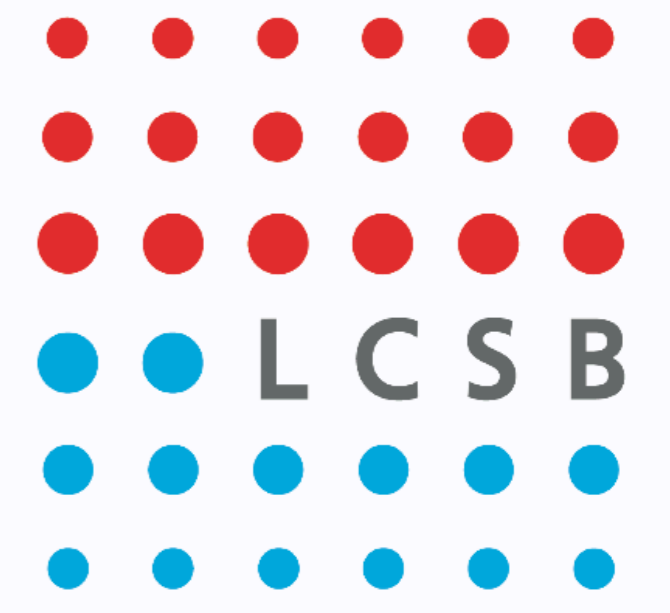


# The Parkinson's Disease Map: A Framework for Integration, Curation and Exploration of Disease-related Pathways

## Luxembourg Centre for Systems Biomedicine



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### Literature and bioinformatics databases

#### Curated content:

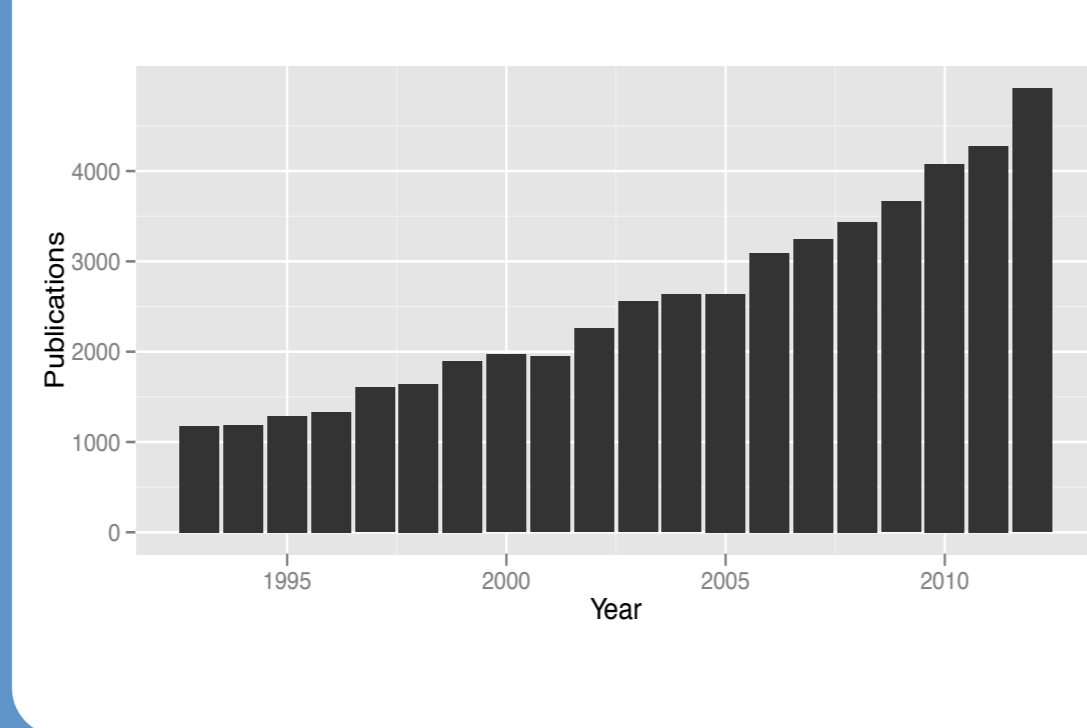
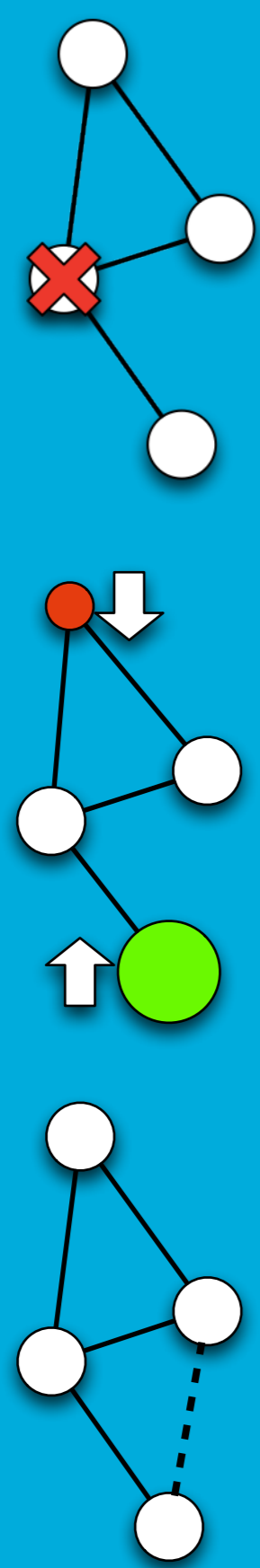
- 2285 elements
- 989 reactions
- 429 papers
- 223 Reactome reactions
- 31 KEGG reactions
- SBML/SBGN standard<sup>3</sup>

### Community curation

- Access by the PD research community
- Collecting remarks using web-based engine Payao<sup>12</sup>
- Moderation of collected feedback
- Update of the map

### Experimental data

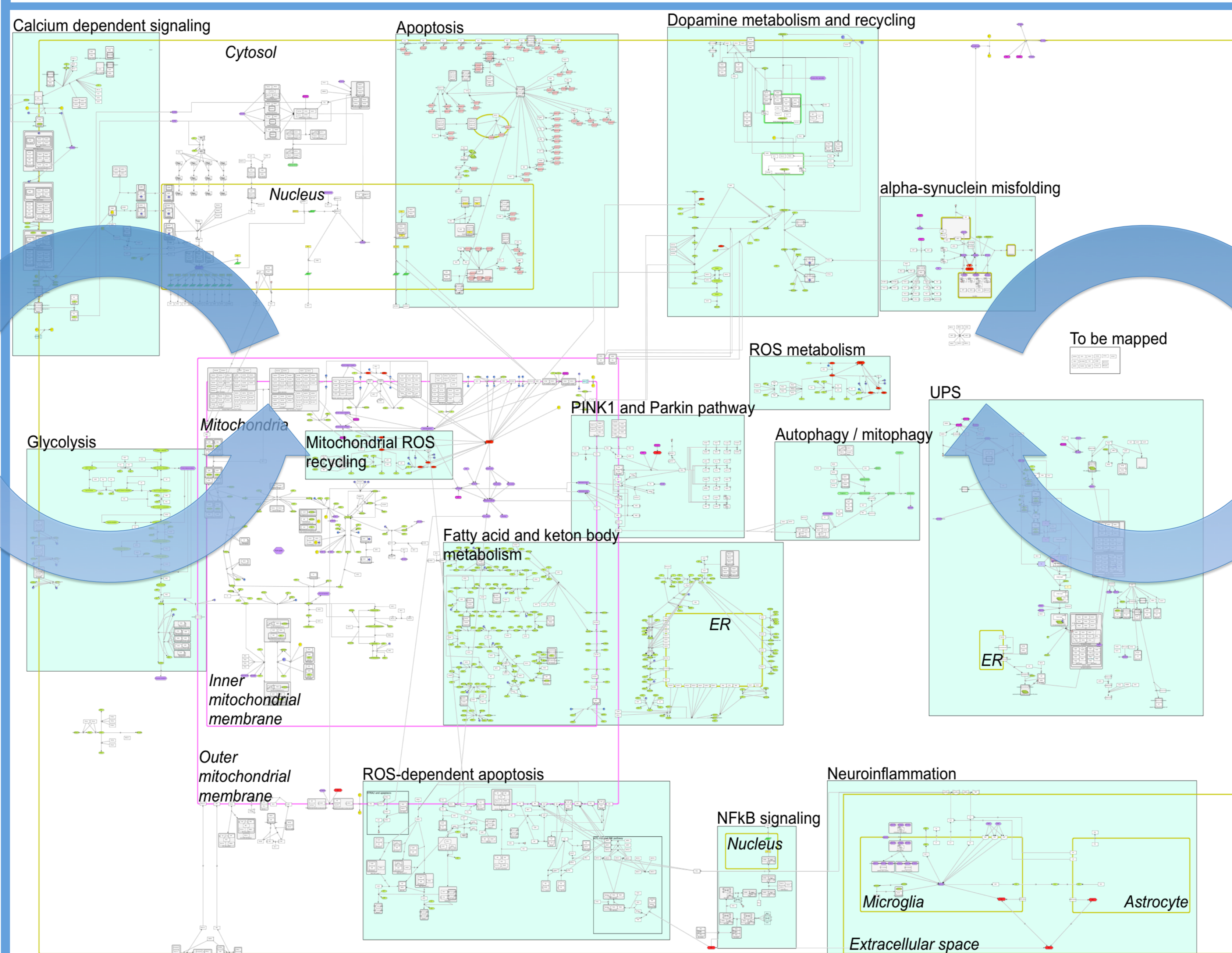
- GWAS
- Genetic variation
- Perturbation experiments
- Gene and protein expression
- Metabolomics
- Protein-protein interaction data



### Problem statement

- Number of publications on PD grows continuously
- Many molecular pathways are implicated in PD
- Molecular pathology of PD is likely multi-factorial<sup>1,2</sup>
- Exploration and analysis of molecular pathways require integration of literature and experimental data

### Parkinson's disease map



#### Focus:

- Mitochondrial dysfunction
- Neuroinflammation
- Protein misfolding
- Synaptic dysfunction
- Failure of protein degradation

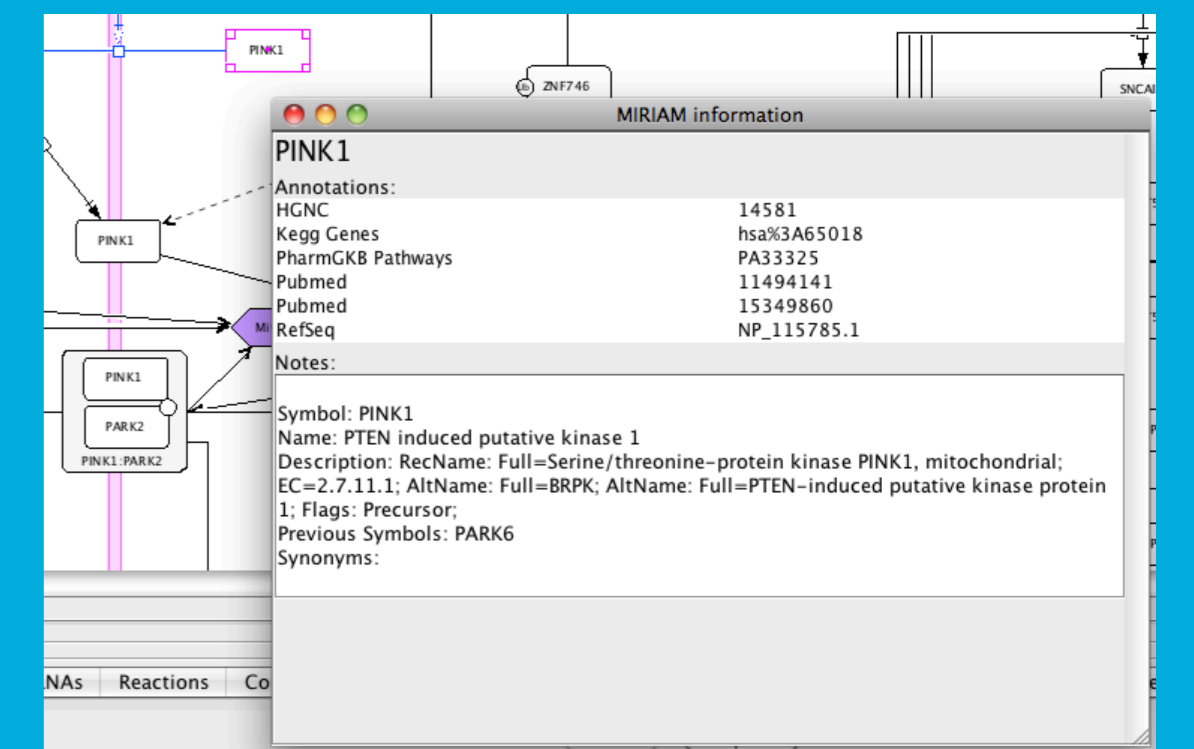
#### Components:

- Gene regulation
- Protein-protein interaction
- Metabolic interactions
- Phenotypic information

### Outcomes

- PD map is a rich resource of molecular pathways implicated in PD
- Access to knowledge on PD pathways using tools for browsing, annotation and integration of experimental data
- The map is open for analysis by systems biology approaches, providing insight into its global structure
- Text mining and community curation are invaluable for efficient map enrichment

### Annotation



Constantly updated and accessible bioinformatics annotation

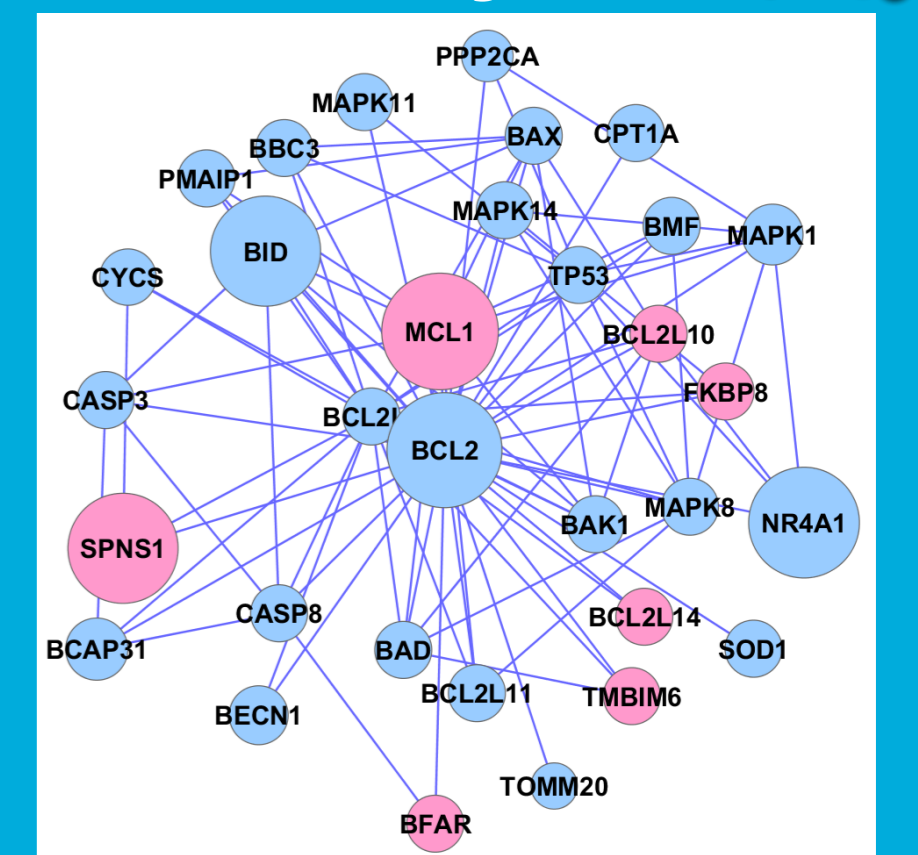
### Text mining

- 50 000 full text publications
- PD-related text
- Co-occurrences<sup>11</sup>
- Contextualized search

DJ-1, but not its K130R mutant, inhibits p53 transcriptional activity on Bax promoter.<sup>10</sup>

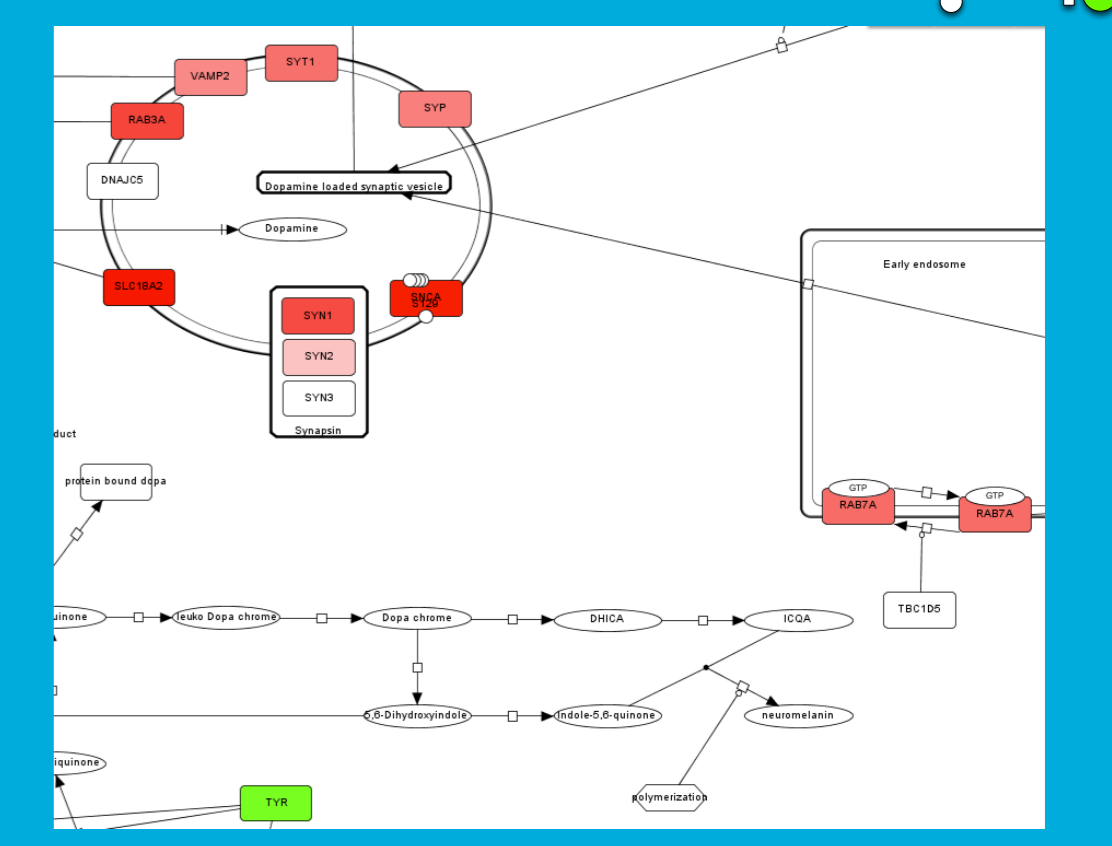
- Human in the loop
- Syntax analysis

### Analysis



New map elements (PathExpand<sup>4</sup>), hubs, inter-modular links and critical pathways

### Enrichment



8 datasets of human PD SNpc<sup>5-8</sup> jointly analysed<sup>9</sup> for differentially expressed genes and mapped

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in collaboration with:

