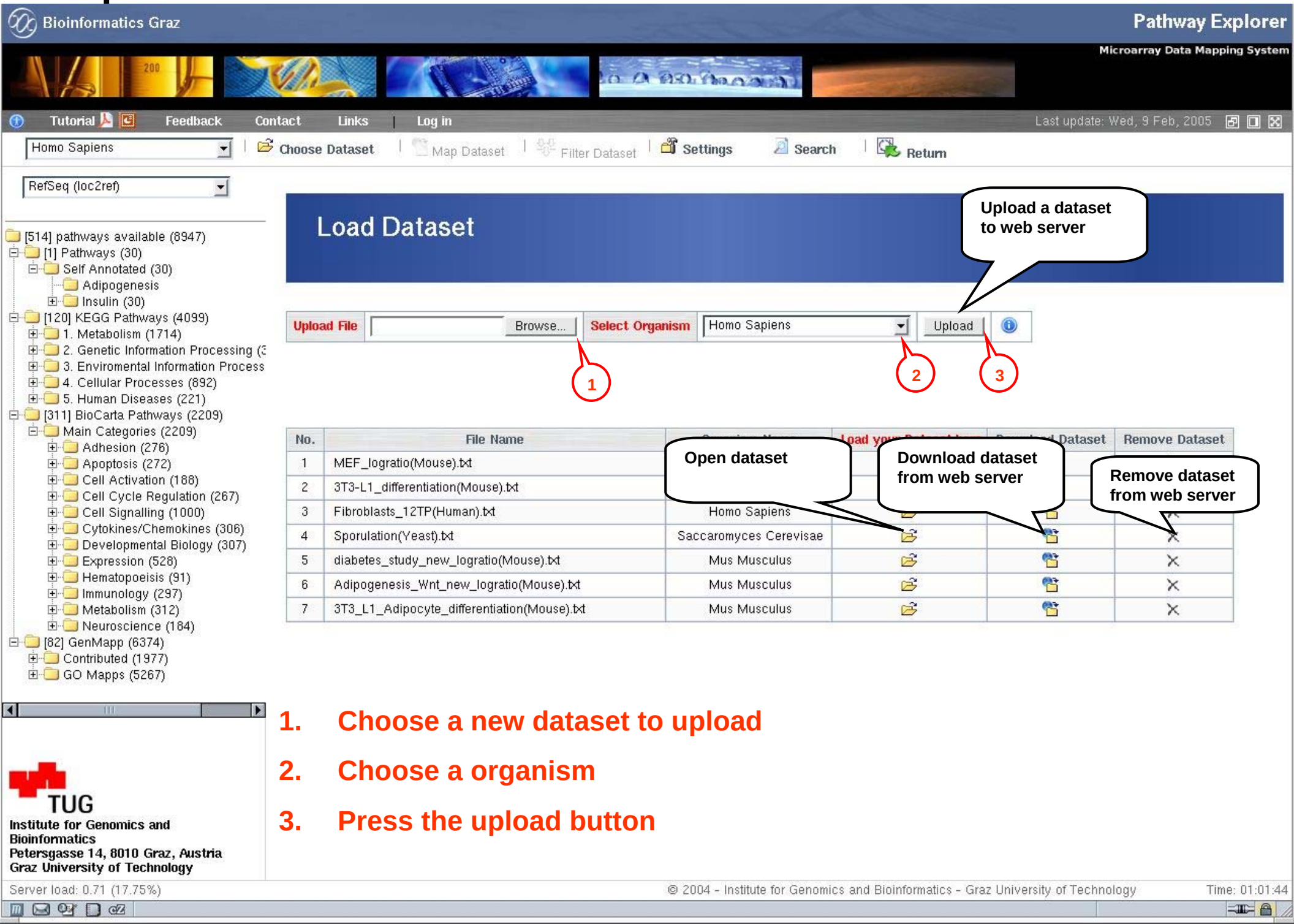
3. Upload a dataset

Dataset Format:

	A	B	C	D	E
1	UniqueID	Name	TP1 (day-2)	TP2 (day0-0hr)	TP3 (day0-8hr)
2	NM_014232	vesicle-associated membrane protein 2 (synaptobrevin 2); vamp2	-0.18725334	0.1531857	-0.051753625
3	NM_000668	class i alcohol dehydrogenase, beta subunit; adh1b	-0.005982075	0.34848127	0.93900555
4	NM_003240	transforming growth factor, beta 4; ebaf	-0.112653494	-0.0135629885	0.16890651
5	NM_018443	zinc finger znf140-like protein; znf302	0.08047339	NaN	NaN
6	NM_004138	type i hair keratin 3a; krtha3a	-0.2854154	-0.40987158	-0.43591157

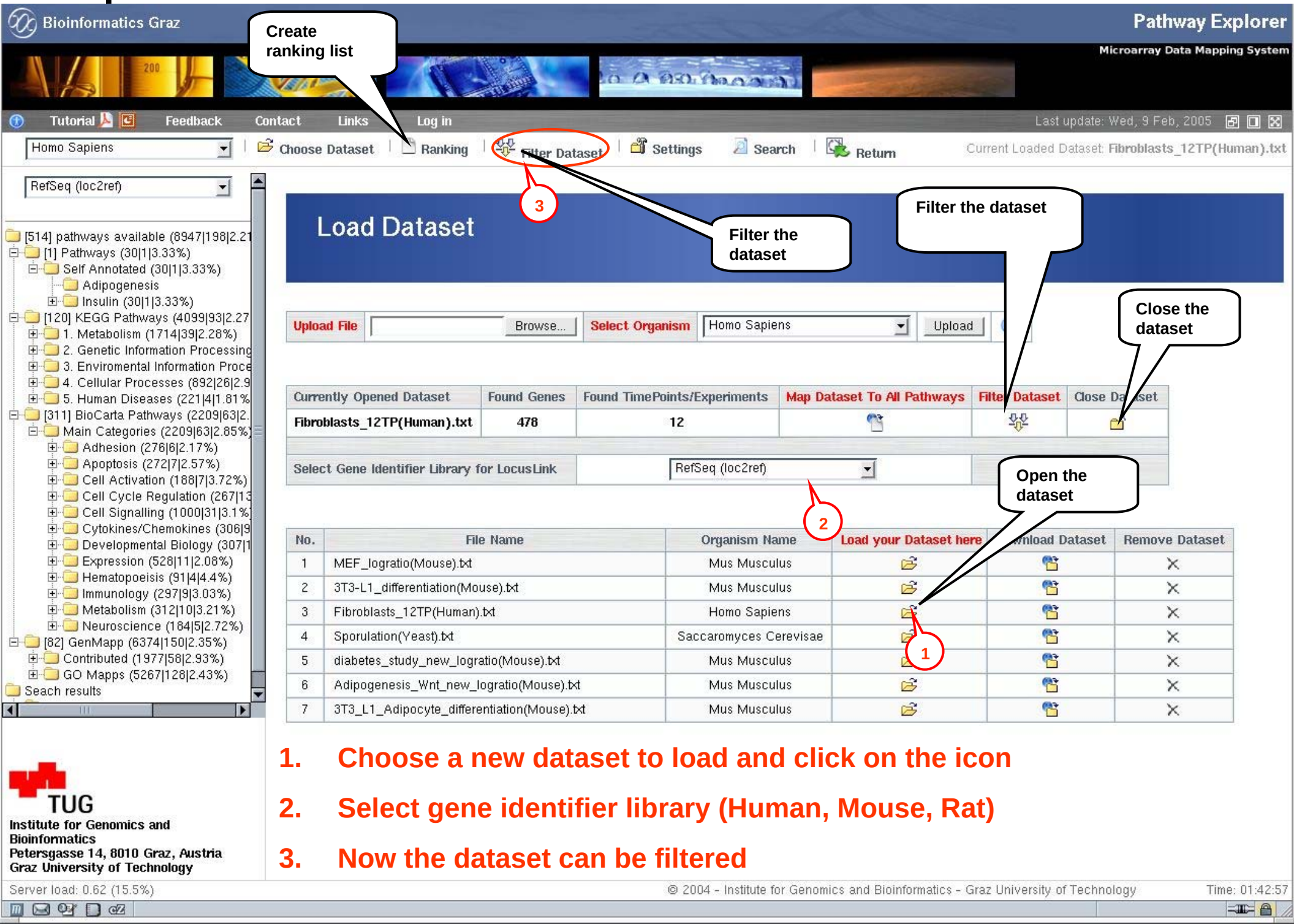
1. All fields must be tab delimited
2. 1st column must contain the UNIQID as ‘RefSeq‘ and/or ‘GenBank‘, ‘UniGene‘, ‘GeneOntology‘.
3. 2nd column must contain the gene name
4. The other columns may contain the expression data

3. Upload a dataset



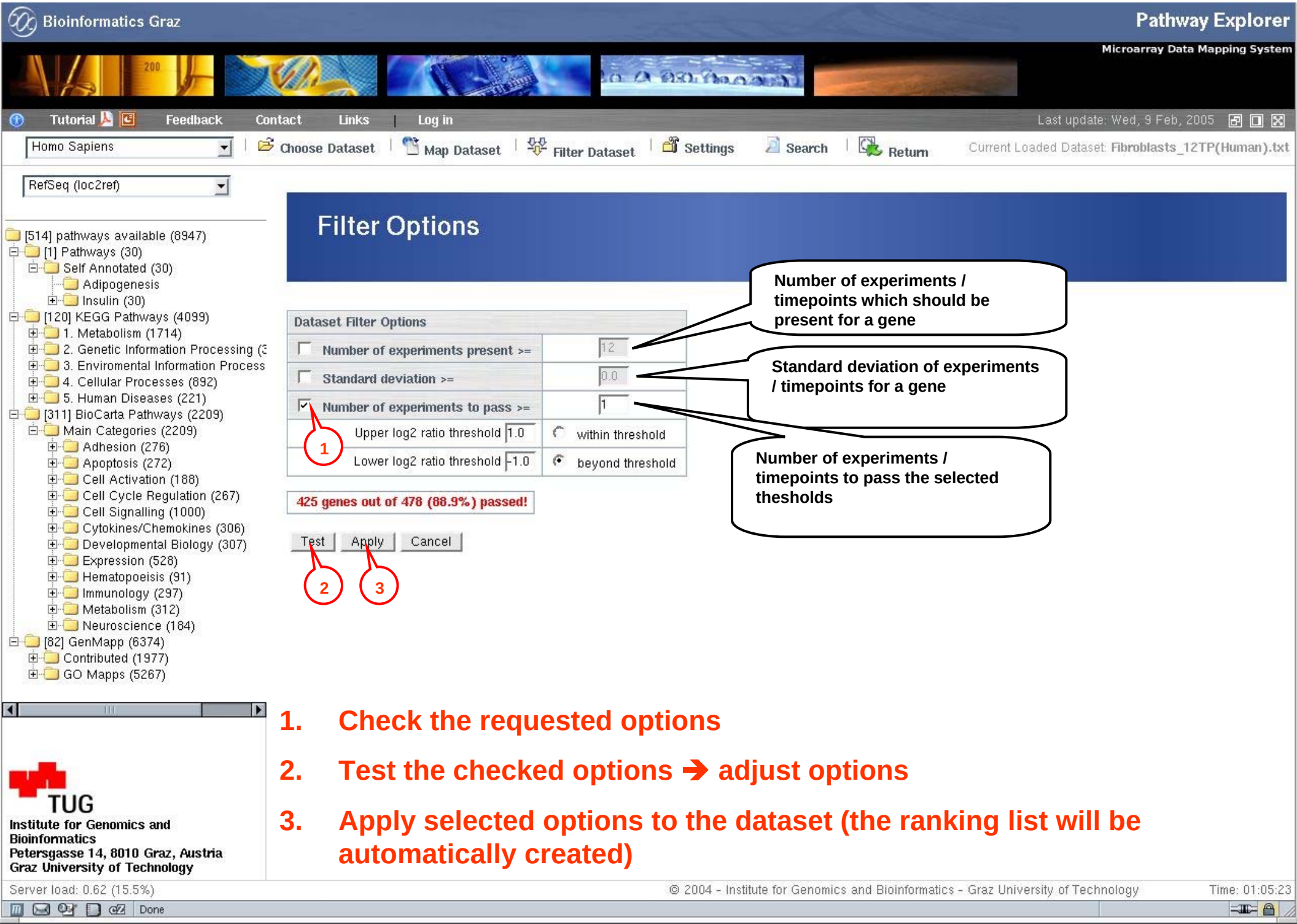
1. Choose a new dataset to upload
2. Choose a organism
3. Press the upload button

4. Open a dataset



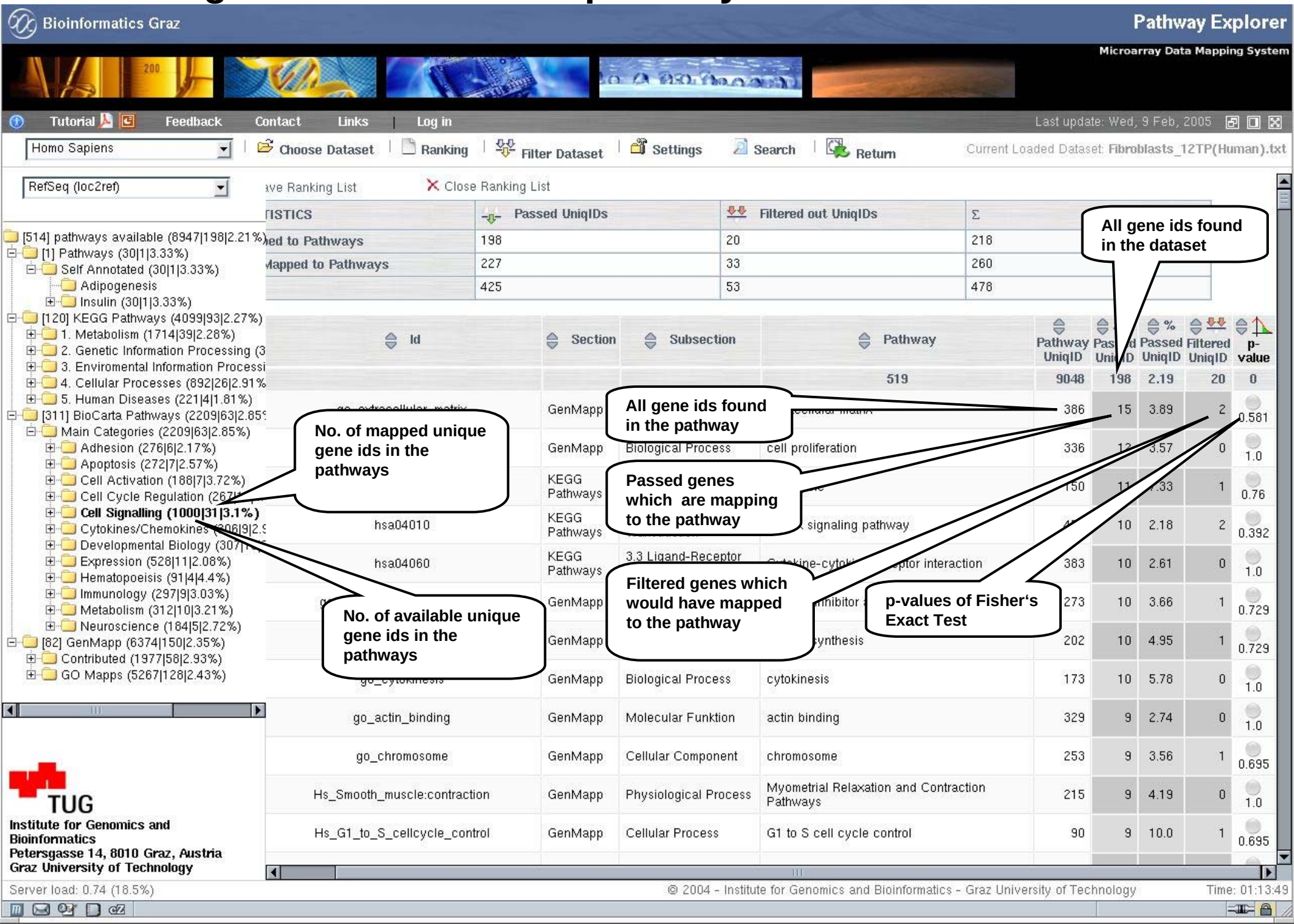
1. Choose a new dataset to load and click on the icon
2. Select gene identifier library (Human, Mouse, Rat)
3. Now the dataset can be filtered

5. Filter the dataset

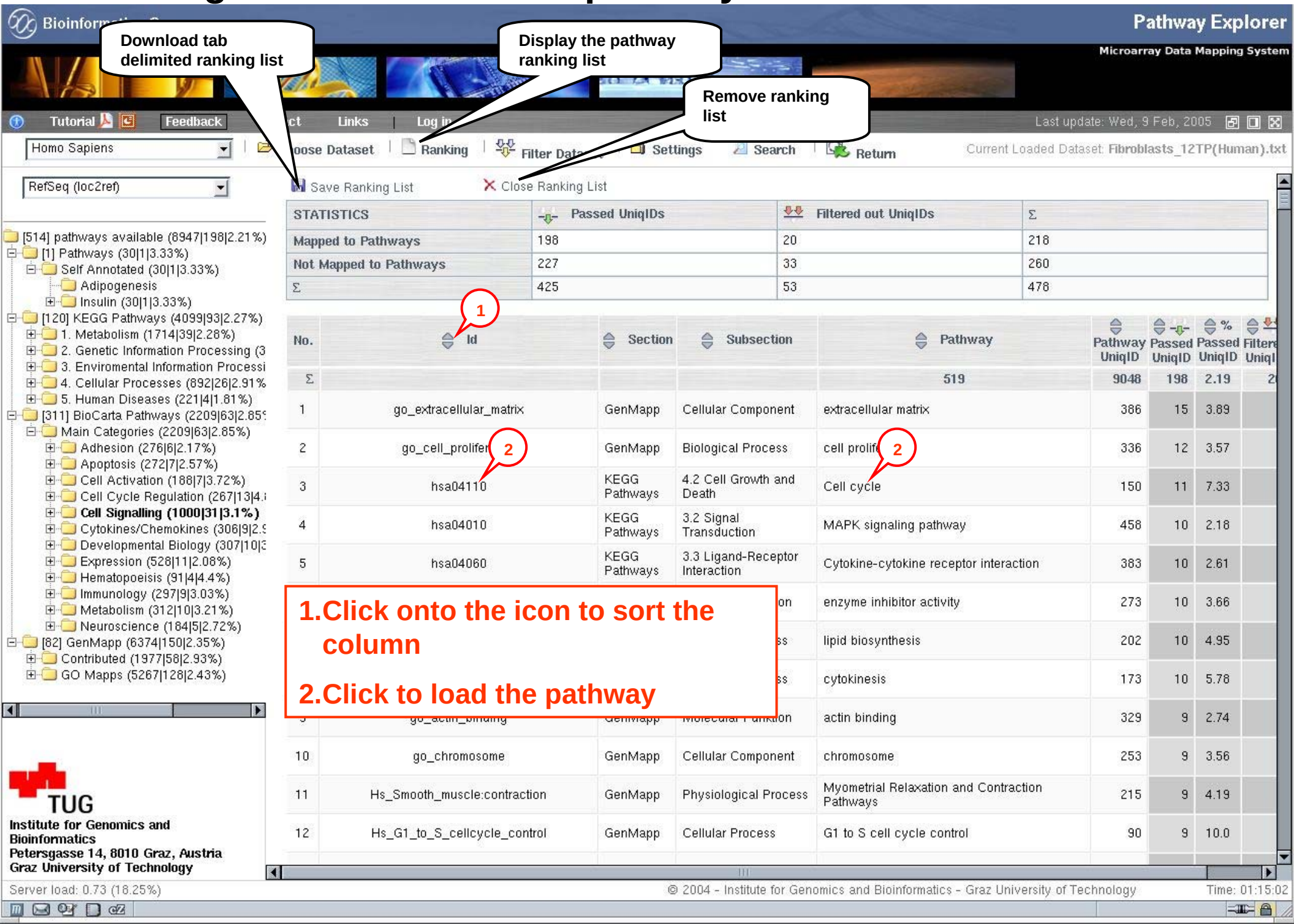


1. **Check the requested options**
2. **Test the checked options ➔ adjust options**
3. **Apply selected options to the dataset (the ranking list will be automatically created)**

6. Ranking list of all available pathways



6. Ranking list of all available pathways

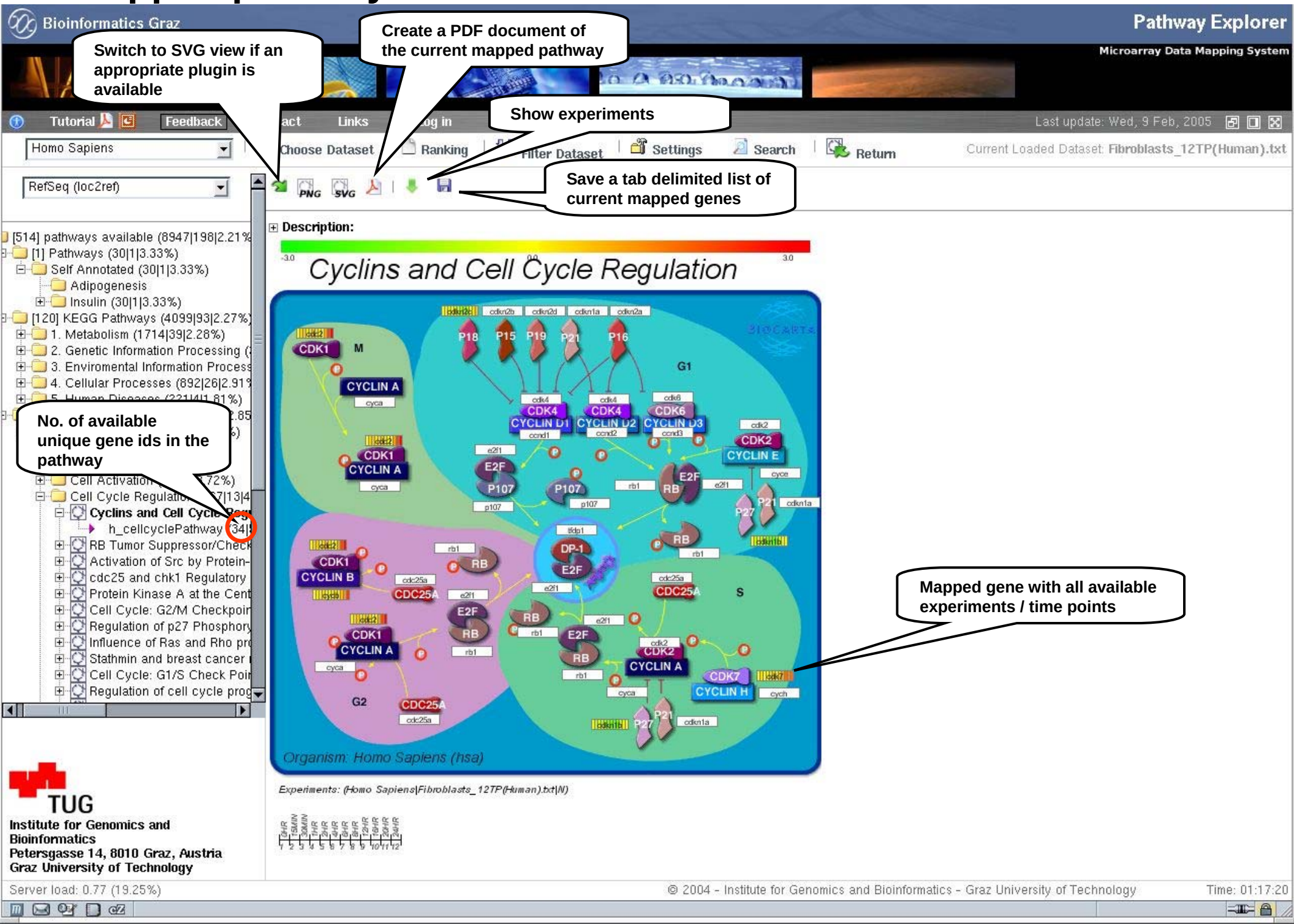


STATISTICS	Passed UniqIDs	Filtered out UniqIDs	Σ
Mapped to Pathways	198	20	218
Not Mapped to Pathways	227	33	260
Σ	425	53	478

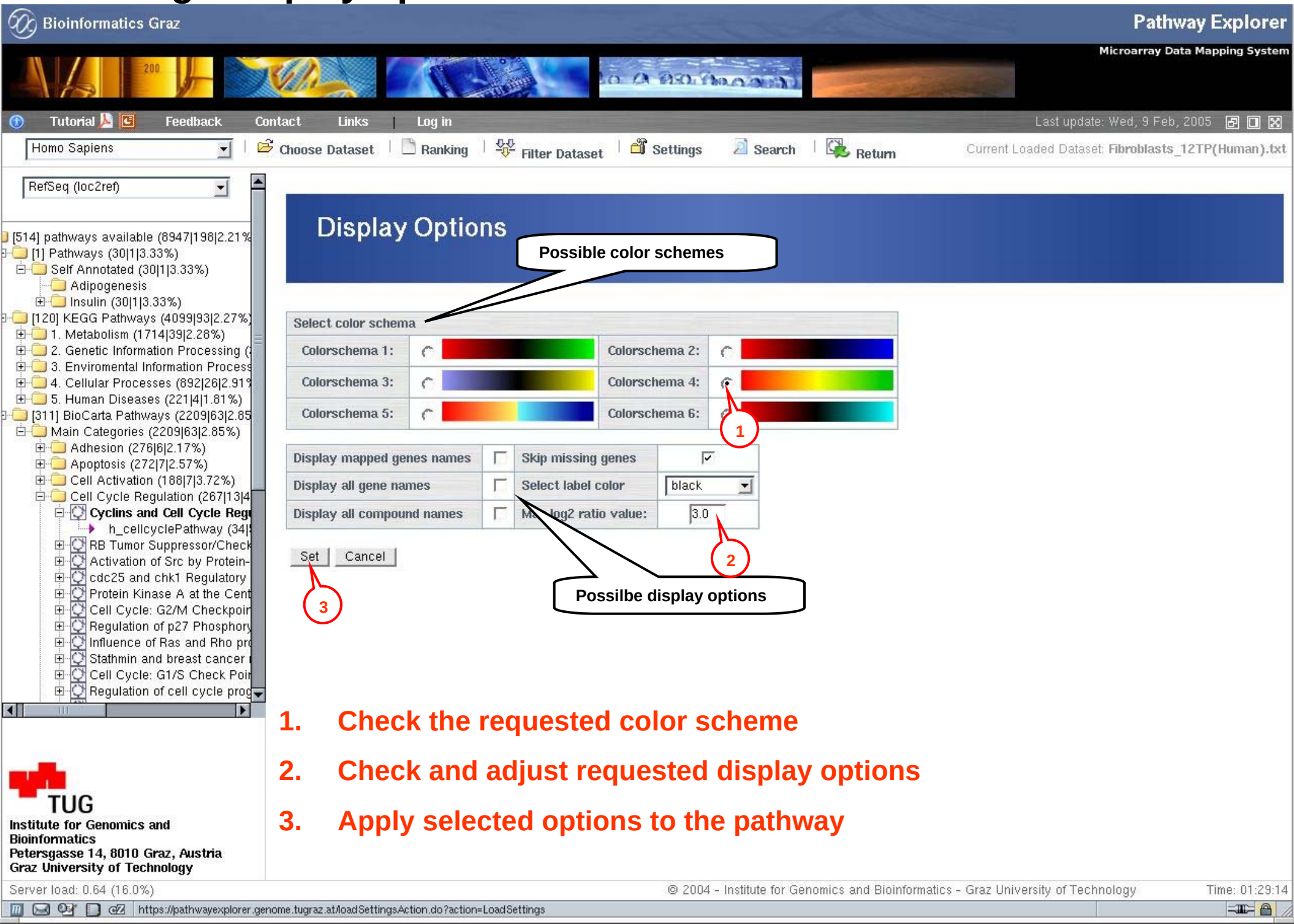
No.	Id	Section	Subsection	Pathway	Pathway UniqID	Passed UniqID	% Passed UniqID	Filtered UniqID
Σ				519	9048	198	2.19	2
1	go_extracellular_matrix	GenMapp	Cellular Component	extracellular matrix	386	15	3.89	
2	go_cell_proliferation	GenMapp	Biological Process	cell proliferation	336	12	3.57	
3	hsa04110	KEGG Pathways	4.2 Cell Growth and Death	Cell cycle	150	11	7.33	
4	hsa04010	KEGG Pathways	3.2 Signal Transduction	MAPK signaling pathway	458	10	2.18	
5	hsa04060	KEGG Pathways	3.3 Ligand-Receptor Interaction	Cytokine-cytokine receptor interaction	383	10	2.61	
				enzyme inhibitor activity	273	10	3.66	
				lipid biosynthesis	202	10	4.95	
				cytokinesis	173	10	5.78	
				actin binding	329	9	2.74	
10	go_chromosome	GenMapp	Cellular Component	chromosome	253	9	3.56	
11	Hs_Smooth_muscle:contraction	GenMapp	Physiological Process	Myometrial Relaxation and Contraction Pathways	215	9	4.19	
12	Hs_G1_to_S_cellcycle_control	GenMapp	Cellular Process	G1 to S cell cycle control	90	9	10.0	

1. Click onto the icon to sort the column
2. Click to load the pathway

7. Mapped pathway

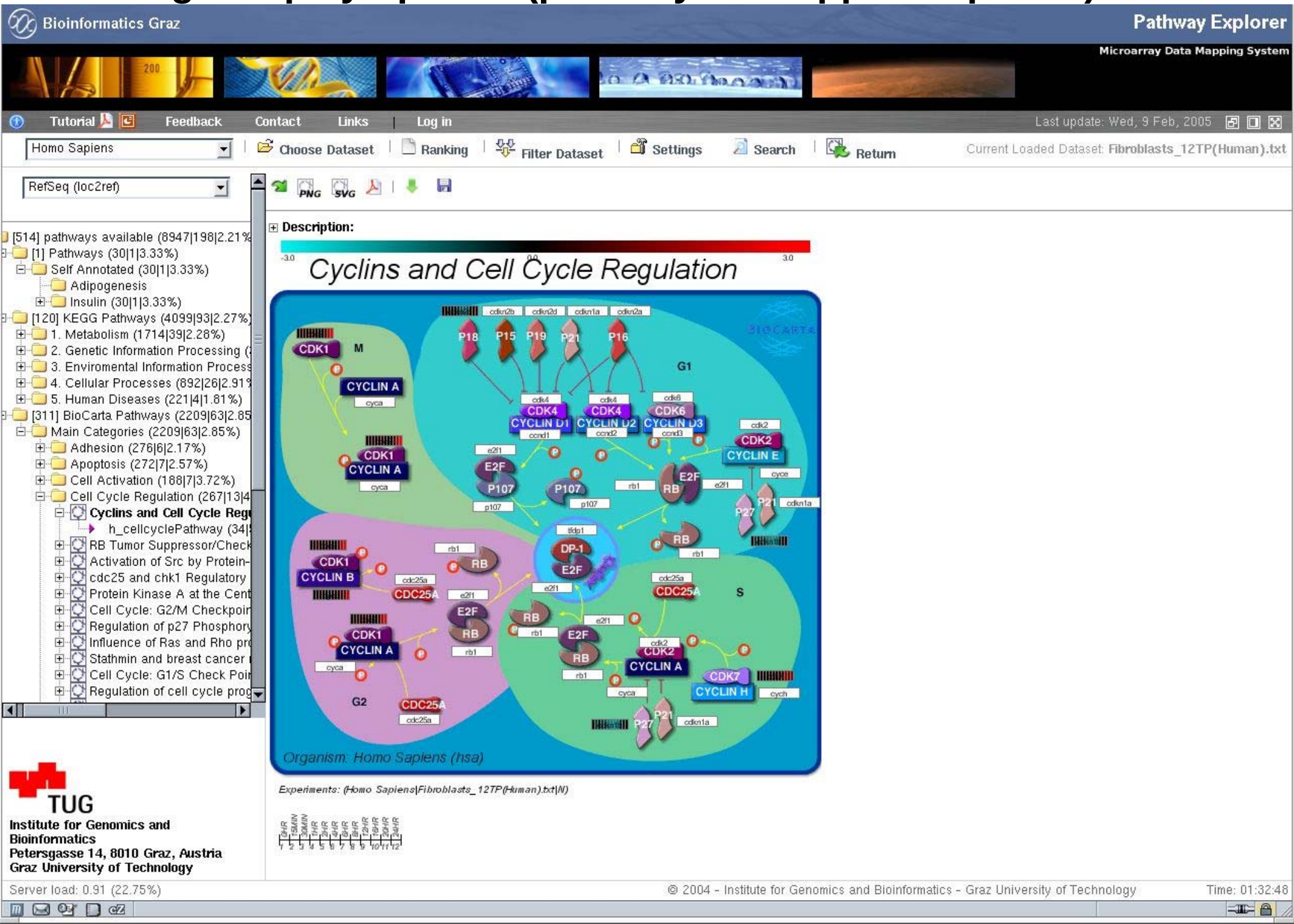


8. Change display options

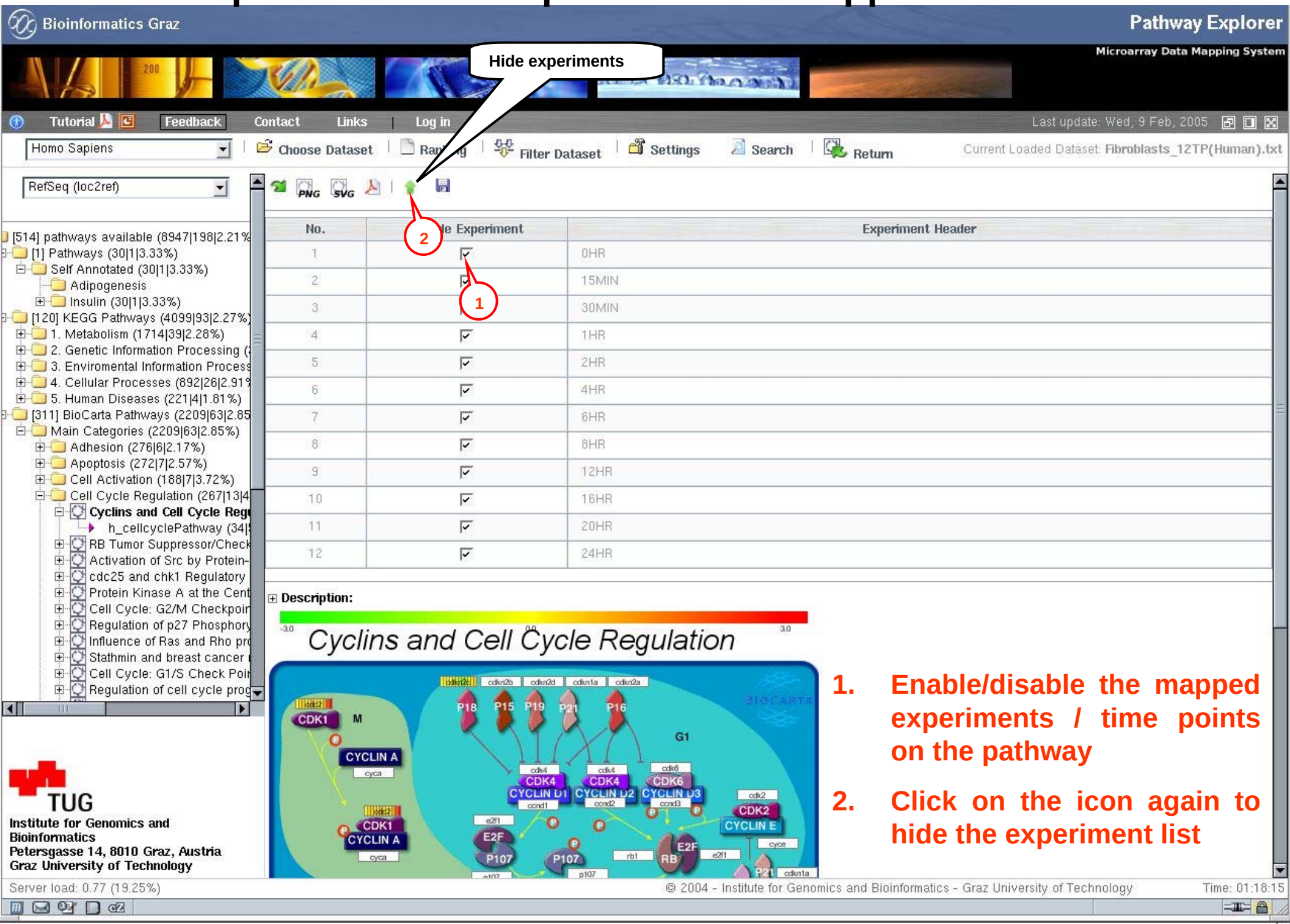


1. Check the requested color scheme
2. Check and adjust requested display options
3. Apply selected options to the pathway

8. Change display options (pathway with applied options)



9. Show experiments / time points of the mapped dataset



10. Show pathway description

Bioinformatics Graz — Pathway Explorer — Microarray Data Mapping System

Hide the pathway description again

Tutorial | Feedback | ntact | Links | Log in — Last update: Wed, 9 Feb, 2005

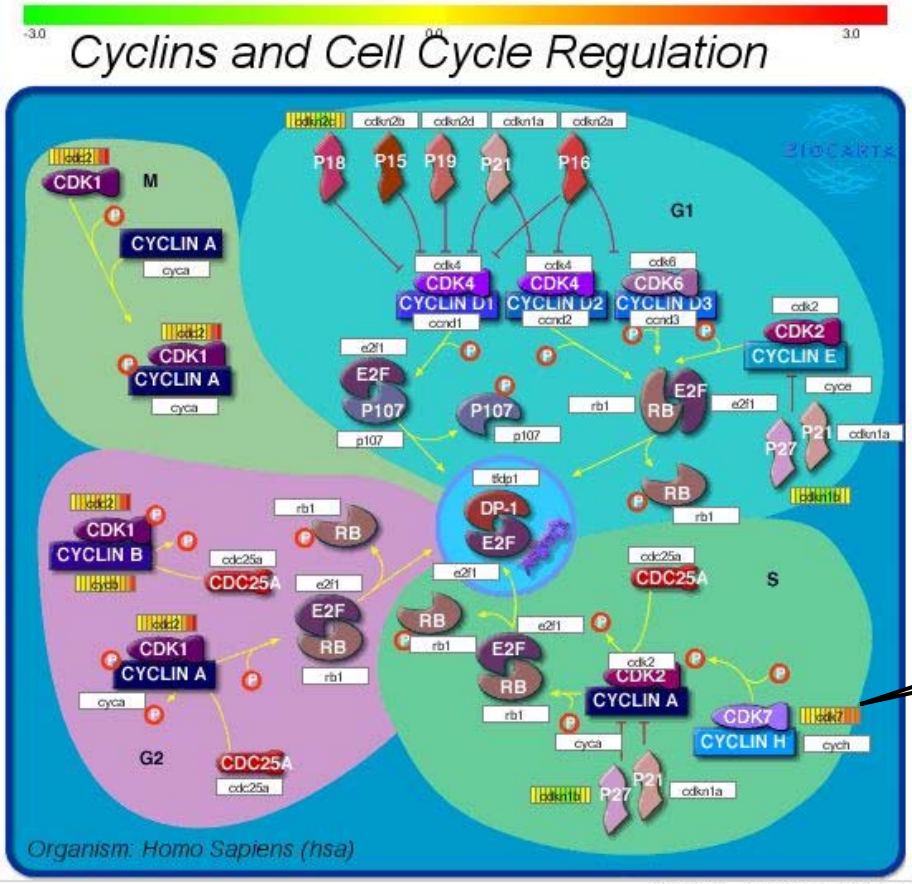
Homo Sapiens | Choose Dataset | Ranking | Filter Dataset | Settings | Search | Return — Current Loaded Dataset: Fibroblasts_12TP(Human).txt

RefSeq (loc2ref) | PNG | SVG

- [514] pathways available (8947|198|2.21%)
  - [1] Pathways (30|1|3.33%)
    - Self Annotated (30|1|3.33%)
      - Adipogenesis
      - Insulin (30|1|3.33%)
  - [120] KEGG Pathways (4099|93|2.27%)
    - 1. Metabolism (1714|39|2.28%)
    - 2. Genetic Information Processing (
    - 3. Enviromental Information Process
    - 4. Cellular Processes (892|26|2.91%
    - 5. Human Diseases (221|4|1.81%)
  - [311] BioCarta Pathways (2209|63|2.85
    - Main Categories (2209|63|2.85%)
      - Adhesion (276|6|2.17%)
      - Apoptosis (272|7|2.57%)
      - Cell Activation (188|7|3.72%)
      - Cell Cycle Regulation (267|13|4
        - **Cyclins and Cell Cycle Regu**
          - h_cellcyclePathway (34|
        - RB Tumor Suppressor/Check
        - Activation of Src by Protein-
        - cdc25 and chk1 Regulatory
        - Protein Kinase A at the Cent
        - Cell Cycle: G2/M Checkpoir
        - Regulation of p27 Phosphory
        - Influence of Ras and Rho pr
        - Stathmin and breast cancer
        - Cell Cycle: G1/S Check Poi
        - Regulation of cell cycle prog

Description:

The cell cycle is regulated by the interplay of many molecules. Key among these are the cyclins which are expressed and then degraded in a concerted fashion to drive the stages of the cell cycle. Cyclins combine with cyclin dependent kinases (cdks) to form activated kinases that phosphorylate targets leading to cell cycle regulation. A breakdown in the regulation of this cycle can lead to out of control growth and contribute to tumor formation. Defects in many of the molecules that regulate the cell cycle have been implicated in cancer. Key among these are p53, the cdk inhibitors (p15, p16, p18, p19, p21, p27), and Rb, all of which act to keep the cell cycle from progressing until all repairs to damaged DNA have been completed.



Mapped gene with all available experiments / time points. Click on the mapped gene to get more information.

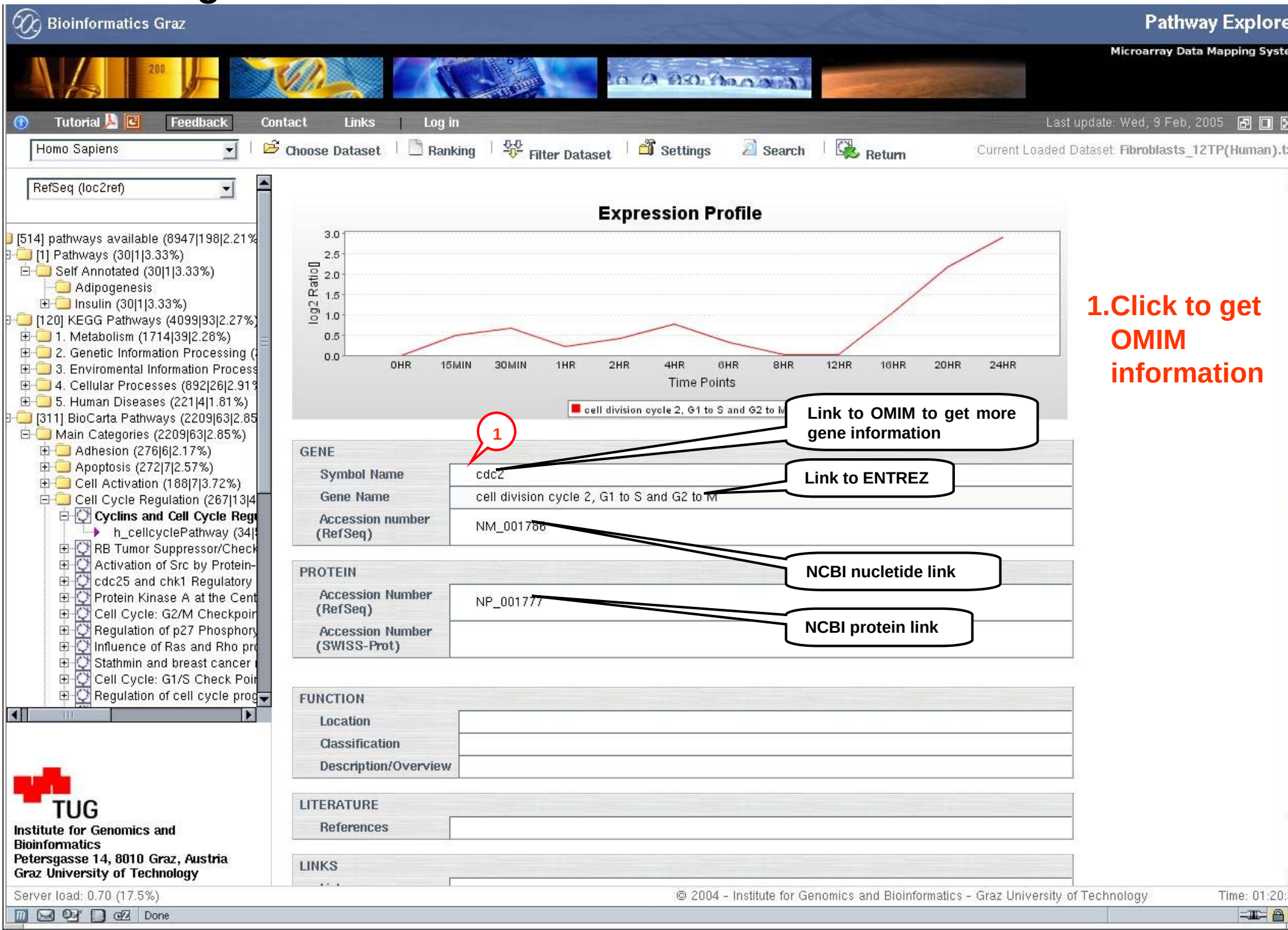
TUG
Institute for Genomics and Bioinformatics
Petersgasse 14, 8010 Graz, Austria
Graz University of Technology

Server load: 0.77 (19.25%)

Time: 01:19:04

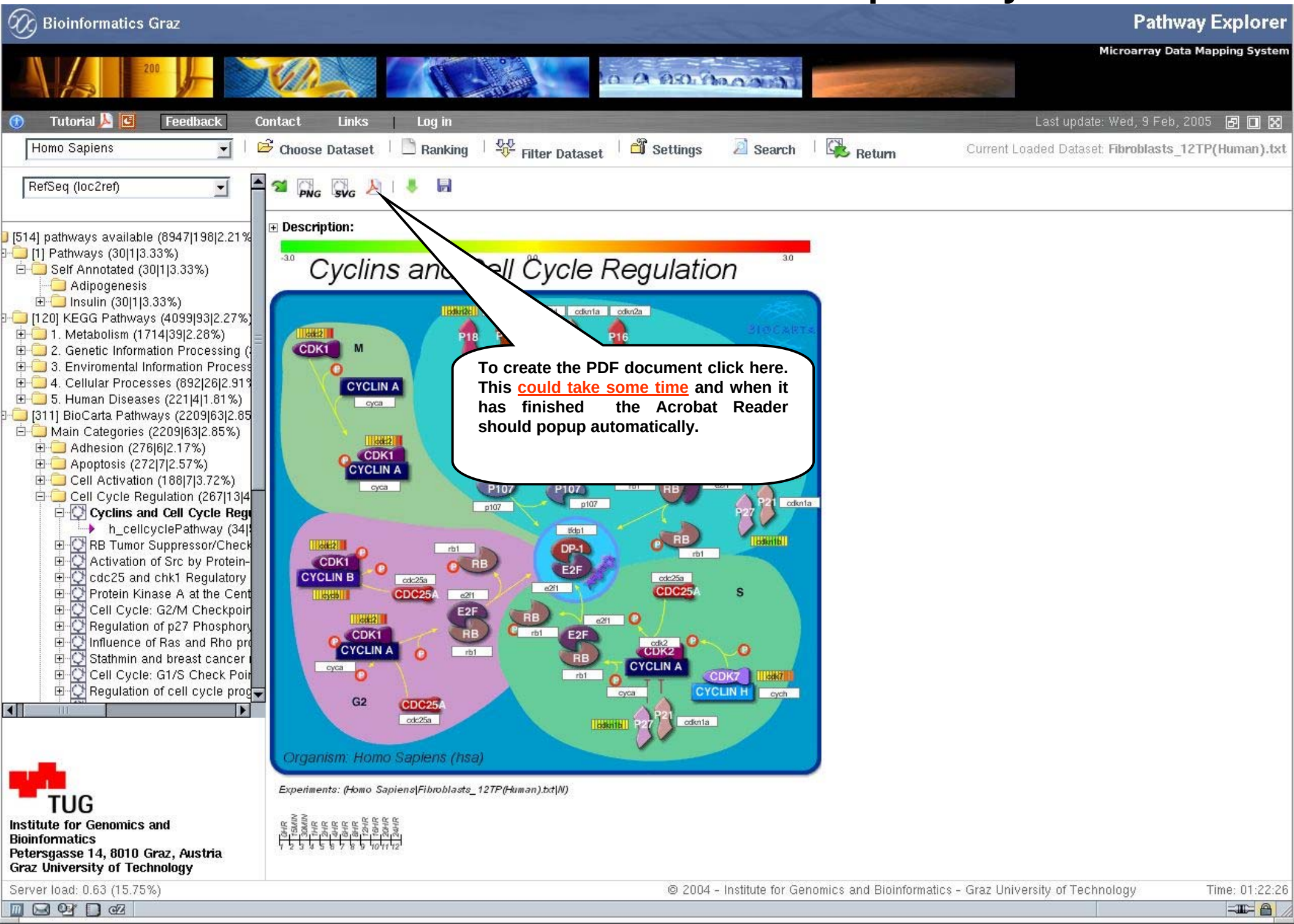
Waiting for pathwayexplorer.genome.tugraz.at...

11. Show gene information

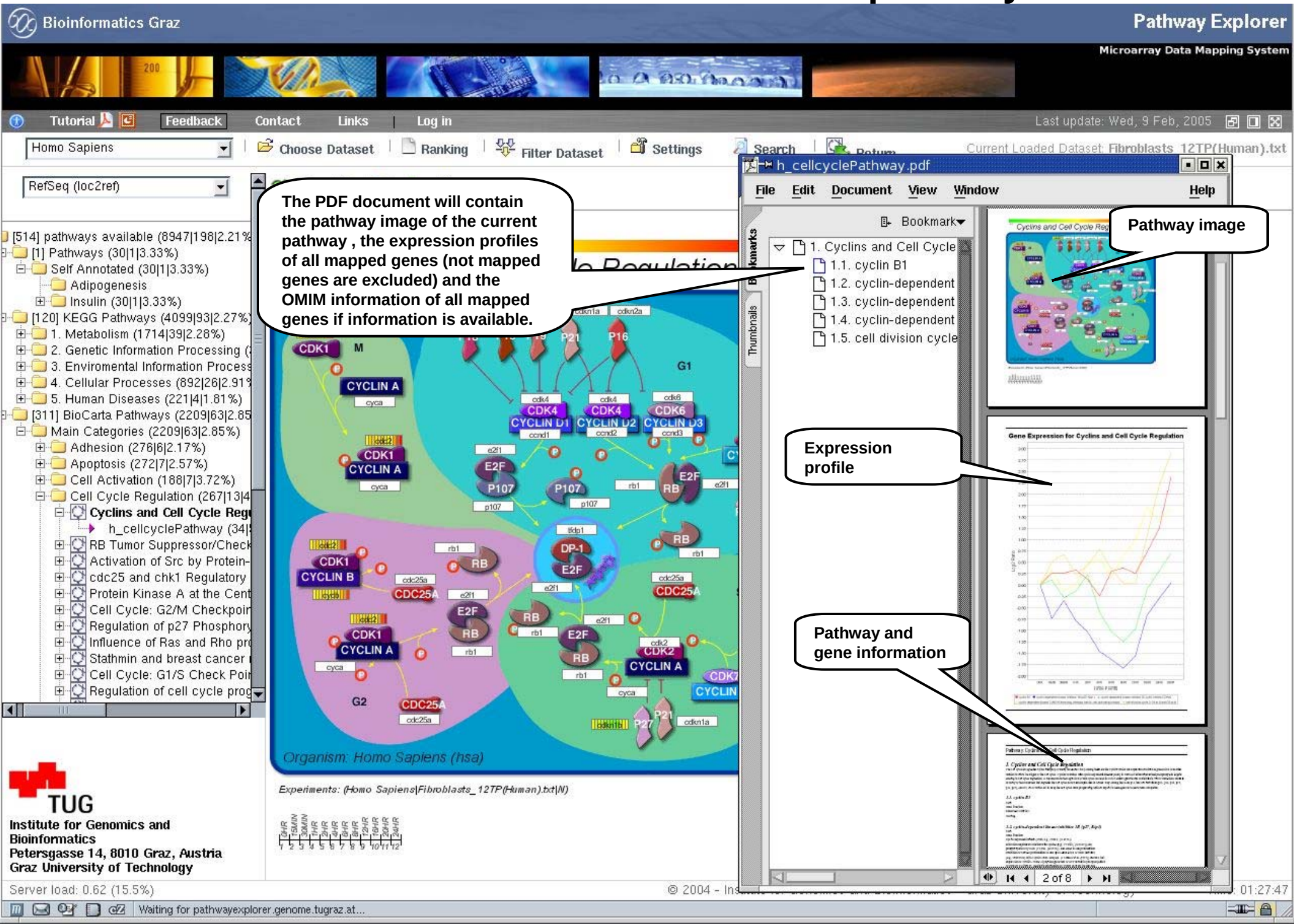


12. Display OMIM gene information

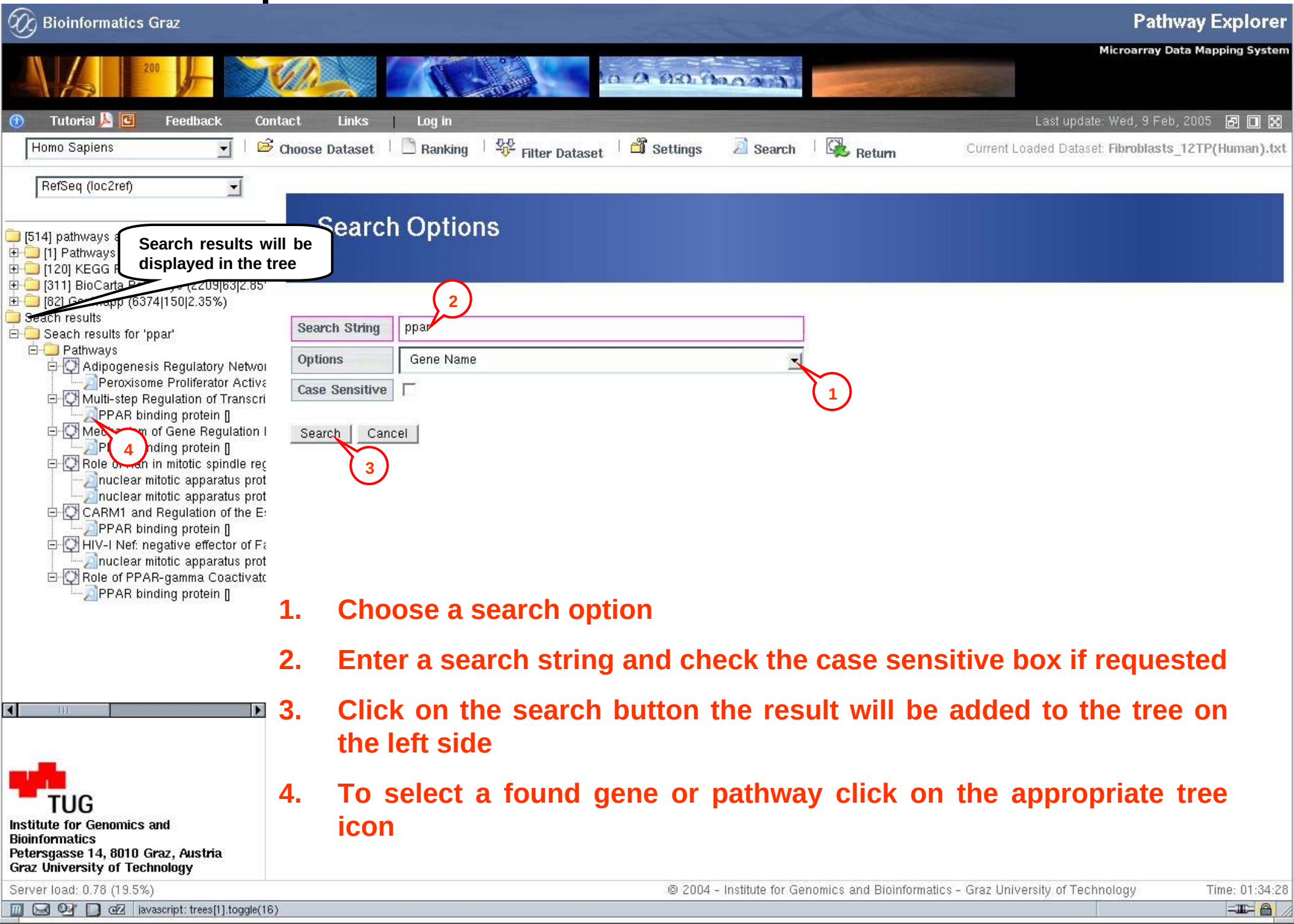
13. Create a PDF document with all available pathway information



13. Create a PDF document with all available pathway information



15. Search options



1. Choose a search option
2. Enter a search string and check the case sensitive box if requested
3. Click on the search button the result will be added to the tree on the left side
4. To select a found gene or pathway click on the appropriate tree icon

14. Search option (results)