

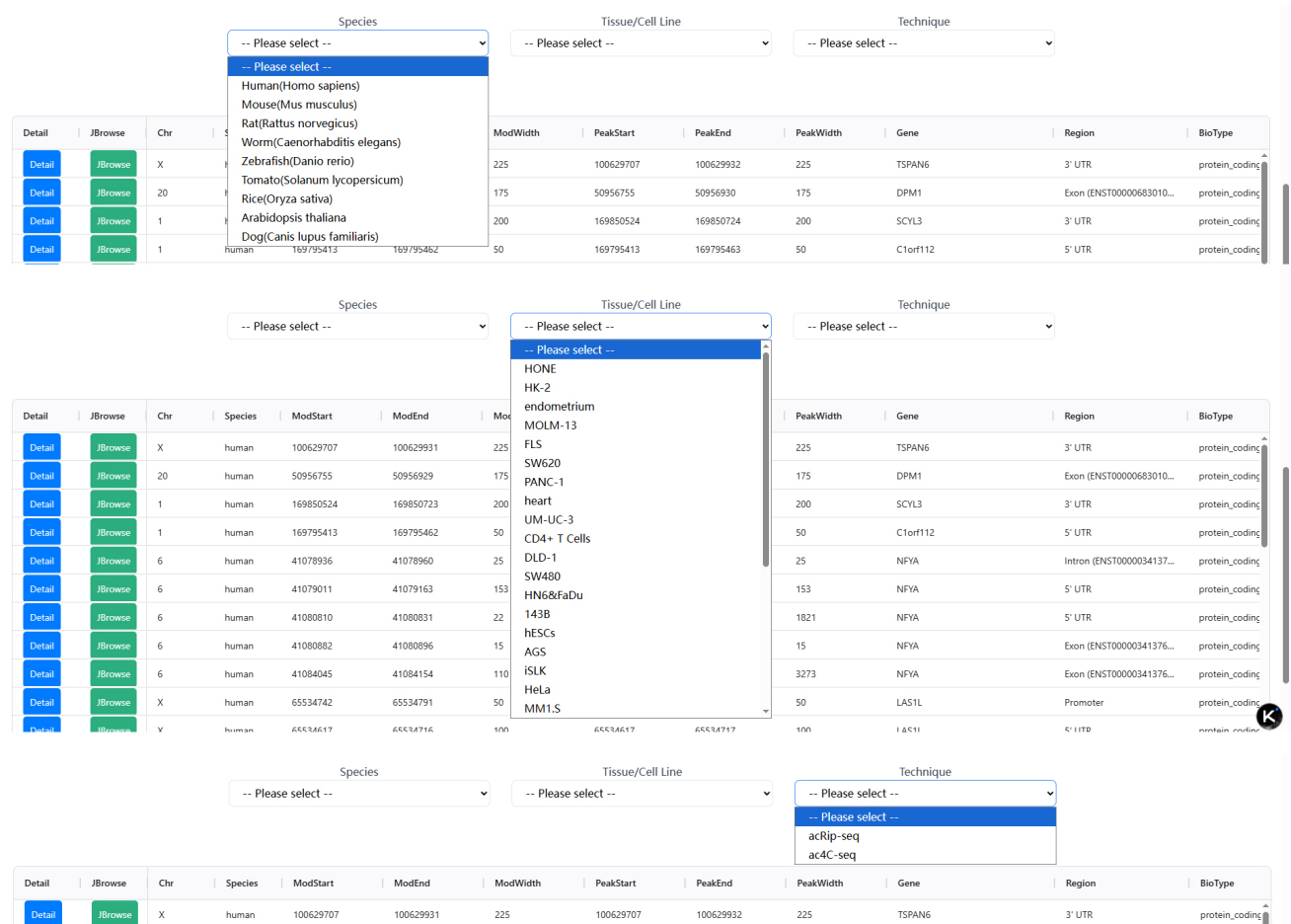
Instruction Manual

ac4CDB and ac4CDiseaseDB

1.Click on the "ac4CDB" section in the navigation bar on the homepage to enter the database.



2.After selecting Species, Tissue/Cell Line and Technique based on your interest, the web page will automatically redirect to the corresponding data table.



3.Clicking on the word "Chart" on the page will adjust the table to fit the screen. Additionally, when the mouse hovers over the title of each column in the data table, a multi-functional menu bar icon will appear. Clicking on the icon will reveal three options. The leftmost function bar includes the functions of locking columns (left or right) and adjusting column width to fit content.

Detail	JBrowse	Chr		ModEnd	ModWidth	PeakStart	PeakEnd	PeakWidth	Gene	Region	BioType
Detail	JBrowse	X	Pin Column	100629931	225	100629707	100629932	225	TSPAN6	3' UTR	protein_coding
Detail	JBrowse	20	Autosize This Column	50956929	175	50956755	50956930	175	DPM1	Exon (ENST00000683010...	protein_coding
Detail	JBrowse	1	Autosize All Columns	169850723	200	169850524	169850724	200	SCYL3	3' UTR	protein_coding
Detail	JBrowse	1	Reset Columns	169795462	50	169795413	169795463	50	C1orf112	5' UTR	protein_coding
Detail	JBrowse	6	human	41078936	41078960	41078936	41078961	25	NFYA	Intron (ENST0000034137...	protein_coding
Detail	JBrowse	6	human	41079011	41079163	41079011	41080832	153	NFYA	5' UTR	protein_coding
Detail	JBrowse	6	human	41080810	41080831	41080810	41080832	1821	NFYA	5' UTR	protein_coding
Detail	JBrowse	6	human	41080882	41080896	41080882	41084155	15	NFYA	Exon (ENST00000341376...	protein_coding
Detail	JBrowse	6	human	41084045	41084154	41080882	41084155	3273	NFYA	Exon (ENST00000341376...	protein_coding
Detail	JBrowse	X	human	65534742	65534791	65534742	65534792	50	LAS1L	Promoter	protein_coding
Detail	JBrowse	X	human	65534617	65534716	65534617	65534717	100	LAS1L	5' UTR	protein_coding
Detail	JBrowse	X	human	65529742	65529877	65529742	65529877	136	LAS1L	3' UTR	protein_coding
Detail	JBrowse	X	human	65531356	65531437	65529742	65532567	1696	LAS1L	3' UTR	protein_coding
Detail	JBrowse	X	human	65532560	65532566	65529742	65532567	2825	LAS1L	3' UTR	protein_coding
Detail	JBrowse	X	human	65523679	65523728	65523679	65523729	50	LAS1L	3' UTR	protein_coding
Detail	JBrowse	X	human	65523629	65523653	65523629	65523654	25	LAS1L	3' UTR	protein_coding
Detail	JBrowse	X	human	65518129	65518478	65518129	65518479	350	LAS1L	3' UTR	protein_coding
Detail	JBrowse	7	human	92243267	92243341	92243267	92243342	75	KRIT1	5' UTR	protein_coding
Detail	JBrowse	7	human	92200447	92200571	92200447	92200572	125	KRIT1	3' UTR	protein_coding
Detail	JBrowse	11	human	64276931	64277042	64276931	64284344	112	BAD	Promoter	protein_coding

4.The middle function bar has different filtering functions for character columns and numeric columns.

Detail	JBrowse	Chr		ModEnd	ModWidth	PeakStart	PeakEnd	PeakWidth	Gene	Region	BioType
Detail	JBrowse	X	Contains	100629931	225	100629707	100629932	225	TSPAN6	3' UTR	protein_coding
Detail	JBrowse	20	Filter...	50956929	175	50956755	50956930	175	DPM1	Exon (ENST00000683010...	protein_coding
Detail	JBrowse	1	human	169850524	169850723	169850524	169850724	200	SCYL3	3' UTR	protein_coding
Detail	JBrowse	1	human	169795413	169795462	169795413	169795463	50	C1orf112	5' UTR	protein_coding

Detail	JBrowse	Chr		ModEnd	ModWidth	PeakStart	PeakEnd	PeakWidth	Gene	Region	BioType
Detail	JBrowse	X	Contains	100629931	225	100629707	100629932	225	TSPAN6	3' UTR	protein_coding
Detail	JBrowse	20	Does not contain	50956929	175	50956755	50956930	175	DPM1	Exon (ENST00000683010...	protein_coding
Detail	JBrowse	1	Equals	169850524	169850723	169850524	169850724	200	SCYL3	3' UTR	protein_coding
Detail	JBrowse	1	Does not equal	169795413	169795462	169795413	169795463	50	C1orf112	5' UTR	protein_coding
Detail	JBrowse	6	Begins with	41078936	41078960	41078936	41078961	25	NFYA	Intron (ENST0000034137...	protein_coding
Detail	JBrowse	6	Ends with	41079011	41079163	41079011	41080832	153	NFYA	5' UTR	protein_coding
Detail	JBrowse	6	Blank	41080810	41080831	41080810	41080832	1821	NFYA	5' UTR	protein_coding
Detail	JBrowse	6	Not blank	41080882	41080896	41080882	41084155	15	NFYA	Exon (ENST00000341376...	protein_coding

Detail	JBrowse	Chr	Species	ModStart	ModEnd	PeakEnd	PeakWidth	Gene	Region	BioType
Detail	JBrowse	X	human	100629707	100629931	100629932	225	TSPAN6	3' UTR	protein_coding
Detail	JBrowse	20	human	50956755	50956929	50956930	175	DPM1	Exon (ENST00000683010...	protein_coding
Detail	JBrowse	1	human	169850524	169850723	169850524	200	SCYL3	3' UTR	protein_coding
Detail	JBrowse	1	human	169795413	169795462	169795413	50	C1orf112	5' UTR	protein_coding
Detail	JBrowse	6	human	41078936	41078960	41078936	25	NFYA	Intron (ENST0000034137...	protein_coding
Detail	JBrowse	6	human	41079011	41079163	41079011	153	NFYA	5' UTR	protein_coding
Detail	JBrowse	6	human	41080810	41080831	41080810	1821	NFYA	5' UTR	protein_coding
Detail	JBrowse	6	human	41080882	41080896	41080882	15	NFYA	Exon (ENST00000341376...	protein_coding
Detail	JBrowse	6	human	41084045	41084154	41080882	3273	NFYA	Exon (ENST00000341376...	protein_coding
Detail	JBrowse	X	human	65534742	65534791	65534742	50	LAS1L	Promoter	protein_coding

5.For any column, users can click on the column name to sort in ascending or descending order.

Detail	JBrowse	Width	PeakStart	BioType	PeakEnd	PeakWidth	Gene	Region	TissueORCell	targetNumber	RBPNumber
Detail	JBrowse		41079011	protein_coding	41080832	153	NFYA	5' UTR	HK-2	0	9
Detail	JBrowse		41079011	protein_coding	41080832	1821	NFYA	5' UTR	HK-2	0	1
Detail	JBrowse		41080882	protein_coding	41084155	15	NFYA	Exon (ENST00000341376...	HK-2	0	0
Detail	JBrowse		41080882	protein_coding	41084155	3273	NFYA	Exon (ENST00000341376...	HK-2	0	19
Detail	JBrowse		65534742	protein_coding	65534792	50	LAS1L	Promoter	HK-2	0	7
Detail	JBrowse		65534617	protein_coding	65534717	100	LAS1L	5' UTR	HK-2	0	82
Detail	JBrowse		65529742	protein_coding	65532567	136	LAS1L	3' UTR	HK-2	0	98
Detail	JBrowse		65529742	protein_coding	65532567	1696	LAS1L	3' UTR	HK-2	0	28
Detail	JBrowse	Width	PeakStart	BioType	PeakEnd	PeakWidth	Gene	Region	TissueORCell	targetNu...	RBPNumber
Detail	JBrowse		72199075	protein_coding	72199375	300	PKM	3' UTR	HK-2	33	764
Detail	JBrowse		6555090	protein_coding	6555240	150	TNFSF9	3' UTR	HK-2	32	37
Detail	JBrowse		49586362	protein_coding	49586387	25	RPS29	Promoter	HK-2	32	49
Detail	JBrowse		68609880	protein_coding	68609980	100	PPP6R3	Promoter	HK-2	32	49
Detail	JBrowse		82078387	protein_coding	82078687	300	FASN	3' UTR	HK-2	31	315
Detail	JBrowse		37174483	protein_coding	37174583	100	PIM1	3' UTR	HK-2	30	103
Detail	JBrowse		82841787	protein_coding	82842297	510	SEC31A	Exon (ENST00000395310...	HK-2	30	118
Detail	JBrowse		400211	protein_coding	400411	200	NME4	3' UTR	HK-2	27	159
Detail	JBrowse		39521825	protein_coding	39522075	250	ATF4	3' UTR	HK-2	24	544
Detail	JBrowse		37184230	protein_coding	37184280	50	RPN2	5' UTR	HK-2	24	93
Detail	JBrowse		81511355	protein_coding	81511580	225	ACTG1	3' UTR	HK-2	24	437
Detail	JBrowse		184242325	protein_coding	184242911	586	ALG3	3' UTR	HK-2	24	66

6. After clicking the "Detail" button on the far left of the data table, the page will redirect to the detailed information page of that row. The page includes all the annotation information of the site, as well as a preview of the secondary structure, miRNA Target, RNA Binding Protein, ClinVar Annotation (from ac4CDiseaseDB), and other information.

Record Details - ID: 7632

Chr	11
Species	human
ModStart	68,609,880
ModEnd	68,609,979
ModWidth	100
PeakStart	68,609,880
PeakEnd	68,609,980
PeakWidth	100
Gene	PPP6R3
Region	Promoter
BioType	protein_coding
GeneStart	68,609,951
GeneEnd	68,613,538
GeneLength	3,588
GenelId	ENSG00000110075
BlockCount	1
BlockSizes	100
BlockStarts	0
Infold	IdDbHm0000007632
Source	GSE248203
Strand	+
TissueORCell	HK-2
ExtractStart	68,609,880
ExtractEnd	68,609,979
ModSequence	UGCCUGUCAUCCUCUUUACUGCAGUGAGGAAGGAAACUGUCUACCUCUCAAGAUGCUGCUUGUAAAGACGC AGAGGAGUGUCCCGAGACUGCAGAGGCG
SecStru	.((((((.....)))))).....))))))(((.....))))).(-29.60)
targetidlist	ID:3375,3376,5262,5263,6201,6202,7145,7146,145103,145104,166890,166891,547,548,1490,1491,2432,2433,4319,4320,8422,8423,148
targetNumber	32
RBPidlist	ID:6837818,6837819,6837820,6837821,6837822,6837823,6837824,6837825,6837826,6837827,6837828,6837829,6837830,6837831,683
RBPNumber	49

[Open in JBrowse](#)

Previous 1 2 3 4 Next

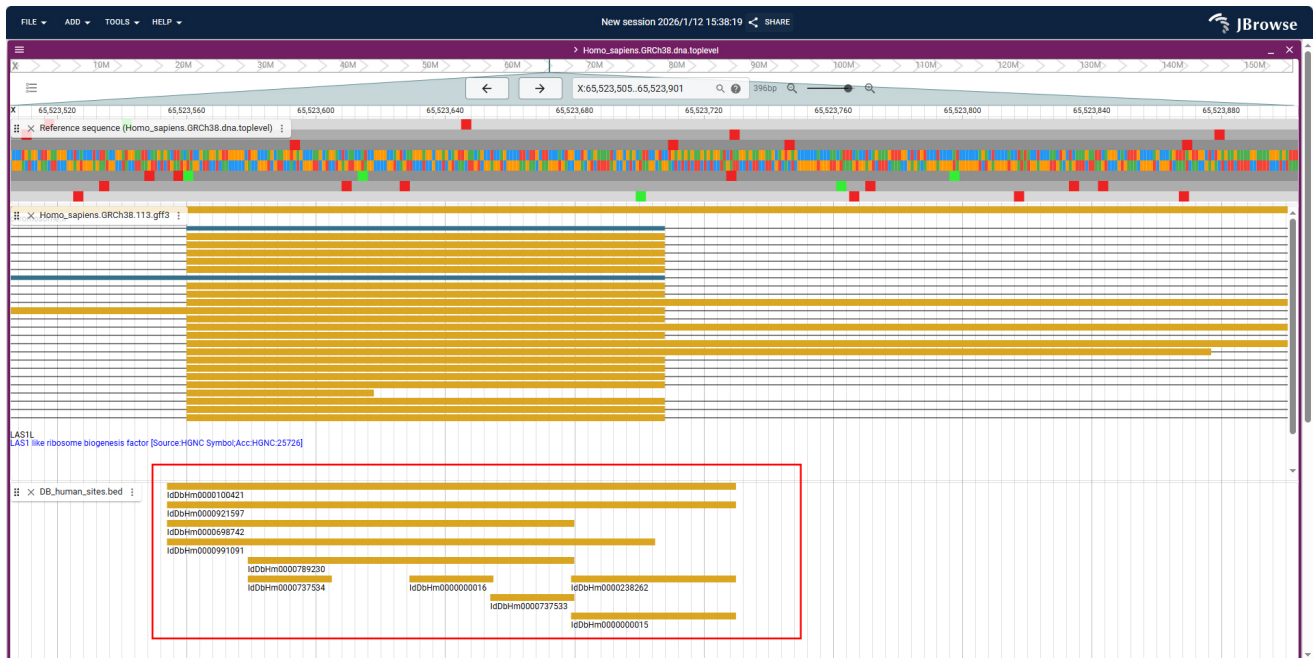
id	chromosome	start	end	RBPid	RBP
6837818	chr11	68609904	68609905	human_RBP_CLIPdb_3171634	PTBP1
6837819	chr11	68609905	68609941	Human_RBP_POSTAR3_1138433	AGO2
6837820	chr11	68609907	68609908	human_RBP_CLIPdb_3171635	YTHDC1
6837821	chr11	68609907	68609908	human_RBP_CLIPdb_3171636	PTBP1
6837822	chr11	68609908	68609909	human_RBP_CLIPdb_3171637	RBM15B
6837823	chr11	68609908	68609909	Human_RBP_POSTAR2update_928889	RBM15B
6837824	chr11	68609909	68609946	Human_RBP_POSTAR3_1138434	AGO2
6837825	chr11	68609912	68609932	human_RBP_CLIPdb_3171638	NUDT21
6837826	chr11	68609912	68609945	Human_RBP_POSTAR3_1138435	AGO2
6837827	chr11	68609912	68609950	Human_RBP_POSTAR3_1138436	AGO2

ClinVar Annotation

A total of 4 records were found, currently displaying records 1 - 4

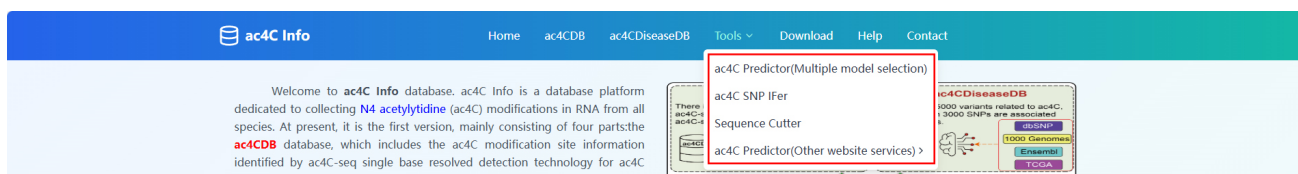
id	ClinicalSignificance	RSid(dbSNP)	RCVaccession	PhenotypeList
461993	Benign/Likely benign	373021819	RCV000421695 RCV000540568 RCV001017652	not specified Peutz-Jeghers syndrome Hereditary can
601117	Benign/Likely benign	373021819	RCV000571229 RCV000879771 RCV001356806	Hereditary cancer-predisposing syndrome Peutz-Jegh
609189	Benign/Likely benign	373021819	RCV000581348 RCV000632867	Hereditary cancer-predisposing syndrome Peutz-Jegh
4995594	Uncertain significance	865941858	RCV004007811	Peutz-Jeghers syndrome

7. Click the JBrowse button to enter the genome browser to view the location information of the site in the genome.



Tools

1. Analysis tools ac4C Predictor and ac4C SNP Ifer and auxiliary tool Sequence Cutter are all located in the drop-down menu of this menu bar. Clicking on them will redirect you to the corresponding functions. At the same time, links to some tools developed by the original author are provided for jumping.



2. In the ac4C Predictor tool, select the appropriate parameters (such as the prediction model), and at the same time, choose to upload or paste the sequence (Standard FASTA format) into the input box below. Click "Submit" to start the calculation.

ac4C Predictor

Support rapid ac4C site prediction with multiple models options

parameter configuration

Current filtering criteria

Species: Human

Prediction model: LSA-ac4C

Threshold: 0.5

Length: 201

Species / Genome

Human/hg38

Threshold

0.5 Default

Prediction model

LSA-ac4C

Sequence length

201

[Upload files](#)

Paste sequence

Examples

Drag and drop files or click to upload

Supports FASTA format (.fa, .fasta, .txt)

Choose local file

Reset

Submit

ac4C Predictor

Support rapid ac4C site prediction with multiple models options

parameter configuration

Current filtering criteria

Species: Human

Prediction model: LSA-ac4C

Threshold: 0.5

Length: 201

Species / Genome

Human/hg38

Threshold

0.5 Default

Prediction model

LSA-ac4C

LSA-ac4C

TransAC4C

ERNIE-ac4C

Voting-ac4C

DLC-ac4C

DeepAc4C

NBCR-ac4C

STM-ac4C

TransCNN

Sequence length

201

 Examples



es or click to upload

ormat (.fa, .fasta, .txt)

Choose local file

ac4C Predictor

Support rapid ac4C site prediction with multiple models options

parameter configuration

Current filtering criteria

Species: Human

Prediction model: LSA-ac4C

Threshold: 0.5

Length: 201

Species / Genome

Human/hg38

Threshold

0.5 Default

Prediction model

LSA-ac4C

Sequence length

201

 Upload files

 Paste sequence

 Examples

FASTA

```
>gene1
```

[illegible]

```
>gene2
```

[illegible]

```
>qgene3
```

[illegible]

Please use the standard FASTA format: a description line starting with > followed by sequence lines

 Reset

Submit

3.While the program is running, users can copy the link provided on the page. Even if the web page is closed, we can continue to access and check the running status of the project by pasting the link into the browser. After a short while, the result page will appear.

ac4C Predictor

Support rapid ac4C site prediction with multiple models options

Current filtering criteria

Species: Human

Length: 201

Threshold: 0.5

Prediction Model: LSA-ac4C

Program running status

Process ID: sub_696466cd87ef00.33241598

Current website address: http://172.18.185.193:8099/tools/tool1.php?submission_id=sub_696466cd87ef00.33241598

If you are worried about forgetting or not being able to find the process address, you can copy the current URL and paste it into the browser

[Verify input file](#)

4. On the result page, users can click the download button to download the analysis results to their local device.

ac4C Predictor

Support rapid ac4C site prediction with multiple models options

Current filtering criteria

Species: Human

Length: 201

Threshold: 0.5

Prediction Model: LSA-ac4C

Results

Finsh!

 Download results

View Results (100 lines):

NAME	POSITION	BASE	AC4C PROBABILITY	AC4C
gene1	101	C	85.63%	Yes
gene2	101	C	84.16%	Yes
gene3	101	C	82.52%	Yes
gene4	101	C	80.63%	Yes
gene5	101	C	80.36%	Yes
gene6	101	C	78.88%	Yes
gene7	101	C	78.03%	Yes
gene8	101	C	79.27%	Yes
gene9	101	C	86.15%	Yes

5.The usage method of ac4C SNP IFer is basically similar to that of the ac4C Predictor tool. Please explore it by yourself.(The input is in the standard VCF file format.)

ac4C SNP IFer

A real-time analysis module to assess the degree of influence of gene variations on acetylation modification

parameter configuration

Current filtering criteria

Species: Human

Threshold: 0.5

Prediction model: LSA-ac4C

Length: 201

Species / Genome

Human/hg38

Threshold

0.5 Default

Prediction model

LSA-ac4C

Sequence length

201

Upload files

Paste sequence

Examples

Standard vcf format:

```
##fileformat=VCFv4.2
##reference=file:///hg38.no_alt.fa.gz
#CHROM POS ID REF ALT QUAL FILTER INFO
chr20 63239375 chr20-63239375-SNV-GC G C . . .
chr5 80631216 chr5-80631216-SNV-TC T C . . .
chr5 181200936 chr5-181200936-SNV-TC T C . . .
chr11 65117191 chr11-65117191-SNV-CT C T . . .
chr18 13488804 chr18-13488804-SNV-CT C T . . .
chr10 55278211 chr10-55278211-SNV-CT C T . . .
```

Please use the standard vcf format: For details, please refer to the example.

Reset

Submit

6.The auxiliary tool Sequence Cutter is used to generate the input for ac4C Predictor. After entering the tool, set the length of sequence cutting and the center base(The selection of parameters should be based on the input requirements of the ac4C Predictor's prediction model.).

Sequence Cutter

Cut the sequence according to your length

Sequence Processing Configuration

Parameters

Sequence length

201

Central base

C

 [Upload File](#)

 [Paste Sequence](#)



Drag and drop files or click to upload

Supports FASTA format (.fa, .fasta, .txt)

Select File

 Clear

 Submit

Downloads

1.The Download page offers one-click download for all datasets.

Downloads

Download our datasets,instruction manual.



ac4CDB Datasets



ac4CDisease Datasets



Instruction Manual

ac4CDB Datasets

 Arabidopsis Thaliana Seedlings.rar

 2.76MB  rar

 Download

 Zebrafish Zebrafish.rar

 1.14MB  rar

 Download

 Dog WRD.rar

 11.96MB  rar

 Download

 Human 143B.rar

 3.06MB  rar

 Download

 Human A549.rar

 19.42MB  rar

 Download