

TRAINING COURSE IN Computational Methods for Epitranscriptomics

Bari, 26th-28th April 2023



RNA editing databases and REDIportal

**Introduction to
biological databases for RNA editing
and
practice with REDIportal**

- NGS technologies allowed identification of RNA editing
- Different types of RNA editing found in virtually all organisms
- A-to-I editing abundant in the human transcriptome
- Growth of novel data on RNA editing instances
 - =>
 - non-uniform data in research articles

- **REDIdb** (http://srv00.recas.ba.infn.it/py_script/REDIdb/)
RNA editing in plant organellars
- **DARNED** (<http://darned.ucc.ie/>)
A-to-I in human, mouse and fruit fly
(not provide editing levels - not updated since 2013)
- **RADAR** (<http://rnaedit.com/>)
A-to-I in human, mouse and fly
incorporates editing levels for 38% of stored positions
data from cellular lines
- **REDIportal** (<http://srv00.recas.ba.infn.it/atlas/>)
A-to-I changes (4.5 millions) from Inosinome ATLAS and RADAR database
more than 2,500 GTEx RNAseq experiments from 55 body sites of 147 individuals with WGS data
available embedded specific genome browser (JBrowse)

REDIdb (http://srv00.recas.ba.infn.it/py_script/REDIdb/)



Organism

Location

Gene

RefSeq Exons Full Orfs

- mostly C to U conversion
- 26618 RNA editing events
- 281 organisms and 85 complete organellar genomes

REDIdb (http://srv00.recas.ba.infn.it/py_script/REDIdb/)

Abies holophylla
Acorus calamus
Actinostachys pennula
Adiantum capillus-veneris
Adiantum sp. Qiu 95118
Aegilops crassa
Akashiwo sanguinea
Akashiwo sp. AP-LIS1
Alexandrium tamarense
Allium cepa

--Organism--

REDIdb (http://srv00.recas.ba.infn.it/py_script/REDIdb/)

Organism

--Organism--

Location

--Location--

Gene

--Location--

able/Disable

mitochondrion

RefSeq

chloroplast

Orfs

Submit

Reset

Organism

--Org--

Location

atpB

Gene

--Gene--

Enable/Disable

RefSeq

Exons

Full Orfs

Submit

Reset

REDIdb (http://srv00.recas.ba.infn.it/py_script/REDIdb/)

Organism

Nelumbo nucifera

Location

mitochondrion

Gene

cox2

[Enable/Disable](#)

RefSeq Exons Full Orfs

[Submit](#)

[Reset](#)

Query

Results

Show 10 entries

Search:

[Copy](#) [Print](#) [Column visibility](#) [PDF](#) [CSV](#)

Genbank	Organism	Taxonomy	Genome	Location	Source	Gene_name	Editing_type	Details	Number_of_events
NC_030753	Nelumbo nucifera	T	G	mitochondrion	gene F	cox2	S	C->U,U->C	23, 1
KR610474	Nelumbo nucifera	T	G	mitochondrion	gene F	cox2	S	C->U,U->C	23, 1

REDIdb (http://srv00.recas.ba.infn.it/py_script/REDIdb/)

GENERAL INFORMATIONS

ORGANISM *Nelumbo nucifera*

DIVISION Eukaryota, Viriplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, Proteales, Nelumbonaceae, *Nelumbo*

LOCATION mitochondrion

STATUS complete genome

SEQUENCE Full

SOURCE gene

NAME cox2

GENBANK NC_030753

PUBMED 27444405

GO Gene Ontology

MOLECULAR FUNCTION GO:0004129 cytochrome-c oxidase activity

BIOLOGICAL PROCESS GO:0022900 electron transport chain

CELLULAR COMPONENT GO:0016020 membrane

EDITING FEATURES

Genomic position	cDNA position	Genomic codon	Edited codon	Genomic AA	Edited AA
105715	161	tCa	tTa	S	L

REDIdb (http://srv00.recas.ba.infn.it/py_script/REDIdb/)

100829

742

Cgg

Tgg

R

W

SEQUENCES

GENOMIC SEQUENCE 783 bp [FASTA](#)

BASE COUNT 214a 169c 159g 241t

```
1 ATGATTGTT TAGAATGGCT ATTCCCTACA ATCGCTCTT GTGATGCTGC GGAACCAGG CAATTAGGAT CTCAGACGC AGCAACACCT ATGATGCAAG GAATAATGGA CTTACATCAC
121 GATATCTTT TCTTCCTCAT TCTGATTTTG GTTTCGTAT CACGGATGTT GGTTCGCGCT TTATGGCATT TCCACTATCA AACGAACCCA ATCCCGCAAA GGATTGTTCA TGGAACTACT
241 ATCGAGATTG TTTGGACCAT ATTTCTAGT ATCATCCCGA TGTTCTTGC TATACCATCA TTTGCTCTGT TATACTCAAT GGACGAGGTA GTAGTAGATC CAGCCATTAC TATCAAAGCT
361 ATTGGACATC AATGGTATCG GACTTATGAG TATTCGGACT ATAACAGTTC CGATGAACAG TCACTCACT TTGACAGTTA TACGATTCCA GAAGATGATC CAGAATTGGG TCAATCACGT
481 TTATTAGAAG TGGACAATAG AGTGGTTGTA CCAGCCAAAA CTAATCTACG TATTATTGTA ACACCTGCTG ATGACCTCA TAGTTGGCT GTACCTTCCT CAGGTGTCAA ATGTGATGCT
601 GTACCTGGTC GTTAAATCA GACCTCTATT TCGGTACAAAC GAGAAGGAGT TTACTATGGT CAGTGCAGTG AGATTGTTGG AACTAATCAT GCCTCTACGT CTATCGTCGT AGAAGCTGTT
721 CCTAAGAAAAG ATTATGGTT TC000TATCC AATCAATTAA TCCCCCAAAAC CGGGGAAAGCT TAA
```

cDNA SEQUENCE 783 bp [FASTA](#) [MSA](#)

BASE COUNT 214a 147c 159g 263t

```
1 ATGATTGTT TAGAATGGCT ATTCCCTACA ATTGCTCTT GTGATGCTGC GGAACCAGG CAATTAGGAT TTCAAGACGC AGCAACACCT ATGATGCAAG GAATAATGGA CTTACATCAC
121 GATATCTTT TCTTCCTCAT TCTGATTTTG GTTTCGTAT TATGGATGTT GGTTCGCGCT TTATGGCATT TCCACTATCA AACGAACCCA ATCCCGCAAA GGATTGTTCA TGGAACTACT
241 ATCGAGATTG TTTGGACCAT ATTTCTAGT ATCATCTCGA TGTTCTTGC TATACCATCA TTTGCTCTGT TATACTCAAT GGACGAGGTA GTAGTAGATC CAGCCATTAC TATTAAGCT
361 ATTGGACATC AATGGTATTG GACTTATGAG TATTCGGACT ATAACAGTTC CGATGAACAG TCACTCACT TTGACAGTTA TATGATTCCA GAAGATGATT TAGAATTGGG TCAATTACGT
481 TTATTAGAAG TGGACAATAG AGTGGTTGTA CCAGCCAAAA CTAATCTACG TATTATTGTA ACATCTGCTG ATGACTTCA TAGTTGGCT GTACCTTCCT TAGGTGTCAA ATGTGATGCT
601 GTACCTGGTC GTTAAATCA GACCTCTATT TTGGTACAAAC GAGAAGGAGT TTACTATGGT CAGTGCAGTG AGATTGTTGG AACTAATCAT GCCTTTATGC CTATCGTCGT AGAAGCTGTT
721 TCTAAGAAAAG ATTATGGTT TC000TATCC AATCAATTAA TCCCCCAAAAC CGGGGAAAGCT TAA
```

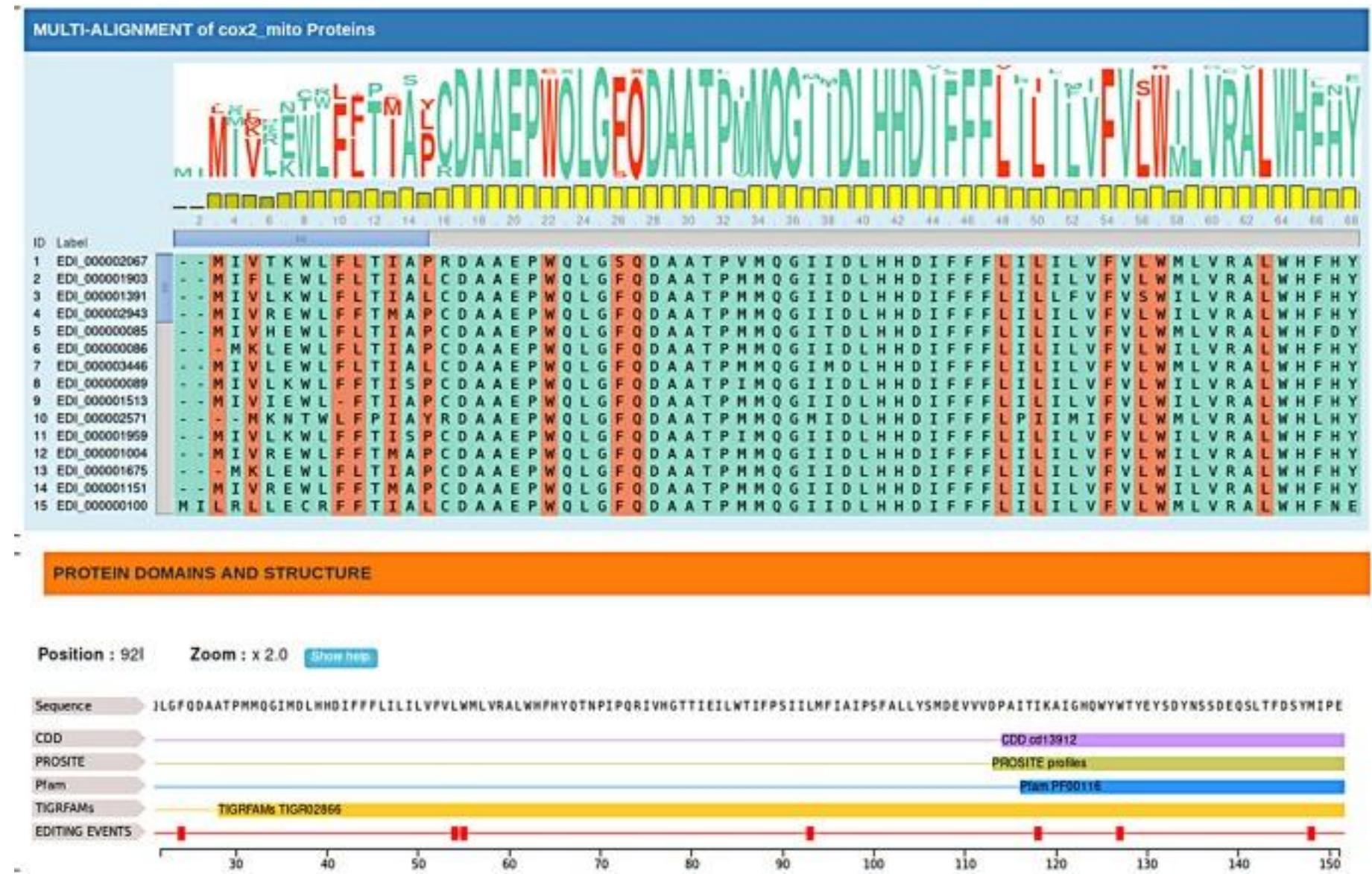
PROTEIN SEQUENCE 261 AA [FASTA](#) [MSA](#) [DOMAINS](#)

```
1 mivlewlflt ialcdaaaepw qlgfqdaatp mmqgimdlhh dfffflllll vfvliwmhvra lwhfhyqtvp ipqrivhggt ieilwtifps iilmfiaips fallysmdev vvdpaithka
121 ighqwywtye ysdynssdeq sltdfsymip eddlelgqlr llevdnrvvv paktnlriiv tsadvlhsmw vpslgvkcds vpgrlnqtsi lvqregvyyg qcseicgtnh afmpivveav
241 srkdygswvs nqlipqtgea x
```

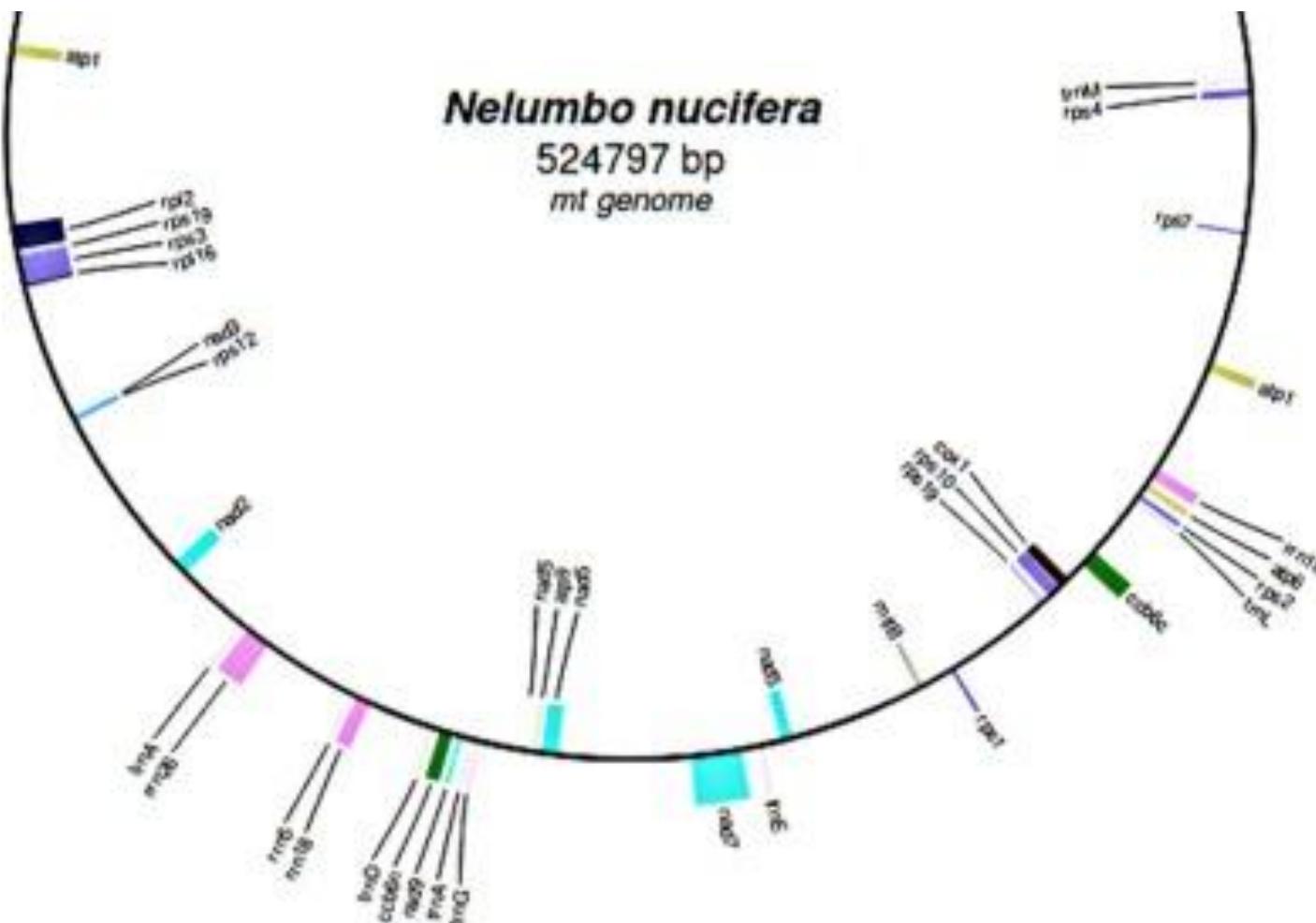
REDIdb (http://srv00.recas.ba.infn.it/py_script/REDIdb/)

integrated
MSAViewer:

- logo and bar charts;
- multialignment;
- domains.



REDIdb (http://srv00.recas.ba.infn.it/py_script/REDIdb/)



Legend:

- | | | | | |
|---------------|---------------------------|----------------------------|------------------|---------------|
| ■ Complex IV | ■ ATP synthase | ■ Ribosomal proteins (SSU) | ■ maturase | ■ ORFs |
| ■ Complex II | ■ Complex I | ■ Ribosomal proteins (LSU) | ■ Transfer RNAs | ■ Other genes |
| ■ Complex III | ■ Cytochrome c biogenesis | ■ RNA polymerase | ■ Ribosomal RNAs | |

DARNED

(<https://darned.ucc.ie/>)



Human

Assembly	Chromosome	Start	End
HG18 <input type="button" value=""/>	Chr1 <input type="button" value=""/>	<input type="text"/>	<input type="text"/>
Limit the search to a particular type of sequence		Flanking Sequence Length Around Editing Sites.	
All <input type="button" value=""/>	<input type="text"/>	<input type="text"/>	
Limit the search by the source (tissue/cell line) in which RNA editing is known to be supported			
<input type="text"/>			
<input type="button" value="Submit"/>			

- mostly A to I editing
- ~ 650000 in humans
(mainly from LCL)
- ~ 2300 in flies
- ~ 8500 in mice

DARNED

(<https://darned.ucc.ie/>)

✓ Human
Drosophila
Mouse

Region Based

Gene Based

Sequence Based

Assembly

Chromosome

Start

End

✓ HG18
HG19

✓ Chr1
Chr2
Chr3
Chr4
Chr5
Chr6

of

Flanking Sequence Length Around Editing Sites.

✓ All
Exon
Intron
Other

Limit the search

Source (tissue/cell line) in which RNA editing is known to be supported

Submit

DARNED

(<https://darned.ucc.ie/>)

Human ▾ Region Based Gene Based Sequence Based

Assembly	Type of Gene	Name
HG19 ▾	✓ RefGene RefSeq	<input type="text"/>

Submit

DARNED

[\(https://darned.ucc.ie/\)](https://darned.ucc.ie/)

Search Criteria::: Assembly:hg18, Chrom: chr3, Start:3999005, End:39990015, Flank: 2 , Results found: 883

Coordinates	Strand	Changes	Source	SNP	Gene	Alu	Data Sets
3.3999009	-	A[C]-To-I	LYMPHOBLASTOID CELL LINE		[O]		Peng,2012(PubMed)
3.3999018	-	A[G]-To-I	LYMPHOBLASTOID CELL LINE		[O]		Peng,2012(PubMed)
3.3999409	-	A[C]-To-I	LYMPHOBLASTOID CELL LINE		[O]		Peng,2012(PubMed)
3.37288911	+	A-To-I	BREAST CANCER [2]		GOLGA4[J]	SINE	Bahn,2012(PubMed)[2]

« previous 1 2 3 4 ... 79 80 81 82 next »

DARNED

(<https://darned.ucc.ie/>)

Coordinate: chromosome and coordinate in the reference genome (links to UCSC and ENSEMBL browsers)

Strand: + or -

Changes: RNA editing in form **Observed base[Reference genomic base]-to-Edited base**

Source: tissue source (available for human only, for multiple sources the number is indicated in parentheses)

SNP: RefSNP corresponding to this coordinate (for human only, link to entry in the NCBI database; superscript "u" if validation is unknown)

InGene: gene name or "O" if not part of intron or exon. (additional info for gene: I to intron, E to exon, 5 to 5'UTR, 3 to 3'UTR and C to CDS)

ALU: type of repeat

Data Set: reference information and link to PubMed entry.

DARNED

(<https://darned.ucc.ie/>)

Human ▾

Region Based

Gene Based

Sequence Based

Enter your Sequence:

2L:8997721-8998534 +

2L:8997641-8997668 +

Alignment region

Aligned Sequence

Editing site

Query 577 GGGCGTTCGCGACATTAAGGACCTGAAGGTCTGGCGGCCGAAAATGGA 626

|||||

Sbjct 8998271 GGGCGTTCGCGACATTAAGGACCTGAAGGTCTGGCGGCCGAAAATGGA 8998320

Query 627 CTGCAGCTGGAAAAGCTCGTCAAGA TCCTGAC 676

|||||

Sbjct 8998321 CTGCAGCTGGAAAAGCTCGTCAAGA TCCTGAC 8998370

Query 677 CTGGCTAAAGCTATAAAGTAGTGCACTAGACTAAGGCTATTGGGGCGCTA 726

|||||

Sbjct 8998371 CTGGCTAAAGCTATAAAGTAGTGCACTAGACTAAGGCTATTGGGGCGCTA 8998420

RADAR

a rigorously annotated database of A-to-I RNA editing

(<http://rnaedit.com/>)

- site unreachable -

At release:

- DARNED dataset + manually curated annotations and information about tissue-specific editing levels
- 1.379.403 A-to-I in humans
- 2.698 in flies
- 8.108 in mice

RADAR

a rigorously annotated database of A-to-I RNA editing

(<http://rnaedit.com/>)

Search for A-to-I RNA editing sites(hg19/mm9/dm3):

Species: Human

Chromosome:

Start:

End:

Gene Name:

Genic location: All Nonsynonymous Synonymous 5'UTR 3'UTR ncRNA Intronic Intergenic

Repetitive Element: All Alu Repetitive non-Alu Nonrepetitive

Editing Conservation: Human Chimpanzee Rhesus Mouse

Search

RADAR

a rigorously annotated database of A-to-I RNA editing

(<http://rnaedit.com/>)

The screenshot shows a search results page for 'human htr2c nonsynonymous'. At the top, it says 'You searched for: human htr2c nonsynonymous' and 'Found 5 sites:'. Below is a table with columns: Chromosome, Position, Gene, Strand, Genic region, Repetitive Element, Conservation, Reference, and Editing Levels. Red arrows highlight specific data points: one arrow points to the 'Position' column header, another to the first 'Position' value (14082682), and a third to the 'Editing Levels' column header. Within the table, red circles highlight the 'Position' values 14082682, 114082684, 114082688, 114082689, and 114082694; the 'Gene' values HTR2C; the 'Strand' values '+'; the 'Genic region' values 'Nonsyn Ile->Val', 'Nonsyn Ile->Met', 'Nonsyn Asn->Asp', 'Nonsyn Asn->Ser', and 'Nonsyn Ile->Val'; the 'Repetitive Element' values 'Nonrepetitive'; the 'Conservation' values 'Chimpanzee Rhesus Mouse', 'Rhesus Mouse', 'Chimpanzee', 'Chimpanzee Mouse', and 'Chimpanzee Rhesus Mouse'; the 'Reference' values 'Burns et al. 1997', 'Burns et al. 1997', 'Niswender et al. 1998', 'Burns et al. 1997', and 'Burns et al. 1997'; and the 'Editing Levels' values 'Link', 'Link', 'N/A', 'Link', and 'Link'. A red arrow also points from the bottom of the 'Editing Levels' column to the bottom of the table row.

Chromosome	Position	Gene	Strand	Genic region	Repetitive Element	Conservation	Reference	Editing Levels
chrX	14082682	HTR2C	+	Nonsyn Ile->Val	Nonrepetitive	Chimpanzee Rhesus Mouse	Burns et al. 1997	Link
chrX	114082684	HTR2C	+	Nonsyn Ile->Met	Nonrepetitive	Rhesus Mouse	Burns et al. 1997	Link
chrX	114082688	HTR2C	+	Nonsyn Asn->Asp	Nonrepetitive		Niswender et al. 1998	N/A
chrX	114082689	HTR2C	+	Nonsyn Asn->Ser	Nonrepetitive	Chimpanzee Mouse	Burns et al. 1997	Link
chrX	114082694	HTR2C	+	Nonsyn Ile->Val	Nonrepetitive	Chimpanzee Rhesus Mouse	Burns et al. 1997	Link

RADAR

(<http://rnaedit.com/>)

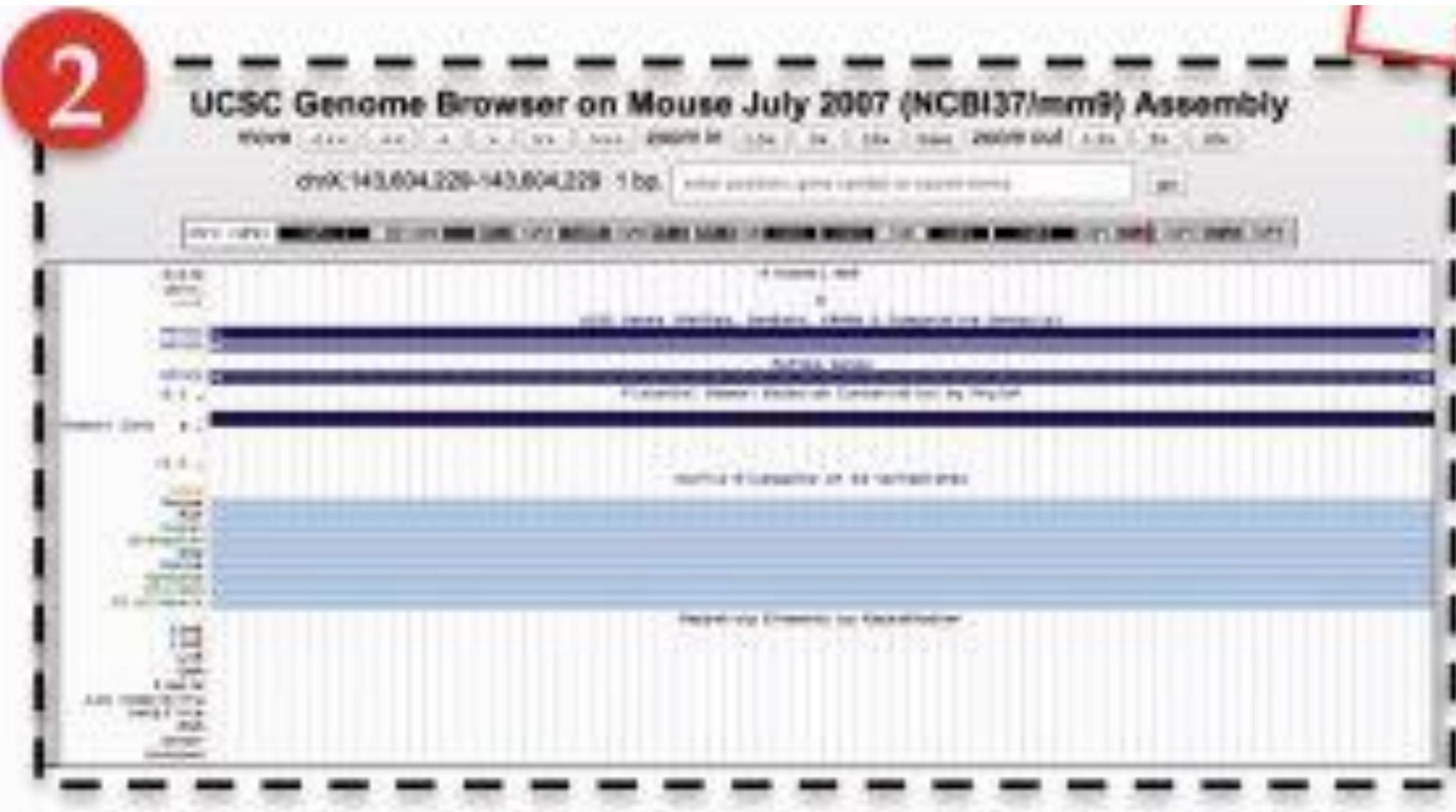
UCSC link



RADAR

(<http://rnaedit.com/>)

conservation
link
to UCSC



reference
link
to PubMed

RADAR
(<http://rnaedit.com/>)

3

Key Settings Abstract Send To:

Nature. 1997 May 15;387(6630):303-8.

Regulation of serotonin-2C receptor G-protein coupling by RNA editing.

Burns GM, Chu H, Buetow KH, Hutchinson JK, Carlton HS, Sanders-Bush E, Ericson SB.

Department of Pharmacology, Vanderbilt University School of Medicine, Nashville, Tennessee 37232-6800, USA.

Abstract

The neurotransmitter serotonin (5-hydroxytryptamine, 5-HT) elicits a wide array of physiological effects by binding to several receptor subtypes. The 5-HT₂ family of receptors belongs to a large group of seven-transmembrane-spanning G-protein-coupled receptors and includes three receptor subtypes (5-HT_{2A}, 5-HT_{2B} and 5-HT_{2C}) which are linked to phospholipase C, promoting the hydrolysis of membrane phospholipids and a subsequent increase in the intracellular levels of inositol phosphates and diacylglycerol. Here we show that transcripts encoding the 2C subtype of serotonin receptor (5-HT_{2C}R) undergo RNA editing events in which genetically encoded adenosine residues are converted to inosines by the action of double-stranded RNA adenosine deaminase(s). Sequence analysis of complementary DNA isolates from dissected brain regions have indicated the tissue-specific expression of seven major 5-HT_{2C} receptor isoforms encoded by eleven distinct RNA species. Editing of 5-HT_{2C}R messenger RNAs alters the amino-acid coding potential of the predicted second intracellular loop of the receptor and can lead to a 10-15-fold reduction in the efficacy of the interaction between receptors and their G proteins. These observations indicate that RNA editing is a new mechanism for regulating serotonergic signal transduction and suggest that this post-translational modification may be critical for modulating the different cellular functions that are mediated by other members of the G-protein-coupled receptor superfamily.

Comment in:
RNA editing: Message change for a fat controller. [Nature. 1997]

PMID: 9103207 (PubMed - Indexed for MEDLINE)

Editing level
data and
link to
reference

RADAR
(<http://rnaedit.com/>)

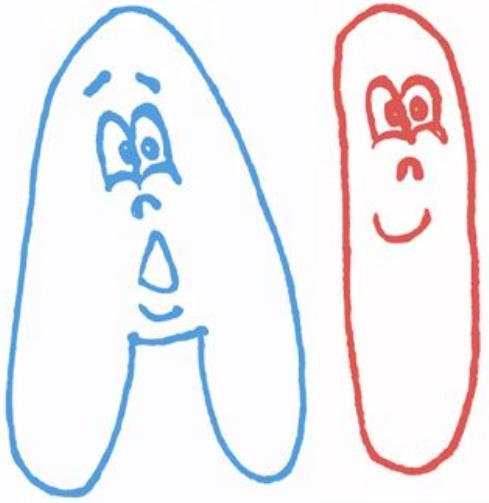
4

RNA editing site: chrX:114082682 in human

Found 2 datapoints:

[Download results](#)

Reference	Tissue	Sequencing Coverage	Editing level (%)
Ramaswami et al 2013	Illumina Bodymap 4	75	
Ramaswami et al 2013	Brain	17	88.2



REDIportal v2.0

An ATLAS of A-to-I RNA editing events in human and other organisms
(<http://srv00.recas.ba.infn.it/atlas/>)

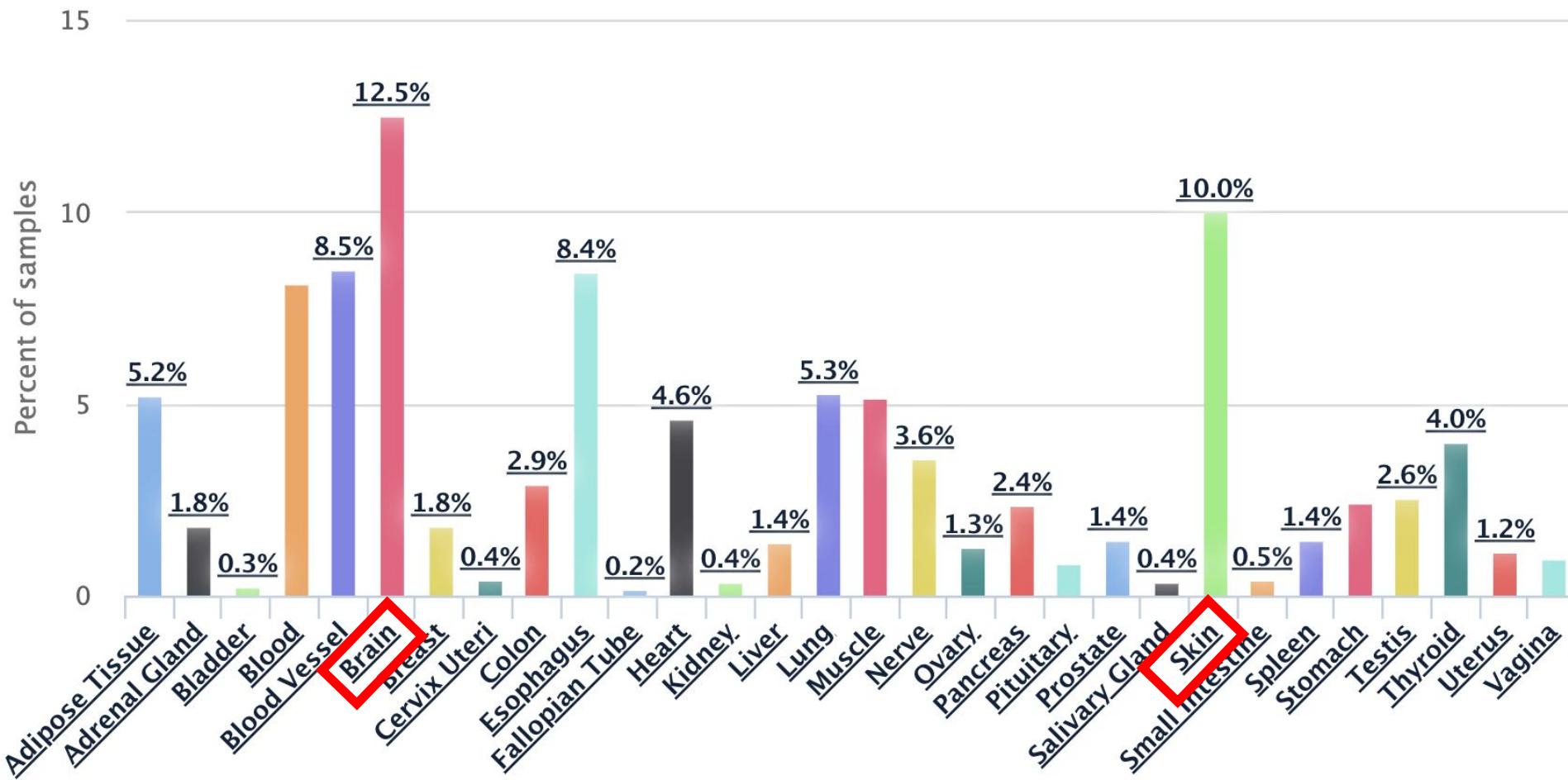
- **16 millions in humans**
 - 9642 RNAseq samples
 - 549 individuals
 - 31 tissues
 - 54 body sites
 - from the GTEx project
- **107,094 in mice**
 - 2 tissues (brain, bone marrow)

REDIportal

(<http://srv00.recas.ba.infn.it/atlas/>)

Human Tissues loaded in the ATLAS

Click the columns to view body sites.



REDIportal

(<http://srv00.recas.ba.infn.it/atlas/>)

Search RNA Editing Sites By:

Organism Name:	<input type="text" value="Homo sapiens"/>
Genome Version:	<input type="text" value="hg19"/>
Genomic Region:	<input type="text" value="Coordinates like chr4:158149690-158282538"/>
Gene Name:	<input type="text" value="Gene Symbol like GRIA2, TP53, SOD1 ..."/> <input type="checkbox"/> Exact Match
Location:	<input type="text" value="Any"/>
Genic Region:	<input type="text" value="Any"/>
AA change:	<input type="text" value="Any"/>
Tissue:	<input type="text" value="Choose one or more tissues"/>
Body Site:	<input type="text" value="Choose one or more sites"/>

 **SEARCH**

 **CLEAN**

 **EXAMPLE**

REDIportal

[\(http://srv00.recas.ba.infn.it/atlas/\)](http://srv00.recas.ba.infn.it/atlas/)

Show 10 rows Column visibility Download

		Chr	Position	Ref	Ed	Strand	dbSNP	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn
		Chr	Position	Ref	Ed	Strand	dbSNP	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn
		chr20	36035570	T	C	-		ALU	SINE/AluJo	SRC;BLCAP	intergenic	2		0	A
		chr20	36035593	T	C	-		ALU	SINE/AluJo	SRC;BLCAP	intergenic	0		0	A
		chr20	36035600	T	C	-		ALU	SINE/AluJo	SRC;BLCAP	intergenic	1		0	A
		chr20	36035609	T	C	-		ALU	SINE/AluJo	SRC;BLCAP	intergenic	5		0	A
		chr20	36035617	A	G	+		ALU	SINE/AluJo	SRC;BLCAP	intergenic	1		0	A
		chr20	36035622	T	C	-		ALU	SINE/AluJo	SRC;BLCAP	intergenic	12		0	A
		chr20	36035623	T	C	-		ALU	SINE/AluJo	SRC;BLCAP	intergenic	6		0	A
		chr20	36035628	T	C	-		ALU	SINE/AluJo	SRC;BLCAP	intergenic	20		0	A
		chr20	36035632	T	C	-		ALU	SINE/AluJo	SRC;BLCAP	intergenic	9		0	A
		chr20	36035643	A	G	+		ALU	SINE/AluJo	SRC;BLCAP	intergenic	13		0	A

REDIportal

(<http://srv00.recas.ba.infn.it/atlas/>)

- link to UCSC genome browser
- genomic position
- reference and edited nucleotide
- strand
- dbSNP accession
- editing location
- repeated element
- gene symbol according to Gencode v19
- genic region
- number of edited samples
- potential amino acid change
- PhastCons conservation score across 46 organisms
- flag indicating source db (ATLAS, RADAR or DARNED)

REDIportal

[\(http://srv00.recas.ba.infn.it/atlas/\)](http://srv00.recas.ba.infn.it/atlas/)

		Show 10 rows	Column visibility		Download																																																											
		Chr	Position	Ref	Ed	Strand	dbSNP	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn																																																	
		chr4	158257875	A	G	+		NONREP	-/-	GRIA2	exonic	550		777																																																		
<div style="display: flex; justify-content: space-around;"> Heat-Map Box Plot Alternative Annotations Editing Details </div>																																																																
<h3>RNA Editing Heat-Map</h3> <p>Level Variation Across Tissues</p> <p>Brain - Cortex Mean Editing: 0.95</p> <table border="1"> <tr> <td>...ose -Subcut...</td><td>Adipose -Viscera...</td><td>Artery -Adrenal Gland</td><td>Artery -Aorta...</td><td>Artery -Coronary</td><td>Artery -Tibial</td><td>Bladder</td><td>Brain -Amygdala</td><td>Brain -Anterior c...</td><td>Brain -Caudate (...</td><td>Brain -Cerebellar...</td><td>Brain -Cerebellum</td><td>Brain -Frontal Co...</td><td>Brain -Hippocam...</td><td>Brain -Nucleus a...</td><td>Brain -Putamen (...</td><td>Brain -Spinal cor...</td><td>Breast -Mammari...</td><td>Cells -EBV-trans...</td><td>Cells -Transform...</td><td>Cervix -Ectocervix</td><td>Colon -Endocervi...</td><td>Colon -Sigmoid</td><td>Colon -Transverse</td><td>Esophagus -Gast...</td><td>Esophagus -Muc...</td><td>Fallopian Tube</td><td>Heart -Atrial App...</td><td>Heart -Left Ventr...</td><td>Kidney</td><td>Lung</td><td>Minor Salivary Gl...</td><td>Muscle -Abdomi...</td><td>Muscle -Skeletal</td><td>Nerve - Tibial</td><td>Ovary</td><td>Pancreas</td><td>Pituitary</td><td>Prostate</td><td>Skin -Not Sun Ex...</td><td>Skin -Sun Expos...</td><td>Small Intestine -...</td><td>Spleen</td><td>Stomach</td><td>Tes...</td><td>Thyroid</td><td>Uterus</td><td>Vagina</td><td>Whole Blood</td></tr> </table> <p>Click Here to see details</p>																...ose -Subcut...	Adipose -Viscera...	Artery -Adrenal Gland	Artery -Aorta...	Artery -Coronary	Artery -Tibial	Bladder	Brain -Amygdala	Brain -Anterior c...	Brain -Caudate (...	Brain -Cerebellar...	Brain -Cerebellum	Brain -Frontal Co...	Brain -Hippocam...	Brain -Nucleus a...	Brain -Putamen (...	Brain -Spinal cor...	Breast -Mammari...	Cells -EBV-trans...	Cells -Transform...	Cervix -Ectocervix	Colon -Endocervi...	Colon -Sigmoid	Colon -Transverse	Esophagus -Gast...	Esophagus -Muc...	Fallopian Tube	Heart -Atrial App...	Heart -Left Ventr...	Kidney	Lung	Minor Salivary Gl...	Muscle -Abdomi...	Muscle -Skeletal	Nerve - Tibial	Ovary	Pancreas	Pituitary	Prostate	Skin -Not Sun Ex...	Skin -Sun Expos...	Small Intestine -...	Spleen	Stomach	Tes...	Thyroid	Uterus	Vagina	Whole Blood
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		chr4	158257879	A	G	+		NONREP	-/-	GRIA2	exonic	484		777																																																		
		chr4	158281294	A	G	+		NONREP	-/-	GRIA2	exonic	591		711																																																		
		Chr	Position	Ref	Ed	Strand	dbSNP	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn																																																	

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		Chr	Position	Ref	Ed	Strand	dbSNP	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn
		chr4	158257875	A	G	+		NONREP	-/-	GRIA2	exonic			777	
Heat-Map Box Plot (circled in red) Alternative Annotations Editing Details															
Box Plot Of RNA Editing values <p>RNA Editing Levels</p> <p>Body Sites</p> <p>Highcharts.com</p> <p>RNA Editing Levels</p> <p>Maximum: 1 Upper quartile: 0.88 Median: 0.94 Lower quartile: 0.98 Minimum: 0.96</p>															
		chr4	158257879	A	G	+		NONREP	-/-	GRIA2	exonic			777	
		chr4	158281294	A	G	+		NONREP	-/-	GRIA2	exonic			711	
		Chr	Position	Ref	Ed	Strand	dbSNP	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn

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		Chr	Position	Ref	Ed	Strand	dbSNP	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn		
➡	U	chr4	158257875	A	G	+	S	NONREP	-/-	GRIA2	exonic	550	N	777	A R		
Heat-Map		Box Plot		Alternative Annotations		Editing Details											
RefSeq Annotation																	
Gene	Region	ExFun				Transcript			ExonNumber		cDNAchange		ProteinChange				
GRIA2	exonic	nonsynonymous SNV				NM_000826			exon11		c.A1820G		p.Q607R				
GRIA2	exonic	nonsynonymous SNV				NM_001083619			exon11		c.A1820G		p.Q607R				
GRIA2	exonic	nonsynonymous SNV				NM_001083620			exon11		c.A1679G		p.Q560R				
UCSC Annotation																	
Gene	Region	ExFun				Transcript			ExonNumber		cDNAchange		ProteinChange				
GRIA2	exonic	nonsynonymous SNV				uc003ipk.4			exon11		c.A1679G		p.Q560R				
GRIA2	exonic	nonsynonymous SNV				uc003ipl.4			exon11		c.A1820G		p.Q607R				
GRIA2	exonic	nonsynonymous SNV				uc003ipm.4			exon11		c.A1820G		p.Q607R				
GRIA2	exonic	nonsynonymous SNV				uc011cit.2			exon11		c.A1679G		p.Q560R				
➡	U	chr4	158257879	A	G	+	S	NONREP	-/-	GRIA2	exonic	484	S	777	A R		
➡	U	chr4	158281294	A	G	+	S	NONREP	-/-	GRIA2	exonic	591	N	711	A R		
	Chr	Position		Ref	Ed	Strand	dbSNP	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn		

Showing 1 to 3 of 3 entries (filtered from 4,668,508 total entries)

rv00_recas_ba_infn_it/cgi/atlas/getpage.py?query1=&query2=GRIA2&query3=NONREP&query4=exonic&query5=#C_C

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	Chr	Position	Ref	Ed	Strand	dbSNP	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn
	U chr4	158257875	A	G	+		NONREP	-/-	GRIA2	exonic			777	

Heat-Map Box Plot Alternative Annotations Editing Details

N. Samples	N. Tissues	N. Body Sites
550	19	36

Click Here for Editing details

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Showing 1 to 3 of 3

RNAseq Run	WGS Run	Tissue	BodySite	n.As	n.Gs	EditingFreq	gCoverage	gFreq
SRR1068687	SRR2165675	Esophagus	Esophagus - Gastroesophageal Junction	0	6	1.00	33	0.00
SRR1069048	SRR2170756	Skin	Skin - Not Sun Exposed (Suprapubic)	8	4	0.33	46	0.00
SRR1069376	SRR2166912	Blood Vessel	Artery - Aorta	0	39	1.00	32	0.00
SRR1069714	SRR2165091	Stomach	Stomach	0	14	1.00	31	0.00
SRR1070086	SRR2165027	Nerve	Nerve - Tibial	2	14	0.88	42	0.00
SRR1070111	SRR2166639	Blood Vessel	Artery - Aorta	0	21	1.00	41	0.00
SRR1070159	SRR2166642	Nerve	Nerve - Tibial	2	5	0.71	30	0.00
SRR1070260	SRR2157441	Breast	Breast - Mammary Tissue	6	2	0.25	20	0.00
SRR1070597	SRR2165469	Nerve	Nerve - Tibial	3	5	0.62	42	0.00
SRR1070641	SRR2164775	Blood Vessel	Artery - Aorta	0	99	1.00	24	0.00

Select Select Select Select n.As n.Gs EditingFreq gCoverage gFreq

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Chr Position Ref Ed Strand dbSNP Location
 Repeats Gene Region EditedIn ExFun Phast KnownIn

	Chr	Position	Ref	Ed	Strand	Location	Repeats	Gene	Region	EditedIn	ExFun	Phast	KnownIn	
1	chr8	103842440	T	C	-	ALU	SINE/AluSz6	AZIN1	intronic	10	U	0	A	
2	chr8	103842451	T	C	-	S	ALU	SINE/AluSz6	AZIN1	intronic	24	U	0	A
3	chr8	103842466	T	C	-	S	ALU	SINE/AluSz6	AZIN1	intronic	20	U	0	A R
4	chr8	103842486	T	C	-	S	ALU	SINE/AluSz6	AZIN1	intronic	47	U	0	A R
5	chr8	103842492	T	C	-	S	ALU	SINE/AluSz6	AZIN1	intronic	39	U	0	A R
6	chr8	103842502	T	C	-	S	ALU	SINE/AluSz6	AZIN1	intronic	41	U	243	A R
7	chr8	103842506	T	C	-	S	ALU	SINE/AluSz6	AZIN1	intronic	38	U	243	A R
8	chr8	103842514	T	C	-	S	ALU	SINE/AluSz6	AZIN1	intronic	7	U	243	A
9	chr8	103842522	T	C	-	S	ALU	SINE/AluSz6	AZIN1	intronic	48	U	0	A R
10	chr8	103842531	T	C	-	S	ALU	SINE/AluSz6	AZIN1	intronic	20	U	0	R

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Search RNA Editing By Sample:

Organism:

Genome Version:

Sample Name:

Data Source:

Data Status:

Data Type:

Tissue:

Body Site:

≤ AEI (%)

≤ ADAR expr (TPM)

≤ ADARB1 expr (TPM)

≤ ADARB2 expr (TPM)

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EXAMPLE

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		Show 10 rows		CSV	Excel	PDF	Select all	Deselect all																Search:	
		Sample	WGS/WES	Source	Organism	Events	Hyper	Body Site	Status	Type	AEI	REI	ADAR	ADARB1	ADARB2										
	<input type="checkbox"/>	SRR1069188	NA			91267	74935	Brain - Cerebellum	normal		2.501	4.222	95.077	59.382	7.696										
	<input type="checkbox"/>	SRR1070986	SRR8233641			86257	53929	Brain - Nucleus accumbens (basal ganglia)	normal		2.116	2.077	68.416	12.565	10.562										
	<input type="checkbox"/>	SRR1071289	SRR8233649			12684	12440	Brain - Hypothalamus	normal		1.766	1.326	9.100	1.050	3.966										
	<input type="checkbox"/>	SRR1071880	SRR8233643			66042	40439	Brain - Hypothalamus	normal		1.942	1.013	66.078	18.685	13.820										
	<input type="checkbox"/>	SRR1072178	SRR8233659			86836	0	Brain - Caudate (basal ganglia)	normal		2.411	1.929	56.810	7.694	24.295										
	<input type="checkbox"/>	SRR1072367	SRR8233659			52840	29987	Brain - Frontal Cortex (BA9)	normal		1.870	0.835	51.555	4.681	64.410										
	<input type="checkbox"/>	SRR1072504	SRR8233641			92239	53140	Brain - Hypothalamus	normal		2.068	2.462	100.380	16.618	11.893										
	<input type="checkbox"/>	SRR1072797	SRR8233650			55321	46360	Brain - Hypothalamus	normal		2.183	4.615	177.233	23.630	8.741										
	<input type="checkbox"/>	SRR1073143	SRR8233650			51426	33528	Brain - Anterior cingulate cortex (BA24)	normal		2.064	2.895	79.414	22.118	9.168										
	<input type="checkbox"/>	SRR1073755	SRR8233492			51633	42367	Brain - Spinal cord (cervical c-1)	normal		2.055	0.728	40.243	2.532	20.203										
		Filter	WGS/WES	Source	Organism	Events	Hyper	Body Site	Status	Type	AEI	REI	ADAR	ADARB1	ADARB2										

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