west_map

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Contents

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1. Introduction

1.1 Function

The purpose of 'west_map' is to extend the functional capability of BioMart to Python. BioMart, further described below, is designed to "facilitate the scientific discovery process" (www.biomart.org). Perhaps the most useful component of BioMart is the ability to map biological elements to each other through the BioMart API. This API, while setup for easy and widespread use, has a widespread selection of limited tools.

This tool, created for linux or as a set of Python 3 libraries, is focused on the quick mapping of biological elements through the API. Currently, its functionality includes file conversion and the creation of new map files given a list of Ids. Use 'west_map' if you have a file with Ids that need converted or if you want to create a map between two Id types. Since 'west_map' uses the BioMart database, the capabilities extend to current BioMart structure.

1.2 Installation

The files are available on pypi.python.org after searching for "west_map". Any further questions on access or updates to the package can be sent to the authors email on the title page. At the current state, there is no alternate URL, yet one is coming.

The downloadable tarball houses the source code, documentation (including this document), test files, the license, and a version update file.

1.2.1 Dependencies

The source code is written in Python 3.2 and has been tested successfully in Python 3.4 and Python 2.7. The non-'west_map' imports within the program include 'getopt', 'os', 'collections', 'itertools', 'sys', and 'requests'. Each of these are included within the standard Python libraries. Setuptools is required to install the package. For further setuptools documentation, see https://pypi.python.org/pypi/setuptools.

1.2.2 How to install

After downloading the tarball, use standard 'setup.py' commands to install on the machine. For instance, if installing on a local linux account:

tar xzvf west_map-0.1.tar.gz

cd west_map-0.1

python setup.py install –user

       This will install in the ~/.local/bin directory and store the libraries in the ~/.local/lib. The path can be renamed to install anywhere, but the prefix must be manually changed in the setup.py command. To use the 'west_map' command in any directory make sure to add the /bin to PATH. Add to .bashrc if one would like this command to carry over to future sessions.

export PATH=$PATH:~/.local/bin

2. BioMart structure and 'west_map'

2.1 BioMart

2.1.1 Database Structure

The BioMart central portal uses a combination of 4 qualifiers to determine query results: a database (or mart), a dataset, filters, and attributes. The database is the highest level qualifier and determines the overall location that the information is coming from. The default database for 'west_map' is "ensembl" which corresponds to the Ensembl 78 Genes database. The dataset is a subset of the database and usually identifies the type of data being used. The default dataset is the "hsapiens_gene_ensembl" dataset under the "ensembl" database. Finally, filters are a list of qualifiers that describe the query values. They are dependent on the database and the dataset. Attributes are the qualifiers that the user would like to be returned. In 'west_map', the filter is automatically included within the mapping file, but not included in a converted file.

For conversion or mapping, all four qualifiers must be specified. For "--show_marts", no qualifiers are necessary. For "--show_datasets", marts must be specified. For "--show_filters" or "--show_attributes", both a mart and a dataset must be specified (or defaults will be used).

2.1.2 API Setup

The BioMart API has a REST API, SOAP API, and Java API. The processors available are TSV, CSV, and JSON. 'west_map' uses the REST API with XML queries. The XML query is created using Python string manipulation and submitted to the REST API using the Python "requests" package. The API 'west_map' response requires either a 200 or 400. In the first case, the response is processed. In the latter, the query is too long. So the query is cut in half and then resubmitted.

2.1.3 Data Characteristics

When the data is returned by BioMart, it is represented in multiple patterns. In the case of REST API through 'west_map', the response-object text-attribute is a simple string, delineating a table through '\n' and '\t'. The Ids to be converted often have multiple values for an attribute or a set of attributes. The results are filter dependent and not attribute dependent. So, they will include multiple lines to reflect these multiple relationships. As BioMart retrieves its data via source databases, any incomplete data is a consequence of the individual data source, the improper structure of the query, or the Ids to be converted/mapped.

2.2 'west_map'

2.2.1 Connection to BioMart

As stated above, 'west_map' connects to the BioMart REST API through XML Queries using the Python package "requests". The connection is made through the sub-package 'west_map.biomart', through the module 'west_map.biomart.control' which submits user requests and data to either 'west_map.biomart.get_lists' (which gets available BioMart lists for marts, datasets, filters, and attributes) or 'west_map.biomart.query' (which iteratively sends XML queries requesting Id conversion).

2.2.2 Retrieval from BioMart

The 'west_map.biomart.get_lists' object does not directly use the BioMart API. Rather it sends requests to either "http://www.biomart.org/biomart/martservice" or "http://www.biomart.org/biomart/martservice/marts" using parameters which return html text that is parsed within the 'get_lists' methods.

The 'west_map.biomart.query' formulates XML queries for the BioMart API in the following format:

<Query client='biomartclient' processor='TSV' limit='-1' header='0'>

<Dataset name='[dataset name]' config='[mart name]'>

<Filter name='[filter name]'/>

<Attribute name='[attribute name 1]'/>

<Attribute name='[attribute name 2]'/>

…

</Dataset>

</Query>

2.2.3 Limitations and constraints

The 'west_map' package does not handle most API returned status codes (404, 405, 500). The mapping output is CSV, but the XML and input file handle can only use TSV. The "--show_datasets" command line argument uses parsing code written only for the "ensembl"

3. Using 'west_map' functionality

3.1 Functionality

The package 'west_map' has a single command but two overall functionalities. In the first version, the package can convert a tab delimted text file with Ids to alternate BioMart Ids. In this case, the column with the Ids is specified by the user within the command line. If an Id corresponds to multiple Ids (or if there are multiple columns locations within a line, each with multiple corresponding Ids) additional lines are added where everything but the Ids are duplicated so that the exaustive product of the sets of new Ids are added. For instance, the mapping

id1	newid-a	newid-b
id2	newid-c	newid-d	newid-e

will convert the line

id1	id2	1.34	aerosol

to

newid-a	newid-c	1.34	aerosol
newid-a	newid-d	1.34	aerosol
newid-a	newid-e	1.34	aerosol
…			
newid-b	newid-e	1.34	aerosol

Whereas the mapping function would output:

id1,newid-a,newid-b

id2,newid-c,newid-d,newid-e

3.2 Inputs

Required for Conversion or Mapping:

-i	--input=	Input file where the ids are that need to be converted.
-o	--output=	Name of the file where the converted Ids will be, regardless of version
-d	--dataset=	Name of the BioMart datasets

-f	--filter=	Name of the BioMart filter (singular in current version)
-a	--attributes=	List of the names of the BioMart attributes, separated with ','
-m	--mart=	Name of the BioMart mart
-c	--columns=	List separated with ',' of the columns of the input file with the Ids
-v	--version=	"convert" [default] or "map" to delineate function

Non-required:

-h	--help	
-n	--header	Add to signify a single line header in the input file
-r	--show_marts	List all BioMart marts (overrides mapping/conversion functionality)
-s	--show_datasets	List all BioMart datasets given a [-m, --mart] (overrides mapping/ conversion functionality)
-l	--show_filters	List all BioMart filters given [-m, --mart], [-d, --dataset] (overrides mapping/conversion functionality)
-b	--show_attributes	List all BioMart attributes given [-m, --mart], [-d, --dataset] (overrides mapping/conversion functionality)

3.3 Examples

3.3.1 Task: Converting .dyn network file of Affymetrix coexpressions to HGNC Symbols

west_map --input=network.dyn --output=converted_network.dyn --mart=ensembl --dataset=hsapiens_gene_ensembl --filter=affy_hg_u133_v2 --attributes=hgnc_symbol --columns=1,2 --version=convert

Here, the input network is "network.dyn" and the output network is "converted_network.dyn". In this example the network Ids from the original .dyn belong to H. Sapiens, so we use the "hsapiens_gene_ensembl" dataset for the "ensembl" mart. The Affymetrix arrays have multiple probesets, so it is important to pick a probeset that is representative of the MicroArray platform used.

3.3.2 Task: Create a file with the start and end sequence positions within the human genome for a list of Entrez Ids (One column)

west_map --input=entrez_ids.txt --output=mapping_file.txt --mart=ensembl

--dataset=hsapiens_gene_ensembl --filter=gene_id

--attributes=chromosome_name,start_position,end_position --columns=1 --version=map

3.3.3 Task: Show list of all attributes available for the "ensembl" mart and the "hsapiens_gene_ensembl" datasets

west_map --mart=ensembl --dataset=hsapiens_gene_ensembl --show_attributes

3.3.4 Task: Show list of all available BioMart martservice

west_map --show_marts

3.3.5 Task: Export list of filters to a file.txt

west_map --mart=ensembl --dataset=hsapiens_gene_ensembl --show_filters > filters.txt

4. Using 'west_map' Python library

4.1 Directory structure

4.2 Useful Libraries

4.2.1 'biomart.control'

biomart.control(mart, dataset, filters, attribute)

1. 'biomart.control.show_marts()' - Prints all BioMart available marts to stdout.

2. 'biomart.control.show_datasets()' - Prints all BioMart datasets for a given mart to stdout. Requires the initialization of 'biomart.control.mart'.

3. 'biomart.control.show_filters()' - Prints all BioMart filters for a given mart and dataset to stdout. Requires the initialization of 'biomart.control.mart' and 'biomart.control.dataset'.

4. 'biomart.control.show_attributes()' - Prints all BioMart attributes for a given mart and dataset to stdout. Requires the intialization of 'biomart.control.mart' and 'biomart.control.dataset'.

5. 'biomart.control.get_converstion(ids)' – Accepts a list of ids that correspond to self.filter. Returns a dictionary of lists where dictionary[id] = [list of corresponding ids]. Requires the intialization of 'biomart.control.mart', 'biomart.control.dataset', 'biomart.control.filters', and 'biomart.control.attribute'.

4.2.2 'map.control'

1. 'map.control.help()' - Prints directions to 'west_map' functionality to stdout.

4.2.3 'map.contact'

1. 'map.contact.parse(inputloc, columns, header)' – given an input file location (string), a list of columns (list of int), and a header flag (boolean), saves a non-redundant list of ids to convert as 'map.contact.ids'.

2. 'map.contact.export(inputloc, columns, header, outputloc, conversion)' – given an input file location (string), a list of columns (list of int), a header flag (boolean), an output file location (string), and a conversion object (dictionary of lists created from 'biomart.control.get_conversion(ids)'), exports an updated file with converted ids instead of original ids.

3. 'map.contact.mapping(inputloc, columns, header, outputloc, conversion)' – given (see previous), exports a comma separated mapping file for filter and attributes.

4.3 Examples

4.3.1 Task: show attributes for "ensembl" and "hsapiens_gene_ensembl"

import west_map

c = west_map.biomart.control(mart='ensembl', dataset='hsapiens_gene_ensembl')

c.show_attributes()

4.3.2 Task: obtain list of ids from second column in "input.txt"

import west_map

cont = west_map.map.contact()

 # inputfile location, list of columns, boolean for header

ids = cont.parse('input.txt', [2], False)

4.3.3 Task: obtain conversion object (dictionary of lists) for previously obtained list

c = west_map.biomart.control(mart='ensembl', dataset='hsapiens_gene_ensembl', filters=['affy_u133_plus2'], attribute=['hgnc_symbol'])

conversion = c.get_conversion(ids) # "ids" from previous task

4.3.4 Task: export "output.txt" a converted file from "input.txt' in the previous example

inputfile location, list of columns, boolean for header, output file location, conversion object

cont.export('input.txt', [2], False, 'output.txt', conversion)

5. Appendix

5.1 Available BioMart marts

Breast_mart_69	BCCTB Bioinformatics Portal (UK and Ireland)
EMAGE browse repository	EMAGE BROWSE REPOSITORY
EMAGE gene expression	EMAGE GENE EXPRESSION
EMAP anatomy ontology	EMAP ANATOMY ONTOLOGY
ENSEMBL_MART_ONTOLOGY	Ontology
ENSEMBL_MART_PLANT	GRAMENE 40 ENSEMBL GENES (CSHL/CORNELL US)
ENSEMBL_MART_PLANT_SEQUENCE	Sequence
ENSEMBL_MART_PLANT_SNP	GRAMENE 40 VARIATION (CSHL/CORNELL US)
Eurexpress Biomart	EUREXPRESS (MRC EDINBURGH UK)
GermOnline	GERMONLINE
HapMap_rel27	HAPMAP 27 (NCBI US)
Hsmm_Hmec	Predictive models of gene regulation from processed high-throughput epigenomics data: Hsmm vs. Hmec
K562_Gm12878	Predictive models of gene regulation from processed high-throughput epigenomics data: K562 vs. Gm12878
Pancreas63	PANCREATIC EXPRESSION DATABASE (BARTS CANCER INSTITUTE UK)
Prod_BOFUB	Botrytis cinerea B0510, genes functional annotation
Prod_BOTRYTISEDIT	Botrytis cinerea T4, genes functional annotation
Prod_LMACULANSEDIT	Leptosphaeria maculans, genes functional annotation
Prod_POPLAR	Populus trichocarpa, genes functional annotation
Prod_POPLAR_V2	Populus trichocarpa, genes functional annotation V2.0
Prod_TOMATO	Tomato, stuctural and functional annotation
Prod_WHEAT	Wheat, stuctural annotation with Genetic maps (genetic markers..)
Public_MAIZE	Zea mays ZmB73, genes functional annotation
Public_OBIOMARTPUB	Multi-species: marker, QTL, SNP, gene, germplasm, phenotype, association, with Gene annotations
Public_TAIRV10	Arabidopsis Thaliana TAIRV10, genes functional annotation
Public_VITIS	Grapevine 8x, stuctural annotation with Genetic maps (genetic markers..)
Public_VITIS_12x	Grapevine 12x.0, stuctural and functional annotation with Genetic maps (genetic markers..)
Sigenae Oligo Annotation (Ensembl 56)	SIGENAE OLIGO ANNOTATION (ENSEMBL 56)
Sigenae Oligo Annotation (Ensembl 59)	SIGENAE OLIGO ANNOTATION (ENSEMBL 59)
Sigenae_Oligo_Annotation_Ensembl_61	SIGENAE OLIGO ANNOTATION (ENSEMBL 61)

WS220	WORMBASE 220 (CSHL US)
biblioDB	PARAMECIUM BIBLIOGRAPHY (CNRS FRANCE)
biomart	MGI (JACKSON LABORATORY US)
biomartDB	PARAMECIUM GENOME (CNRS FRANCE)
cg_mart_02	PROTEOMICS (UNIVERSITY OF CAMBRIDGE - UK)
ensembl	ENSEMBL GENES 79 (SANGER UK)
example	FANTOM5 phase1.1 (RIKEN CSLST Japan)
expression	VectorBase Expression
fungi_mart_26	ENSEMBL FUNGI 26 (EBI UK)
fungi_sequence_mart_26	
fungi_variations_26	ENSEMBL FUNGI VARIATION 26 (EBI UK)
genomic_features	ENSEMBL GENOMIC FEATURES 79 (SANGER UK)
htgt	WTSI MOUSE GENETICS PROJECT (SANGER UK)
ikmc	IKMC GENES AND PRODUCTS (IKMC)
metazoa_genomic_features_mart_26	
metazoa_mart_26	ENSEMBL METAZOA 26 (EBI UK)
metazoa_sequence_mart_26	
metazoa_variations_26	ENSEMBL METAZOA VARIATION 26 (EBI UK)
metazome_mart	Metazome
metazome_sequence_mart	Sequences
msd	MSD (EBI UK)
oncomodules	INTOGEN ONCOMODULES
ontology	Ontology Mart
parasite_mart	ParaSite Mart (EBI UK)
parasite_sequences	ParaSite Mart Sequences
phytozome_mart	Phytozome
plants_mart_26	ENSEMBL PLANTS 26 (EBI UK)
plants_sequence_mart_26	
plants_variations_26	ENSEMBL PLANTS VARIATION 26 (EBI UK)
pride	PRIDE (EBI UK)
prod-intermart_1	INTERPRO (EBI UK)
protists_mart_25	ENSEMBL PROTISTS 25 (EBI UK)
protists_sequence_mart_26	
protists_variations_26	ENSEMBL PROTISTS VARIATION 26 (EBI UK)
regulation	ENSEMBL REGULATION 79 (SANGER UK)
sequence	ENSEMBL SEQUENCE 79 (SANGER UK)
sequence_mart	Sequences
snp	ENSEMBL VARIATION 79 (SANGER UK)
unimart	UNIPROT (EBI UK)
vb_gene_mart_1502	VectorBase Genes
vb_genomic_features_mart_1502	Genomic Features 1502

vb_ontology_mart_1502	Ontology Mart 1502
vb_sequence_mart_1502	VectorBase Sequence Mart
vb_snp_mart_1502	VectorBase Variation
vega	VEGA 59 (SANGER UK)

5.2 Available BioMart datasets for "ensembl"

dnovemcinctus_gene_ensembl	Dasypus novemcinctus genes (Dasnov3.0)	Dasnov3.0	2015-03-03 14:20:47
cjacchus_gene_ensembl	Callithrix jacchus genes (C_jacchus3.2.1)	C_jacchus3.2.1	2015-03-03 14:20:11
vpacos_gene_ensembl	Vicugna pacos genes (vicPac1)	vicPac1	2015-03-03 14:20:20
ggallus_gene_ensembl	Gallus gallus genes (Galgal4)	Galgal4	2015-03-03 14:20:51
tsyrichta_gene_ensembl	Tarsius syrichta genes (tarSyr1)	tarSyr1	2015-03-03 14:20:48
mlucifugus_gene_ensembl	Myotis lucifugus genes (myoLuc2)	myoLuc2	2015-03-03 14:21:21
nleucogenys_gene_ensembl	Nomascus leucogenys genes (Nleu1.0)	Nleu1.0	2015-03-03 14:20:36
amexicanus_gene_ensembl	Astyanax mexicanus genes (AstMex102)	AstMex102	2015-03-03 14:20:31
gaculeatus_gene_ensembl	Gasterosteus aculeatus genes (BROADS1)	BROADS1	2015-03-03 14:20:17
amelanoleuca_gene_ensembl	Ailuropoda melanoleuca genes (ailMel1)	ailMel1	2015-03-03 14:21:09
acarolinensis_gene_ensembl	Anolis carolinensis genes (AnoCar2.0)	AnoCar2.0	2015-03-03 14:20:41
sscrofa_gene_ensembl	Sus scrofa genes (Sscrofa10.2)	Sscrofa10.2	2015-03-03 14:20:29
mfuro_gene_ensembl	Mustela putorius furo genes (MusPutFur1.0)	MusPutFur1.0	2015-03-03 14:19:55
olatipes_gene_ensembl	Oryzias latipes genes (HdrR)	HdrR	2015-03-03 14:20:59
ogarnettii_gene_ensembl	Otolemur garnettii genes (OtoGar3)	OtoGar3	2015-03-03 14:20:37
psinensis_gene_ensembl	Pelodiscus sinensis genes (PelSin_1.0)	PelSin_1.0	2015-03-03 14:20:58
xtropicalis_gene_ensembl	Xenopus tropicalis genes (JGI4.2)	JGI4.2	2015-03-03 14:21:26
pmarinus_gene_ensembl	Petromyzon marinus genes (Pmarinus_7.0)	Pmarinus_7.0	2015-03-03 14:20:02
aplatyrhynchos_gene_ensembl	Anas platyrhynchos genes (BGI_duck_1.0)	BGI_duck_1.0	2015-03-03 14:19:59
csavignyi_gene_ensembl	Ciona savignyi genes (CSAV2.0)	CSAV2.0	2015-03-03 14:20:15
panubis_gene_ensembl	Papio anubis genes (PapAnu2.0)	PapAnu2.0	2015-03-03 14:21:31

oanatinus_gene_ensembl	Ornithorhynchus anatinus genes (OANA5)	OANA5	2015-03-03 14:21:16
xmaculatus_gene_ensembl	Xiphophorus maculatus genes (Xipmac4.4.2)	Xipmac4.4.2	2015-03-03 14:20:24
ecaballus_gene_ensembl	Equus caballus genes (EquCab2)	EquCab2	2015-03-03 14:20:34
ocuniculus_gene_ensembl	Oryctolagus cuniculus genes (OryCun2.0)	OryCun2.0	2015-03-03 14:20:53
cintestinalis_gene_ensembl	Ciona intestinalis genes (KH)	KH	2015-03-03 14:21:34
pcapensis_gene_ensembl	Procavia capensis genes (proCap1)	proCap1	2015-03-03 14:21:24
meugenii_gene_ensembl	Macropus eugenii genes (Meug_1.0)	Meug_1.0	2015-03-03 14:20:19
scerevisiae_gene_ensembl	Saccharomyces cerevisiae genes (R64-1-1)	R64-1-1	2015-03-03 14:21:30
pformosa_gene_ensembl	Poecilia formosa genes (PoeFor_5.1.2)	PoeFor_5.1.2	2015-03-03 14:21:04
oniloticus_gene_ensembl	Oreochromis niloticus genes (Orenil1.0)	Orenil1.0	2015-03-03 14:21:03
saraneus_gene_ensembl	Sorex araneus genes (sorAra1)	sorAra1	2015-03-03 14:21:11
pvampyrus_gene_ensembl	Pteropus vampyrus genes (pteVam1)	pteVam1	2015-03-03 14:20:43
gmorhua_gene_ensembl	Gadus morhua genes (gadMor1)	gadMor1	2015-03-03 14:21:28
oaries_gene_ensembl	Ovis aries genes (Oar_v3.1)	Oar_v3.1	2015-03-03 14:21:05
itridecemlineatus_gene_ensembl	Ictidomys tridecemlineatus genes (spetri2)	spetri2	2015-03-03 14:21:01
cporcellus_gene_ensembl	Cavia porcellus genes (cavPor3)	cavPor3	2015-03-03 14:21:25
drerio_gene_ensembl	Danio rerio genes (Zv9)	Zv9	2015-03-03 14:21:07
tnigroviridis_gene_ensembl	Tetraodon nigroviridis genes (TETRAODON8.0)	TETRAODON8.0	2015-03-03 14:19:56
lafricana_gene_ensembl	Loxodonta africana genes (loxAfr3)	loxAfr3	2015-03-03 14:21:19
etelfairi_gene_ensembl	Echinops telfairi genes (TENREC)	TENREC	2015-03-03 14:20:49
dmelanogaster_gene_ensembl	Drosophila melanogaster genes (BDGP6)	BDGP6	2015-03-03 14:21:14
rnorvegicus_gene_ensembl	Rattus norvegicus genes (Rnor_5.0)	Rnor_5.0	2015-03-03 14:20:56
fcatus_gene_ensembl	Felis catus genes (Felis_catus_6.2)	Felis_catus_6.2	2015-03-03 14:20:27
loculatus_gene_ensembl	Lepisosteus oculatus genes (LepOcu1)	LepOcu1	2015-03-03 14:19:58
eeuropaeus_gene_ensembl	Erinaceus europaeus genes (eriEur1)	eriEur1	2015-03-03 14:21:22
tbelangeri_gene_ensembl	Tupaia belangeri genes	tupBel1	2015-03-03 14:20:21

	(tupBel1)		
cfamiliaris_gene_ensembl	Canis familiaris genes (CanFam3.1)	CanFam3.1	2015-03-03 14:20:40
mdomestica_gene_ensembl	Monodelphis domestica genes (monDom5)	monDom5	2015-03-03 14:20:30
mmusculus_gene_ensembl	Mus musculus genes (GRCm38.p3)	GRCm38.p3	2015-03-03 14:21:33
mmurinus_gene_ensembl	Microcebus murinus genes (micMur1)	micMur1	2015-03-03 14:19:53
choffmanni_gene_ensembl	Choloepus hoffmanni genes (choHof1)	choHof1	2015-03-03 14:20:54
falbicollis_gene_ensembl	Ficedula albicollis genes (FicAlb_1.4)	FicAlb_1.4	2015-03-03 14:20:04
ggorilla_gene_ensembl	Gorilla gorilla genes (gorGor3.1)	gorGor3.1	2015-03-03 14:20:25
mgallopavo_gene_ensembl	Meleagris gallopavo genes (UMD2)	UMD2	2015-03-03 14:20:10
hsapiens_gene_ensembl	Homo sapiens genes (GRCh38.p2)	GRCh38.p2	2015-03-03 14:20:14
lchalumnae_gene_ensembl	Latimeria chalumnae genes (LatCha1)	LatCha1	2015-03-03 14:20:57
csabaeus_gene_ensembl	Chlorocebus sabaeus genes (ChlSab1.1)	ChlSab1.1	2015-03-03 14:20:23
tguttata_gene_ensembl	Taeniopygia guttata genes (taeGut3.2.4)	taeGut3.2.4	2015-03-03 14:21:17
pabelii_gene_ensembl	Pongo abelii genes (PPYG2)	PPYG2	2015-03-03 14:20:32
ptroglodytes_gene_ensembl	Pan troglodytes genes (CHIMP2.1.4)	CHIMP2.1.4	2015-03-03 14:19:54
trubripes_gene_ensembl	Takifugu rubripes genes (FUGU4.0)	FUGU4.0	2015-03-03 14:20:45
sharrisii_gene_ensembl	Sarcophilus harrisii genes (DEVIL7.0)	DEVIL7.0	2015-03-03 14:20:38
oprinceps_gene_ensembl	Ochotona princeps genes (OchPri2.0)	OchPri2.0	2015-03-03 14:20:08
mmulatta_gene_ensembl	Macaca mulatta genes (MMUL_1)	MMUL_1	2015-03-03 14:20:01
btaurus_gene_ensembl	Bos taurus genes (UMD3.1)	UMD3.1	2015-03-03 14:20:42
celegans_gene_ensembl	Caenorhabditis elegans genes (WBcel235)	WBcel235	2015-03-03 14:20:07
dordii_gene_ensembl	Dipodomys ordii genes (dipOrd1)	dipOrd1	2015-03-03 14:21:20
ttruncatus_gene_ensembl	Tursiops truncatus genes (turTru1)	turTru1	2015-03-03 14:20:05

5.3 Attributes for "ensembl" and "hsapiens_gene_ensembl"

Most of the following attributes can be used as filters as well (not anything organism specific

other than H. sapiens).

ensembl_gene_id	Ensembl Gene ID
ensembl_transcript_id	Ensembl Transcript ID
ensembl_peptide_id	Ensembl Protein ID
ensembl_exon_id	Ensembl Exon ID
description	Description
chromosome_name	Chromosome Name
start_position	Gene Start (bp)
end_position	Gene End (bp)
strand	Strand
band	Band
transcript_start	Transcript Start (bp)
transcript_end	Transcript End (bp)
transcription_start_site	Transcription Start Site (TSS)
transcript_length	Transcript length
transcript_tsl	Transcript Support Level (TSL)
transcript_gencode_basic	GENCODE basic annotation
transcript_appris_pi	APPRIS principal isoform annotation
external_gene_name	Associated Gene Name
external_gene_source	Associated Gene Source
external_transcript_name	Associated Transcript Name
external_transcript_source_name	Associated Transcript Source
transcript_count	Transcript count
percentage_gc_content	% GC content
gene_biotype	Gene type
transcript_biotype	Transcript type
source	Source (gene)
transcript_source	Source (transcript)
status	Status (gene)
transcript_status	Status (transcript)
version	Version (gene)
transcript_version	Version (transcript)
phenotype_description	Phenotype description
source_name	Source name
study_external_id	Study External Reference
go_id	GO Term Accession
name_1006	GO Term Name
definition_1006	GO Term Definition
go_linkage_type	GO Term Evidence Code
namespace_1003	GO domain

goslim_goa_accession	GOSlim GOA Accession(s)
goslim_goa_description	GOSlim GOA Description
arrayexpress	ArrayExpress
chembl	ChEMBL ID(s)
clone_based_ensembl_gene_name	Clone based Ensembl gene name
clone_based_ensembl_transcript_name	Clone based Ensembl transcript name
clone_based_vega_gene_name	Clone based VEGA gene name
clone_based_vega_transcript_name	Clone based VEGA transcript name
ccds	CCDS ID
dbass3_id	Database of Aberrant 3' Splice Sites (DBASS3) IDs
dbass3_name	DBASS3 Gene Name
dbass5_id	Database of Aberrant 5' Splice Sites (DBASS5) IDs
dbass5_name	DBASS5 Gene Name
embl	EMBL (Genbank) ID
ens_hs_gene	Ensembl Human Gene IDs
ens_hs_transcript	Ensembl Human Transcript IDs
ens_hs_translation	Ensembl Human Translation IDs
ens_lrg_gene	LRG to Ensembl link gene
ens_lrg_transcript	LRG to Ensembl link transcript
entrezgene	EntrezGene ID
entrezgene_transcript_name	EntrezGene transcript name ID
hpa	Human Protein Atlas Antibody ID
ottg	VEGA gene ID(s) (OTTG)
ottt	VEGA transcript ID(s) (OTTT)
ottp	VEGA protein ID(s) (OTTP)
hgnc_id	HGNC ID(s)
hgnc_symbol	HGNC symbol
hgnc_transcript_name	HGNC transcript name
merops	MEROPS ID
pdb	PDB ID
mim_morbid_accession	MIM Morbid Accession
mim_morbid_description	MIM Morbid Description
mim_gene_accession	MIM Gene Accession
mim_gene_description	MIM Gene Description
mirbase_accession	miRBase Accession(s)
mirbase_id	miRBase ID(s)
mirbase_transcript_name	miRBase transcript name
protein_id	Protein (Genbank) ID
refseq_mrna	RefSeq mRNA [e.g. NM_001195597]
refseq_mrna_predicted	RefSeq mRNA predicted [e.g. XM_001125684]
refseq_ncrna	RefSeq ncRNA [e.g. NR_002834]

refseq_ncrna_predicted	RefSeq ncRNA predicted [e.g. XR_108264]
refseq_peptide	RefSeq Protein ID [e.g. NP_001005353]
refseq_peptide_predicted	RefSeq Predicted Protein ID [e.g. XP_001720922]
rfam	Rfam ID
rfam_transcript_name	Rfam transcript name
ucsc	UCSC ID
unigene	Unigene ID
uniparc	UniParc
uniprot_sptrembl	UniProt/TrEMBL Accession
uniprot_swissprot	UniProt/SwissProt ID
uniprot_swissprot_accession	UniProt/SwissProt Accession
uniprot_genename	UniProt Gene Name
uniprot_genename_transcript_name	Uniprot Genename Transcript Name
wikigene_name	WikiGene Name
wikigene_id	WikiGene ID
wikigene_description	WikiGene Description
efg_agilent_sureprint_g3_ge_8x60k	Agilent SurePrint G3 GE 8x60k probe
efg_agilent_sureprint_g3_ge_8x60k_v2	Agilent SurePrint G3 GE 8x60k v2 probe
efg_agilent_wholegenome_4x44k_v1	Agilent WholeGenome 4x44k v1 probe
efg_agilent_wholegenome_4x44k_v2	Agilent WholeGenome 4x44k v2 probe
affy_hc_g110	Affy HC G110 probeset
affy_hg_focus	Affy HG FOCUS probeset
affy_hg_u133_plus_2	Affy HG U133-PLUS-2 probeset
affy_hg_u133a_2	Affy HG U133A_2 probeset
affy_hg_u133a	Affy HG U133A probeset
affy_hg_u133b	Affy HG U133B probeset
affy_hg_u95av2	Affy HG U95AV2 probeset
affy_hg_u95b	Affy HG U95B probeset
affy_hg_u95c	Affy HG U95C probeset
affy_hg_u95d	Affy HG U95D probeset
affy_hg_u95e	Affy HG U95E probeset
affy_hg_u95a	Affy HG U95A probeset
affy_hugenefl	Affy HuGene FL probeset
affy_hta_2_0	Affy HTA-2_0 probeset
affy_huex_1_0_st_v2	Affy HuEx 1_0 st v2 probeset
affy_hugene_1_0_st_v1	Affy HuGene 1_0 st v1 probeset
affy_hugene_2_0_st_v1	Affy HuGene 2_0 st v1 probeset
affy_primeview	Affy primeview
affy_u133_x3p	Affy U133 X3P probeset
agilent_cgh_44b	Agilent CGH 44b probe
codelink	Codelink probe

illumina_humanwg_6_v1	Illumina HumanWG 6 v1 probe
illumina_humanwg_6_v2	Illumina HumanWG 6 v2 probe
illumina_humanwg_6_v3	Illumina HumanWG 6 v3 probe
illumina_humanht_12_v3	Illumina Human HT 12 V3 probe
illumina_humanht_12_v4	Illumina Human HT 12 V4 probe
illumina_humanref_8_v3	Illumina Human Ref 8 V3 probe
phalanx_onearray	Phalanx OneArray probe
family	Ensembl Protein Family ID(s)
family_description	Ensembl Family Description
pirsf	PIRSF SuperFamily ID
superfamily	Superfamily ID
smart	SMART ID
profile	PROFILE ID
prints	PRINTS ID
pfam	PFAM ID
tigrfam	TIGRFam ID
interpro	Interpro ID
interpro_short_description	Interpro Short Description
interpro_description	Interpro Description
low_complexity	Low complexity
transmembrane_domain	Transmembrane domain
signal_domain	Signal domain
ncoils	Ncoils
ensembl_gene_id	Ensembl Gene ID
ensembl_transcript_id	Ensembl Transcript ID
ensembl_peptide_id	Ensembl Protein ID
chromosome_name	Chromosome Name
start_position	Gene Start (bp)
end_position	Gene End (bp)
transcript_start	Transcript Start (bp)
transcript_end	Transcript End (bp)
transcription_start_site	Transcription Start Site (TSS)
transcript_length	Transcript length
strand	Strand
external_gene_name	Associated Gene Name
external_gene_source	Associated Gene Source
5_utr_start	5' UTR Start
5_utr_end	5' UTR End
3_utr_start	3' UTR Start
3_utr_end	3' UTR End
cds_length	CDS Length

transcript_count	Transcript count
description	Description
gene_biotype	Gene type
exon_chrom_start	Exon Chr Start (bp)
exon_chrom_end	Exon Chr End (bp)
is_constitutive	Constitutive Exon
rank	Exon Rank in Transcript
phase	phase
cdna_coding_start	cDNA coding start
cdna_coding_end	cDNA coding end
genomic_coding_start	Genomic coding start
genomic_coding_end	Genomic coding end
ensembl_exon_id	Ensembl Exon ID
cds_start	CDS Start
cds_end	CDS End
ensembl_gene_id	Ensembl Gene ID
ensembl_transcript_id	Ensembl Transcript ID
ensembl_peptide_id	Ensembl Protein ID
chromosome_name	Chromosome Name
start_position	Gene Start (bp)
end_position	Gene End (bp)
strand	Strand
band	Band
external_gene_name	Associated Gene Name
external_gene_source	Associated Gene Source
transcript_count	Transcript count
percentage_gc_content	% GC content
description	Description
vpacos_homolog_ensembl_gene	Alpaca Ensembl Gene ID
vpacos_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
vpacos_homolog_ensembl_peptide	Alpaca Ensembl Protein ID
vpacos_homolog_chromosome	Alpaca Chromosome Name
vpacos_homolog_chrom_start	Alpaca Chromosome Start (bp)
vpacos_homolog_chrom_end	Alpaca Chromosome End (bp)
vpacos_homolog_orthology_type	Homology Type
vpacos_homolog_subtype	Ancestor
vpacos_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
vpacos_homolog_perc_id	% Identity with respect to query gene
vpacos_homolog_perc_id_r1	% Identity with respect to Alpaca gene
pformosa_homolog_ensembl_gene	Amazon molly Ensembl Gene ID
pformosa_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID

pformosa_homolog_ensembl_peptide	Amazon molly Ensembl Protein ID
pformosa_homolog_chromosome	Amazon molly Chromosome Name
pformosa_homolog_chrom_start	Amazon molly Chromosome Start (bp)
pformosa_homolog_chrom_end	Amazon molly Chromosome End (bp)
pformosa_homolog_orthology_type	Homology Type
pformosa_homolog_subtype	Ancestor
pformosa_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
pformosa_homolog_perc_id	% Identity with respect to query gene
pformosa_homolog_perc_id_r1	% Identity with respect to Amazon molly gene
acarolinensis_homolog_ensembl_gene	Anole Lizard Ensembl Gene ID
acarolinensis_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
acarolinensis_homolog_ensembl_peptide	Anole Lizard Ensembl Protein ID
acarolinensis_homolog_chromosome	Anole Lizard Chromosome Name
acarolinensis_homolog_chrom_start	Anole Lizard Chromosome Start (bp)
acarolinensis_homolog_chrom_end	Anole Lizard Chromosome End (bp)
acarolinensis_homolog_orthology_type	Homology Type
acarolinensis_homolog_subtype	Ancestor
acarolinensis_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
acarolinensis_homolog_perc_id	% Identity with respect to query gene
acarolinensis_homolog_perc_id_r1	% Identity with respect to Anole Lizard gene
acarolinensis_homolog_dn	dN
acarolinensis_homolog_ds	dS
dnovemcinctus_homolog_ensembl_gene	Armadillo Ensembl Gene ID
dnovemcinctus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
dnovemcinctus_homolog_ensembl_peptide	Armadillo Ensembl Protein ID
dnovemcinctus_homolog_chromosome	Armadillo Chromosome Name
dnovemcinctus_homolog_chrom_start	Armadillo Chromosome Start (bp)
dnovemcinctus_homolog_chrom_end	Armadillo Chromosome End (bp)
dnovemcinctus_homolog_orthology_type	Homology Type
dnovemcinctus_homolog_subtype	Ancestor
dnovemcinctus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
dnovemcinctus_homolog_perc_id	% Identity with respect to query gene
dnovemcinctus_homolog_perc_id_r1	% Identity with respect to Armadillo gene
dnovemcinctus_homolog_dn	dN
dnovemcinctus_homolog_ds	dS
gmorhua_homolog_ensembl_gene	Atlantic Cod Ensembl Gene ID
gmorhua_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
gmorhua_homolog_ensembl_protein	Atlantic Cod Ensembl Protein ID
gmorhua_homolog_chromosome	Atlantic Cod Chromosome Name
gmorhua_homolog_chrom_start	Atlantic Cod Chromosome Start (bp)
gmorhua_homolog_chrom_end	Atlantic Cod Chromosome End (bp)

gmorhua_homolog_orthology_type	Homology Type
gmorhua_homolog_subtype	Ancestor
gmorhua_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
gmorhua_homolog_perc_id	% Identity with respect to query gene
gmorhua_homolog_perc_id_r1	% Identity with respect to Atlantic Cod gene
ogarnettii_homolog_ensembl_gene	Bushbaby Ensembl Gene ID
ogarnettii_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
ogarnettii_homolog_ensembl_peptide	Bushbaby Ensembl Protein ID
ogarnettii_homolog_chromosome	Bushbaby Chromosome Name
ogarnettii_homolog_chrom_start	Bushbaby Chromosome Start (bp)
ogarnettii_homolog_chrom_end	Bushbaby Chromosome End (bp)
ogarnettii_homolog_orthology_type	Homology Type
ogarnettii_homolog_subtype	Ancestor
ogarnettii_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
ogarnettii_homolog_perc_id	% Identity with respect to query gene
ogarnettii_homolog_perc_id_r1	% Identity with respect to Bushbaby gene
ogarnettii_homolog_dn	dN
ogarnettii_homolog_ds	dS
celegans_homolog_chrom_start	Caenorhabditis elegans Chromosome Start (bp)
celegans_homolog_ensembl_gene	Caenorhabditis elegans Ensembl Gene ID
celegans_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
celegans_homolog_ensembl_peptide	Caenorhabditis elegans Ensembl Protein ID
celegans_homolog_chromosome	Caenorhabditis elegans Chromosome Name
celegans_homolog_chrom_end	Caenorhabditis elegans Chromosome End (bp)
celegans_homolog_orthology_type	Homology Type
celegans_homolog_subtype	Ancestor
celegans_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
celegans_homolog_perc_id	% Identity with respect to query gene
celegans_homolog_perc_id_r1	% Identity with respect to Caenorhabditis elegans gene
celegans_homolog_dn	dN
celegans_homolog_ds	dS
fcatus_homolog_ensembl_gene	Cat Ensembl Gene ID
fcatus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
fcatus_homolog_ensembl_peptide	Cat Ensembl Protein ID
fcatus_homolog_chromosome	Cat Chromosome Name
fcatus_homolog_chrom_start	Cat Chromosome Start (bp)
fcatus_homolog_chrom_end	Cat Chromosome End (bp)
fcatus_homolog_orthology_type	Homology Type
fcatus_homolog_subtype	Ancestor
fcatus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
fcatus_homolog_perc_id	% Identity with respect to query gene

fcatus_homolog_perc_id_r1	% Identity with respect to Cat gene
fcatus_homolog_dn	dN
fcatus_homolog_ds	dS
amexicanus_homolog_ensembl_gene	Cave fish Ensembl Gene ID
amexicanus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
amexicanus_homolog_ensembl_peptide	Cave fish Ensembl Protein ID
amexicanus_homolog_chromosome	Cave fish Chromosome Name
amexicanus_homolog_chrom_start	Cave fish Chromosome Start (bp)
amexicanus_homolog_chrom_end	Cave fish Chromosome End (bp)
amexicanus_homolog_orthology_type	Homology Type
amexicanus_homolog_subtype	Ancestor
amexicanus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
amexicanus_homolog_perc_id	% Identity with respect to query gene
amexicanus_homolog_perc_id_r1	% Identity with respect to Cave fish gene
ggallus_homolog_ensembl_gene	Chicken Ensembl Gene ID
ggallus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
ggallus_homolog_ensembl_peptide	Chicken Ensembl Protein ID
ggallus_homolog_chromosome	Chicken Chromosome Name
ggallus_homolog_chrom_start	Chicken Chromosome Start (bp)
ggallus_homolog_chrom_end	Chicken Chromosome End (bp)
ggallus_homolog_orthology_type	Homology Type
ggallus_homolog_subtype	Ancestor
ggallus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
ggallus_homolog_perc_id	% Identity with respect to query gene
ggallus_homolog_perc_id_r1	% Identity with respect to Chicken gene
ggallus_homolog_dn	dN
ggallus_homolog_ds	dS
ptroglodytes_homolog_ensembl_gene	Chimpanzee Ensembl Gene ID
ptroglodytes_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
ptroglodytes_homolog_ensembl_peptide	Chimpanzee Ensembl Protein ID
ptroglodytes_homolog_chromosome	Chimpanzee Chromosome Name
ptroglodytes_homolog_chrom_start	Chimpanzee Chromosome Start (bp)
ptroglodytes_homolog_chrom_end	Chimpanzee Chromosome End (bp)
ptroglodytes_homolog_orthology_type	Homology Type
ptroglodytes_homolog_subtype	Ancestor
ptroglodytes_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
ptroglodytes_homolog_perc_id	% Identity with respect to query gene
ptroglodytes_homolog_perc_id_r1	% Identity with respect to Chimpanzee gene
ptroglodytes_homolog_dn	dN
ptroglodytes_homolog_ds	dS
psinensis_homolog_ensembl_gene	Chinese softshell turtle Ensembl Gene ID

psinensis_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
psinensis_homolog_ensembl_peptide	Chinese softshell turtle Ensembl Protein ID
psinensis_homolog_chromosome	Chinese softshell turtle Chromosome Name
psinensis_homolog_chrom_start	Chinese softshell turtle Chromosome Start (bp)
psinensis_homolog_chrom_end	Chinese softshell turtle Chromosome End (bp)
psinensis_homolog_orthology_type	Homology Type
psinensis_homolog_subtype	Ancestor
psinensis_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
psinensis_homolog_perc_id	% Identity with respect to query gene
psinensis_homolog_perc_id_r1	% Identity with respect to Chinese softshell turtle gene
psinensis_homolog_dn	dN
psinensis_homolog_ds	dS
cintestinalis_homolog_ensembl_gene	Ciona intestinalis Ensembl Gene ID
cintestinalis_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
cintestinalis_homolog_ensembl_peptide	Ciona intestinalis Ensembl Protein ID
cintestinalis_homolog_chromosome	Ciona intestinalis Chromosome Name
cintestinalis_homolog_chrom_start	Ciona intestinalis Chromosome Start (bp)
cintestinalis_homolog_chrom_end	Ciona intestinalis Chromosome End (bp)
cintestinalis_homolog_orthology_type	Homology Type
cintestinalis_homolog_subtype	Ancestor
cintestinalis_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
cintestinalis_homolog_perc_id	% Identity with respect to query gene
cintestinalis_homolog_perc_id_r1	% Identity with respect to Ciona intestinalis gene
cintestinalis_homolog_dn	dN
cintestinalis_homolog_ds	dS
csavignyi_homolog_ensembl_gene	Ciona savignyi Ensembl Gene ID
csavignyi_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
csavignyi_homolog_ensembl_peptide	Ciona savignyi Ensembl Protein ID
csavignyi_homolog_chromosome	Ciona savignyi Chromosome Name
csavignyi_homolog_chrom_start	Ciona savignyi Chromosome Start (bp)
csavignyi_homolog_chrom_end	Ciona savignyi Chromosome End (bp)
csavignyi_homolog_orthology_type	Homology Type
csavignyi_homolog_subtype	Ancestor
csavignyi_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
csavignyi_homolog_perc_id	% Identity with respect to query gene
csavignyi_homolog_perc_id_r1	% Identity with respect to Ciona savignyi gene
csavignyi_homolog_dn	dN
csavignyi_homolog_ds	dS
lchalumnae_homolog_ensembl_gene	Coelacanth Ensembl Gene ID
lchalumnae_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
lchalumnae_homolog_ensembl_peptide	Coelacanth Ensembl Protein ID

lchalumnae_homolog_chromosome	Coelacanth Chromosome Name
lchalumnae_homolog_chrom_start	Coelacanth Chromosome Start (bp)
lchalumnae_homolog_chrom_end	Coelacanth Chromosome End (bp)
lchalumnae_homolog_orthology_type	Homology Type
lchalumnae_homolog_subtype	Ancestor
lchalumnae_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
lchalumnae_homolog_perc_id	% Identity with respect to query gene
lchalumnae_homolog_perc_id_r1	% Identity with respect to Coelacanth gene
saraneus_homolog_ensembl_gene	Common Shrew Ensembl Gene ID
saraneus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
saraneus_homolog_ensembl_peptide	Common Shrew Ensembl Protein ID
saraneus_homolog_chromosome	Common Shrew Chromosome Name
saraneus_homolog_chrom_start	Common Shrew Chromosome Start (bp)
saraneus_homolog_chrom_end	Common Shrew Chromosome End (bp)
saraneus_homolog_orthology_type	Homology Type
saraneus_homolog_subtype	Ancestor
saraneus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
saraneus_homolog_perc_id	% Identity with respect to query gene
saraneus_homolog_perc_id_r1	% Identity with respect to Common Shrew gene
btaurus_homolog_ensembl_gene	Cow Ensembl Gene ID
btaurus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
btaurus_homolog_ensembl_peptide	Cow Ensembl Protein ID
btaurus_homolog_chromosome	Cow Chromosome Name
btaurus_homolog_chrom_start	Cow Chromosome Start (bp)
btaurus_homolog_chrom_end	Cow Chromosome End (bp)
btaurus_homolog_orthology_type	Homology Type
btaurus_homolog_subtype	Ancestor
btaurus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
btaurus_homolog_perc_id	% Identity with respect to query gene
btaurus_homolog_perc_id_r1	% Identity with respect to Cow gene
btaurus_homolog_dn	dN
btaurus_homolog_ds	dS
cfamiliaris_homolog_ensembl_gene	Dog Ensembl Gene ID
cfamiliaris_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
cfamiliaris_homolog_ensembl_peptide	Dog Ensembl Protein ID
cfamiliaris_homolog_chromosome	Dog Chromosome Name
cfamiliaris_homolog_chrom_start	Dog Chromosome Start (bp)
cfamiliaris_homolog_chrom_end	Dog Chromosome End (bp)
cfamiliaris_homolog_orthology_type	Homology Type
cfamiliaris_homolog_subtype	Ancestor
cfamiliaris_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]

cfamiliaris_homolog_perc_id	% Identity with respect to query gene
cfamiliaris_homolog_perc_id_r1	% Identity with respect to Dog gene
cfamiliaris_homolog_dn	dN
cfamiliaris_homolog_ds	dS
ttruncatus_homolog_ensembl_gene	Dolphin Ensembl Gene ID
ttruncatus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
ttruncatus_homolog_ensembl_peptide	Dolphin Ensembl Protein ID
ttruncatus_homolog_chromosome	Dolphin Chromosome Name
ttruncatus_homolog_chrom_start	Dolphin Chromosome Start (bp)
ttruncatus_homolog_chrom_end	Dolphin Chromosome End (bp)
ttruncatus_homolog_orthology_type	Homology Type
ttruncatus_homolog_subtype	Ancestor
ttruncatus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
ttruncatus_homolog_perc_id	% Identity with respect to query gene
ttruncatus_homolog_perc_id_r1	% Identity with respect to Dolphin gene
dmelanogaster_homolog_ensembl_gene	Drosophila Ensembl Gene ID
dmelanogaster_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
dmelanogaster_homolog_ensembl_peptide	Drosophila Ensembl Protein ID
dmelanogaster_homolog_chromosome	Drosophila Chromosome Name
dmelanogaster_homolog_chrom_start	Drosophila Chromosome Start (bp)
dmelanogaster_homolog_chrom_end	Drosophila Chromosome End (bp)
dmelanogaster_homolog_orthology_type	Homology Type
dmelanogaster_homolog_subtype	Ancestor
dmelanogaster_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
dmelanogaster_homolog_perc_id	% Identity with respect to query gene
dmelanogaster_homolog_perc_id_r1	% Identity with respect to Drosophila gene
dmelanogaster_homolog_dn	dN
dmelanogaster_homolog_ds	dS
aplatyrhynchos_homolog_ensembl_gene	Duck Ensembl Gene ID
aplatyrhynchos_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
aplatyrhynchos_homolog_ensembl_peptide	Duck Ensembl Protein ID
aplatyrhynchos_homolog_chromosome	Duck Chromosome Name
aplatyrhynchos_homolog_chrom_start	Duck Chromosome Start (bp)
aplatyrhynchos_homolog_chrom_end	Duck Chromosome End (bp)
aplatyrhynchos_homolog_orthology_type	Homology Type
aplatyrhynchos_homolog_subtype	Ancestor
aplatyrhynchos_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
aplatyrhynchos_homolog_perc_id	% Identity with respect to query gene
aplatyrhynchos_homolog_perc_id_r1	% Identity with respect to Duck gene
aplatyrhynchos_homolog_dn	dN
aplatyrhynchos_homolog_ds	dS

lafricana_homolog_ensembl_gene	Elephant Ensembl Gene ID
lafricana_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
lafricana_homolog_ensembl_peptide	Elephant Ensembl Protein ID
lafricana_homolog_chromosome	Elephant Chromosome Name
lafricana_homolog_chrom_start	Elephant Chromosome Start (bp)
lafricana_homolog_chrom_end	Elephant Chromosome End (bp)
lafricana_homolog_orthology_type	Homology Type
lafricana_homolog_subtype	Ancestor
lafricana_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
lafricana_homolog_perc_id	% Identity with respect to query gene
lafricana_homolog_perc_id_r1	% Identity with respect to Elephant gene
lafricana_homolog_dn	dN
lafricana_homolog_ds	dS
mfuro_homolog_ensembl_gene	Ferret Ensembl Gene ID
mfuro_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
mfuro_homolog_ensembl_peptide	Ferret Ensembl Protein ID
mfuro_homolog_chromosome	Ferret Chromosome Name
mfuro_homolog_chrom_start	Ferret Chromosome Start (bp)
mfuro_homolog_chrom_end	Ferret Chromosome End (bp)
mfuro_homolog_orthology_type	Homology Type
mfuro_homolog_subtype	Ancestor
mfuro_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
mfuro_homolog_perc_id	% Identity with respect to query gene
mfuro_homolog_perc_id_r1	% Identity with respect to Ferret gene
mfuro_homolog_dn	dN
mfuro_homolog_ds	dS
falbicollis_homolog_ensembl_gene	Flycatcher Ensembl Gene ID
falbicollis_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
falbicollis_homolog_ensembl_peptide	Flycatcher Ensembl Protein ID
falbicollis_homolog_chromosome	Flycatcher Chromosome Name
falbicollis_homolog_chrom_start	Flycatcher Chromosome Start (bp)
falbicollis_homolog_chrom_end	Flycatcher Chromosome End (bp)
falbicollis_homolog_orthology_type	Homology Type
falbicollis_homolog_subtype	Ancestor
falbicollis_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
falbicollis_homolog_perc_id	% Identity with respect to query gene
falbicollis_homolog_perc_id_r1	% Identity with respect to Flycatcher gene
falbicollis_homolog_dn	dN
falbicollis_homolog_ds	dS
trubripes_homolog_ensembl_gene	Fugu Ensembl Gene ID
trubripes_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID

trubripes_homolog_ensembl_peptide	Fugu Ensembl Protein ID
trubripes_homolog_chromosome	Fugu Chromosome Name
trubripes_homolog_chrom_start	Fugu Chromosome Start (bp)
trubripes_homolog_chrom_end	Fugu Chromosome End (bp)
trubripes_homolog_orthology_type	Homology Type
trubripes_homolog_subtype	Ancestor
trubripes_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
trubripes_homolog_perc_id	% Identity with respect to query gene
trubripes_homolog_perc_id_r1	% Identity with respect to Fugu gene
trubripes_homolog_dn	dN
trubripes_homolog_ds	dS
nleucogenys_homolog_ensembl_gene	Gibbon Ensembl Gene ID
nleucogenys_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
nleucogenys_homolog_ensembl_peptide	Gibbon Ensembl Protein ID
nleucogenys_homolog_chromosome	Gibbon Chromosome Name
nleucogenys_homolog_chrom_start	Gibbon Chromosome Start (bp)
nleucogenys_homolog_chrom_end	Gibbon Chromosome End (bp)
nleucogenys_homolog_orthology_type	Homology Type
nleucogenys_homolog_subtype	Ancestor
nleucogenys_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
nleucogenys_homolog_perc_id	% Identity with respect to query gene
nleucogenys_homolog_perc_id_r1	% Identity with respect to Gibbon gene
nleucogenys_homolog_dn	dN
nleucogenys_homolog_ds	dS
ggorilla_homolog_ensembl_gene	Gorilla Ensembl Gene ID
ggorilla_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
ggorilla_homolog_ensembl_peptide	Gorilla Ensembl Protein ID
ggorilla_homolog_chromosome	Gorilla Chromosome Name
ggorilla_homolog_chrom_start	Gorilla Chromosome Start (bp)
ggorilla_homolog_chrom_end	Gorilla Chromosome End (bp)
ggorilla_homolog_orthology_type	Homology Type
ggorilla_homolog_subtype	Ancestor
ggorilla_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
ggorilla_homolog_perc_id	% Identity with respect to query gene
ggorilla_homolog_perc_id_r1	% Identity with respect to Gorilla gene
ggorilla_homolog_dn	dN
ggorilla_homolog_ds	dS
cporcellus_homolog_ensembl_gene	Guinea Pig Ensembl Gene ID
cporcellus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
cporcellus_homolog_ensembl_peptide	Guinea Pig Ensembl Protein ID
cporcellus_homolog_chromosome	Guinea Pig Chromosome Name

cporcellus_homolog_chrom_start	Guinea Pig Chromosome Start (bp)
cporcellus_homolog_chrom_end	Guinea Pig Chromosome End (bp)
cporcellus_homolog_orthology_type	Homology Type
cporcellus_homolog_subtype	Ancestor
cporcellus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
cporcellus_homolog_perc_id	% Identity with respect to query gene
cporcellus_homolog_perc_id_r1	% Identity with respect to Guinea Pig gene
cporcellus_homolog_dn	dN
cporcellus_homolog_ds	dS
eeuropaeus_homolog_ensembl_gene	Hedgehog Ensembl Gene ID
eeuropaeus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
eeuropaeus_homolog_ensembl_peptide	Hedgehog Ensembl Protein ID
eeuropaeus_homolog_chromosome	Hedgehog Chromosome Name
eeuropaeus_homolog_chrom_start	Hedgehog Chromosome Start (bp)
eeuropaeus_homolog_chrom_end	Hedgehog Chromosome End (bp)
eeuropaeus_homolog_orthology_type	Homology Type
eeuropaeus_homolog_subtype	Ancestor
eeuropaeus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
eeuropaeus_homolog_perc_id	% Identity with respect to query gene
eeuropaeus_homolog_perc_id_r1	% Identity with respect to Hedgehog gene
ecaballus_homolog_ensembl_gene	Horse Ensembl Gene ID
ecaballus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
ecaballus_homolog_ensembl_peptide	Horse Ensembl Protein ID
ecaballus_homolog_chromosome	Horse Chromosome Name
ecaballus_homolog_chrom_start	Horse Chromosome Start (bp)
ecaballus_homolog_chrom_end	Horse Chromosome End (bp)
ecaballus_homolog_orthology_type	Homology Type
ecaballus_homolog_subtype	Ancestor
ecaballus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
ecaballus_homolog_perc_id	% Identity with respect to query gene
ecaballus_homolog_perc_id_r1	% Identity with respect to Horse gene
ecaballus_homolog_dn	dN
ecaballus_homolog_ds	dS
dordii_homolog_ensembl_gene	Kangaroo Rat Ensembl Gene ID
dordii_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
dordii_homolog_ensembl_peptide	Kangaroo Rat Ensembl Protein ID
dordii_homolog_chromosome	Kangaroo Rat Chromosome Name
dordii_homolog_chrom_start	Kangaroo Rat Chromosome Start (bp)
dordii_homolog_chrom_end	Kangaroo Rat Chromosome End (bp)
dordii_homolog_orthology_type	Homology Type
dordii_homolog_subtype	Ancestor

dordii_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
dordii_homolog_perc_id	% Identity with respect to query gene
dordii_homolog_perc_id_r1	% Identity with respect to Kangaroo Rat gene
pmarinus_homolog_ensembl_gene	Lamprey Ensembl Gene ID
pmarinus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
pmarinus_homolog_ensembl_peptide	Lamprey Ensembl Protein ID
pmarinus_homolog_chromosome	Lamprey Chromosome Name
pmarinus_homolog_chrom_start	Lamprey Chromosome Start (bp)
pmarinus_homolog_chrom_end	Lamprey Chromosome End (bp)
pmarinus_homolog_orthology_type	Homology Type
pmarinus_homolog_subtype	Ancestor
pmarinus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
pmarinus_homolog_perc_id	% Identity with respect to query gene
pmarinus_homolog_perc_id_r1	% Identity with respect to Lamprey gene
etelfairi_homolog_ensembl_gene	Lesser hedgehog tenrec Ensembl Gene ID
etelfairi_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
etelfairi_homolog_ensembl_peptide	Lesser hedgehog tenrec Ensembl Protein ID
etelfairi_homolog_chromosome	Lesser hedgehog tenrec Chromosome Name
etelfairi_homolog_chrom_start	Lesser hedgehog tenrec Chromosome Start (bp)
etelfairi_homolog_chrom_end	Lesser hedgehog tenrec Chromosome End (bp)
etelfairi_homolog_orthology_type	Homology Type
etelfairi_homolog_subtype	Ancestor
etelfairi_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
etelfairi_homolog_perc_id	% Identity with respect to query gene
etelfairi_homolog_perc_id_r1	% Identity with respect to Lesser hedgehog tenrec gene
mmulatta_homolog_ensembl_gene	Macaque Ensembl Gene ID
mmulatta_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
mmulatta_homolog_ensembl_peptide	Macaque Ensembl Protein ID
mmulatta_homolog_chromosome	Macaque Chromosome Name
mmulatta_homolog_chrom_start	Macaque Chromosome Start (bp)
mmulatta_homolog_chrom_end	Macaque Chromosome End (bp)
mmulatta_homolog_orthology_type	Homology Type
mmulatta_homolog_subtype	Ancestor
mmulatta_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
mmulatta_homolog_perc_id	% Identity with respect to query gene
mmulatta_homolog_perc_id_r1	% Identity with respect to Macaque gene
mmulatta_homolog_dn	dN
mmulatta_homolog_ds	dS
cjacchus_homolog_ensembl_gene	Marmoset Ensembl Gene ID
cjacchus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
cjacchus_homolog_ensembl_peptide	Marmoset Ensembl Protein ID

cjacchus_homolog_chromosome	Marmoset Chromosome Name
cjacchus_homolog_chrom_start	Marmoset Chromosome Start (bp)
cjacchus_homolog_chrom_end	Marmoset Chromosome End (bp)
cjacchus_homolog_orthology_type	Homology Type
cjacchus_homolog_subtype	Ancestor
cjacchus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
cjacchus_homolog_perc_id	% Identity with respect to query gene
cjacchus_homolog_perc_id_r1	% Identity with respect to Marmoset gene
cjacchus_homolog_dn	dN
cjacchus_homolog_ds	dS
olatipes_homolog_ensembl_gene	Medaka Ensembl Gene ID
olatipes_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
olatipes_homolog_ensembl_peptide	Medaka Ensembl Protein ID
olatipes_homolog_chromosome	Medaka Chromosome Name
olatipes_homolog_chrom_start	Medaka Chromosome Start (bp)
olatipes_homolog_chrom_end	Medaka Chromosome End (bp)
olatipes_homolog_orthology_type	Homology Type
olatipes_homolog_subtype	Ancestor
olatipes_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
olatipes_homolog_perc_id	% Identity with respect to query gene
olatipes_homolog_perc_id_r1	% Identity with respect to Medaka gene
olatipes_homolog_dn	dN
olatipes_homolog_ds	dS
pvampyrus_homolog_ensembl_gene	Megabat Ensembl Gene ID
pvampyrus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
pvampyrus_homolog_ensembl_peptide	Megabat Ensembl Protein ID
pvampyrus_homolog_chromosome	Megabat Chromosome Name
pvampyrus_homolog_chrom_start	Megabat Chromosome Start (bp)
pvampyrus_homolog_chrom_end	Megabat Chromosome End (bp)
pvampyrus_homolog_orthology_type	Homology Type
pvampyrus_homolog_subtype	Ancestor
pvampyrus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
pvampyrus_homolog_perc_id	% Identity with respect to query gene
pvampyrus_homolog_perc_id_r1	% Identity with respect to Megabat gene
mlucifugus_homolog_ensembl_gene	Microbat Ensembl Gene ID
mlucifugus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
mlucifugus_homolog_ensembl_peptide	Microbat Ensembl Protein ID
mlucifugus_homolog_chromosome	Microbat Chromosome Name
mlucifugus_homolog_chrom_start	Microbat Chromosome Start (bp)
mlucifugus_homolog_chrom_end	Microbat Chromosome End (bp)
mlucifugus_homolog_orthology_type	Homology Type

mlucifugus_homolog_subtype	Ancestor
mlucifugus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
mlucifugus_homolog_perc_id	% Identity with respect to query gene
mlucifugus_homolog_perc_id_r1	% Identity with respect to Microbat gene
mlucifugus_homolog_dn	dN
mlucifugus_homolog_ds	dS
mmusculus_homolog_ensembl_gene	Mouse Ensembl Gene ID
mmusculus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
mmusculus_homolog_ensembl_peptide	Mouse Ensembl Protein ID
mmusculus_homolog_chromosome	Mouse Chromosome Name
mmusculus_homolog_chrom_start	Mouse Chromosome Start (bp)
mmusculus_homolog_chrom_end	Mouse Chromosome End (bp)
mmusculus_homolog_orthology_type	Homology Type
mmusculus_homolog_subtype	Ancestor
mmusculus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
mmusculus_homolog_perc_id	% Identity with respect to query gene
mmusculus_homolog_perc_id_r1	% Identity with respect to Mouse gene
mmusculus_homolog_dn	dN
mmusculus_homolog_ds	dS
mmurinus_homolog_ensembl_gene	Mouse Lemur Ensembl Gene ID
mmurinus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
mmurinus_homolog_ensembl_peptide	Mouse Lemur Ensembl Protein ID
mmurinus_homolog_chromosome	Mouse Lemur Chromosome Name
mmurinus_homolog_chrom_start	Mouse Lemur Chromosome Start (bp)
mmurinus_homolog_chrom_end	Mouse Lemur Chromosome End (bp)
mmurinus_homolog_orthology_type	Homology Type
mmurinus_homolog_subtype	Ancestor
mmurinus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
mmurinus_homolog_perc_id	% Identity with respect to query gene
mmurinus_homolog_perc_id_r1	% Identity with respect to Mouse Lemur gene
oniloticus_homolog_ensembl_gene	Nile tilapia Ensembl Gene ID
oniloticus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
oniloticus_homolog_ensembl_peptide	Nile tilapia Ensembl Protein ID
oniloticus_homolog_chromosome	Nile tilapia Chromosome Name
oniloticus_homolog_chrom_start	Nile tilapia Chromosome Start (bp)
oniloticus_homolog_chrom_end	Nile tilapia Chromosome End (bp)
oniloticus_homolog_orthology_type	Homology Type
oniloticus_homolog_subtype	Ancestor
oniloticus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
oniloticus_homolog_perc_id	% Identity with respect to query gene
oniloticus_homolog_perc_id_r1	% Identity with respect to Nile tilapia gene

panubis_homolog_ensembl_gene	Olive baboon Ensembl Gene ID
panubis_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
panubis_homolog_ensembl_peptide	Olive baboon Ensembl Protein ID
panubis_homolog_chromosome	Olive baboon Chromosome Name
panubis_homolog_chrom_start	Olive baboon Chromosome Start (bp)
panubis_homolog_chrom_end	Olive baboon Chromosome End (bp)
panubis_homolog_orthology_type	Homology Type
panubis_homolog_subtype	Ancestor
panubis_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
panubis_homolog_perc_id	% Identity with respect to query gene
panubis_homolog_perc_id_r1	% Identity with respect to Olive baboon gene
panubis_homolog_dn	dN
panubis_homolog_ds	dS
mdomestica_homolog_ensembl_gene	Opossum Ensembl Gene ID
mdomestica_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
mdomestica_homolog_ensembl_peptide	Opossum Ensembl Protein ID
mdomestica_homolog_chromosome	Opossum Chromosome Name
mdomestica_homolog_chrom_start	Opossum Chromosome Start (bp)
mdomestica_homolog_chrom_end	Opossum Chromosome End (bp)
mdomestica_homolog_orthology_type	Homology Type
mdomestica_homolog_subtype	Ancestor
mdomestica_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
mdomestica_homolog_perc_id	% Identity with respect to query gene
mdomestica_homolog_perc_id_r1	% Identity with respect to Opossum gene
mdomestica_homolog_dn	dN
mdomestica_homolog_ds	dS
pabelii_homolog_ensembl_gene	Orangutan Ensembl Gene ID
pabelii_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
pabelii_homolog_ensembl_peptide	Orangutan Ensembl Protein ID
pabelii_homolog_chromosome	Orangutan Chromosome Name
pabelii_homolog_chrom_start	Orangutan Chromosome Start (bp)
pabelii_homolog_chrom_end	Orangutan Chromosome End (bp)
pabelii_homolog_orthology_type	Homology Type
pabelii_homolog_subtype	Ancestor
pabelii_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
pabelii_homolog_perc_id	% Identity with respect to query gene
pabelii_homolog_perc_id_r1	% Identity with respect to Orangutan gene
pabelii_homolog_dn	dN
pabelii_homolog_ds	dS
amelanoleuca_homolog_ensembl_gene	Panda Ensembl Gene ID
amelanoleuca_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID

amelanoleuca_homolog_ensembl_peptide	Panda Ensembl Protein ID
amelanoleuca_homolog_chromosome	Panda Chromosome Name
amelanoleuca_homolog_chrom_start	Panda Chromosome Start (bp)
amelanoleuca_homolog_chrom_end	Panda Chromosome End (bp)
amelanoleuca_homolog_orthology_type	Homology Type
amelanoleuca_homolog_subtype	Ancestor
amelanoleuca_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
amelanoleuca_homolog_perc_id	% Identity with respect to query gene
amelanoleuca_homolog_perc_id_r1	% Identity with respect to Panda gene
amelanoleuca_homolog_dn	dN
amelanoleuca_homolog_ds	dS
sscrofa_homolog_ensembl_gene	Pig Ensembl Gene ID
sscrofa_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
sscrofa_homolog_ensembl_peptide	Pig Ensembl Protein ID
sscrofa_homolog_chromosome	Pig Chromosome Name
sscrofa_homolog_chrom_start	Pig Chromosome Start (bp)
sscrofa_homolog_chrom_end	Pig Chromosome End (bp)
sscrofa_homolog_orthology_type	Homology Type
sscrofa_homolog_subtype	Ancestor
sscrofa_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
sscrofa_homolog_perc_id	% Identity with respect to query gene
sscrofa_homolog_perc_id_r1	% Identity with respect to Pig gene
sscrofa_homolog_dn	dN
sscrofa_homolog_ds	dS
oprinceps_homolog_ensembl_gene	Pika Ensembl Gene ID
oprinceps_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
oprinceps_homolog_ensembl_peptide	Pika Ensembl Protein ID
oprinceps_homolog_chromosome	Pika Chromosome Name
oprinceps_homolog_chrom_start	Pika Chromosome Start (bp)
oprinceps_homolog_chrom_end	Pika Chromosome End (bp)
oprinceps_homolog_orthology_type	Homology Type
oprinceps_homolog_subtype	Ancestor
oprinceps_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
oprinceps_homolog_perc_id	% Identity with respect to query gene
oprinceps_homolog_perc_id_r1	% Identity with respect to Pika gene
xmaculatus_homolog_ensembl_gene	Platyfish Ensembl Gene ID
xmaculatus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
xmaculatus_homolog_ensembl_peptide	Platyfish Ensembl Protein ID
xmaculatus_homolog_chromosome	Platyfish Chromosome Name
xmaculatus_homolog_chrom_start	Platyfish Chromosome Start (bp)
xmaculatus_homolog_chrom_end	Platyfish Chromosome End (bp)

xmaculatus_homolog_orthology_type	Homology Type
xmaculatus_homolog_subtype	Ancestor
xmaculatus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
xmaculatus_homolog_perc_id	% Identity with respect to query gene
xmaculatus_homolog_perc_id_r1	% Identity with respect to Platyfish gene
oanatinus_homolog_ensembl_gene	Platypus Ensembl Gene ID
oanatinus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
oanatinus_homolog_ensembl_peptide	Platypus Ensembl Protein ID
oanatinus_homolog_chromosome	Platypus Chromosome Name
oanatinus_homolog_chrom_start	Platypus Chromosome Start (bp)
oanatinus_homolog_chrom_end	Platypus Chromosome End (bp)
oanatinus_homolog_orthology_type	Homology Type
oanatinus_homolog_subtype	Ancestor
oanatinus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
oanatinus_homolog_perc_id	% Identity with respect to query gene
oanatinus_homolog_perc_id_r1	% Identity with respect to Platypus gene
oanatinus_homolog_dn	dN
oanatinus_homolog_ds	dS
ocuniculus_homolog_ensembl_gene	Rabbit Ensembl Gene ID
ocuniculus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
ocuniculus_homolog_ensembl_peptide	Rabbit Ensembl Protein ID
ocuniculus_homolog_chromosome	Rabbit Chromosome Name
ocuniculus_homolog_chrom_start	Rabbit Chromosome Start (bp)
ocuniculus_homolog_chrom_end	Rabbit Chromosome End (bp)
ocuniculus_homolog_orthology_type	Homology Type
ocuniculus_homolog_subtype	Ancestor
ocuniculus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
ocuniculus_homolog_perc_id	% Identity with respect to query gene
ocuniculus_homolog_perc_id_r1	% Identity with respect to Rabbit gene
ocuniculus_homolog_dn	dN
ocuniculus_homolog_ds	dS
rnorvegicus_homolog_ensembl_gene	Rat Ensembl Gene ID
rnorvegicus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
rnorvegicus_homolog_ensembl_peptide	Rat Ensembl Protein ID
rnorvegicus_homolog_chromosome	Rat Chromosome Name
rnorvegicus_homolog_chrom_start	Rat Chromosome Start (bp)
rnorvegicus_homolog_chrom_end	Rat Chromosome End (bp)
rnorvegicus_homolog_orthology_type	Homology Type
rnorvegicus_homolog_subtype	Ancestor
rnorvegicus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
rnorvegicus_homolog_perc_id	% Identity with respect to query gene

rnorvegicus_homolog_perc_id_r1	% Identity with respect to Rat gene
rnorvegicus_homolog_dn	dN
rnorvegicus_homolog_ds	dS
pcapensis_homolog_ensembl_gene	Rock Hyrax Ensembl Gene ID
pcapensis_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
pcapensis_homolog_ensembl_peptide	Rock Hyrax Ensembl Protein ID
pcapensis_homolog_chromosome	Rock Hyrax Chromosome Name
pcapensis_homolog_chrom_start	Rock Hyrax Chromosome Start (bp)
pcapensis_homolog_chrom_end	Rock Hyrax Chromosome End (bp)
pcapensis_homolog_orthology_type	Homology Type
pcapensis_homolog_subtype	Ancestor
pcapensis_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
pcapensis_homolog_perc_id	% Identity with respect to query gene
pcapensis_homolog_perc_id_r1	% Identity with respect to Rock Hyrax gene
oaries_homolog_ensembl_gene	Sheep Ensembl Gene ID
oaries_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
oaries_homolog_ensembl_peptide	Sheep Ensembl Protein ID
oaries_homolog_chromosome	Sheep Chromosome Name
oaries_homolog_chrom_start	Sheep Chromosome Start (bp)
oaries_homolog_chrom_end	Sheep Chromosome End (bp)
oaries_homolog_orthology_type	Homology Type
oaries_homolog_subtype	Ancestor
oaries_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
oaries_homolog_perc_id	% Identity with respect to query gene
oaries_homolog_perc_id_r1	% Identity with respect to Sheep gene
oaries_homolog_dn	dN
oaries_homolog_ds	dS
choffmanni_homolog_ensembl_gene	Sloth Ensembl Gene ID
choffmanni_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
choffmanni_homolog_ensembl_peptide	Sloth Ensembl Protein ID
choffmanni_homolog_chromosome	Sloth Chromosome Name
choffmanni_homolog_chrom_start	Sloth Chromosome Start (bp)
choffmanni_homolog_chrom_end	Sloth Chromosome End (bp)
choffmanni_homolog_orthology_type	Homology Type
choffmanni_homolog_subtype	Ancestor
choffmanni_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
choffmanni_homolog_perc_id	% Identity with respect to query gene
choffmanni_homolog_perc_id_r1	% Identity with respect to Sloth gene
loculatus_homolog_ensembl_gene	Spotted gar Ensembl Gene ID
loculatus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
loculatus_homolog_ensembl_peptide	Spotted gar Ensembl Protein ID

loculatus_homolog_chromosome	Spotted gar Chromosome Name
loculatus_homolog_chrom_start	Spotted gar Chromosome Start (bp)
loculatus_homolog_chrom_end	Spotted gar Chromosome End (bp)
loculatus_homolog_orthology_type	Homology Type
loculatus_homolog_subtype	Ancestor
loculatus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
loculatus_homolog_perc_id	% Identity with respect to query gene
loculatus_homolog_perc_id_r1	% Identity with respect to Spotted gar gene
itridecemlineatus_homolog_ensembl_gene	Squirrel Ensembl Gene ID
itridecemlineatus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
itridecemlineatus_homolog_ensembl_peptide	Squirrel Ensembl Protein ID
itridecemlineatus_homolog_chromosome	Squirrel Chromosome Name
itridecemlineatus_homolog_chrom_start	Squirrel Chromosome Start (bp)
itridecemlineatus_homolog_chrom_end	Squirrel Chromosome End (bp)
itridecemlineatus_homolog_orthology_type	Homology Type
itridecemlineatus_homolog_subtype	Ancestor
itridecemlineatus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
itridecemlineatus_homolog_perc_id	% Identity with respect to query gene
itridecemlineatus_homolog_perc_id_r1	% Identity with respect to Squirrel gene
itridecemlineatus_homolog_dn	dN
itridecemlineatus_homolog_ds	dS
gaculeatus_homolog_ensembl_gene	Stickleback Ensembl Gene ID
gaculeatus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
gaculeatus_homolog_ensembl_peptide	Stickleback Ensembl Protein ID
gaculeatus_homolog_chromosome	Stickleback Chromosome Name
gaculeatus_homolog_chrom_start	Stickleback Chromosome Start (bp)
gaculeatus_homolog_chrom_end	Stickleback Chromosome End (bp)
gaculeatus_homolog_orthology_type	Homology Type
gaculeatus_homolog_subtype	Ancestor
gaculeatus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
gaculeatus_homolog_perc_id	% Identity with respect to query gene
gaculeatus_homolog_perc_id_r1	% Identity with respect to Stickleback gene
gaculeatus_homolog_dn	dN
gaculeatus_homolog_ds	dS
tsyrichta_homolog_ensembl_gene	Tarsier Ensembl Gene ID
tsyrichta_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
tsyrichta_homolog_ensembl_peptide	Tarsier Ensembl Protein ID
tsyrichta_homolog_chromosome	Tarsier Chromosome Name
tsyrichta_homolog_chrom_start	Tarsier Chromosome Start (bp)
tsyrichta_homolog_chrom_end	Tarsier Chromosome End (bp)
tsyrichta_homolog_orthology_type	Homology Type

tsyrichta_homolog_subtype	Ancestor
tsyrichta_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
tsyrichta_homolog_perc_id	% Identity with respect to query gene
tsyrichta_homolog_perc_id_r1	% Identity with respect to Tarsier gene
sharrisii_homolog_ensembl_gene	Tasmanian Devil Ensembl Gene ID
sharrisii_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
sharrisii_homolog_ensembl_peptide	Tasmanian Devil Ensembl Protein ID
sharrisii_homolog_chromosome	Tasmanian Devil Chromosome Name
sharrisii_homolog_chrom_start	Tasmanian Devil Chromosome Start (bp)
sharrisii_homolog_chrom_end	Tasmanian Devil Chromosome End (bp)
sharrisii_homolog_orthology_type	Homology Type
sharrisii_homolog_subtype	Ancestor
sharrisii_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
sharrisii_homolog_perc_id	% Identity with respect to query gene
sharrisii_homolog_perc_id_r1	% Identity with respect to Tasmanian Devil gene
sharrisii_homolog_dn	dN
sharrisii_homolog_ds	dS
tnigroviridis_homolog_ensembl_gene	Tetraodon Ensembl Gene ID
tnigroviridis_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
tnigroviridis_homolog_ensembl_peptide	Tetraodon Ensembl Protein ID
tnigroviridis_homolog_chromosome	Tetraodon Chromosome Name
tnigroviridis_homolog_chrom_start	Tetraodon Chromosome Start (bp)
tnigroviridis_homolog_chrom_end	Tetraodon Chromosome End (bp)
tnigroviridis_homolog_orthology_type	Homology Type
tnigroviridis_homolog_subtype	Ancestor
tnigroviridis_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
tnigroviridis_homolog_perc_id	% Identity with respect to query gene
tnigroviridis_homolog_perc_id_r1	% Identity with respect to Tetraodon gene
tnigroviridis_homolog_dn	dN
tnigroviridis_homolog_ds	dS
tbelangeri_homolog_ensembl_gene	Tree Shrew Ensembl Gene ID
tbelangeri_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
tbelangeri_homolog_ensembl_peptide	Tree Shrew Ensembl Protein ID
tbelangeri_homolog_chromosome	Tree Shrew Chromosome Name
tbelangeri_homolog_chrom_start	Tree Shrew Chromosome Start (bp)
tbelangeri_homolog_chrom_end	Tree Shrew Chromosome End (bp)
tbelangeri_homolog_orthology_type	Homology Type
tbelangeri_homolog_subtype	Ancestor
tbelangeri_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
tbelangeri_homolog_perc_id	% Identity with respect to query gene
tbelangeri_homolog_perc_id_r1	% Identity with respect to Tree Shrew gene

mgallopavo_homolog_ensembl_gene	Turkey Ensembl Gene ID
mgallopavo_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
mgallopavo_homolog_ensembl_peptide	Turkey Ensembl Protein ID
mgallopavo_homolog_chromosome	Turkey Chromosome Name
mgallopavo_homolog_chrom_start	Turkey Chromosome Start (bp)
mgallopavo_homolog_chrom_end	Turkey Chromosome End (bp)
mgallopavo_homolog_orthology_type	Homology Type
mgallopavo_homolog_subtype	Ancestor
mgallopavo_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
mgallopavo_homolog_perc_id	% Identity with respect to query gene
mgallopavo_homolog_perc_id_r1	% Identity with respect to Turkey gene
mgallopavo_homolog_dn	dN
mgallopavo_homolog_ds	dS
csabaeus_homolog_ensembl_gene	Vervet-AGM Ensembl Gene ID
csabaeus_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
csabaeus_homolog_ensembl_peptide	Vervet-AGM Ensembl Protein ID
csabaeus_homolog_chromosome	Vervet-AGM Chromosome Name
csabaeus_homolog_chrom_start	Vervet-AGM Chromosome Start (bp)
csabaeus_homolog_chrom_end	Vervet-AGM Chromosome End (bp)
csabaeus_homolog_orthology_type	Homology Type
csabaeus_homolog_subtype	Ancestor
csabaeus_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
csabaeus_homolog_perc_id	% Identity with respect to query gene
csabaeus_homolog_perc_id_r1	% Identity with respect to Vervet-AGM gene
csabaeus_homolog_dn	dN
csabaeus_homolog_ds	dS
meugenii_homolog_ensembl_gene	Wallaby Ensembl Gene ID
meugenii_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
meugenii_homolog_ensembl_peptide	Wallaby Ensembl Protein ID
meugenii_homolog_chromosome	Wallaby Chromosome Name
meugenii_homolog_chrom_start	Wallaby Chromosome Start (bp)
meugenii_homolog_chrom_end	Wallaby Chromosome End (bp)
meugenii_homolog_orthology_type	Homology Type
meugenii_homolog_subtype	Ancestor
meugenii_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
meugenii_homolog_perc_id	% Identity with respect to query gene
meugenii_homolog_perc_id_r1	% Identity with respect to Wallaby gene
xtropicalis_homolog_ensembl_gene	Xenopus Ensembl Gene ID
xtropicalis_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
xtropicalis_homolog_ensembl_peptide	Xenopus Ensembl Protein ID
xtropicalis_homolog_chromosome	Xenopus Chromosome Name

xtropicalis_homolog_chrom_start	Xenopus Chromosome Start (bp)
xtropicalis_homolog_chrom_end	Xenopus Chromosome End (bp)
xtropicalis_homolog_orthology_type	Homology Type
xtropicalis_homolog_subtype	Ancestor
xtropicalis_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
xtropicalis_homolog_perc_id	% Identity with respect to query gene
xtropicalis_homolog_perc_id_r1	% Identity with respect to Xenopus gene
xtropicalis_homolog_dn	dN
xtropicalis_homolog_ds	dS
scerevisiae_homolog_ensembl_gene	Yeast Ensembl Gene ID
scerevisiae_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
scerevisiae_homolog_ensembl_peptide	Yeast Ensembl Protein ID
scerevisiae_homolog_chromosome	Yeast Chromosome Name
scerevisiae_homolog_chrom_start	Yeast Chromosome Start (bp)
scerevisiae_homolog_chrom_end	Yeast Chromosome End (bp)
scerevisiae_homolog_orthology_type	Homology Type
scerevisiae_homolog_subtype	Ancestor
scerevisiae_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
scerevisiae_homolog_perc_id	% Identity with respect to query gene
scerevisiae_homolog_perc_id_r1	% Identity with respect to Yeast gene
scerevisiae_homolog_dn	dN
scerevisiae_homolog_ds	dS
tguttata_homolog_ensembl_gene	Zebra Finch Ensembl Gene ID
tguttata_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
tguttata_homolog_ensembl_peptide	Zebra Finch Ensembl Protein ID
tguttata_homolog_chromosome	Zebra Finch Chromosome Name
tguttata_homolog_chrom_start	Zebra Finch Chromosome Start (bp)
tguttata_homolog_chrom_end	Zebra Finch Chromosome End (bp)
tguttata_homolog_orthology_type	Homology Type
tguttata_homolog_subtype	Ancestor
tguttata_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
tguttata_homolog_perc_id	% Identity with respect to query gene
tguttata_homolog_perc_id_r1	% Identity with respect to Zebra Finch gene
tguttata_homolog_dn	dN
tguttata_homolog_ds	dS
drerio_homolog_ensembl_gene	Zebrafish Ensembl Gene ID
drerio_homolog_canonical_transcript_protein	Canonical Protein or Transcript ID
drerio_homolog_ensembl_peptide	Zebrafish Ensembl Protein ID
drerio_homolog_chromosome	Zebrafish Chromosome Name
drerio_homolog_chrom_start	Zebrafish Chromosome Start (bp)
drerio_homolog_chrom_end	Zebrafish Chromosome End (bp)

drerio_homolog_orthology_type	Homology Type
drerio_homolog_subtype	Ancestor
drerio_homolog_orthology_confidence	Orthology confidence [0 low, 1 high]
drerio_homolog_perc_id	% Identity with respect to query gene
drerio_homolog_perc_id_r1	% Identity with respect to Zebrafish gene
drerio_homolog_dn	dN
drerio_homolog_ds	dS
hsapiens_paralog_ensembl_gene	Human Paralog Ensembl Gene ID
hsapiens_paralog_canonical_transcript_protein	Canonical Protein or Transcript ID
hsapiens_paralog_ensembl_peptide	Human Paralog Ensembl Protein ID
hsapiens_paralog_chromosome	Human Paralog Chromosome Name
hsapiens_paralog_chrom_start	Human Paralog Chr Start (bp)
hsapiens_paralog_chrom_end	Human Paralog Chr End (bp)
hsapiens_paralog_orthology_type	Homology Type
hsapiens_paralog_subtype	Ancestor
hsapiens_paralog_paralogy_confidence	Paralogy confidence [0 low, 1 high]
hsapiens_paralog_perc_id	% Identity with respect to query gene
hsapiens_paralog_perc_id_r1	% Identity with respect to Human gene
hsapiens_paralog_dn	dN
hsapiens_paralog_ds	dS
ensembl_gene_id	Ensembl Gene ID
ensembl_transcript_id	Ensembl Transcript ID
ensembl_peptide_id	Ensembl Protein ID
chromosome_name	Chromosome Name
start_position	Gene Start (bp)
end_position	Gene End (bp)
strand	Strand
band	Band
external_gene_name	Associated Gene Name
external_gene_source	Associated Gene Source
transcript_count	Transcript count
percentage_gc_content	% GC content
description	Description
variation_name	Variation Name
germ_line_variation_source	Variation Source
source_description	Variation source description
allele	Variant Alleles
validated	Evidence status
mapweight	Mapweight
minor_allele	Minor allele
minor_allele_freq	Minor allele frequency

minor_allele_count	Minor allele count
clinical_significance	Clinical significance
transcript_location	Transcript location (bp)
snp_chromosome_strand	Variation Chromosome Strand
peptide_location	Protein location (aa)
chromosome_location	Chromosome Location (bp)
polyphen_prediction_2076	PolyPhen prediction
polyphen_score_2076	PolyPhen score
sift_prediction_2076	SIFT prediction
sift_score_2076	SIFT score
distance_to_transcript_2076	Distance to transcript
cds_start_2076	CDS Start
cds_end_2076	CDS End
peptide_shift	Protein Allele
synonymous_status	Consequence Type (Transcript Variation)
allele_string_2076	Consequence specific allele
somatic_variation_name	Variation Name
somatic_source_name	Variation Source
somatic_source_description	Variation source description
somatic_allele	Variant Alleles
somatic_validated	Evidence status
somatic_mapweight	Mapweight
somatic_minor_allele	Minor allele
somatic_minor_allele_freq	Minor allele frequency
somatic_minor_allele_count	Minor allele count
somatic_clinical_significance	Clinical significance
somatic_transcript_location	Transcript location (bp)
somatic_snp_chromosome_strand	Variation Chromosome Strand
somatic_peptide_location	Protein location (aa)
somatic_chromosome_location	Chromosome Location (bp)
mart_transcript_variation_som__dm_polyphen_prediction_2076	PolyPhen prediction
mart_transcript_variation_som__dm_polyphen_score_2076	PolyPhen score
mart_transcript_variation_som__dm_sift_prediction_2076	SIFT prediction
mart_transcript_variation_som__dm_sift_score_2076	SIFT score
mart_transcript_variation_som__dm_distance_to_transcript_2076	Distance to transcript
somatic_cds_start_2076	CDS Start
somatic_cds_end_2076	CDS End
somatic_peptide_shift	Protein Allele
somatic_synonymous_status	Consequence Type (Transcript Variation)

mart_transcript_variation_som__dm_allele_string_2076	Consequence specific allele
transcript_exon_intron	Unspliced (Transcript)
gene_exon_intron	Unspliced (Gene)
transcript_flank	Flank (Transcript)
gene_flank	Flank (Gene)
coding_transcript_flank	Flank-coding region (Transcript)
coding_gene_flank	Flank-coding region (Gene)
5utr	5' UTR
3utr	3' UTR
gene_exon	Exon sequences
cdna	cDNA sequences
coding	Coding sequence
peptide	Protein
upstream_flank	upstream_flank
downstream_flank	downstream_flank
ensembl_gene_id	Ensembl Gene ID
description	Description
external_gene_name	Associated Gene Name
external_gene_source	Associated Gene Source
chromosome_name	Chromosome Name
start_position	Gene Start (bp)
end_position	Gene End (bp)
gene_biotype	Gene type
family	Ensembl Protein Family ID(s)
cdna_coding_start	CDS start (within cDNA)
cdna_coding_end	CDS end (within cDNA)
5_utr_start	5' UTR Start
5_utr_end	5' UTR End
3_utr_start	3' UTR Start
3_utr_end	3' UTR End
ensembl_transcript_id	Ensembl Transcript ID
ensembl_peptide_id	Ensembl Protein ID
transcript_biotype	Transcript type
strand	Strand
transcript_start	Transcript Start (bp)
transcript_end	Transcript End (bp)
transcription_start_site	Transcription Start Site (TSS)
transcript_length	Transcript length
cds_length	CDS Length
cds_start	CDS Start
cds_end	CDS End

ensembl_exon_id	Ensembl Exon ID
exon_chrom_start	Exon Chr Start (bp)
exon_chrom_end	Exon Chr End (bp)
strand	Strand
rank	Exon Rank in Transcript
phase	phase
cdna_coding_start	cDNA coding start
cdna_coding_end	cDNA coding end
genomic_coding_start	Genomic coding start
genomic_coding_end	Genomic coding end
is_constitutive	Constitutive Exon