

SNPs affect RNA protein interactions or binding sites of Alzheimer's disease and related dementia

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Study Background

❖ Alzheimer's Disease

- A progressive disease that destroys memory and other important mental functions.

❖ RNA binding proteins(RBP)

- proteins that bind to the double or single stranded RNA in cells and participate in forming ribonucleoprotein complexes
- RBP normally are present in the nucleus. Under conditions of cell stress, these RBP translocate to the cytoplasm where they form stress granules, which function in part to sequester specialized transcript and promote translation of protective proteins.

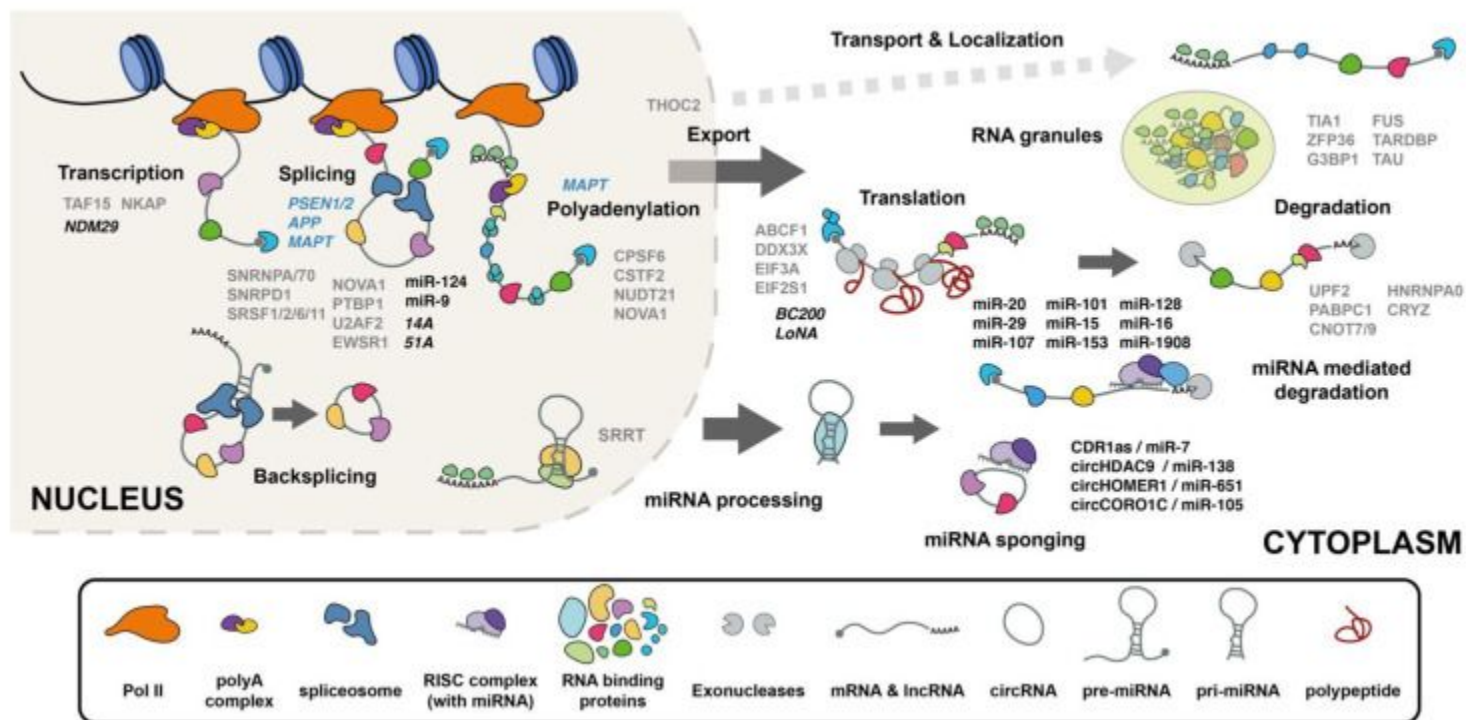


Figure.1. Rybak-Wolf, Agnieszka, and Mireya Plass. "RNA Dynamics in Alzheimer's Disease." Molecules (Basel, Switzerland) vol. 26,17 5113. 24 Aug. 2021, doi:10.3390/molecules26175113

Study Background



Locus



A locus is a specific, fixed position on a chromosome where a particular gene or genetic marker is located.



SNP



A single-nucleotide polymorphism is a germline substitution of a single nucleotide at a specific position in the genome



eCLIP



An enhanced version of the crosslinking and immunoprecipitation (CLIP) assay, and is used to identify the binding sites of RNA binding proteins (RBPs)

Study Background

- ❖ **Genome-wide association studies (GWAS)** have identified >50 susceptibility loci showing robust evidence for association with late-onset Alzheimer's disease (AD).
- ❖ A striking fraction of these loci implicate RNA metabolism. **Some loci code for RNA binding proteins (RBPs)**, which regulate RNA splicing.
- ❖ Understanding the effect of these same-sense SNPs has wide-ranging implications for understanding AD.

Questions to be answered:

- ❖ Investigate the relationship between SNPs and their effect on RBP binding
- ❖ Number of loci on each specific RNA and the function of each Loci
- ❖ Do AD-related SNPs impact on RNA-binding protein?

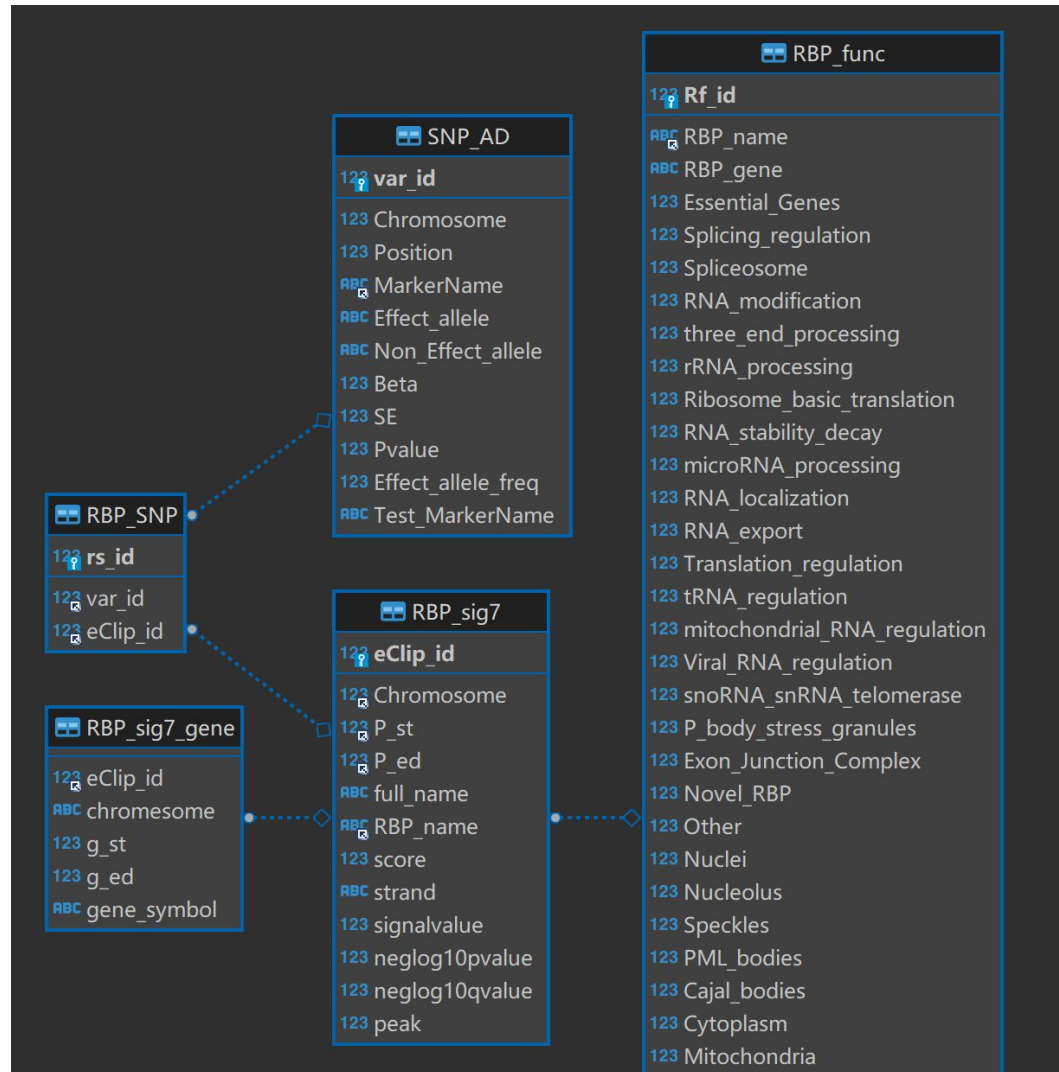
Database Working Pipeline

- ❖ Gather and extract data from ENCODE
- ❖ Create database
- ❖ Design the web interface
- ❖ HTML/Javascript/AJAX
- ❖ Use query to access the data in the database
- ❖ Create CGI program

Datasource

1. Single nucleotide polymorphisms (SNPs) data comes from The **International Genomics of Alzheimer's Project (IGAP)** (Alzheimer's disease GWAS of Kunkle et al. , Nat Genet, 2019).
2. RNA-binding proteins (RBPs) data is download from **ENCSR456FVU**(Reference: A large-scale binding and functional map of human RNA-binding proteins, Nature)
3. Extra DATA: to find the targeted genes, we use bamtools to find the RBP target genes

Build Database



Relationship 1(SNP and RBP)

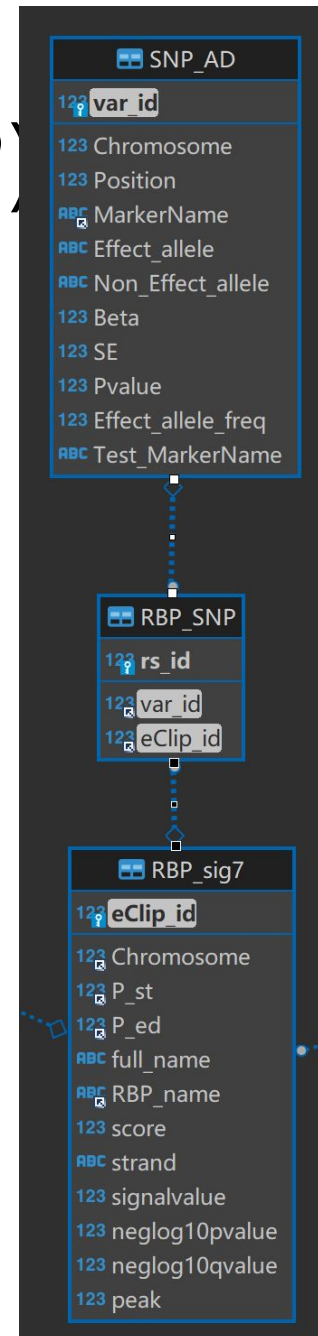
Many to Many Relationships

Both **partial participation**

One SNP could be on a Gene regulated by **more than one** RBP

The genes regulated by **one** RBP could have **more than one** SNPs

Not every SNP is regulated by a RBP, Not every RBP regulate a gene having SNP



Relationship 1(SNP and RBP)

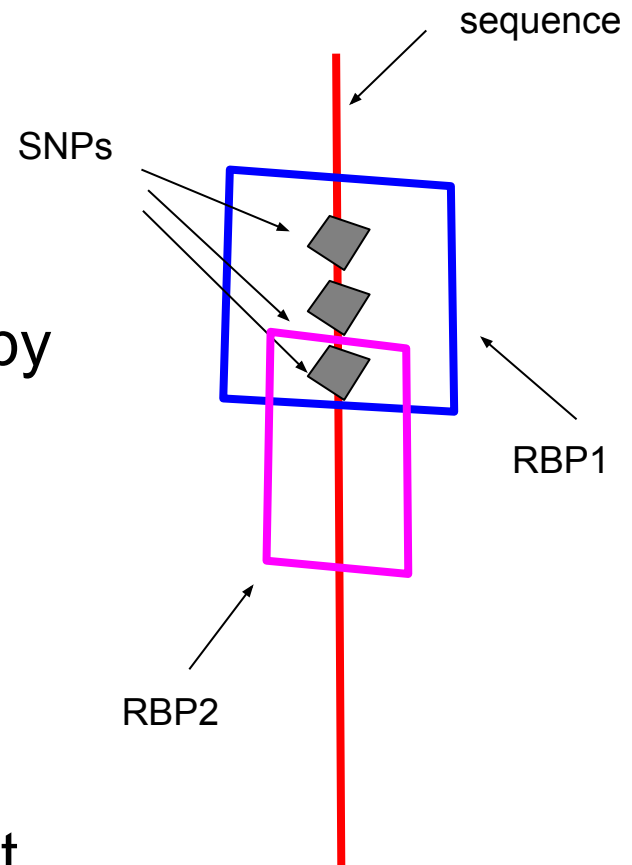
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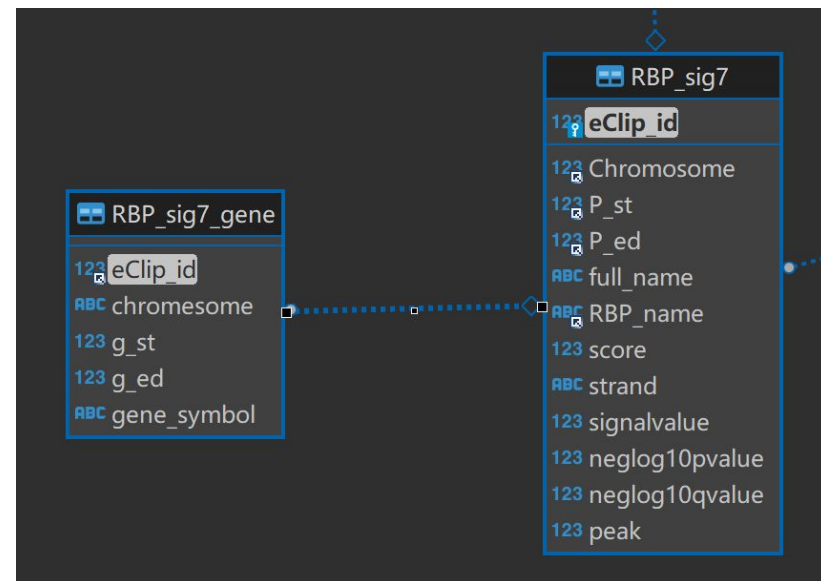
Not every SNP is regulated by a RBP, Not every RBP regulate a gene having SNP



Relationship 2 (RBP and its target genes)

one to many relationship

A targeted gene could be regulated by different RBPs.

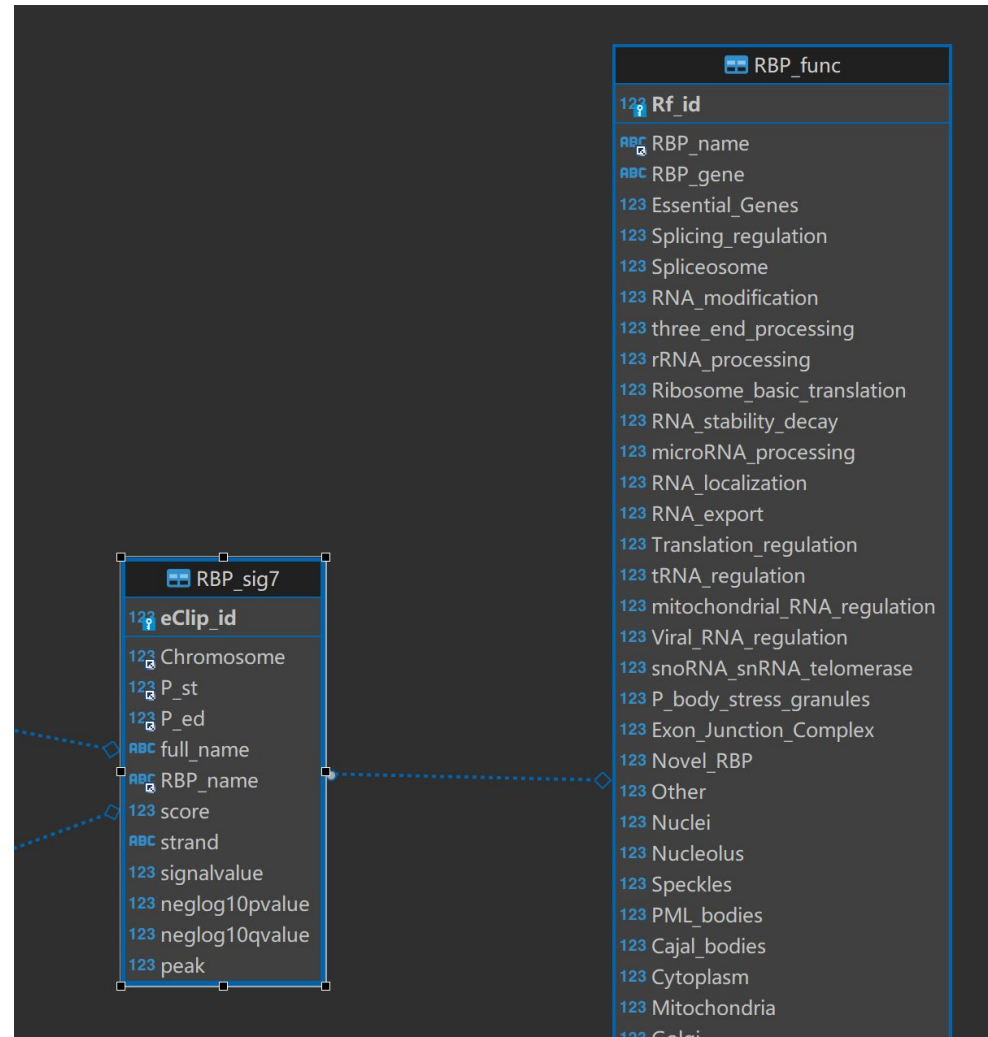


Relationship 3 (RBP and its function)

one to many
Relationship

A RBP must belongs to
a function cluster

A function cluster could
have **more than one**
RBP



Something interesting we met

How to build the many to many relationship for SNP and RBP?

If we use sql to build the relationship table

Data size:

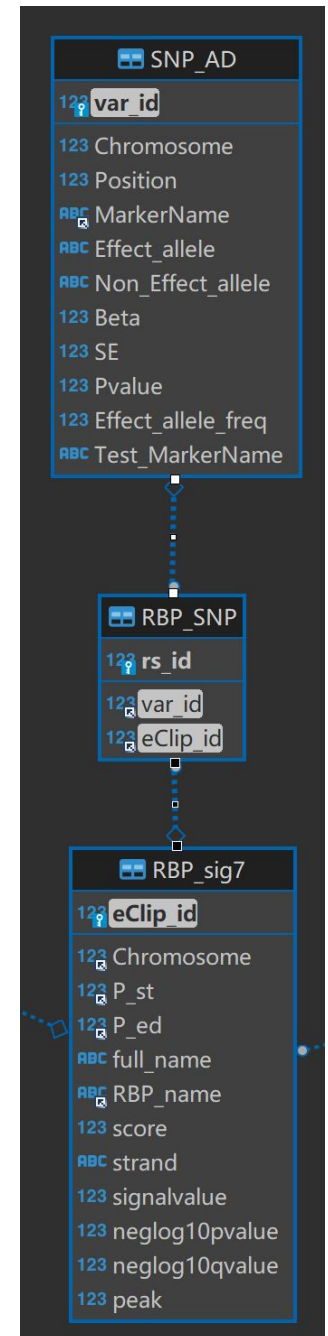
SNP: 676,450 rows; RBP: 6,517,506 rows

If we use join directly(using index at the same time)

the complexity is $O(n \log m) = 676,450 \log(6,517,506) = 10^8$



Theoretically, it would not take more than 1 seconds



Something interesting we met

How to build the many to many relationship for SNP and RBP?

However, it takes a lot of time using sql.(more than three hours and we did not receive any result)

We finally decide to build a Balanced tree to get the relationship table.



Code available:

https://github.com/Rey572/BF768_FinalProjectTree

```
1 #include <cstdlib>
2 #include <iostream>
3
4 using namespace std;
5 struct tree
6 {
7     int val,fix,weight,size;
8     tree *left,*right;
9 };
10 int resize(tree *tr)
11 {
12     if (tr==NULL) return 0;
13     else return tr->size;
14 }
15 void turnleft(tree *&x)
16 {
17     tree *y=x->right;
18     x->right=y->left;
19     y->left=x;
20     x=y;
21     y=x->left;
22     y->size=resize(y->right)+resize(y->left)+y->weight;
23     x->size=resize(x->left)+resize(x->right)+x->weight;
24 }
25 void turnright(tree *&x)
26 {
27     tree *y=x->left;
28     x->left=y->right;
29     y->right=x;
30     x=y;
31     y=x->right;
32     y->size=resize(y->right)+resize(y->left)+y->weight;
33     x->size=resize(x->left)+resize(x->right)+x->weight;
34 }
35 void insert(tree *&head,int item)
36 {
37     if (head==NULL)
38     {
39         head=new tree;
40         head->val=item;
41         head->right=NULL;
```

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SNP-RNA Protein Interactions for Alzheimer's Disease and Related Dementia

Genome-wide association studies (GWAS) have identified more than 50 susceptibility loci showing robust evidence for association with late-onset Alzheimer's disease (AD). A striking fraction of these loci implicates RNA metabolism. Some loci code for RNA binding proteins (RBPs), which regulate RNA splicing. Other susceptibility loci contain polymorphisms that alter splicing of the gene or contain altered splicing patterns associated with AD. Overall, more than 90% of SNPs identified from GWAS occur in non-coding regions. Non-coding SNPs can appear in noncoding RNAs, introns, or in 5' and 3' untranslated regions (UTRs). Our goal is to understand the effect of these non-coding or same-sense SNPs and their wide-ranging implications for understanding AD.

About us

This page is developed at Boston University as part of BF768 Biological Database Systems, Spring 2022 by students Benyu Zhou, Katherine Tu, Mintao Lin, Qinrui Wu, and Xiaojing Peng and guided by instructor G. Benson and professor Xiaoling Zhang from the Department of Medicine at Boston University.



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Home **AD-related SNP-RBP binding** Loci Number AD-related RBP function DIY Help

AD-related SNP-RBP binding

Select p-value

- ☒ 0.05
☐ 0.01

submit

Description

Table

Plot

Description summary:

the number of SNP,
the number of RBP



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Home **AD-related SNP-RBP binding** Loci Number AD-related RBP function DIY Help

AD-related SNP-RBP binding

Select p-value

☒ 0.05

☐ 0.01

submit

Description

Table

Plot

SNP-chr	SNP position	SNP marker name	SNP P-value	RBP Name	P-value	Output gene



Download table

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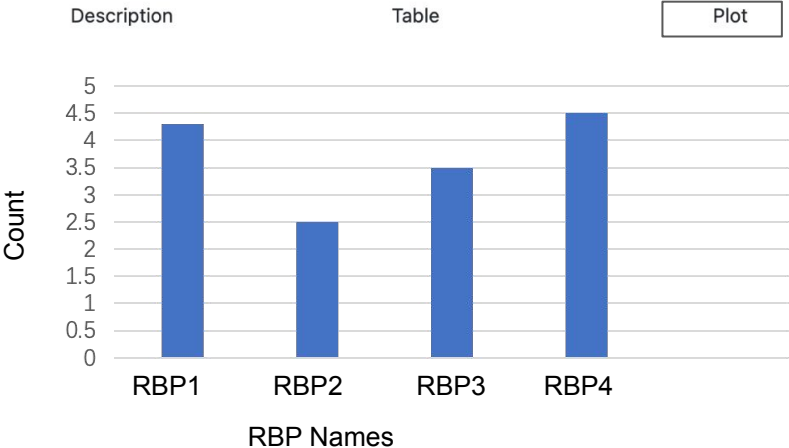
Home **AD-related SNP-RBP binding** Loci Number AD-related RBP function DIY Help

AD-related SNP-RBP binding

Select p-value

- ☒ 0.05
☐ 0.01

submit



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Loci Number

Input RBP name (e.g. BUD13):

Table

Plot

Description summary:

The number of SNP,
Genes annotated to loci



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Home AD-related SNP-RBP binding **Loci Number** AD-related RBP function DIY Help

Loci Number

Input RBP name (e.g. BUD13):

submit

Description

Table

Plot

SNP chromosome	SNP position	SNP marker name	P-value for SNP	Target Gene
				APOBEC3C

Download table



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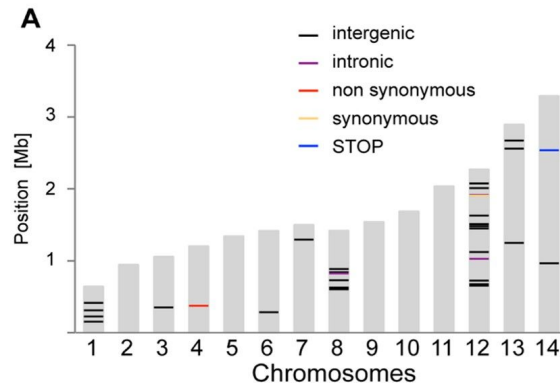
Loci Number

Input RBP name (e.g. BUD13):

Description

Table

Example graph:
Bopp et al. PLOS Genetics
2013;9(2):e1003293



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AD-related RBP function

Input SNP:

[Table](#)

[Plot](#)

Description summary:

Beta value of the SNP

Whether a Risk/Protective SNP

The number of RBPs that target the SNP



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AD-related RBP function

Input SNP:

Description

Plot

RBP Name	RBP Gene	Function	Target



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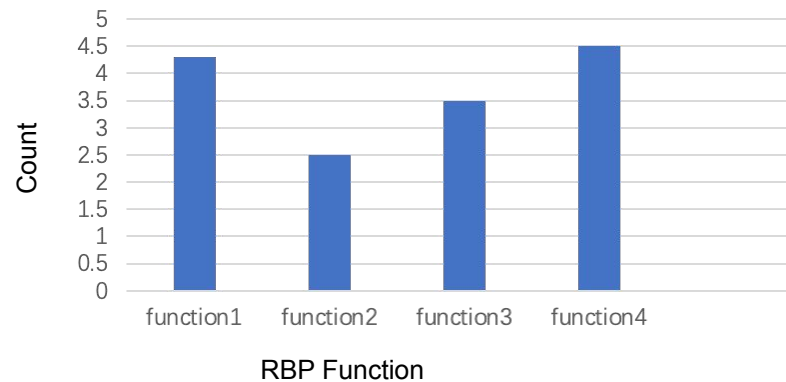
Home AD-related SNP-RBP binding Loci Number DIY Help

AD-related RBP function

Input SNP:

Description

Table



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DIY query

Input query:

Submit

Table



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Under construction...



CGI

❖ APIDB.py

- Application Programming Interface to our database.
- In this py file, a class named APIDB is defined that connects to the database on bioed and performs all queries based on selectors.

❖ api_main.py

- This py file contains main CGI structure that receives html form input and use the APIDB class to returns query results in json form to html.

Reference

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5. Bopp SER, Manary MJ, Bright AT, Johnston GL, Dharia NV, Luna FL, et al. (2013) Mitotic Evolution of *Plasmodium falciparum* Shows a Stable Core Genome but Recombination in Antigen Families. *PLoS Genet* 9(2): e1003293. <https://doi.org/10.1371/journal.pgen.1003293>