

## BloodChIP REST Interface

### EXPORT FUNCTION - CSV FILE WITH GENE(S) BOUND BY SPECIFIC TF(S)

[http://149.171.101.136/python/BloodChIP/server.php?csv\\_hdr=CSV\\_HEADER&search\\_type=TYPE&search=SEARCH&join=BINDING\\_PROFILES&exp\\_cell\\_type=CELLTYPE1&exp\\_cell\\_type\\_0=CELLTYPE\\_0&exp\\_fold=FOLD\\_CHANGE &foldchange=FOLD\\_VALUE](http://149.171.101.136/python/BloodChIP/server.php?csv_hdr=CSV_HEADER&search_type=TYPE&search=SEARCH&join=BINDING_PROFILES&exp_cell_type=CELLTYPE1&exp_cell_type_0=CELLTYPE_0&exp_fold=FOLD_CHANGE &foldchange=FOLD_VALUE)

#### Description

- **CSV\_HEADER** field corresponds to each of the columns of the CSV file to be created. The structure is fixed and is equivalent to the structure of the database set in the server.

*GeneSymbol,chr,peak\_s,peak\_e,CD34\_FLI1,SKNO1\_FLI1,MK\_FLI1,CD34\_ERG,SKNO1\_ERG,K562\_ERG,CD34\_GATA2,MK\_GATA2,K562\_GATA2,CD34\_RUNX1,SKNO1\_RUNX1,MK\_RUNX1,K562\_RUNX1,CD34\_SCL,MK\_SCL,K562\_SCL,CD34\_LYL1,CD34\_LMO2,CD34\_SMAD1,K562\_SMAD1,CD34\_TCF7L2,K562\_TCF7L2,CD34\_H3K27ac,CD34\_H3K4me1,CD34\_H3K4me3,CD34\_footprint,K562\_H3K27ac,K562\_H3K4me1,K562\_H3K4me3,K562\_footprint,txStart,txEnd,Size(bp)*

- **TYPE** field defines the type of request to perform

1-> Coordinate(s)

0->Gene(s)

- **SEARCH (optional)** defines the set of Gene(s)/Coordinate(s) to search (separated by comma).

e.g.

**For Type= 0** (gene(s))

**Format:** ERG,A2LD1,RUNX1,....

**For Type=1** (coordinate(s))

**Format:** chr21:39751949-40033704,chr21:36160097-36260987,...

- **BINDING PROFILES (optional)** defines the conditions to look up Genes bound by specific transcription factor(s)

<TF1>%20<condition1>%20<TF2>%20<condition2>%20<TF3>%20<condition3>%20<TF4>%20  
....<condition(m-1)>%20<TFm>

Where <TF(x)> correspond to one of the following values according to the cell types and binding profiles available:

| CD34          | Megacaroocytes | SKNO-1        | K562          |
|---------------|----------------|---------------|---------------|
| CD34_FLI1=1   | MK_FLI1=1      | SKNO1_FLI1=1  |               |
| CD34_ERG=1    |                | SKNO1_ERG=1   | K562_ERG=1    |
| CD34_GATA2=1  | MK_GATA2=1     |               | MK_GATA2=1    |
| CD34_RUNX1=1  | MK_RUNX1=1     | SKNO1_RUNX1=1 | K562_RUNX1=1  |
| CD34_SCL=1    | MK_SCL=1       |               | K562_SCL=1    |
| CD34_LYL1=1   |                |               |               |
| CD34_LMO2=1   |                |               |               |
| CD34_SMAD=1   |                |               | K562_SMAD=1   |
| CD34_TCF7L2=1 |                |               | K562_TCF7L2=1 |

On the other hand, **<condition(x)>** refers to the relationship between the binding profiles to retrieve. It can be AND or OR.

**Note:** SEARCH and BINDING\_PROFILES fields do not depend on each other. It is, requests can be made using both or either of the two parameters. When one of the parameters is not considered, this parameter goes empty within the API (i.e. ...search=&... or ...&join=&...)

- **CELLTYPE1 & CELLTYPE0** fields correspond to any two available cell types that want to be compared regarding gene expression. If FOLD\_CHANGE is empty, no filter by expression is implemented and therefore these fields will not be considered in the search (i.e. the fields can be empty in the API).

Possible values (with **CELLTYPE1 != CELLTYPE0**)

- cd34 (i.e. CD34)
  - skno (i.e. SKNO1)
  - mega (i.e. Megakaryocytes)
  - k562 (i.e. K562)
- **FOLD\_VALUE** defines how large is the relation between gene expression of **CELLTYPE1** and the corresponding in **CELLTYPE0**. The possible value is to be larger or equal to 1. If **FOLD\_CHANGE** is empty, it means no filter by expression is implemented and therefore the field will not be considered in the search (i.e. it can be empty in the API).
  - **FOLD\_CHANGE** is used if filter by expression is required. The value corresponds to the relation of the gene expression between **CELLTYPE1** and **CELLTYPE0**. The following values are available

| <b>Option</b>                    | <b>Value in API</b> | <b>Meaning</b>  |
|----------------------------------|---------------------|---|
| <i>Greater than or less than</i> | ><                  | <i>CELLTYPE1 is FOLD_VALUE <b>greater than or less than</b> CELLTYPE0</i> |
| <i>Less than</i>                 | <                   | <i>CELLTYPE1 is FOLD_VALUE <b>less than</b> CELLTYPE0</i>                 |
| <i>Greater than</i>              | >                   | <i>CELLTYPE1 is FOLD_VALUE <b>greater than</b> CELLTYPE0</i>              |

If no filter by expression is required, the field needs to go empty in the API (i.e. ...&foldchange=&...).

## EXPORT FUNCTION - CSV FILE WITH GENE EXPRESSION

### API STRUCTURE

#### Description

In order to obtain the raw data for the gene expression of a set of genes, in the structure of the query above, change the name and value for the first value of the expression within the API

(i.e. Instead of ...csv\_hdr=**CSV\_HEADER**... use ...csv\_expression\_hdr=**EXPRESSION\_HDR**...),

where **EXPRESSION\_HDR** corresponds to each of the columns of the CSV file to be created. The structure is fixed and is equivalent to the structure of the database set in the server.

*GeneSymbol,k562\_1,k562\_2,k562\_3,CD34\_1,CD34\_2,'CD34\_3,CD34\_4,CD34\_5,CD34\_6,CD34\_7,'  
CD34\_8,CD34\_9,CD34\_10,CD34\_11,CD34\_12,CD34\_13,CD34\_14,CD34\_15,CD34\_16,CD34\_17,C  
D34\_18,CD34\_19,CD34\_20,CD34\_21,CD34\_22,CD34\_23,CD34\_24,CD34\_25,CD34\_26,CD34\_27,'  
CD34\_28,CD34\_29,CD34\_30,CD34\_31,Mega1,Mega2,Mega3,Mega4,SKNO1,SKNO2,SKNO3,SKN  
O4,Fold-Change(k562 vs. mega),Fold-Change(k562 vs. skno),Fold-Change(cd34 vs. mega),Fold-  
Change(cd34 vs. skno),Fold-Change(mega vs. skno),Fold-Change(k562 vs. cd34).*

Although the remaining variables in the API (e.g. **BINDING\_PROFILES,CELLTYPE1**,...) might not be required to perform the query, they do need to be part of this in order for the export function to work.

Therefore, include the variables in the string, but assign no value to them

(e.g. ...&join=&exp\_cell\_type=&exp\_cell\_type\_0=&exp\_fold=&foldchange=...).