

The design of the feature table in xlsx format refers to the TBL in text format from [NCBI](#). Consistent with TBL, xlsx's annotation of sequences follows the INSDC standard. Users can get tips from different feature and qualifier combinations in the table, including examples, formats and their definitions.

## Locations

- 1) Chr.
  - Header of each sequence, starting with the **Feature** field
- 2) Start and end.
  - Start and end coordinates of each feature in the sequence
  - Coordinate should be a value of integer type
  - If the end is greater than the starting coordinate, the feature is considered to be located in the **reverse strand** of the sequence
- 3) Completeness
  - Whether the feature is complete. For example, if it is a coding gene, all CDS features of the gene should be divided by 3.
  - If incomplete, mark the incomplete direction, 5', 3', or both ends.

## Attributes

- 4) Feature
  - Name of feature within the coordinate range.
  - All available features are listed in the drop-down box.
  - For the feature name within the coordinate range, we suggest that each coding locus should have **[gene]** features as the basic unit, even if the feature can be omitted in some cases.
  - If the feature has more than one qualifier, the feature column **should be empty** when these qualifiers are listed under the feature, which indicates that these qualifiers belong to the same feature block.
- 5) Qualifier
  - Annotations for multiple dimensions of the feature
  - All available qualifiers of this feature are listed in the drop-down box after selecting the corresponding feature.
  - We hope you can describe the characteristics of this locus in as much detail as possible, even though this position can sometimes be omitted.
  - When there is more than one qualifier, all qualifiers should be listed **below the line declaring the feature**, and the feature column on the left should be empty.
- 6) Qualifier value
  - After declaring the corresponding qualifier, the user should fill in the specific contents of the qualifier
  - The user can be prompted in **qualifier hints** for the filling specification and definition of this value.

## Qualifier hints

- 7) Type and example
  - For each qualifier, qualifier hints give written suggestions including examples, formats and definitions according to the INSDC standard.

- [Qualifier hints] are only used for type hints. No matter what its content is, it **will not affect** the format verification and conversion of xlsx

definition	feature	qualifiers	type	comment
1) region at the 3' end of a mature transcript (following the stop codon) that is not translated into a protein; 2) region at the 3' end of an RNA virus (following the last stop codon) that is not translated into a protein;	<b>3'UTR</b>	allele	text	
		citation	[number]	
		db_xref	<database>:<identifier>	
		experiment	[CATEGORY:]text	
		function	text	
		gene	text	
		gene_synonym	text	
		inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	Na
		locus_tag	text (single token)	
		map	text	
		note	text	
		old_locus_tag	text (single token)	
		standard_name	text	
		trans_splicing	boolean	
1) region at the 5' end of a mature transcript (preceding the initiation codon) that is not translated into a protein; 2) region at the 5' end of an RNA virus genome (preceding the first initiation codon) that is not translated into a protein;	<b>5'UTR</b>	allele	text	
		citation	[number]	
		db_xref	<database>:<identifier>	
		experiment	[CATEGORY:]text	
		function	text	
		gene	text	
		gene_synonym	text	
		inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	NA
		locus_tag	text (single token)	
		map	text	
		note	text	
		old_locus_tag	text (single token)	
		standard_name	text	
		trans_splicing	boolean	
coding sequence; sequence of nucleotides that corresponds with the sequence of amino acids in a protein (location includes stop codon); feature includes amino acid	<b>CDS</b>	allele	text	/codon_start has valid value of 1 or 2 or 3, indicating the offset at which the first complete codon of a coding feature can be found, relative to the first base of that feature; /transl_table defines the genetic code table used if other than the universal genetic code table; genetic code exceptions outside the range of the specified tables is reported in
		artificial_location	[artificial_location_value]	
		circular_RNA	boolean	
		citation	[number]	
		codon_start	<1 or 2 or 3>	
		db_xref	<database>:<identifier>	
		EC_number	text	
		exception	[exception_value]	
		experiment	[CATEGORY:]text	
		function	text	
		gene	text	

conceptual translation.	gene_synonym	text	/transl_except qualifier;
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	/protein_id consists of a stable ID portion (from the end of 2018 new accessions may be extended to a 3+7 accession format with 3 position letters and 7 numbers; existing data before the end of 2018 uses a 3+5 format) plus a version number after the decimal point; when the protein sequence encoded by the CDS changes, only the version number of the /protein_id value is incremented; the stable part of the /protein_id remains unchanged and as a result will permanently be associated with a given protein;
	locus_tag	text (single token)	
	map	text	
	note	text	
	number	unquoted text (single token)	
	old_locus_tag	text (single token)	
	operon	text	
	product	text	
	protein_id	<identifier>	
	pseudo	boolean	
	pseudogene	TYPE	
	ribosomal_slippage	boolean	
	standard_name	text	
	translation	text	
	transl_except	(pos:<location>,aa:<amino_acid> )	
	transl_table	<integer>	
	trans_splicing	boolean	
constant region of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; includes one or more exons depending on the particular chain	allele	text	
	citation	[number]	
	db_xref	<database>;<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	NA
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	product	text	
displacement loop; a region within mitochondrial DNA in which a short stretch of RNA is paired with one	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	allele	text	
	citation	[number]	
	db_xref	<database>;<identifier>	
	experiment	[CATEGORY:]text	NA
D-loop	gene	text	
	gene_synonym	text	

<p>strand of DNA, displacing the original partner  DNA strand in this region; also used to describe the displacement of a region of one strand of duplex DNA by a single stranded invader in the reaction catalyzed by RecA protein</p>	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
<p>Diversity segment of immunoglobulin heavy chain, and T- cell receptor beta chain;</p>	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	NA
	locus_tag	text (single token)	
	map	text	
	note	text	
<p>joining segment of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains;</p>	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	NA

	pseudogene	TYPE	
	standard_name	text	
extra nucleotides inserted between rearranged immunoglobulin segments.	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	NA
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
sequence tagged site; short, single-copy DNA sequence that characterizes a mapping landmark on the genome and can be detected by PCR; a region of the genome can be mapped by determining the order of a series of STSs;	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	STS location to include primer(s) in primer_bind key or primers.
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	standard_name	text	
switch region of immunoglobulin heavy chains; involved in the rearrangement of heavy chain DNA leading to the expression of a different immunoglobulin	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	NA
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	

	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
variable region of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; codes for the variable amino terminal portion; can be composed of V_segments, D_segments, N_regions, and J_segments;	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	NA
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
variable segment of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; codes for most of the variable region (V_region) and the last few amino acids of the leader peptide;	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	NA
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
gap between two components of a genome or transcriptome assembly;	(Mandatory) estimated_length	unknown or <integer>	the location span of the assembly_gap feature for an unknown gap has to be specified by the submitter; the specified gap length has to be reasonable (less or = 1000) and will be
	assembly_gap	is "within scaffold", "repeat within scaffold" or "contamination". If there are multiple types of	
		gap_type	

		linkage_evidence they will appear as multiple	indicated as "n"'s in sequence. However, the value for the estimated_length of assembly_gap features within a single (non-CON) transcriptome record must be an integer and can not be "unknown";
	(Mandatory) linkage_evidence	TYPE (Note: Mandatory only if the qualifier is invalid.)	
region of biological interest identified as a centromere and which has been experimentally characterized;	<b>centromere</b>	citation [number] db_xref <database>:<identifier> experiment [CATEGORY:]text inference [CATEGORY:]TYPE[(same species)][:EVIDENCE_BASIS] note text standard_name text	the centromere feature describes the interval of DNA that corresponds to a region where chromatids are held and a kinetochore is formed
region of genome that codes for portion of spliced mRNA, rRNA and tRNA; may contain 5'UTR, all CDSs and 3' UTR;	<b>exon</b>	allele text citation [number] db_xref <database>:<identifier> EC_number text experiment [CATEGORY:]text function text gene text gene_synonym text inference [CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS] locus_tag text (single token) map text note text number unquoted text (single token) old_locus_tag text (single token) product text pseudo boolean pseudogene TYPE standard_name text trans_splicing boolean	NA
gap in the sequence	<b>gap</b>	experiment [CATEGORY:]text inference [CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS] map text note text	the location span of the gap feature for an unknown gap is 100 bp, with the 100 bp indicated as 100 "n"'s in the sequence. Where estimated length is indicated by an integer, this is indicated by the same number of "n"'s in the sequence. No upper

		or lower limit is set on the size of the gap.
region of biological interest identified as a gene and for which a name has been assigned;	<b>gene</b>	<p>allele text</p> <p>citation [number]</p> <p>db_xref &lt;database&gt;:&lt;identifier&gt;</p> <p>experiment [CATEGORY:]text</p> <p>function text</p> <p>gene text</p> <p>gene_synonym text</p> <p>inference [CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]</p> <p>locus_tag text (single token)</p> <p>map text</p> <p>note text</p> <p>old_locus_tag text (single token)</p> <p>operon text</p> <p>product text</p> <p>pseudo boolean</p> <p>pseudogene TYPE</p> <p>phenotype text</p> <p>standard_name text</p> <p>trans_splicing boolean</p>
intervening DNA; DNA which is eliminated through any of several kinds of recombination;	<b>iDNA</b>	<p>allele text</p> <p>citation [number]</p> <p>db_xref &lt;database&gt;:&lt;identifier&gt;</p> <p>experiment [CATEGORY:]text</p> <p>function text</p> <p>gene text</p> <p>gene_synonym text</p> <p>inference [CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]</p> <p>locus_tag text (single token)</p> <p>map text</p> <p>note text</p> <p>number unquoted text (single token)</p> <p>old_locus_tag text (single token)</p> <p>standard_name text</p>
a segment of DNA that is transcribed, but removed from within the transcript by splicing together the sequences	<b>intron</b>	<p>allele text</p> <p>citation [number]</p> <p>db_xref &lt;database&gt;:&lt;identifier&gt;</p> <p>experiment [CATEGORY:]text</p> <p>function text</p> <p>gene text</p>

(exons) on either side of it;	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	number	unquoted text (single token)	
	old_locus_tag	text (single token)	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	trans_splicing	boolean	
mRNA messenger RNA; includes 5'untranslated region (5'UTR), coding sequences (CDS, exon) and 3'untranslated region (3'UTR);	allele	text	
	artificial_location	[artificial_location_value]	
	circular_RNA	boolean	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	NA
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	operon	text	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	trans_splicing	boolean	
mat_pepti mature peptide or protein coding sequence; coding sequence for the mature or final peptide or protein product following post-translational modification; the location does not	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	EC_number	text	
	experiment	[CATEGORY:]text	NA
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	

include the stop codon (unlike the corresponding CDS);	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
any transcript or RNA product that cannot be defined by other RNA keys (prim_transcript, precursor_RNA, mRNA, 5'UTR, 3'UTR, exon, CDS, sig_peptide, transit_peptide, mat_peptide, intron, polyA_site, ncRNA, rRNA and tRNA);	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
<b>misc_RNA</b>	locus_tag	text (single token)	NA
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	operon	text	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	trans_splicing	boolean	
<b>misc_binding</b>	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
<b>misc_difference</b>	note	text	
	old_locus_tag	text (single token)	
	allele	text	
	citation	[number]	
feature sequence is different from that presented in the	clone	text	the misc_difference feature key should be used to describe variability that arises as a result

entry and cannot be described by any other difference key (old_sequence, variation, or modified_base);	compare	[accession-number.sequence-version]	of genetic manipulation (e.g. site directed mutagenesis); use /replace="" to annotate deletion, e.g. misc_difference 412..433 /replace=""
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	phenotype	text	
	replace	text	
	standard_name	text	
	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
region of biological interest which cannot be described by any other feature key; a new or rare feature;	function	text	this key should not be used when the need is merely to mark a region in order to comment on it or to use it in another feature's location
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	number	unquoted text (single token)	
	old_locus_tag	text (single token)	
	phenotype	text	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
site of any generalized, site-specific or replicative recombination event where there is a breakage and reunion of duplex DNA that cannot be	experiment	[CATEGORY:]text	NA
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	

described by other recombination keys or qualifiers of source key (/proviral);	map	text	
	note	text	
	old_locus_tag	text (single token)	
	recombination_class	TYPE	
	standard_name	text	
	allele	text	
	citation	[number]	
	db_xref	<database>;<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
any secondary or tertiary nucleotide structure or conformation that cannot be described by other Structure keys (stem_loop and D-loop);	gene	text	
	gene_synonym	text	NA
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	standard_name	text	
	allele	text	
	citation	[number]	
region of genome containing mobile elements;	db_xref	<database>;<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	NA
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
the indicated nucleotide is a modified nucleotide and should be substituted for by the indicated molecule (given in	rpt_family	text	
	rpt_type	<repeat_type>	
	standard_name	text	
	allele	text	
	citation	[number]	
	db_xref	<database>;<identifier>	value is limited to the restricted vocabulary for modified base abbreviations;
	experiment	[CATEGORY:]text	
	frequency	text	
	gene	text	
	gene_synonym	text	

the mod_base qualifier value)	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
a non-protein- coding gene, other than ribosomal RNA and transfer RNA, the functional molecule of which is the RNA transcript;	allele	text	
	citation	[number]	
	db_xref	<database>;<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	operon	text	
ncRNA	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	trans_splicing	Example	
	ncRNA_class	TYPE	
	allele	text	
	db_xref	<database>;<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	/replace="" is used to annotate deletion, e.g. old_sequence
	gene_synonym	text	12..15 /replace="" NOTE: This feature key is not valid in entries/records created from 15- Oct-2007.
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
the presented sequence revises a previous version of the sequence at this location;	map	text	
	note	text	
	old_locus_tag	text (single token)	
	replace	text	
	allele	text	
	citation	[number]	
	db_xref	<database>;<identifier>	NA
region containing polycistronic transcript including a cluster of genes that are under the	experiment	[CATEGORY:]text	
	function	text	
	map	text	
	note	text	

control of the same regulatory sequences/promoter and in the same biological pathway	<table border="1"> <tr><td>inference</td><td>[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]</td></tr> <tr><td>map</td><td>text</td></tr> <tr><td>note</td><td>text</td></tr> <tr><td>phenotype</td><td>text</td></tr> <tr><td>pseudo</td><td>boolean</td></tr> <tr><td>pseudogene</td><td>TYPE</td></tr> <tr><td>standard_name</td><td>text</td></tr> </table>	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	map	text	note	text	phenotype	text	pseudo	boolean	pseudogene	TYPE	standard_name	text					
inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]																			
map	text																			
note	text																			
phenotype	text																			
pseudo	boolean																			
pseudogene	TYPE																			
standard_name	text																			
origin of transfer; region of a DNA molecule where transfer is initiated during the process of conjugation or mobilization	<table border="1"> <tr><td>allele</td><td>text</td></tr> <tr><td>bound_moiety</td><td>text</td></tr> <tr><td>citation</td><td>[number]</td></tr> <tr><td>db_xref</td><td>&lt;database&gt;:&lt;identifier&gt;</td></tr> <tr><td>direction</td><td>value</td></tr> <tr><td>experiment</td><td>[CATEGORY:]text</td></tr> <tr><td>gene</td><td>text</td></tr> <tr><td>gene_synonym</td><td>text</td></tr> <tr><td>inference</td><td>[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]</td></tr> </table>	allele	text	bound_moiety	text	citation	[number]	db_xref	<database>:<identifier>	direction	value	experiment	[CATEGORY:]text	gene	text	gene_synonym	text	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	rep_origin should be used for origins of replication; /direction has legal values RIGHT, LEFT and BOTH, however only RIGHT and LEFT are valid when used in conjunction with the oriT feature; origins of transfer can be present in the chromosome; plasmids can contain multiple origins of transfer
allele	text																			
bound_moiety	text																			
citation	[number]																			
db_xref	<database>:<identifier>																			
direction	value																			
experiment	[CATEGORY:]text																			
gene	text																			
gene_synonym	text																			
inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]																			
<b>oriT</b>	<table border="1"> <tr><td>locus_tag</td><td>text (single token)</td></tr> <tr><td>map</td><td>text</td></tr> <tr><td>note</td><td>text</td></tr> <tr><td>old_locus_tag</td><td>text (single token)</td></tr> <tr><td>rpt_family</td><td>text</td></tr> <tr><td>rpt_type</td><td>&lt;repeat_type&gt;</td></tr> <tr><td>rpt_unit_range</td><td>&lt;base_range&gt;</td></tr> <tr><td>rpt_unit_seq</td><td>text</td></tr> <tr><td>standard_name</td><td>text Molecule Scope DNA</td></tr> </table>	locus_tag	text (single token)	map	text	note	text	old_locus_tag	text (single token)	rpt_family	text	rpt_type	<repeat_type>	rpt_unit_range	<base_range>	rpt_unit_seq	text	standard_name	text Molecule Scope DNA	
locus_tag	text (single token)																			
map	text																			
note	text																			
old_locus_tag	text (single token)																			
rpt_family	text																			
rpt_type	<repeat_type>																			
rpt_unit_range	<base_range>																			
rpt_unit_seq	text																			
standard_name	text Molecule Scope DNA																			
site on an RNA transcript to which will be added adenine residues by post-transcriptional polyadenylation;	<table border="1"> <tr><td>allele</td><td>text</td></tr> <tr><td>citation</td><td>[number]</td></tr> <tr><td>db_xref</td><td>&lt;database&gt;:&lt;identifier&gt;</td></tr> <tr><td>experiment</td><td>[CATEGORY:]text</td></tr> <tr><td>gene</td><td>text</td></tr> <tr><td>gene_synonym</td><td>text</td></tr> <tr><td>inference</td><td>[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]</td></tr> </table>	allele	text	citation	[number]	db_xref	<database>:<identifier>	experiment	[CATEGORY:]text	gene	text	gene_synonym	text	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	NA				
allele	text																			
citation	[number]																			
db_xref	<database>:<identifier>																			
experiment	[CATEGORY:]text																			
gene	text																			
gene_synonym	text																			
inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]																			
any RNA species that is not yet the mature RNA	<table border="1"> <tr><td>allele</td><td>text</td></tr> <tr><td>citation</td><td>[number]</td></tr> <tr><td>db_xref</td><td>&lt;database&gt;:&lt;identifier&gt;</td></tr> </table>	allele	text	citation	[number]	db_xref	<database>:<identifier>	used for RNA which may be the result of post-transcriptional processing; if the RNA in												
allele	text																			
citation	[number]																			
db_xref	<database>:<identifier>																			

product; may include ncRNA, rRNA, tRNA, 5' untranslated region (5'UTR), coding sequences (CDS, exon), intervening sequences (intron) and 3' untranslated region (3'UTR);	experiment	[CATEGORY:]text	question is known not to have been processed, use the prim_transcript key.
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	operon	text	
	product	text	
	standard_name	text	
	trans_splicing	boolean	
	allele	text	
primary (initial, unprocessed) transcript; may include ncRNA, rRNA, tRNA, 5' untranslated region (5'UTR), coding sequences (CDS, exon), intervening sequences (intron) and 3' untranslated region (3'UTR);	citation	[number]	NA
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	operon	text	
	standard_name	text	
non-covalent primer binding site for initiation of replication, transcription, or reverse transcription; includes site(s) for synthetic e.g., PCR primer elements;	allele	text	used to annotate the site on a given sequence to which a primer molecule binds - not intended to represent the sequence of the primer molecule itself; PCR components and reaction times may be stored under the "/PCR_conditions" qualifier; since PCR reactions most often involve pairs of primers, a single primer_bind key may use the order() operator with two locations, or a pair of primer_bind keys may be used.
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	standard_name	text	
	PCR_conditions	text	

	allele	text	
	citation	[number]	
	db_xref	<database>;<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
propeptide  propeptide coding sequence; coding sequence for the domain of a proprotein that is cleaved to form the mature protein product.	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	NA
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	allele	text	
	citation	[number]	
	db_xref	<database>;<identifier>	
protein_binder  non-covalent protein binding site on nucleic acid;	experiment	[CATEGORY:]text	
	function	text	
	gene	text	note that feature key regulatory with
	gene_synonym	text	/regulatory_class="ribosome_binder_site" should be used for
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	ribosome binding sites.
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	operon	text	
	standard_name	text	
rRNA  mature ribosomal RNA; RNA component of the ribonucleoprotein particle (ribosome) which assembles amino acids into proteins.	allele	text	
	citation	[number]	
	db_xref	<database>;<identifier>	
	experiment	[CATEGORY:]text	
	function	text	rRNA sizes should be annotated with the /product qualifier.
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	
	map	text	

	note	text	
	old_locus_tag	text (single token)	
	operon	text	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
any region of sequence that functions in the regulation of transcription, translation, replication or chromatin structure;	allele	text	
	bound_moiety	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	This feature has replaced the following Feature Keys on 15-DEC-2014: enhancer, promoter, CAAT_signal, TATA_signal, -35_signal, -10_signal, RBS, GC_signal, polyA_signal, attenuator, terminator, misc_signal.
	locus_tag	text (single token)	
region of genome containing repeating units;	map	text	
	note	text	
	old_locus_tag	text (single token)	
	operon	text	
	phenotype	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	allele	text	
	citation	[number]	
repeat_region	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	NA
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	rpt_family	text	
	rpt_type	<repeat_type>	
	rpt_unit_range	<base_range>	
	rpt_unit_seq	text	

	<b>satellite</b>	<satellite_type>[:<class>][ <identifier>]
	<b>standard_name</b>	text
	<b>allele</b>	text
	<b>citation</b>	[number]
	<b>db_xref</b>	<database>:<identifier>
	<b>experiment</b>	[CATEGORY:]text
	<b>function</b>	text
	<b>gene</b>	text
	<b>gene_synonym</b>	text
	<b>inference</b>	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]
signal peptide coding sequence; coding sequence for an N-terminal domain of a secreted protein; this domain is involved in attaching nascent polypeptide to the membrane leader sequence;	<b>e</b>	NA
	<b>locus_tag</b>	text (single token)
	<b>map</b>	text
	<b>note</b>	text
	<b>old_locus_tag</b>	text (single token)
	<b>product</b>	text
	<b>pseudo</b>	boolean
	<b>pseudogene</b>	TYPE
	<b>standard_name</b>	text
	<b>altitude</b>	text
identifies the biological source of the specified span of the sequence; this key is mandatory; more than one source key per sequence is allowed; every entry/record will have, as a minimum, either a single source key spanning the entire sequence or multiple source keys, which together, span the entire sequence.	<b>bio_material</b>	[<institution-code>:<collection-code>:]<material_id>
	<b>cell_line</b>	text
	<b>cell_type</b>	text
	<b>chromosome</b>	text
	<b>citation</b>	[number]
	<b>clone</b>	text
	<b>clone_lib</b>	text
	<b>collected_by</b>	text
	<b>collection_date</b>	text
	<b>country</b>	<country_value>[:<region>][,<locality>]
<b>source</b>	<b>cultivar</b>	text
	<b>culture_collection</b>	<institution-code>:<collection-code>:<culture_id>
	<b>db_xref</b>	<database>:<identifier>
	<b>dev_stage</b>	text
	<b>ecotype</b>	text
	<b>environmental_sample</b>	boolean
	<b>focus</b>	boolean

	germline	boolean	
	haplogroup	text	
	haplotype	text	
	host	text	
	identified_by	text	
	isolate	text	
	isolation_source	text	
	lab_host	text	
	lat_lon	text	
	macronuclear	boolean	
	map	text	
	mating_type	text	
	metagenome_source	text	
	note	text	
	organelle	<organelle_value>	
		[fwd_name: XXX, ]fwd_seq:	
	PCR_primers	xxxxx, [rev_name: YYYY, ]rev_seq: yyyy	
	plasmid	text	
	pop_variant	text	
	proviral	boolean	
	rearranged	boolean	
	segment	text	
	serotype	text	
	serovar	text	
	sex	text	
	specimen_voucher	[<institution-code>:[<collection- code>:]]<specimen_id>	
	strain	text	
	sub_clone	text	
	submitter_seqid	text	
	sub_species	text	
	sub_strain	text	
	tissue_lib	text	
	tissue_type	text	
	transgenic	boolean	
	type_material	<type-of-type> of <organism name>	
	variety	text	
hairpin; a double- helical region formed by base-	stem_loop	allele	text
		citation	[number]
		db_xref	<database>;<identifier>
			NA

pairing between adjacent (inverted) complementary sequences in a single strand of RNA or DNA.	experiment [CATEGORY:]text function text gene text gene_synonym text inference [CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS] locus_tag text (single token) map text note text old_locus_tag text (single token) operon text standard_name text	
mature transfer RNA, a small RNA molecule (75-85 bases long) that mediates the translation of a nucleic acid sequence into an amino acid sequence;	allele text anticodon (pos:<location>,aa:<amino_acid>,seq:<text>) circular_RNA boolean citation [number] db_xref <database>:<identifier> experiment [CATEGORY:]text function text gene text gene_synonym text inference [CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS] NA locus_tag text (single token) map text note text old_locus_tag text (single token) operon text product text pseudo boolean pseudogene TYPE standard_name text trans_splicing boolean	
region of biological interest identified as a telomere and which has been experimentally characterized;	citation [number] db_xref <database>:<identifier> experiment [CATEGORY:]text note text inference [CATEGORY:]TYPE[(same species)][:EVIDENCE_BASIS] note text rpt_type <repeat_type> rpt_unit_range <base_range>	the telomere feature describes the interval of DNA that corresponds to a specific structure at the end of the linear eukaryotic chromosome which is required for the integrity and maintenance of the end; this region is unique compared to the rest of the

	rpt_unit_seq	text	chromosome and represent the physical end of the chromosome;
	standard_name	text	
transfer messenger RNA; tmRNA acts as a tRNA first, and then as an mRNA that encodes a peptide tag; the ribosome translates this mRNA region of tmRNA and attaches the encoded peptide tag to the C-terminus of the unfinished protein; this attached tag targets the protein for destruction or proteolysis;	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	
	locus_tag	text (single token)	NA
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
	tag_peptide	<base_range>	
transit peptide coding sequence; coding sequence for an N-terminal domain of a nuclear-encoded organellar protein; this domain is involved in post-translational import of the protein into the organelle;	allele	text	
	citation	[number]	
	db_xref	<database>:<identifier>	
	experiment	[CATEGORY:]text	
	function	text	
	gene	text	
	gene_synonym	text	
	inference	[CATEGORY:]TYPE[ (same species)][:EVIDENCE_BASIS]	NA
	locus_tag	text (single token)	
	map	text	
	note	text	
	old_locus_tag	text (single token)	
	product	text	
	pseudo	boolean	
	pseudogene	TYPE	
	standard_name	text	
a small region of sequenced bases, generally 10 or fewer in its length, which could not be confidently	allele	text	
	citation	[number]	
	compare	[accession-number.sequence-version]	use /replace="" to annotate deletion, e.g. unsure
	db_xref	<database>:<identifier>	11..15 /replace=""
	experiment	[CATEGORY:]text	

identified. Such a region might contain called bases (A, T, G, or C), or a mixture of called-bases and uncalled-bases ('N'). The unsure feature should not be used when annotating gaps in genome assemblies. Please refer to assembly\_gap feature for gaps within the sequence of an assembled genome. For annotation of gaps in other sequences than assembled genomes use the gap feature.

gene	text
gene_synonym	text
inference	[CATEGORY:JTYPE[ (same species)][:EVIDENCE_BASIS]
locus_tag	text (single token)
map	text
note	text
old_locus_tag	text (single token)

replace text

a related strain contains stable mutations from the same gene (e.g., RFLPs, polymorphisms, etc.) which differ from the presented sequence at this location (and possibly others);

allele	text	
citation	[number]	
compare	[accession-number.sequence-version]	
db_xref	<database>:<identifier>	used to describe alleles, RFLP's, and other naturally occurring mutations and polymorphisms; variability arising as a result of genetic manipulation (e.g. site directed mutagenesis) should be described with the misc_difference feature; use /replace="" to annotate deletion, e.g. variation 4..5 /replace=""
experiment	[CATEGORY:Jtext	
frequency	text	
gene	text	
gene_synonym	text	
inference	[CATEGORY:JTYPE[ (same species)][:EVIDENCE_BASIS]	
locus_tag	text (single token)	
map	text	
note	text	
old_locus_tag	text (single token)	
phenotype	text	
product	text	
replace	text	
standard_name	text	