

PART ONE

Table SMO. Overview of the sequence features and sequence attributes (based on the Sequence Ontology project) identified by the GenomeContent from the gene annotation files (GTF* or GFF*) of 461 eukaryotic genome projects

Lozada-Chávez I., Stadler,P.F., and Prohaska, S.J. (2018). bioRxiv,doi.org/10.1101/283549. Re-submitted (2022)

Genome-wide features of introns are evolutionary decoupled among themselves and from genome size throughout Eukarya

<https://www.biorxiv.org/content/early/2018/03/18/283549>

Sequence Ontology project: <https://github.com/The-Sequence-Ontology/SO-Ontologies>

Official SO sequence features (e.g., "gene", "CDS", "mRNA") and attributes (e.g., "Parent", "gene_id", "ID", "name") in columns 2, 3 and 9 are recognized from the **SOFA.obo** file:

https://github.com/The-Sequence-Ontology/SO-Ontologies/blob/master/Ontology_Files/subsets/SOFA.owl

