

This document is an anonymized version of the original project plan used during development of the REPAIRtoire database (document from early 2010). When mentioning this document, please refer to:

Milanowska K, Krwawicz J, Papaj G, Kosinski J, Poleszak K, Lesiak J, Osinska E, Rother K, Bujnicki JM. REPAIRtoire--a database of DNA repair pathways. Nucleic Acids Res. 2011 Jan;39(Database issue):D788-92. Epub 2010 Nov 4.

Project Description: "REPAIRtoire web site first version"

Team:

Kaja M. ([email@deleted](#))
Asia K. ([email@deleted](#))
Grzesiek P. ([email@deleted](#))
Jan K. ([email@deleted](#))
Poleszak K. ([email@deleted](#))
Justyna L. ([email@deleted](#))
Ewelina O. ([email@deleted](#))
Kristian R. ([email@deleted](#))
Janusz M.B. ([email@deleted](#))

Project objective (short):

Publish REPAIRtoire in NAR DB issue 2011.

Task description:

Important missing features in REPAIRtoire are implemented. A detailed, comprehensive, and checked set of data is available for multiple pathways. The website is optimized to look nice. A full set of automatically created annotation is used to enrich the data.

Expected results:

The web server runs, and is liked by J.M.B., our peers (<< 6 names deleted >>, recipients of the conference in << deleted >>) and they like it.

Server URLs:

Development: <http://150.254.121.231:8001>

Production: <http://repairtoire.genesilico.pl>

Milestones:

- DONE Decided which tables of the data model are going to be curated manually (all)
- DONE DrawRepair interface is working.
- DONE KR sent GP his final version of curated data.
- DONE The metadata model has been implemented in the data model.
- DONE All curated data has been loaded to build the initial database.
- DONE The website represents all data that is in the initial database.
- DONE A picture has been created for each repair step in the database.
- DONE Manually assembled the pictures for a pathway to a single PNG file.
- DONE REPAIRtoire has been transferred and is running on a public server.

Tasks:

- MMR pathway complete (Kosa) (S.cerevisiae, DONE E.coli, DONE H.sapiens)
- NER pathway complete for E.coli, H.sapiens (AK), S.cerevisiae (?)
- NHEJ pathway complete for E.coli (DOES NOT EXIST), H.sapiens (AK), S.cerevisiae (?)
- HR pathway complete for E.coli (AK), H.sapiens (AK?), S.cerevisiae (?)

- BER pathway complete for E.coli, H.sapiens (AK), S.cerevisiae (?)
- curate damages to highest level of detail, no generalizations except keywords (KR)
- add images to damages (KR)
- Link damages to pathways (AK)
- Annotated proteins, pathways, damages, and repair processes by keywords.
- Update UML diagrams (KM/ZB)
- Add protein structures (this could be also done with wiki-like formatting) - ??? (java error while loading structures from pdb)
- Document the App 'Nucleotides' (tables Modifications, ChemicalGroup, Nucleotide) explicitly. (KM)
- Delete Activity table. (KM)
- Documentation of code (KM)
- improvements in Protein table (according Kosa's suggestions below). (KM)
- Go through Kosas suggestions << removed >>. (KM)

Done between 1.10.2009 until 6.11.2009

- DONE Add app to add publications.
- DONE add icons from homepage in 5 subpages
- DONE Show protein:references as table containing author, year, title, journal.
- DONE Improve view of Protein sequences
- DONE Added protein structure information.
- DONE add HTML views for damages, diseases etc. (KM)
- DONE Annotated proteins by automatic data.
- DONE REPAIRtoire has been transferred to the a public server.
- DONE Ticket system is established and acknowledged by all participants.
- DONE Web interface integrated into the generalized Django architecture.
- DONE Editing on the development server acknowledged by all participants.
- DONE New data model ready for editing
- DONE Improved online picture drawing tool.
- DONE add mol structures to damages (KR)

Optional or later:

- Possibility to show crosstalk of repair mechanisms (important!)
- Wiki-like pages for proteins - waiting for feedback
- XML format for RNA
- Decide that web templates look good enough (JMB: Yeah, good enough. For the time being, we are not changing the looks. We will come back to this in the future, when other more important things are done. 10/2009)
- Exchange formats for Systems biology
- Include information about protein-protein information. As a minimum: in the Protein page list all other proteins the given protein interacts with (and provide a field for optional indication of the type of interaction: physical, genetic, etc. and whether experimentally determined and how, or predicted theoretical etc.). This would serve as a proxy for linking different pathways.