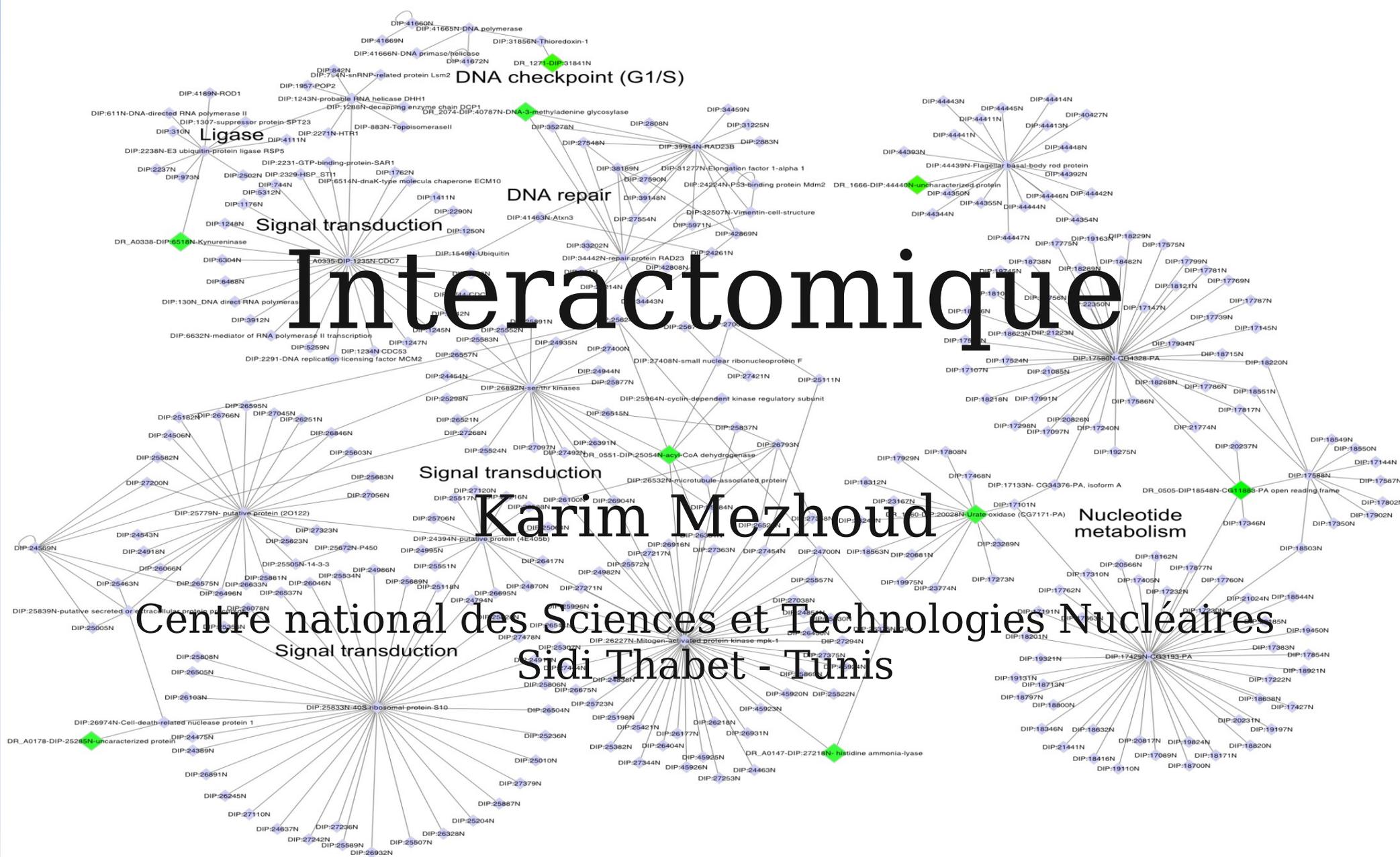


Interactomique



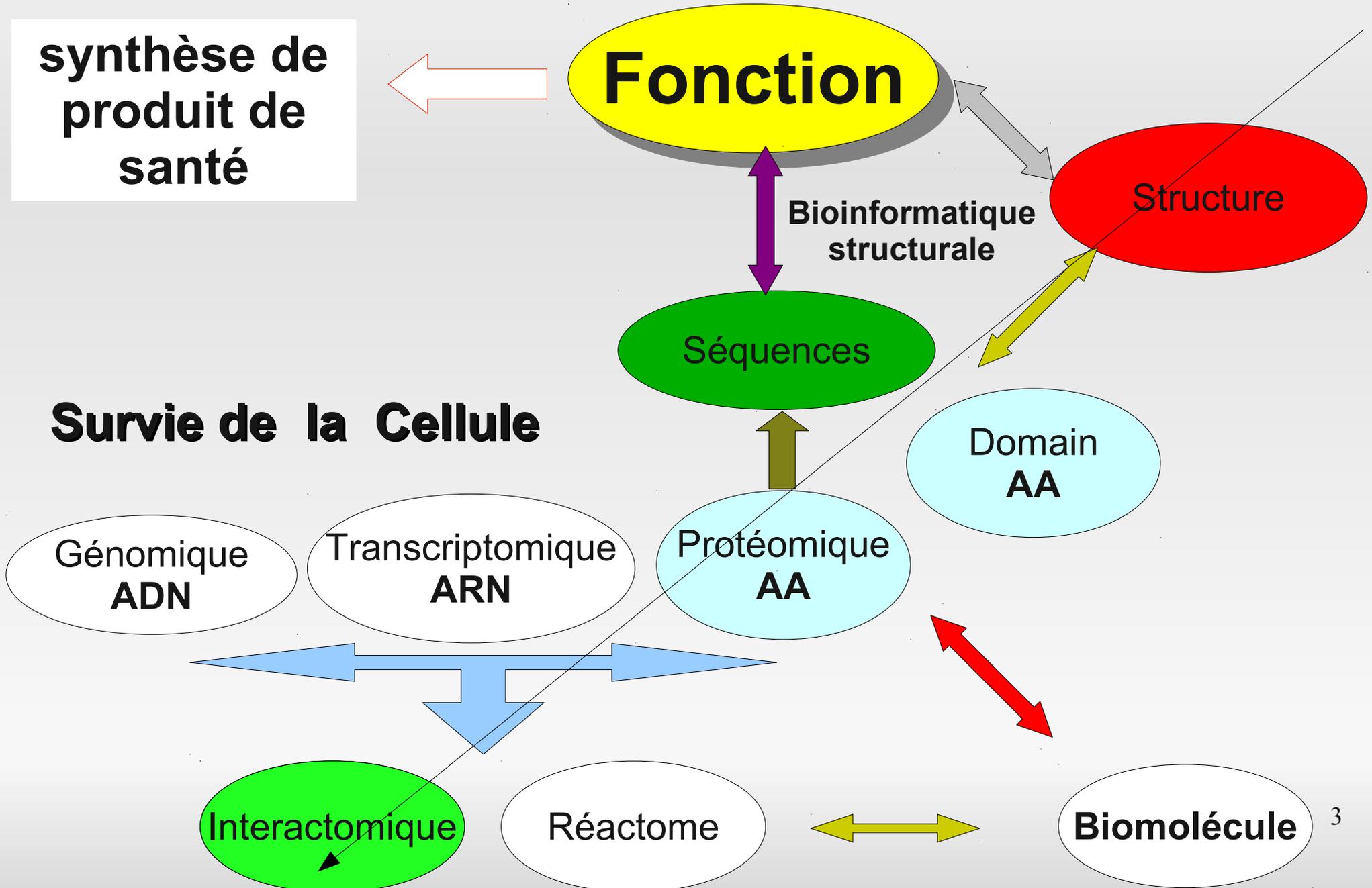
Karim Mezhoud

Centre national des Sciences et Technologies Nucléaires
Sidi Thabet - Tunis

Définition

L'interactomique est l'étude des voies de signalisation intracellulaire induites par les protéines. Elle consiste à lister les protéines existantes dans les bases de données, possédant des interactions avec d'autres protéines. Ces interactions sont généralement démontrées expérimentalement et peuvent être interpolées entre espèces. L'interaction Protein-protein peut être plus précise et devient une interaction domain-domain.

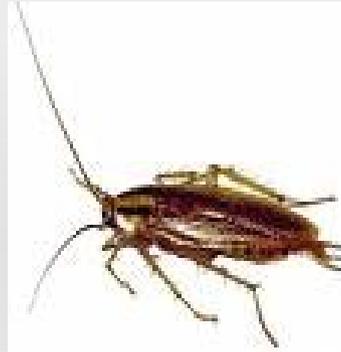
Prédiction de fonction



Apparition des espèces radio-résistantes



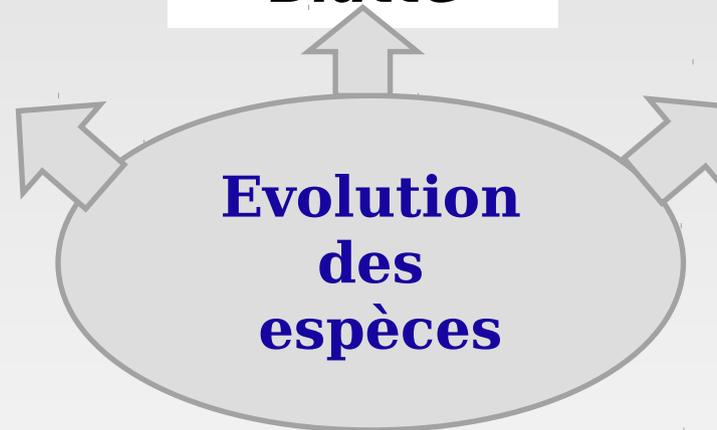
Scorpion



Blatte



**Bactérie
*Deinococcus
radiodurans***



Comment ces organismes résistent aux rayonnements ionisants?

La réparation de l'ADN



***OH**



**Dompage de
l'ADN**

**Réparation
de l'ADN**

**Mort
cellulaire**

Mutation



Survie

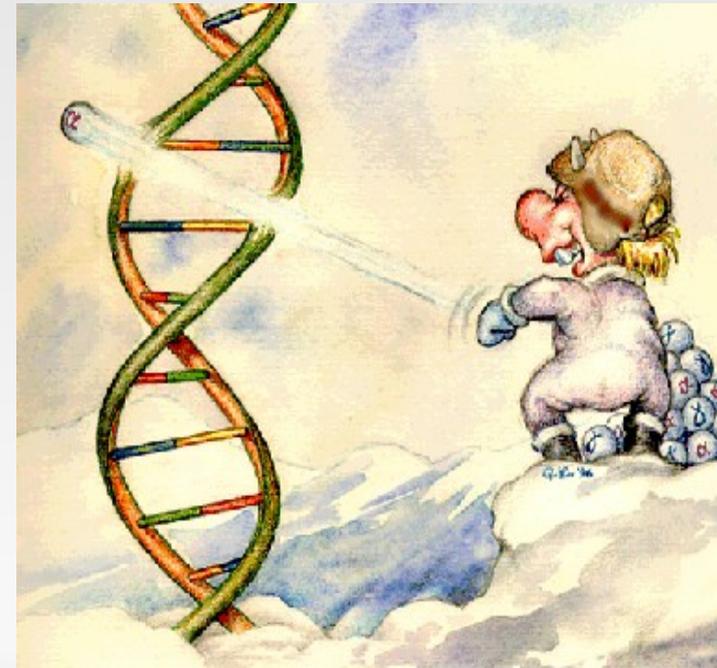


Cancer

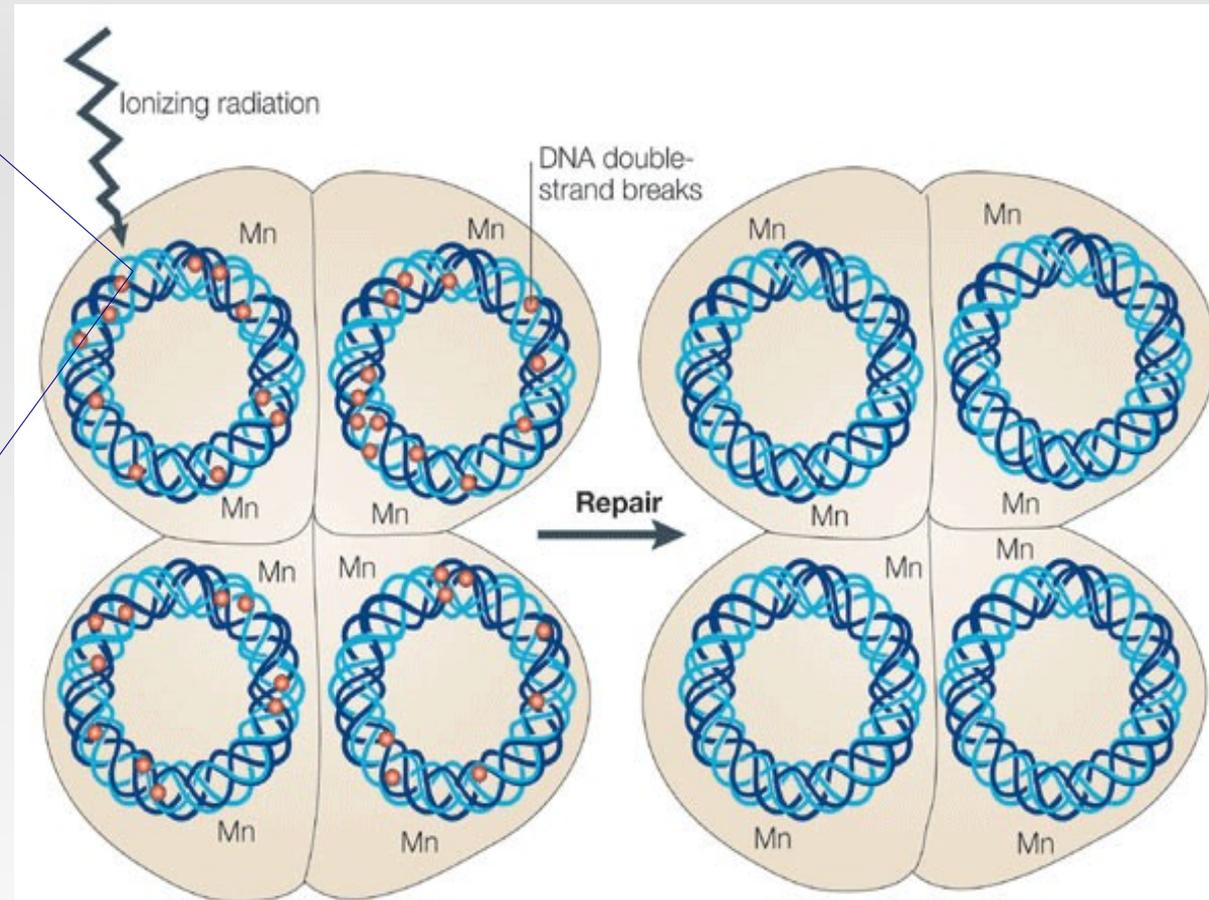
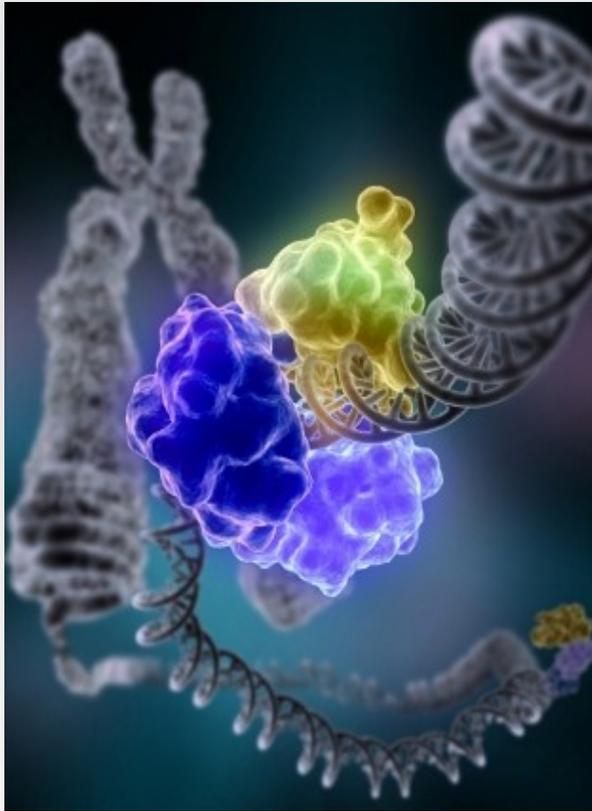
Radiosensible

**La radiorésistance est
due:**

1. Neutraliser les *OH
2. Détecter et réparer les cassures de l'ADN

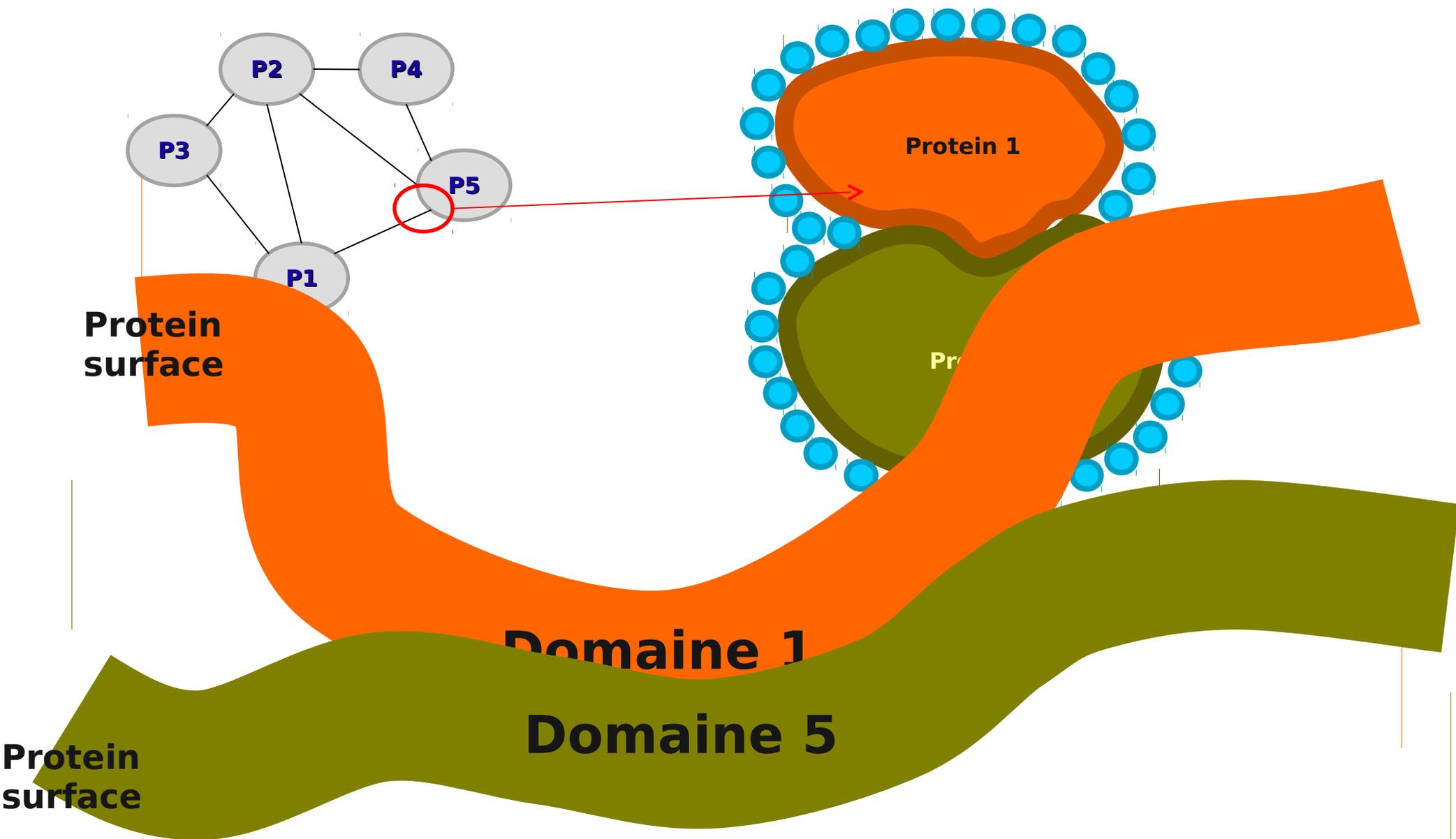


Exemple



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Interactomique



Comparaison génomique (Sghaier et al., 2008)

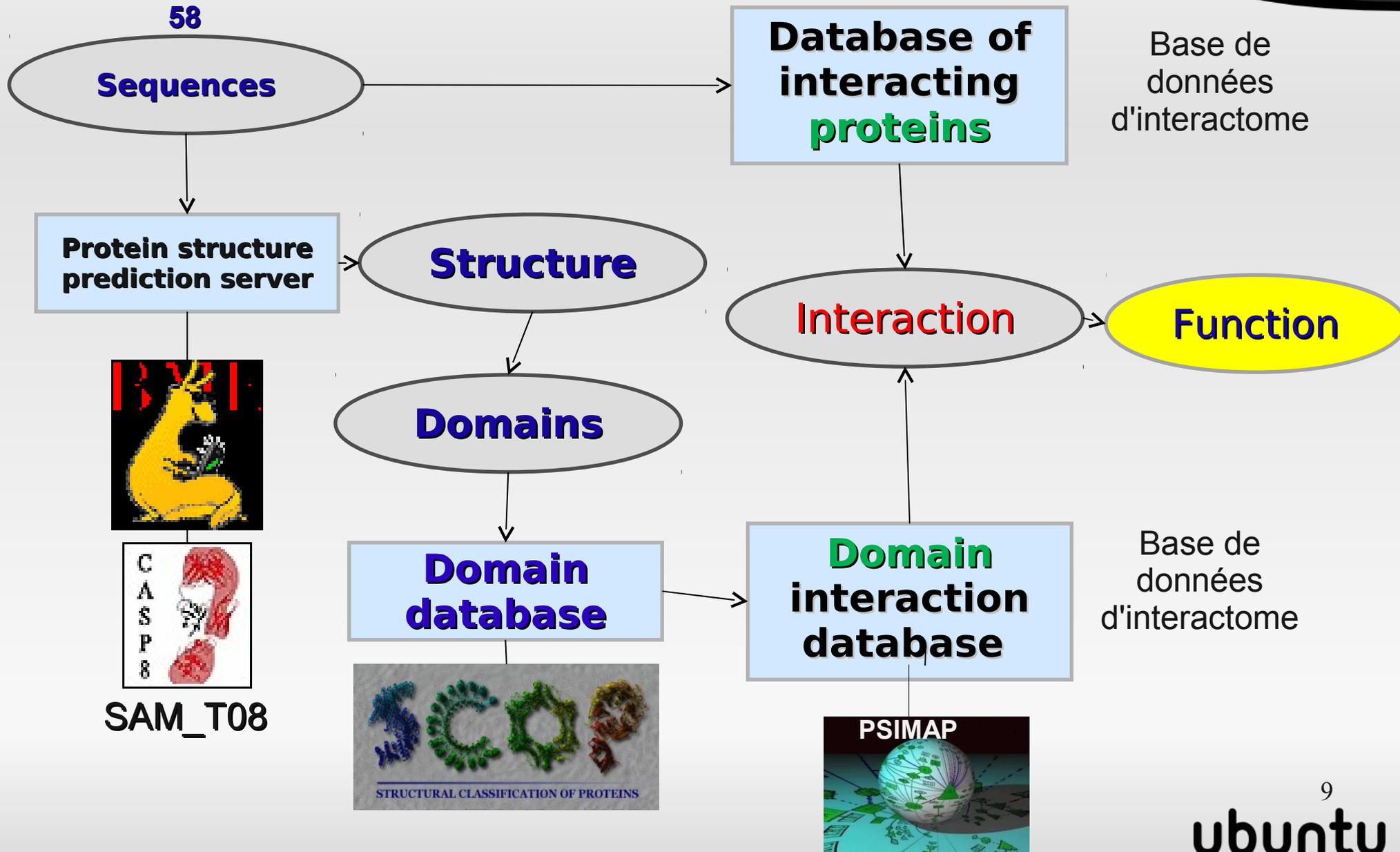


**Génomes de
Bactéries
Radiorésistantes**

58 gènes

**Génomes de
Bactéries
Radiosensibles**

Méthodologie



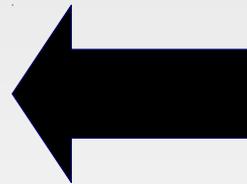
Principe et méthodes



Bases de données Interactome

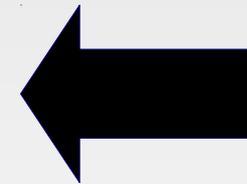
P 1- P 2
P3- P 4
.
.
.
P 1001 – P
546
.
.
.
P n – P N-2

Interaction



P 1
P 2
P 3
Protéine 4
.
.
.
.
P 1001
.
.
.
P 42600 1581
page

Sequences
DIP



Protéome

Protéine 1
Protéine 2
Protéine 3
Protéine 4
.
.
.
.
Protéine 1001
.
.
.
Protéine 3181

Nos
Sequences₀

ubuntu

Séquence de protéine



>DR_A0368-Q9RYF0

MSHALRPLCPPPEQFRPHDGRRPVVASCSTQAPALLVLSHLRWNFVFQRPQHLMTRAARTRRVFFIEEPV
FGEDADRLEMVTDASGVTVCTPHVESGHSPAESQARTARLLTQLVQSEGLDYLWVYTPMELPVAAGLTP
RLTVYDCMDELANFRGAPPELREREQQLFEQAGVVFTGGHRLYEAKCLQHGNYVFPSSVEVEHFAQARQD
LADPADQRELPRPRLGFYGVIDERFDTALIGELARRRPEWQIVLLGPVVKIDPAELPQAPNLHYLGQKTYA
ELPQYLAHWDVALLPFALNPSTEFISPTKTPEYLAAGVPVVSTGIRDVIRPYGEGEMVRVADGVDAFEAAC
AAALDEAGTAQATERQQRADAYLAGLSWDRTWNEMQAAMESAVQTQOSAAPAPLRESADD

Méthodologie



Mettre la base de donnée de séquences en format avec la commande suivante: `formatdb -i nom-du-fichier`

58_proteins.txt

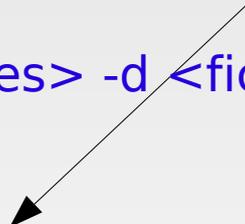


58_proteins.txt
_sans_chariot



dip20080918B.seq
dip20080918B.seq.phr
dip20080918B.seq.pin
dip20080918B.seq.psq
formatdb.log

`blastall -p blastp -i <fichier séquences> -d <fichier database> -o <fichier output>`



```
Query= DR_A0361-Q9RYF7
      (375 letters)
Database: dip20080918B.seq
         42,562 sequences; 23,571,726 total letters
Searching.....done

Sequences producing significant alignments:
dip:DIP-14663N|refseq:NP_215755          87  4e-17
dip:DIP-38858N|refseq:XP_001713086|uniprot:013779 64  3e-10
dip:DIP-1184N|refseq:NP_014511|uniprot:Q08269   51  2e-06
```

Méthodologie



Blast 1

```
Query= DR_A0361-Q9RYF7
      (375 letters)
Database: dip20080918B.seq
         42,562 sequences; 23,571,726 total letters
Searching.....done
```

	Score (bits)	E Value
Sequences producing significant alignments:		
dip:DIP-14663N refseq:NP_215755	87	4e-17
dip:DIP-38858N refseq:XP_001713086 uniprot:013779	64	3e-10
dip:DIP-1184N refseq:NP_014511 uniprot:Q08269	51	2e-06



Blast 2 = filtration de Blast 1: on récupère que le meilleur score

Query= DR_A0363-Q9RYF5		
dip:DIP-14862N refseq:NP_215948	369	e-102
Query= DR_A0361-Q9RYF7		
dip:DIP-14663N refseq:NP_215755	87	4e-17
Query= DR_A0338-Q9RYH5		
dip:DIP-6518N refseq:NP_013332 uniprot:Q05979	114	3e-25

Méthodologie



Fichier 1 = Blast 2

```
Query= DR_A0363-Q9RYF5
dip:DIP-14862N|refseq:NP_215948          369    e-102
Query= DR_A0361-Q9RYF7
dip:DIP-14663N|refseq:NP_215755        87     4e-17
Query= DR_A0338-Q9RYH5
dip:DIP-6518
```

Fichier 2 = base de données interactomique DIP

```
DIP-1E  DIP-328N    Q07817  NP_612815  DIP-232N    Q07812    3    DIP-110851X:SS  DIP-1X:SS    DIP-93495X:SS
DIP-2E  DIP-1043N    P10415  NP_000624  DIP-14663N  P04049    NP_002871    3    DIP-108783X:HT  DIP-76062X:SS  DIP-2X:SS
```

Fichier 3

```
Query= DR_A0361-Q9RYF7- dip:DIP-14663N|refseq:NP_215755
DIP-2E  DIP-1043N    P10415  NP_000624  DIP-14663N  P04049    NP_002871    3    DIP-108783X:HT  DIP-76062X:SS  DIP-2X:SS
```

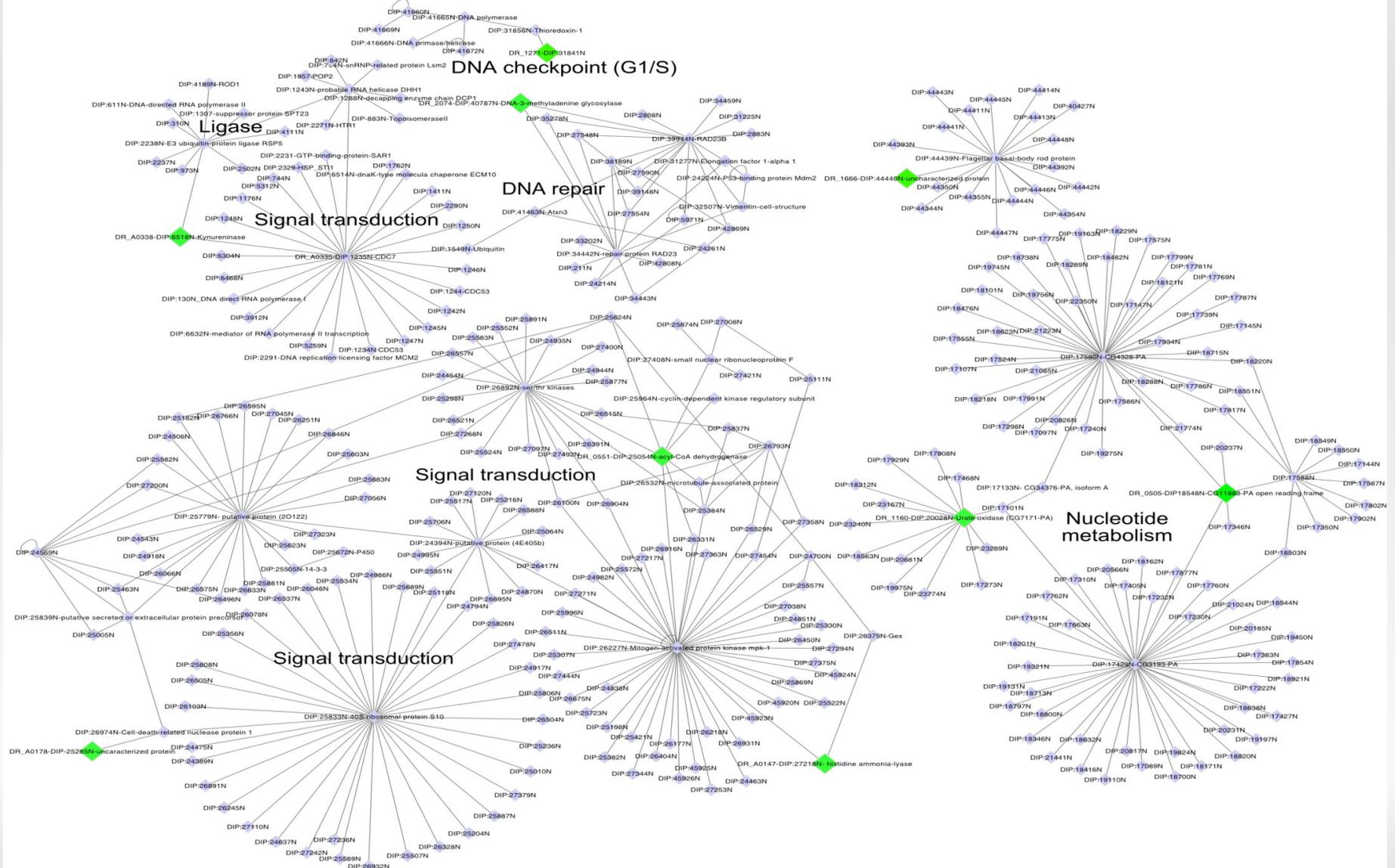
blast 3



blast 3

DR_A0338-Q9RYH5	-DIP-6518N							
DIP-11720E	DIP-1235N	P06243	NP_010267	DIP-6518N	Q05979	NP_013332	1	DIP-14154X:HT
DIP-63815E	DIP-6518N	Q05979	NP_013332	DIP-2238N	P39940	NP_011051	0	
DR_A0178-Q9RYX6	-DIP-25285N							
DIP-81944E	DIP-25285N	017892	NP_502747	DIP-26974N	Q9N3T2	NP_491168	1	DIP-109393X:HT

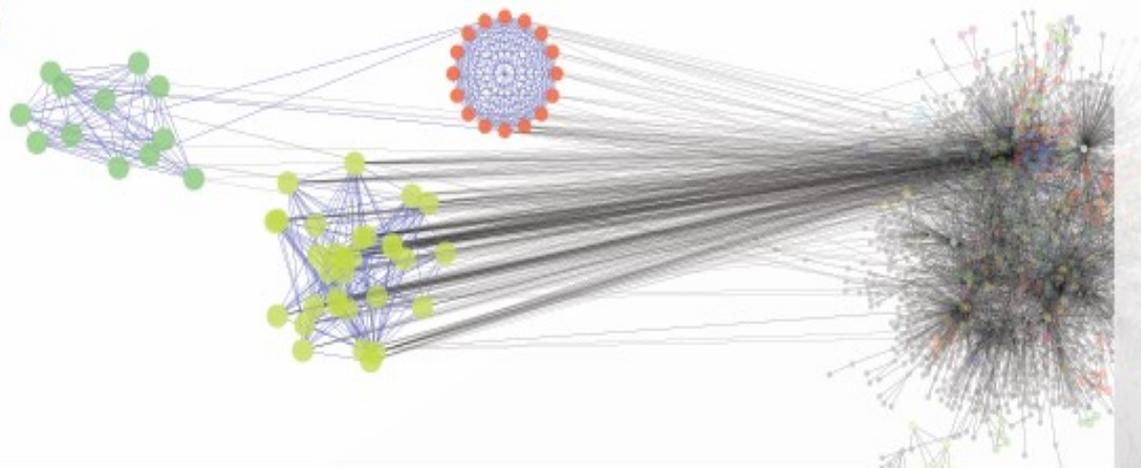
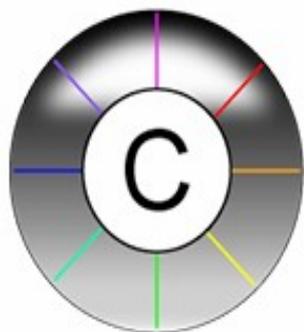
Exemple de resultats



Logiciel d'interactomique



Cytoscape



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About Cytoscape

Cytoscape is an open source bioinformatics software platform for **visualizing** molecular interaction networks and **integrating** these interactions with gene expression profiles and other state data.

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Online Tutorials

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Manual

[HTML format](#) or [PDF format](#), explains all basic features of Cytoscape. Get [Acrobat reader](#)

Developers

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Installation du Plugin MiSink



DIP SOFTWARE: MiSink Plugin

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Installation

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[Documentation](#)

[FAQ](#)

[Help](#)

To install MiSink plugin on your computer follow the steps below:

1. Install the most recent version of [Cytoscape](#).

MiSink is an add-on module for Cytoscape and therefore proper installation of Cytoscape is compulsory. Please, try to remember the directory Cytoscape will be installed as this information will be needed later on.

NOTE: In case Cytoscape has been already installed, please, make sure it is version 2.3 or above and check what directory it has been installed in.

2.A. Cytoscape version 2.5 and newer:

- a. Open Plugins->Manage Plugins menu within Cytoscape and select 'Change Download Site'.
- b. Click on 'Add Site', chose 'plugins' (instead of 'networks') within the top pulldown and click on 'Add'.
- c. Enter a name (arbitrary - DIP, MiSink, whatever...) and URL:

```
http://dip.doe-mbi.ucla.edu/misink/cplug.xml
```

then click on 'Add' followed by 'Ok' within Network manager dialog.

- d. Select the name you used in the 'Plugin Downloads Sites' dialog and click 'Ok'. There should be now one plugin listed as available for download - unfold the folder tree to get to MiSink plugin, select it and click on 'Install'.

Interaction firefox – cytoscape par MiSink



ZOOM

A

B

C

D

I Add nodes/edges

II Check references

III Find neighbours

UniProt
the universal protein resource

UniProtKB Entry - UniProt [E...]

UniProtKB Entry: P13108

ENTRY INFORMATION

ENTRY NAME	HSC2L_YEAST
ACCESSION NUMBER	P13108
Integrated into Swiss-Prot on	1990-04-01
Sequence was first modified on	1996-10-01 (Sequence version 3)
Annotations were last modified on	2006-10-01 (Entry version 61)

NAME AND ORIGIN OF THE PROTEIN

PROTEIN NAME	ATP-dependent endonuclease HSC2
Synonyms	Heat shock protein Hsp90 coactivator isoforms; H2 Lids heat shock regulator protein
GENE NAME	Main: HSC2; Original locus name: YMR180W; ORF name: YR-8015.16
SOURCE ORGANISM	Saccharomyces cerevisiae
TAXONOMY ID	4912 [NCBI: NCNT]
LINEAGE	Eukaryota; Opisthokonta; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycotinae; Saccharomycotinales; Saccharomycotini

REFERENCES

[1] Berkovich KA, Parsley PW, Finkelman DB, Tindes J, Lindayer B. Hsp92 is an essential protein that is required in higher concentrations for growth of *ce* at temperatures. 1993. *Mol Cell Biol.* 9: 3919-3920.