



A PUBLIC DATABASE OF TRANSCRIPTION FACTOR AND REGULATORY SEQUENCE ANNOTATION

Stuart Lithwick logged in. [Log Out](#)

- LOGIN
- REGISTER
- MY PROJECTS
- SUBMIT
- SEARCH
- + OVERVIEW
- + XML FORMAT
- + GFF FORMAT
- + CONTACTS

WELCOME TO PAZAR MALL!

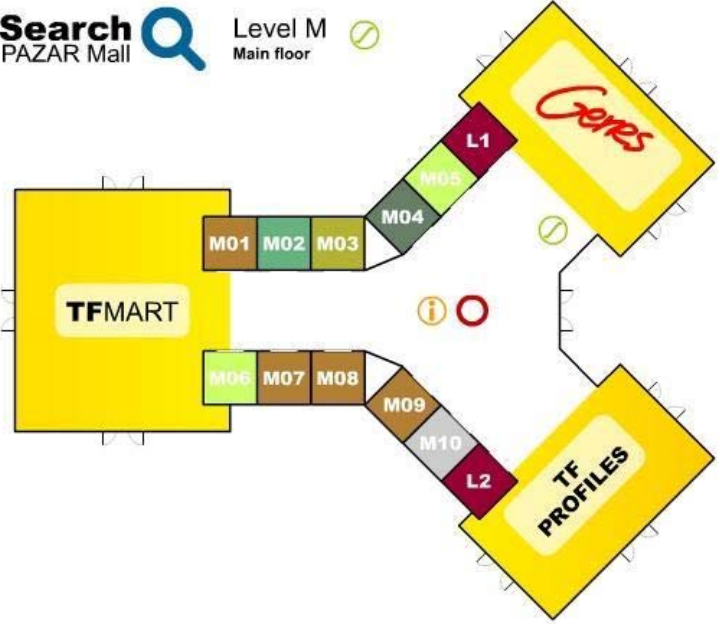
PAZAR can be searched by [Gene](#), [Transcription Factor](#) or [Profile](#) by clicking on one of the department stores below.

Each project in PAZAR is a boutique in the mall. You can limit your search to a specific project by clicking on the corresponding boutique on the mall map.

If you own restricted projects, log in and they will appear in the mall map. If you just created a project and it does not appear on the mall map, please log out and log in again.

Search PAZAR Mall

Level M
Main floor



« scroll left scroll right »

Level M - Main floor	Level 1 - First floor
M01 - muscle set	101 - For Lease
M02 - liver set	102 - For Lease
M03 - jasper_core	103 - For Lease
M04 - are_project	104 - For Lease
M05 - pleiades genes	105 - For Lease
M06 - test	106 - For Lease
M07 - For Lease	107 - For Lease
M08 - For Lease	108 - For Lease
M09 - For Lease	109 - For Lease
M10 - For Lease	110 - For Lease

Escalator
Use the escalator to go to a different floor

Information booth
Here you can find friendly staff members who are happy to help you

You are here:

Submission entry form - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Submission entry form Submission entry form



A PUBLIC DATABASE OF TRANSCRIPTION FACTOR AND REGULATORY SEQUENCE ANNOTATION
Shant Litwick logged in. [Log Out](#)

PAZAR - Data Submission

Some hints:

- You can use this interface to enter data to an already existing project or to a new one. For the latter, you just have to create a new project below and it will be added in your list of existing projects.
- TF centric submissions are based on a specific Transcription Factor from which you want to annotate binding sites.
- CRE centric submissions are annotations of a Cis Regulatory Element (CRE) from which you have experimental evidence of a role in gene regulation (binding or other).

Submit to Project:

Create A New Project

Name	<input type="text"/>
Status	<input type="text" value="restricted"/>
Description	<input type="text"/>
Administrator Password	<input type="text"/>
Re-enter Admin Password	<input type="text"/>
<input type="button" value="Create New Project"/>	



Stuart Lithwick logged in. [Log Out](#)

- LOGIN
- REGISTER
- MY PROJECTS
- SUBMIT
- SEARCH
- OVERVIEW
- XML FORMAT
- GFF FORMAT
- CONTACTS

Describe your Cis Regulatory Element

Genomic Sequence Artificial Sequence

CRE genome location data

Enter here unique genome identification parameters in chromosome coordinates.
The chromosome coordinates should be correct for the current Ensembl release and the respective genome build.
The best way to set those is through the 'Get chromosome coordinates' button.

sequence

name (optional) quality

start end

chromosome strand

organism

Gene ID Gene DB

Gene Description (optional)

Representative Transcript (optional) Transcript DB

Transcription Start Region Start (optional) Transcription Start Region End (optional)

Artificial Sequence data

sequence

construct name

comment

Transcription factor/complex binding to this CRE (if known)

Interaction Evidence with an unknown factor (e.g. nuclear extract)

Other Experimental Evidence for a Role of this CRE in Regulating Gene Expression

Get Chromosome Coordinates - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Gene ID Gene DB

approximate position of the element relative to the most common transcription start site

sequence

Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Gene symbol: S100B
Gene ENSG00000160307 (Ensembl)
Gene 6285 (EntrezGene)
Species: homo sapiens

Please choose the appropriate combination (transcript, position, sequence) and click the submit button

ENST00000291700 -702(46848722) TATGGCCAGGTAGACCAGATAGCACTTAGGCTGCATGG
ENSG00000160307 -702(46848722) TATGGCCAGGTAGACCAGATAGCACTTAGGCTGCATGG

CRE analysis: Experimental Evidence - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

Experimental Evidence for a role in regulating Gene Expression

Method Name

OR Enter a New Method:

New Method Name

New Method Description

If the experiment is not *in vitro*, enter the cell/tissue information below.

Cell Name OR

Cell Status

Tissue OR

Organism (e.g. Homo sapiens)

Reference (PubMed ID) describing this specific experiment

Comments concerning this specific experiment

Explain specific conditions (if any). Please do not fill anything if not applicable.

Development Time/Timepoint

Exactly OR Range-start Range-end

Scale

Description

Physiological conditions

Condition Concentration/Quantity/Stage Scale

Environmental Conditions

Chemical compound Concentration/Quantity Scale

Effect description

qualitative

quantitative

quantitative

scale

qualitative

Mutation Information - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

http://www.pazar.info/cgi-bin/sW1/addmutation.cgi

UCSC NCBI ENSEMBL TFCAT/PAZAR/PLEIA... UBC/CMMT Brain Resources Ontologies Genomics Resources

Describe your Mutation

Original Sequence

```

1   ACAGCTGGAC TTCTCCTTCC TCAGGCTGGC TGGAGGCTTC AGCAAGGGGG
51  CACACCGTCC ACACGCCTCT GTAAAACAGC GTTCGAACGG GACATCTCTA
101 AGGCATCGTC CAACTCTGAG AGTCTGTGAC CTTCCACCCCT GGGGTGGAGG
151 GAAAGGCCTT GGGATACAGT CCACACATCA CGTTTTCCCC TAAAAGTACC
201 ACCCGTTTTA GTCCCTGCAG ACACTGGCCCT CAGCAGCTTC TCTGAGGCAG
251 CCCCCTTGAG CCCAGGGCTG ACCACAGACA AGCACTACTG TCCACAGAAC
301 TTCACGCCCA GTGGGGCCAG ACTTGGAGGA TGGCAGAGGA GAGAAGCTCC
351 AGGGGCCCTC CCATTAGAAA CCAACTTGCA GGCCACTTAA TCTCCTATGC
401 TCAGCCTGTA CTTGGAAGCT GCTTGTTCCT GGCTGCACAT TTGCTTTGTT
451 TGAATCAATT AATCCAAGTC TCTCTCCTCT CCCCACCCCC AACCTTGCCT
501 TTAGGGTGAC ATCAATATTC ATGTAATAAA GAAATCGCAC AAAAAGCTGA
551 CTCGCCACTT CCTGCCCTAC AGGCCCTTTT TTCTTCTCA GCCCATGTGC
601 AATCCTGGCT CCCAGCAAGT CCCCAGGGCT GCTTGGCAA TGCAGCCCTG
651 TGTGAGGCC TGGCAGCCCT GCCACCCCGC CCTTGGCTC CCATTGGCTG
701 CCACGGCCTG CAGTGGGCTG CACCAGGGTT CATCCATCCT CCCTGGGCAG
751 AGGGAATAAG AGGCTGCCTC TGCCCAACCA TCCTGCCGCC CAGGACCCGC
801 AGCAGAGACG ACGCCTGCAG CAAGGAGACC AGGAAGGGGT GAGACAAGGA
851 AGAGGTGAGA AAGAGCCAGG CCAAGAGGAC GCTCAGGAAG AAAATGGTCT
901 TTTCTTTTGG GTGGAACCGA ATGGAGGGGT AGAAACTAAG TGGTAGCTTA
951 AAAAGCCCTT TTAGGACAA TTGGCAGCATT TCAGAAGTGT CAATAGGATG
1001 ATGTGTTTTA ATCTCCACAT TACTGCTGCT TTGTGGACAC CTGACTGCAT
1051 CAGCCCTAGA CAGCTAGAGG TGTGTTTTGC CATAAATCAG AGAAACGTCA
1101 GGTTCATGCG CCCAGAAAGT ATTGTGACA TTTTCCAGC GGTACTACAA
1151 ATACTGCCTC TTCTGTAACT ATTTGAAGAG TAAAGATTTT GCTTCCCACT
1201 GGGGCTAAAA ATGATGGAGA ACCTAATGCT AGTTTAGTCC TATATCATAA
1251 ATAAATGCTT CCCTTTTCTC CTTATATTTT TTCCACCCGC CTGGGTAAGT
1301 AACTCTTCAG TTTTCCAGTT TCCCTCAGTT TGAAGTGCCA GGGTCCCAC
1351 AGCCCCAGGA CGCCACTCAG AAATTACGTA ACAATTACAA ATAAATTGGG
1401 TCAAGAAAT CGGGGTTTTG GTGGGTTTTA ACTTTCTCA GTCTCACAGT
1451 TTCTCAGGGA GGTGAAACCC CTTCCTTAGA GGGATC

```

Mutation Information

Mutant Name (optional)

Deletion
Enter the coordinates of the region(s) deleted from the original sequence:
 (use nucleotide numbering scheme displayed above: e.g. 130-500;1000-1500)

Point Mutation
Enter the coordinate(s) of the mutated nucleotide(s), relative to the original sequence, followed by the mutant nucleotide:
 (use nucleotide numbering scheme displayed above: e.g. 54A;55T;58G)

Comments (if any)

Check the resulting Mutant Sequence

Method used to make the mutation

Method Name

OR Enter a New Method:

New Method Name

New Method Description

Reference (PubMed ID) describing this mutant

Effect of this mutation on the expression

qualitative

quantitative

quantitative

scale:

qualitative:

CRE analysis: TF complexes - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

http://www.pazar.info/cgi-bin/sw1/TFcomplex.cgi

UCSC NCBI ENSEMBL TFCAT/PAZAR/PLEIA... UBC/CMMT Brain Resources Ontologies Genomics Resources

If the exact TF is unknown, you can describe a biological sample used (e.g. nuclear extract)

Sample Type

Sample Cell Name OR

Sample Cell Status

Sample Tissue OR

Sample Organism (e.g. Homo sapiens)

Sample Development Time/Timepoint

Exactly OR Range-start Range-end

Scale

Sample Time Description

Interaction type between the sample and this sequence

qualitative

quantitative

quantitative

scale

qualitative

Method Name

OR Enter a New Method:

New Method Name

New Method Description

If the experiment is not *in vitro*, enter the cell/tissue information below.

Cell Name OR

Cell Status

Tissue OR

Organism (e.g. Homo sapiens)

Reference (PubMed ID) describing this specific experiment

Comments concerning this specific experiment

CRE analysis: TF complexes - Mozilla Firefox

File Edit View Go Bookmarks Tools Help

http://www.pazar.info/cgi-bin/SWI/TFComplex.cgi

UCSC NCBI ENSEMBL TFCAT/PAZAR/PLEIA... UBC/CMMT Brain Resources Ontologies Genomics Resources

TF complex components

Select from my TFs:

Select from existing TFs

Enter a new TF:

TF complex name

Pubmed (if published)

TF TF Database

class OR

family OR

modifications (Optional)

Interaction type between the TF complex (factor) and this sequence

qualitative

quantitative

quantitative

scale

qualitative

Method Name

OR Enter a New Method:

New Method Name

New Method Description

If the experiment is not *in vitro*, enter the cell/tissue information below.

Cell Name OR

Cell Status

Tissue OR

Organism (e.g. Homo sapiens)

Reference (PubMed ID) describing this specific experiment

Comments concerning this specific experiment