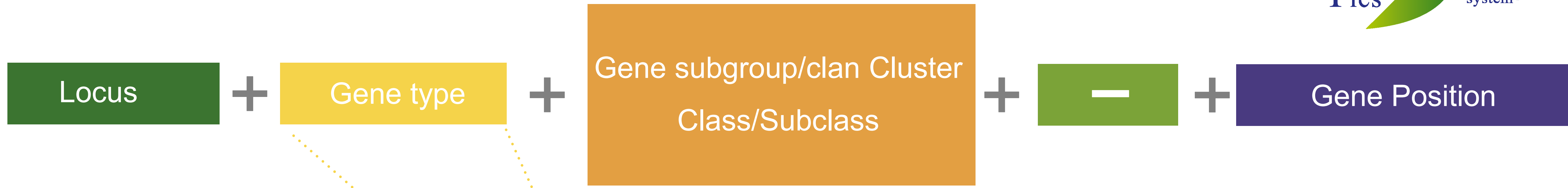
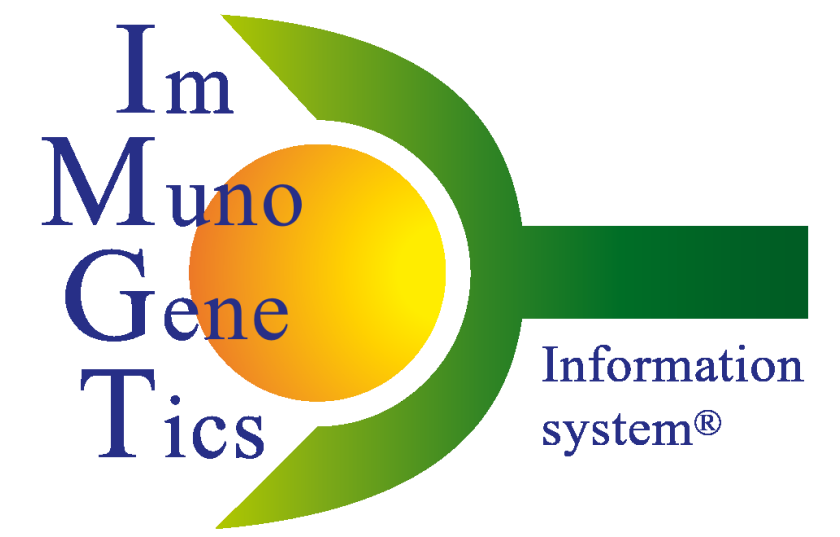


# TR General rules for Gene names



Examples

TRG	C	1	-	1
TRD	V	1	-	3
TRB	J	2	-	2
TRA	V	1	-	

# TR General rules for Gene names

## Locus

If T-cell receptor gamma chain

- Use TRG

If T-cell receptor delta chain

- Use TRD

If T-cell receptor beta chain

- Use TRB

If T-cell receptor alpha chain

- Use TRA

## Gene type

If V-GENE

- Use V

If D-GENE

- Use D

If J-GENE

- Use J

If C-GENE

- Use C

## Gene subgroup, Cluster or Subclass

If V-GENE

- If nucleotide sequence identity in V-REGION  $\geq 75\%$ 
  - Assign to subgroup defined by Arabic positive number
  - Subgroup number determination: compare subgroups of the most phylogenetically related IMGT-annotated species, if possible. Create a species-specific subgroup, if needed. In ambiguous cases, consider CDR-IMGT lengths, L-V-GENE-UNIT sequences, and promoter components.
- If nucleotide sequence identity in V-REGION  $< 75\%$ 
  - Identified by an uppercase latin letter by comparison with the closest species, or by alphabetic order from 5' to 3' for distant species.

If D-GENE

- Assign to a Cluster or set
- Cluster or set number determination : based on nucleotide sequence identity and position

If J-GENE

- Cluster or set number determination : based on nucleotide sequence identity and position and consider positions in D-J-C or J-C clusters

If C-GENE

- Class/subclass determination: based on exon sequence identity %, prototypes, and gene order compared to closest species

→ For TRG

- Assign cluster number based on J-C cluster positions

→ For TRD

- Assign TRDC

→ For TRB

- Assign cluster number based on D-J-C cluster positions

→ For TRA

- Assign TRAC

## Gene Position

if mapped gene in case of several genes in a given subgroup and/or set/cluster

- If V-GENES: Use dash and relative position from 5' end of locus
- If D-GENES: Use dash and relative position within the D-J-C clusters from 5' end of locus
- If J-GENES:
  - For TRG Use relative position within the J-C or D-J-C clusters from 5' end of the locus
  - For TRD Use relative position within the J-C or D-J-C clusters from 5' end of the locus
  - For TRB Use dash and relative position within the J cluster from 5' end of locus
  - For TRA Use relative position within the D-J-C clusters from 5' end of locus
- If C-GENES: Use relative position within C group, or C clusters or J-C clusters or cassettes from 5' end of locus

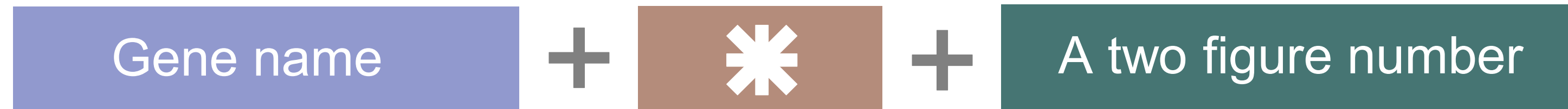
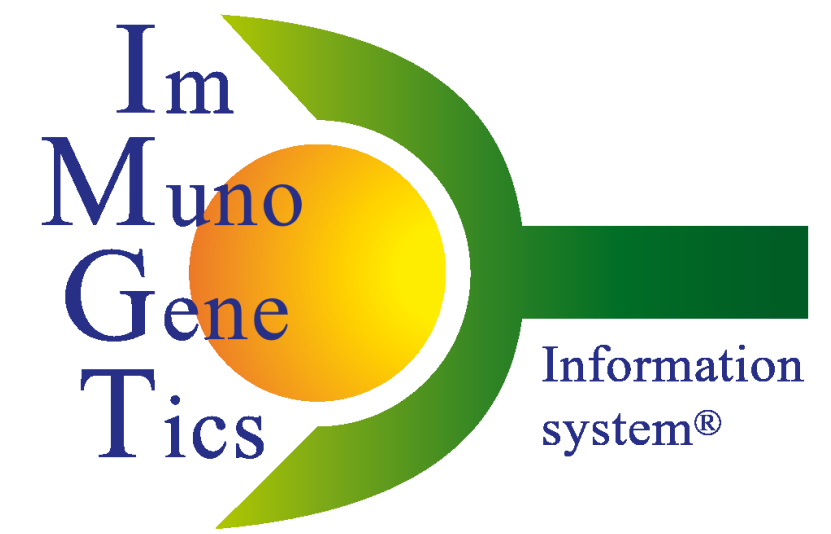
if unmapped gene

- Use "S" and incremented number for temporary designation

if orphon gene

- Use "/OR", chromosome number, dash and specific gene number/letter

# TR General rules for Allele names



Examples

TRGJ1	*	02
TRBC2	*	01
TRDV2	*	03

The first allele has the number \*01 and is considered as reference sequence; other alleles are designated by increasing numbers (\*02, \*03, ...) based, if possible, on chronological order of their publication, and/or confirmation of data by different authors.