



DELIVERABLE 1.2

Standards for collecting and displaying genetic data

Call identifier: PRO-GRACE Grant agreement no: 101094738

Promoting a plant genetic resource community for Europe

Deliverable No. D1.2

Standards for collecting and displaying genetic data Contractual delivery date: M11

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Responsible partner: CSIC Contributing partners: (CSIC, CREA, UNITO, ENEA, INIAV, MAICH, NASC, CNR, NORDGEN, UEB)



This project has received funding from the European Union's Horizon Europe research and innovation programme under grant agreement No 101094738.

Grant agreement no.	Horizon Europe – 101094738
Project full title	PRO-GRACE – Promoting a plant genetic resource community for Europe
Deliverable number	2 10

	01.2
Deliverable title	Standards for collecting and displaying genetic data
Туре	R – Document, report
Dissemination level	Public
Work package number	WP1
Author(s)	CSIC (Clara Pons, Antonio Granell, Bruno Contreras Moreira, Ernesto Igartua Arregui, Luis Guash), IPK (Catherine Hazel Aguilar, Stephan Weise) with the contribution of CREA, UNITO, ENEA, INIAV, MAICH, NASC, CNR, NORDGEN, UEB
Keywords	

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The research leading to these results has received funding from the European Union's Horizon Europe research and innovation programme under grant agreement No 101094738.

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1. Introduction

Plant genetic resources (PGR) are crucial for sustainable crop production and for ensuring food and nutrition security both, today and in the future. To support efficient conservation and accessibility, the integration of genetic data has become essential through practices known as 'next-generation genebanking' (van Treuren and van Hintum, 2014; Wambugu *et al.*, 2018; Nybom and Lācis, 2021; Aubry, 2023).

The European Search Catalogue for Plant Genetic Resources (EURISCO; http://eurisco.ecpgr.org/) serves as a pivotal component of the European PGR information system. Developed within the European Cooperative Programme for Plant Genetic Resources (ECPGR; https://www.ecpgr.cgiar.org/), EURISCO acts as a centralized repository for passport and phenotypic data related to plant genetic resources conserved in European collections. However, it currently lacks representation of genetic data, which has seen significant advancements over the last two decades through EU-funded projects. Such valuable genetic information remains scattered across literature, specific websites, and databases from different projects, highlighting the pressing need for its integration into EURISCO.

Genetic data and metadata encompasses a wide array of types generated using diverse technologies, including whole genome sequencing, reduced genome sequencing (exome sequencing, genotyping, target sequencing, transcriptome sequencing), single nucleotide polymorphisms (SNP), simple sequence repeats (SSR), structural variations (SV), copy number variation (CNV), epigenomics, alternative splicing, gene expression, QTLs and GWAs trait-associated variants are some examples of genetic data produced using different technologies. Harmonizing, integrating, and making this genetic data FAIR (findable, accessible, interoperable, and re-usable) (Wilkinson et al., 2016) has been a shared goal within the scientific community since 2000. To achieve this, employing Permanent Unique Identifiers, standardized metadata with controlled vocabularies, and open-source communication protocols and databases are essential.

By linking genetic data with EURISCO and adhering to FAIR principles (FAIRification, (Welter *et al.*, 2023)), researchers and stakeholders can leverage high-quality, curated data for better decisionmaking and sustainable use of plant genetic resources, contributing to global food security. Two models for data FAIRification exist: create new standards or exploiting (rather than replacing) existing resources and promote their use. In this deliverable we comprehensively reviewed existing standards and public repositories for nucleotide sequence, genetic polymorphisms, makers and, variants to identify currently implemented standards, requirements, and features related to the management and sharing of genetic data and its metadata. The **overall objective of D1.2 is to find and evaluate solutions to the challenges described above, in line with the ECPGR's Plant Genetic Resources Strategy for Europe, and to develop a viable concept for genetic (meta)data implementation and long-term operation to further establish EURISCO as a trusted open-access repository**.

2. Activities

We organized the D1.2 activities in two phases:

 In the first phase we conducted a survey of the FAIRsharing repository (<u>https://fairsharing.org</u>), a curated catalogue on data and metadata standards, inter-related to databases and data policies (Sansone *et al.*, 2019). The FAIRsharing repository was filtered by the terms "genetic", "nucleotide", "sequence", "DNA", "genomics" to identify the existing standards and databases for genetic data. Standards were then classified in four types according to Sansone (Sansone *et al.*, 2019):

- **Minimum reporting guidelines:** guiding principles or checklists that outline the necessary and sufficient information vital for contextualizing and understanding a digital object
- **Semantic standards:** ranging from dictionaries to ontologies, provide definitions and unambiguous identification for concepts and objects.
- **Model/formats or syntax:** define the structure and relationship of information for a conceptual model and include transmission formats to facilitate the exchange of data between different systems.
- **Identifier schemes:** formal systems for resources and other digital objects that allow their unique and unambiguous identification.

Then standards and databases for genetic data were annotated according to: (i) FAIRsharing status indicators (maintained, ready for use and recommended) (Sansone *et al.*, 2019), (ii) if they are organism-specific or not and, (iii) their source or provider (this only for non-organism specific). In addition, we included ELIXIR's (an European life sciences infrastructure to enable researchers to access and analyse life science data, *elixir-europe.org*) recommended resources for submission of experimental data. In addition, we extended the search for stable identifier schemes to identifiers.org (http://identifiers.org/) a resolving system for persistent identifiers in the form of Compact Identifiers and URLs that enable the referencing of scientific data for the scientific community.

2) In a **second phase**, we reviewed those databases and standards and evaluated which are the more suitable to link genetic data with EURISCO.

3. Results

3.1. FAIRsharing survey to find available databases and standards to store EURISCO genetic data.

In July 2023, FAIRsharing had a comprehensive collection of more than 3,868 entries for databases and standards. Within this collection, related to genetic data, there were 873 databases (knowledgebases and public repositories with standard-compliant data) and 297 standards (minimum reporting guidelines, models/formats or syntax and identifier schemes) (**Table 1** and **Annex 1**). A significant portion of these entries, constituting 32.5%, can handle data and metadata across all species for a particular domain or area of study (genome, molecule- or process-specific databases, variations and others). The remaining 67.5% of available standards and databases were species-specific, taxa-specific or family-specific, predominantly focussed on biomedical research and model species. For plants only, there are 129 entries (115 databases and public repositories and 14 standards) (**Table 1**), most of them capable to manage meta(data) across a wide spectrum of plant species (**Annex 1**).

Table 1. Summary of databases, public repositories and standards in FAIRsharing.org related to geneticinformation

Туре	Total entries FAIRsharing	Maintained	Ready- to-use	Recommended	All spcies data	Plant data	ELIXIR recommended
Knowledgebases & public respositories	873	440	668	117	200	115	13

Standards	297	139	243	25	181	14	5
Identifier schemes	1		1				
Minimum reporting guidelines	50	23	39	10	24	4	
Model/formats or syntax:Format	74	29	66	2	61	1	1
Model/formats or syntax:models/syntax	45	30	36	5	31	2	4
Semantic standards	127	57	101	8	65	7	
Total	1170	579	911	142	381	129	18

Since the ultimate goal of D1.2 is to find a global solution to link genetic data with EURISCO, which comprises 6,737 genera and 45,175 species (Kotni et al., 2023), we excluded species-specific, taxonspecific or family-specific entries related to genetic data to identify standards. In total, 440 databases, public repositories and standards related to genetic data and accepting an unlimited number of species remain. We used this list to review and evaluate the existing standards that can be used to link genetic data with EURISCO. Around 239 databases and 181 standards for genetic data and accepting all species are collected in the FAIRsharing catalogue (Annex 1, Table 1 and Table 2). When we analyzed the sources and providers for databases and standards (Figure 1) related to genetic data accepting diverse range of species, including plants, we found that most are provided by the International Nucleotide Sequence Database Collaboration (INSDC, https://www.insdc.org/) (Nakamura et al., 2013; Cochrane et al., 2016; Karsch-Mizrachi et al., 2018) and its standard-developer collaborators. INSDC partners are (in alphabetical order): the DNA Data Bank of Japan (DDBJ; http://www.ddbj.nig.ac.jp/) at the National Institute for Genetics in Mishima, Japan; the European Nucleotide Archive (ENA, www.ebi.ac.uk/ena) at the EMBL European Bioinformatics Institute (EMBL-EBI) in Cambridge, UK; and GenBank (http://www.ncbi.nlm.nih.gov/genbank) at the National Center for Biotechnology Information (NCBI) in Bethesda, MD, (Nakamura et al., 2013; Cochrane et al., 2016; Karsch-Mizrachi et al., 2018).



Figure 1. Main sources of databases and standards related to genetic (meta)data that accept a diverse range of species, including plants. *EMBL include countries outside EU (see https://www.embl.org/about/member-states/)

The INSDC repositories operate independently but synchronize periodically their data and apply similar quality standards (Nakamura *et al.*, 2013; Cochrane *et al.*, 2016; Karsch-Mizrachi *et al.*, 2018). These repositories are built to accommodate everything from raw data (i.e. next-generation sequencing

reads) to assembly data, experimental design details, taxonomic information, functional annotation and information about the projects and biological samples associated with sequencing efforts (Nakamura *et al.*, 2013; Cochrane *et al.*, 2016; Karsch-Mizrachi *et al.*, 2018). Further, the INSDC repositories work in concert with appropriate standards communities to ensure rich metadata capture for understanding the origin of the sequences (Nakamura *et al.*, 2013; Cochrane *et al.*, 2016; Karsch-Mizrachi *et al.*, 2018). From this primary repositories, source of sequence data, many other secondary and tertiary databases (or knowledge bases) providing much more specific tools and information are constructed (**Table 2**).

Table 2. Main public data repositories and knowledge bases for genetic data accepting all species or all plant species.

Abbreviatio	Name	Туре	Scope	Species	Provide	URL	
n					r/maint		
					ainer		
GenBank	NIH genetic	Repository	raw and annotated	all	NCBI	https://www.ncbi.nlm.nih.gov/genban	
	sequence		sequebce data			k/	
	database						
ENA	European	Repository	nucleotide sequencing	all	EMBL-	https://www.ebi.ac.uk/ena/browser/h	
	Nucleotide		information, covering		EBI	ome	
	Archive		raw sequencing data,				
			sequence assembly				
			functional appotation				
DDBI	DNA Data	Repository		الد	ואחח	https://www.ddbi.nig.ac.in/index-	
0000	Bank of	Repository	including raw data	ali	000	e html	
	lanan		annotated sequences.			Cintin	
	sapan		and metagenomic				
			data				
SRA	Sequence	Repository	high-throughput	all	NCBI	https://www.ncbi.nlm.nih.gov/sra	
	Read		sequencing data,				
	Archive		including raw				
			sequence reads				
EVA	European	Repository	all types of genetic	all	EMBL-	https://www.ebi.ac.uk/eva/	
	Variation		variation data		EBI		
	Archive						
UCSC	UCSC	Knowledgeba	visualizing and	all	NCBI	https://genome.ucsc.edu/	
Genome	Genome	se	analyzing genomic				
Encombl	Encombl	Knowlodgoba	udid	211	EMDI	https://www.opcombl.org	
Ensembl	Elisellibi	KIIOWIEUgeba	analyzing genomic	dli	EIVIDL-	https://www.ensembl.org	
		data			LDI	https://plants.ensembi.org	
ArrayExpre	ArrayExpre	Repository	all functional	all	EMBL-	https://www.ebi.ac.uk/biostudies/arra	
SS	ss		genomics data		EBI	yexpress	
			generated from				
			microarray or next-				
			generation				
sequencing (NGS)							
GEO	GEO Gene Repository all functional		all	NCBI	https://www.ncbi.nlm.nih.gov/geo/		
	Expression		genomics data				
	Omnibus		generated from				
			microarray or next-				
			generation				
Track Hub	Track Hub	Repository	Traks for all kind of	all	FMRI-	https://trackhubregistry.org/	
Registry	Registry	перозногу	genetic data	all	EBI		
PLAZA	PLAZA	Knowledgeba	comparative	plants	GHENT	https://bioinformatics.psb.ugent.be/pl	
		se	genomics, gene		Universi	aza/	
			annotations, and		ty	-,	
			sequence data				
GERMINAT	GERMINAT	Repository	Phenotypic and	plants	The	https://ics.hutton.ac.uk/germinate-	
E	E		genetic data		James	demo/#/home	

						Hutton	
						Institute	
PlantGDB	Plant	Knowledgeba	comparative		plants	NSF	https://www.plantgdb.org/
	Genomics	se	genomics,	gene			
	Database		annotations,	and			
			sequence data				
Gramene	Gramene	Knowledgeba	comparative		plants	NSF	https://www.gramene.org/
		se	genomics,	gene			
			annotations,	and			
			sequence data				

Of course, there are many other databases (see **Table 2**, **Annex 1**) and standards related to genetic data provided by sources other than INSDC. databases or standards are specialized and crucial to the topic. These are typically maintained by researchers who specialize in the subject and are frequently generated as part of genome assembly/annotation projects. The data from these projects is ultimately submitted to INSDC.

3.3 Review of existing standards for models, formats and syntax:

Various scheme and syntax standards are used to structure and define the format of the data. These standards help ensure interoperability, consistent representation, and effective data sharing. They preferably should be widespread and open, readable and usable by a wide number of software and invisible to users (Sansone et al., 2019). A total of 91 standards for models, formats and syntax for genetic data and accepting data for all species are listed in FAIRsharing.

3.3.1 Standard formats

Several models and formats are commonly used for representing and storing genetic data. These models/syntaxes ensure that genetic information can be accurately captured, shared, and analysed across different tools and platforms. The choice of format often depends on the specific type of genetic data and the intended use case. Standard formats to store, interchange and display genetic data already exist for many types of data (see https://genome.ucsc.edu/FAQ/FAQformat.html). Some of these standards such as FASTA, FASTQ, SAM/BAM, GFF3 or VCF are stable, widely adopted and implemented in a diverse range of databases and analysis tools. The most common standards for file formats encoding genetic data are listed in **Table 3**.

	ACRONYM	NAME	Type of data	Codification	Extension
Sequence formats	FASTA	FASTA Sequence Format	nucleotide or peptide sequences	Plain text	.fa (others: .fasta,.fsa)
	FASTQ	FASTQ Sequence And Sequence Quality Format	Nucleotide sequence and PHRED quality scores	Plain text	.fq
	Genbank format	EMBL flat file format	Storing sequences nucleotide or peptide sequences and their associated meta-information, feature coordinates, and annotations	Plain text	.gb or .genebank
EMBL format		EMBL flat file format	Storing sequences nucleotide or peptide sequences and their associated meta-information, feature coordinates, and annotations	Plain text	.embl
	DDBJ format	DDBJ flat file format	Storing sequences nucleotide or peptide sequences and their	Plain text	. ddbj

Table 3. The most common file formats to store genetic data

			associated meta-information, feature coordinates, and annotations		
Alignment formats	SAM	Sequence Alignment/Map Format	Alignments of sequencing reads to a reference genome	Plain text	.sam
	BAM	Binary Alignment Map Format	Alignments of sequencing reads to a reference genome	Binary	.bam
	CRAM	Compressed Reference- oriented Alignment Map	Alignments of sequencing reads to a reference genome	Byte	.cram
	VCF	Variant Call Format	DNA variation	Plain text	.vcf
	BCF2	Binary Variant Call Format version 2	DNA variation	Binary	.bcf
Discrete genomic	BED format	Browser Extensible Data Format	Genomic intervals with additional information	Plain text	.bed
feature data and tracks	Bedgraph	Browser Extensible Graphical Data Format	Genomic intervals with continuous-valued data	Plain text	.bb
	GTrack format	Genomic track	Genomic intervals with additional information	Plain text	.gtrak
	BTrack format	Genomic track	Genomic intervals with additional information	Binary	.btrak
	GFF3	Gene Feature File version 3	Features, positions and meta- feature information		.gff
	GTF	Gene transfer format	Genomic annotation with information and scores		.gtf

Sequence data files:

- FASTA format: created in 1988 (Pearson and Lipman, 1988), FASTA is the standard most implemented by databases and repositories (Sansone et al., 2019). It is a very basic format with two minimum lines to represent either nucleotide or peptide sequences (see Annex 2 for an example of FASTA file). First line referred as comment line starts with '>' and gives basic information about sequence. There is no set format for comment line. Any other line that starts with ';' will be ignored. Lines with ';' are not a common feature of FASTA files. After comment line, sequence of nucleic acid or protein is included in standard one letter code. Any tabulators, spaces, asterisks etc in sequence will be ignored. A sequence file in FASTA format can contain several sequences. Each sequence will be separated by their "header" line, starting by ">".
- FASTQ format: common file format for sharing sequencing read data combining both the sequence and an associated per base quality score (Cock *et al.*, 2010). It is the standard for storing the output of high-throughput sequencing instruments including third-generation sequencing instruments. Sequences are represented by four lines (see Annex 2 for an example of FASTQ file). Line 1 begins with "@" followed by the sequence identifier and optional descriptions. Line 2 is raw sequence letters while Line 3 begins with the "+" character optionally followed by the same sequence identifier and descriptions. Line 4 are PHRED quality scores for nucleotide sequence or the estimated probability for a base to be erroneous (Ewing and Green, 1998; Ewing *et al.*, 1998). PHRED scores use a logarithmic scale, and are represented by ASCII characters, mapping to a quality usually going from 0 to 93. Single ASCII character codes from 33 to 126 are used in place of numeric values to denote the PHRED scores in Line 4. See https://bioinformatics.uconn.edu/resources-and-events/tutorials-2/file-formats-tutorial/ for detailed information of PHRED scores and ASCII characters.
- Genbank/EMBL/DDBJ formats: Each of the INSDC members has a sequence standard file format that was designed to be rich and human readable. Despite some differences in the formatting of information, all of them contain almost the same fields and the same

information, making them interchangeable (see Annex 2 for an example of Genbank/EMBL/DDBJ files). Each sequence entry in the INSDC sequence files is composed of lines (each with their own format) starting with a sequence unique identifier, followed by several annotation lines, the sequence and ended by two slashes ("//"). Annotation lines are used to record the various data including a concise description of the sequence, the scientific name and taxonomy of the source organism, and a table of features with controlled vocabulary (see https://www.insdc.org/submitting-standards/feature-table/ for format details) that identifies coding regions and other sites of biological significance, such as transcription units, sites of mutations or modifications, and repeats, protein translations and bibliographic references. For more details see https://www.ncbi.nlm.nih.gov/Sitemap/samplerecord.html,https://www.ddbj.nig.ac.jp/ddbj /flat-file-e.html https://ena-docs.readthedocs.io/en/latest/submit/fileprep/flat-fileand example.html.

Alignment data files

• SAM format: SAM is the standard for reads alignments against reference sequences (Li et al., 2009). It is a tab-delimited text-based format for storing single- and paired-end reads alignments against reference sequences. It can support short and third generation sequencing long reads produced by different sequencing platforms. The format has been extended to include unmapped sequences, and it may contain other data such as base-call & alignment qualities. The SAM format (see Annex 2 for an example) consists of a header section (~metadata) and an alignment section (raw mapping information). Header lines contain metadata about the reference sequences, read and sample information, and (optionally) processing steps and comments. Each header line begins with @, followed by a two-letter code that distinguishes the different types of metadata records in the header: @HD file level metadata, @SQ reference sequence dictionary, @RG read group, @PG program. Each alignment record in a SAM file contains 11 mandatory fields in tab-separated columns describing the read, quality of the read, and nature alignment of the read to a region of the genome. SAM standard is maintained by the Large Scale Genomics work stream of the Global Alliance for Genomics & Health (GA4GH; <u>https://www.ga4gh.org/</u>). For detailed info see https://samtools.github.io/hts-specs/SAMv1.pdf and

https://pacbiofileformats.readthedocs.io/en/12.0/BAM.html.

- BAM format: It is the lossless compressed binary version of the Sequence Alignment/Map (SAM) format. The data between SAM and BAM are exactly same, but BAM is compacted and indexed. BAM file requires an associated BAM.bai index file. Binary BAM files are small and ideal to store alignment files. BAM is the most commonly used format for submission of reads to INSDC sequence repositories and analysis. BAM is maintained by the Large-Scale Genomics work stream of the Global Alliance for Genomics & Health (GA4GH; https://www.ga4gh.org/). For a detailed info see https://samtools.github.io/hts-specs/SAMv1.pdf.
- CRAM format: CRAM is primarily a reference-based compressed format of SAM file, meaning that only differences between the stored sequences and the reference are stored. Additionally, each column in the SAM format is separated into blocks, improving compression ratio. It holds the same information as their SAM equivalent, offering significantly better lossless compression whilst maintaining backwards compatibility with BAM. Since CRAM files are typically 30 to 60% smaller than their BAM equivalents, some labs and repositories are implementing them. Usually, CRAM files are used to store alignments and converted to the BAM format for processing. CRAM is maintained by the Large-Scale Genomics work stream of

the Global Alliance for Genomics & Health (GA4GH; <u>https://www.ga4gh.org/</u>). For a detailed info see <u>https://samtools.github.io/hts-specs/CRAMv3.pdf</u>.

VCF format: is the standard file format for storing DNA variation data between a reference genome and sequences aligned to it, based on SAM/BAM alignments. VCF is a preferred format for databases and analysis tools because it is unambiguous, scalable and flexible, allowing extra information to be added to the info field and storing many millions of variants. The VCF format is a tab-delimited format that stores individual genotypes and variant calls including SNPs, insertions, deletions and structural variants, together with rich annotations (Danecek et al., 2011). The current version VCF 4.3 consists of two parts: metadata lines and data section (See Annex 2). Metadata lines start with a ##, each line begins with a key=value pairs, and have a description of the settings, samples and general experimental design of the genotyping. The data section begins with a single #; this first line is the header line the eight fixed, mandatory fields, used to record the genotyping calls: chromosome (CHROM), a 1-base position of the start of the variant (POS), unique identifiers of the variant (ID), the reference allele (REF), a comma separated list of alternate non-reference alleles (ALT), a PHRED-scaled quality score (QUAL), site filtering information (FILTER) and a semicolon separated list of additional, user extensible annotation (INFO) and information contained within each subsequent genotype column (FORMAT). After the FORMAT field, the sample IDs define the samples included in the VCF file. The following lines of the data section contain the variant site records. Variant site records do not start with any symbol. VCF data and metadata information have a controlled vocabulary for describing variants, however, the VCF format defines a syntactic format but no vocabulary, unique identifier or recommended content for describing samples and reference genome. Recently, in the frame of ELIXIR, a minimal list of metadata recommended fields (Table 4) to describe plant samples in the VCF file has been proposed (Beier et al., 2022). The goal of these recommendations is to link, through precise sample identifiers provided by BioSample (see below), variant data for plants to other information data sets (e.g. phenotypic, transcriptomic, metabolomic) submitted to EMBL-EBI repositories. The Global Alliance for specification of the VCF. See Genomics & Health (GA4GH) maintains the http://samtools.github.io/hts-specs/ for more details.

	Metadata field	Definition	Format	Example	Cardi nalit Y
1	##fileDate	Creation date of the VCF file	Date (ISO 8601, YYYYMMDD)	##fileDate=20120921	1
i	##bioinfor matics_sour ce	Chains of bioinformatics tools for creating the VCF file	URL, DOI	##bioinformatics_source=" <u>doi.org/10.1038/s41588-018-</u> 0266-x"	1
;	##reference _ac	Accession number of reference genome assembly used in the VCF file	/[(GCA/GCF)_(d){9}\. (0-9)*]/	##reference_ac=GCA_902498975.1	1
÷	##reference _url	URL of the reference genome assembly used in the VCF file	URL, DOI	##reference_url="ftp.ncbi.nlm.nih.gov/genomes/all/GCA /902/498/975/GCA 902498975.1 Morex v2.0/GCA 902 498975.1 Morex v2.0 genomic.fna.gz"	1
ł	##contig	Metadata about a single sequence in the reference genome assembly	Composite (see below)	##contig= <id=chr1h,length=522466905,assembly=gca_9 02498975.1,md5=8d21a35cc68340ecf40e2a8dec9428fa,s pecies=NCBITaxon:4513></id=chr1h,length=522466905,assembly=gca_9 	1:N
		The primary identifier of the sequence	String	ID=chr1H	1
		The length in base pairs (bp) of the sequence	Integer	length=522466905	1
		The assembly accession number this sequence belongs to	/[(GCA/GCF)_(d){9}\. (0-9)*]/	assembly=GCA_902498975.1	1

Table 4. Summary of recommendations for metadata formatting (from Beier et al., 2022)

Metadata field	Definition	Format	Example	Cardi nalit Y
	The md5 checksum of the sequence	MD5	md5=8d21a35cc68340ecf40e2a8dec9428fa	1
	The species of the sequence (NCBI Taxon ID)	/[(NCBITaxon):(\d+)] /	species=NCBITaxon:4513	1
##SAMPLE	Metadata about a single sample genotype that is part of the genotyping experiment in the VCF file	Composite (see below)	##SAMPLE= <id=samea104646767,doi="<u>doi.org/10.2564 2/IPK/GBIS/7811152"></id=samea104646767,doi="<u>	1:N
	The primary identifier (BioSamples Database identifier) of the genotyping sample	/[(SAM)(E N D)(A G)(\d+)]/	ID=SAMEA104646767	1
	The DOI of the genotyping sample (if available)	URL, DOI	DOI=" <u>doi.org/10.25642/IPK/GBIS/7811152</u> "	0-1
	The external identifiers under which this genotyping sample is registered in other databases (either 'FAO- WIEWS_instcode:genus:accession_nu mber' or 'DNS:database_identifier:identifier_s cheme:identifier')	See Definition	ext_ID="DEU146:Hordeum:HOR 1361 BRG" or ext_ID="ipk-gatersleben.de:GBIS:akzessionId:7811152"	0:N

 BCF2 format: is a binary, compressed equivalent of VCF that can be indexed with tabix and can be efficiently decoded from disk or stream. The relationship between BCF and VCF is similar to that between BAM and SAM. The Global Alliance for Genomics & Health (GA4GH) maintains the specification of the VCF. See http://samtools.github.io/hts-specs/ for more details.

Discrete genomic feature data and track files:

- BED format: is a simple, tab-delimited text format for representing track genomic features and their associated annotations linked to the genomic coordinates of a reference genome. Examples of such data are epigenetic DNA methylation data, ChIP-seq peaks, germline or somatic DNA variants, as well as RNA-seq expression levels. BED files are predominantly used for graphical display, but can also be queried by statistical analysis tools. BED files consist of one line per feature, with each line containing a minimum of three mandatory columns (chromosome, start, and end), and nine additional optional tab-separated columns for feature annotations (name, score, strand, etc). A BED file can optionally contain a header. However, there is no official description of the format of the header. It may contain one or more lines placed at the beginning of the list of features affected and be signified by different words or symbols, depending on its functional role or simply descriptive: genome browser options (browser); track name and configuration description (track) and other comments, such as the name of each column (#). BED files do not contain any metadata associated to them excepting the track name. See https://github.com/samtools/hts-specs and http://genome.ucsc.edu/FAQ/FAQformat.html#format1 for more details.
- BedGraph format: is a variation of the BED format used for representing continuous-valued data in track format, such as read coverage or signal intensities, in a genome browser. BedGraph files are tab-delimited text files, but they contain four columns (chromosome, start, end, and value) representing the genomic region and the associated data value. The bedGraph format is line-oriented. BedGraph data are preceded by a track definition line, which adds a number of options for controlling the default display of this track. Strand information is provided in the value column, negative values represent reverse strand, whereas positive

values represent forward strand. For more detailed information see http://genome.ucsc.edu/goldenPath/help/bedgraph.html

- GTrack format: a tabular format developed to provide a uniform representation for tracks of most types of genomic datasets. This track format data file format is capable of representing all 15 track types (Gundersen et al., 2011) since they have a flexible column specification and declaring syntactic properties at the beginning of the file. The GTrack format consists of 5 different line types, distinguished by the leading characters and numbered here by order of appearance in the file. Comments preceded by the character # are ignored by parsers and may be present anywhere in the fil. Header lines, preceded by ##, provide detailed information for the type of track. Column specification line, preceded by ###, provide detailed information about the origin of the track (reference, genome, sample, genomic coordinates, values, graphical representation...). Bounding region specification line, preceded by ####, specifies the region where we have information. Data lines, a tab-separated list of values without any preceding character, are defined by the column definition line. GTrack is able to replace most common track file formats and had the advantage that all GTrack types are supported by the FAIRtracks metadata standard (see below). For more detail see https://github.com/gtrack/gtrack/tree/master/gtrack/spec and https://fairtracks.net/standards/#standards-01-fairtracks.
- **BTrack format**: supports the same variety of informational content as GTrack, but in binary form. See <u>https://fairtracks.net/standards/#standards-01-fairtracks</u>.
- GTF/GFF3 formats: are tab-delimited text file formats used for describe functional regions of genomes. GFF3 is the most widely used format to annotate genomes. GFF/GTF lines have nine required fields that *must* be tab-separated. GFF/GTF share the same structure for the first 7 fields, while differing in the format of the ninth field (See Annex 2). The first seven lines define the sequence name, the source of the sequence, the feature type (Transcripts, exon, intron, promoter, 3' UTR, repetitive elements etc), the start and the end of the feature, the confidence score, the strand and the Frame (GTF) or Phase (GFF3). Column 9 contains attributes pertaining to the described feature. In GFF3 format, it contains a list of feature attributes (name, Id, alias, ontology, feature hierarchy, etc) in the format tag=value. Multiple tag=value pairs are separated by semicolons. In GTF, column 9 contains globally unique identifiers for the genomic locus of the transcript and the predicted transcript, respectively, separated by semicolon. For more details see https://github.com/The-Sequence-Ontology/Specifications/blob/master/gff3.md and

http://genome.ucsc.edu/FAQ/FAQformat.html#format1.

3.3.2. Models/syntax

In FairSharing.org there are 45 models and syntax standards for genetic data storage and exchange across various fields and domains (**Annex 1**). These standards ensure consistency, interoperability, and efficient sharing of data among different systems and users. The most 5common models and syntax standards for genetic data storage and exchange are listed in **Table 5**.

ACRONYM	NAME	Implementing databases or standards	Used for
XML	Extensible Markup Language,	NCBI Entrez Gene, ENA, DDBJ, UniProtKB, INSDC, Gene Expression Omnibus (GEO), InterPro, Phytozome, Gramene, PlantGBD, Planteome, BAR	data export, web services, or specific metadata representation

Table 5. Models and syntax standards most common in genetic databases.

		(Bio-Analytic Resource) Plant Genome Database, MaizeGDB			
RDF	Resource Description Framework	Planteome, Agronomic Linked Data (AgroLD	representing ontologies, linking data, and providing structured metadata		
Json	JavaScript Object Notation	Gramene, PlantGDB, Phytozome	data retrieval and representation, especially when interacting with web- based services		
CHADO, CHADO-XML	Modular scheme for biological database	Gramene, Solgenomics, TAIR	store diverse types of biological data, including sequences, annotations, ontologies, and genetic markers, among others.		
ISA, ISA-TAB	Investigation Study Assay Tabular	EVA, ArrayExpress, MIAME, MINSEQE, MIGS/MIMS	Capturing, describing and exchanging of experimental data and metadata		
OWL	Web Ontology language Format	Planteome, Agronomy Ontology Service (AO), Gene Ontology (GO), Sequence ontology (SO)	define the concepts, relationships, and semantics within these ontologies,		
BRAPI	Breeding API specification for the communication of plant breeding data	The Triticeae Toolbox (T3), CassavaBase, Integrated breeding platform	exchange of plant breeding and agricultural data across different software systems and platforms		

- XML: is a versatile markup language used for structuring and encoding data in a machinereadable format. Several databases that store genetic data use XML to represent, storage and exchange various types of genetic (meta)data, from sequences to annotations (Table 5). It is often chosen for its flexibility in structuring complex data and its compatibility with web-based data exchange. The specific usage of XML can vary between databases. For example, Gramene uses XML to provide structured data about genes, genomes, pathways, and annotations while Planteome uses XML to define and exchange ontology terms, annotations, and relationships. See https://www.w3.org/TR/rdf-syntax-grammar/ for more detailed info
- RDF: is a standard for describing resources on the web, using a graph-based model to represent data and their relationships. It is commonly used in the context of semantic web technologies and linked data, where it enables the creation of interconnected and machine-readable data networks. Some resources related to genomics and plant genetics might use RDF for specific purposes, such as representing ontologies, linking data, and providing structured metadata (Table 5). Planteome uses RDF to represent and provide structured data about plant traits, anatomy, and growth stages. RDF is used to enable the integration of plant phenotype data across different species. For more details see https://www.w3.org/RDF/
- JSON: is a lightweight data interchange format that is easy for both humans and machines to
 read and write. In the field of genomics and plant genetics, JSON is often used for data
 exchange through web services and APIs. It is commonly used to provide structured data to
 users and applications over the internet. While JSON may not be the primary format for data
 storage in these databases, it could be used for certain types of data retrieval and
 representation, especially when interacting with web-based services. For more details see
 https://json-spec.readthedocs.io/index.html
- CHADO/CHADOXML scheme: is a relational database modular scheme designed for storing, managing and integrating biological data. It is capable of representing many of the general classes of data frequently encountered in modern biology such as sequence, sequence comparisons, phenotypes, genotypes, ontologies, publications, and phylogeny (Mungall *et al.*, 2007), particularly genomic and genetic data. It's an open-source scheme that provides a structured framework for representing diverse biological information in a consistent and standardized manner. Chado was developed to address the complex and interconnected nature of biological data and to support integration and querying across various data types and sources. CHADO is part of the Generic Model Organism Database (GMOD) suite

(<u>www.gmod.org</u>), a collection of open source software tools for managing, visualising, storing, and disseminating genetic and genomic data that include tools such as Jbrowse, Galaxy, Biomart or Tripal. For more detail see <u>http://gmod.org/wiki/Chado</u> and <u>http://gmod.org/wiki/Chado XML</u>

- ISA/ISA-tab: The ISA (Investigation/Study/Assay) model is a general-purpose framework for capturing and describing the metadata associated with experiments in various scientific domains, including the life sciences (Sansone et al., 2012). ISA-tab is the original format developed by the ISA team. It's a simple, tabular format for representing investigation, study, and assay metadata. It was developed to provide rich descriptions of experimental metadata (i.e. sample characteristics, technology and measurement types, sample-to-data relationships) so that the resulting data and discoveries are reproducible and reusable. The ISA model is not tied to a specific database or biological standard but rather serves as a flexible structure that can be implemented and adapted by various projects and databases Different databases or standards dealing with genetic data such as EVA, ArrayExpress, MIAME, MINSEQE, MIGS/MIMS have implemented the ISA model with slight variations or customizations to suit their specific needs, but the core principles of capturing experimental metadata in an organized and standardized way remain consistent. See https://isaspecs.readthedocs.io/en/latest/index.html for more details.
- OWL language: is a powerful and expressive language used for creating ontologies—formal models that represent knowledge about a domain and the relationships between different concepts within that domain. OWL provides a rich set of constructs for describing classes, properties, individuals, and relationships between them, supporting the creation of hierarchies of classes and sub-classes, reflecting the inherent structure of the domain being modelled. Further, OWL ontologies can be serialized using RDF (Resource Description Framework), making them compatible with other Semantic Web technologies and allowing for easy integration with existing data. Some genetic resources or projects related to ontologies, functional annotations, and semantic integration currently (?) use OWL, for instance Gene Ontology (GO) and Sequence Ontology (SO). OWL is part of the Semantic Web stack, a set of technologies aimed at enhancing the meaning and interpretation of data on the World Wide Web. For more details see https://www.w3.org/TR/owl-ref/
- BrAPI: is an open standard and API (Application Programming Interface) designed to facilitate
 a standardized exchange of plant breeding and agricultural (meta)data, such as germplasm
 information, phenotypic and genotypic data, trial and experiment details, across different
 software systems and platforms. (Selby *et al.*, 2019). BrAPI is not a database itself but rather a
 set of standardized APIs that various databases and systems can implement to enable data
 exchange and integration. BrAPI re-uses existing data standards as much as possible and is
 compatible with both the FAO Multi-Crop Passport Descriptors and the minimum information
 standards for plant phenotyping. BrAPI aims to improve data interoperability and enable data
 sharing and integration among researchers, breeders, and organizations involved in plant
 breeding and crop improvement. BrAPI has gained popularity in the plant breeding and
 agricultural research communities because it addresses the challenges of data fragmentation,
 lack of interoperability and allow to develop software applications, databases, and tools. For
 more detail see www.brapi.org.

3.4. Identifier (ID) schemes standards

ID scheme standards serve for providing unambiguous and stable identification for individual objects of interest. Fairsharing has over 33 entries registered as ID scheme standards, however none has a direct relation exclusively with genetic data. In the case of Identifiers.org, **there are more than 350 ID scheme related to genetic data or their annotation** (see **Annex 3**). With the exception of centralized repositories and ontologies (Nucleotide Sequence Database, SRA, EVA, RefSeq, Ensembl, UniProt, InterPro, KEGG, Gene Ontology, Sequence ontology, etc), most identifiers in Identifiers.org are species-specific, taxa-specific or family-specific.

ID standards encompass various formats such as text, numbers, URLs/DOIs, and primary keys for genetic related objects that are assigned when the objects (raw sequence, genome, alignment, gene, marker, variant locus, ontology term) are created in the repositories, knowledgebases or in ontologies for a particular domain or area of study.

In the case of INSDC, sequence accession numbers have specific formats that might vary slightly between databases, but they generally follow a similar pattern. Here's the general format for sequence accession numbers in INSDC repositories:

- Prefix: The prefix indicates the type of submission and provides context for the sequence. Different prefixes are assigned to different types of data, such as genomic DNA, mRNA, coding sequences, non-coding RNAs, and more.
- Numbers (Digits): The numeric portion of the accession number follows the prefix and is unique to each sequence entry. It's usually a sequence of digits.

Each type of data is assigned a unique accession number following a specific format. For example:

- Genomes: all INSDC members use a standardized format for annotating genome assemblies. This format involves using the "GCA_XXXX" identifier followed by a unique numerical accession number to represent the entire genome assembly sequence and version of an organism. This standardized format ensures consistency and ease of reference when dealing with genome assemblies across different organisms and databases within the INSDC collaboration.
- Genes and Transcripts: The specific format can vary between databases, but it often includes a prefix that denotes the type of sequence. Accession numbers from GenBank often start with a two-letter prefix followed by digits. For example, "NM_001123456" for a RefSeq mRNA entry or "CP012345" for a genomic DNA entry. Accession numbers from ENA start with a letter prefix followed by digits. For example, "X12345" for a nucleotide sequence or "Y56789" for a transcript. Accession numbers from DDBJ also start with a letter prefix followed by digits. For example, "D12345" for a DNA sequence entry or "AB67890" for a transcript.
- **Splicing Forms:** Splicing forms, which represent alternative splicing isoforms of a gene, are often assigned to unique identifiers that are distinct from the primary gene or transcript accession numbers. These identifiers might include version numbers or other annotations to differentiate between different splicing forms.
- Variants: variants submitted in the context of a genomic study are accessioned with submitted SNP ID number ("ss#", that identifies the taxon, the reference genome, the study, the position and the ref/alt alleles) and a reference SNP ID number ("rs#"; "refSNP cluster"), that identifies a variant class in a genomic location of a taxon genome and which can be reported by one or more studies. Variants, such as single nucleotide polymorphisms (SNPs), insertions, deletions, and structural variants, are typically accessioned using unique identifiers.

Ideally, each genetic object should be assigned to a single ID to avoid confusion. However, most IDs found in Identifiers.org have synonyms in other databases, resulting in the assignation of different IDs to the same object. Detailed info of the IDs, such the pattern of the ID, resource URL and synonyms, used for different ontologies and databases are in **Annex 3**. To deal with multiple IDs, the concept of Persistent Unique Identifiers (PUID) has emerged as a potential solution. **PUIDs are designed to be**

permanent and steadfast identifiers, maintaining their validity on a global scale. It is crucial that PUIDs are never completely deleted but instead deprecated if necessary. Additionally, these identifiers should be effortlessly convertible between local IDs and URIs, allowing for seamless interoperability. A well-known example of a PID is a Digital Object Identifier (DOI) which is used to locate specific digital objects. Recently, the term Digital Genetic Object (DGO) has also been proposed (Manzella *et al.*, 2023), the idea is to create DGOs for each type of genetic information in INSDC repositories (e.g. nucleic acid sequence reads, data about gene expression and function, unsequenced markers and chromosomal segments) and link them to the DOI of the germplasm source material to facilitate discovery interoperability among genomic data and germplasm repositories. This proposal, however, is still in infancy (Manzella *et al.*, 2023).

Special case: Plant gene ID

The standardization description of gene nomenclature is of critical importance. It's important to note that the patterns for gene IDs can vary widely between organisms and databases (see **Annex 3**). The adoption of standardized nomenclature and IDs can be influenced by the research community, the organism's complexity, and the level of annotation available. Each one of the INSDC repositories uses their own centralized and stable ID pattern for genes. The gene ID patterns used in the repositories of the INSDC can vary depending on the organism and the type of gene annotation. Further, organism-specific communities have developed their own gene nomenclature standard system. **Table 6** shows plant gene nomenclature resources. Despite this, common formats and conventions are often followed:

- Locus Tag or Systematic ID: Many organisms use a systematic naming convention that often includes a short prefix followed by numbers. Organisms with well-defined genomes often use locus tags to identify genes in a sequential or systematic manner.
- Gene Name: Some genes are identified by their common or official names. They are often chosen based on their functions, characteristics, or roles in specific biological pathways. For example, the plant gene for Activating Transcription Factor 1 is often referred to as " ATF1."
- Accession Number-Based: Sometimes, genes might be linked to an accession number of a specific gene entry in the database. For instance, in GenBank, genes might be referenced using their associated accession number, such as "NM_001123456" for a RefSeq mRNA entry.
- **Synonyms or Aliases**: Genes might have synonyms or aliases that are used as identifiers. These can include both official and common names, as well as other identifiers used in the literature.
- **Standardized Gene Symbols:** For well-studied organisms, standardized gene symbols might be used. These symbols are usually short and informative names that represent the gene's function or role.
- Unique Identifiers: Some databases assign unique identifiers to genes that are independent of their names or other identifiers. These can be alphanumeric strings or combinations of letters and numbers.

	(, , , ,	, ,, ,,
Database name	URL	Species covered
Alfalfa Breeders Toolbox	alfalfatoolbox.org	Alfalfa
CassavaBase	cassavabase.org	Cassava
Citrus Genome Database	citrusgenomedb.org	Lemons, oranges, and more
Cool Season Food Legume Database	coolseasonfoodlegume.org	Lentil, pea, fava bean, chickpea
CottonGen	cottongen.org	Cotton, many species
Genome Database for Rosaceae	rosaceae.org	Apple, strawberry, rose, plums, pears, and more
Genome Database for Vaccinium	vaccinium.org	Blueberry, cranberry, bilberry, and more
GrainGenes	wheat.pw.usda.gov/GG3	Wheat, barley, oats

Table 6. Plant Gene Nomenclature Resources (Adapted from (Reiser et al., 2018))

Gramene	https://www.gramene.org	Maize, rice
International Grape Genome Program	http://www.vitaceae.org	Gravepine
Hardwood Genomics	hardwoodgenomics.org	Oaks, poplars, maples, chestnuts, and more
KnowPulse	knowpulse.usask.ca	Chickpea, common bean, lentil
Legume Information System	legumeinfo.org	Soybean, Medicago, cowpea, chickpea, and more
MaizeGDB	maizegdb.org	Maize
Medicago truncatula Genome Database	medicagogenome.org	Clover
MusaBase	musabase.org	Banana
Oryzabase, Rap-Db	shigen.nig.ac.jp/rice/oryzabase/	Rice
PeanutBase	peanutbase.org	Peanuts
Solanaceae Genomics Network	solgenomics.net	Tomato, potato, eggplant, petunia, and more
Soybase	soybase.org	Soybean
Sweet Potato Database	sweetpotatobase.org	Sweet potato
Т3	triticeaetoolbox.org/wheat	Wheat, barley, oats
TAIR	arabidopsis.org	Arabidopsis thaliana
TreeGenes	treegenesdb.org	1792 species of trees
YamBase	yambase.org	Yams

One of the main problems with gene ID is that researchers often encounter a mix of INSDC IDs and organism-specific gene IDs, names and gene products, which leads to confusion, missing information, and makes difficult to search or integrate data about genes (Reiser *et al.*, 2018). However, some resources provide cross-reference tools to help you map between different gene ID systems, enabling you to work with the IDs that best suit your research context. Whether to use organism-specific gene IDs or INSDC gene IDs depends on the context of your research and the goals of data integration and analysis. Both types of IDs have their advantages and considerations. Organism-specific gene IDs provide direct information about genes (gene annotations, including functional annotations, pathways, and other relevant data for that organism) in the context of a specific organism. Further, they are more intuitive and familiar to researchers working with that organism. INSDC gene IDs provide standardized access to genes across different organisms. This can be beneficial when working with multiple species or conducting comparative genomics or integrating genetic data from different organisms.

A solution to reduce the number of IDs assigned to the same gene and facilitate the integration gene data could be those used in Ensembl Plants (EMBL-EBI genome-centric portal for *plant* species of scientific interest, see below). Ensembl Plants, with genome for more than 150 species (see **Annex 4**), has adopted a combination of organism-specific gene IDs and INSDC IDs, depending on the gene and the organism being studied. For well-studied model organisms and species with established annotations, Ensembl use organism-specific gene IDs that are consistent with the existing nomenclature for those species. This helps Ensembl users from different organism communities to easily identify and locate genes they are familiar with, within the context of the species they are interested in.

3.5 Review of existing Semantic standards

Semantic standards play a crucial role in organizing, annotating, and exchanging metadata in a structured and machine-readable manner. They range from dictionaries to ontologies and provide definitions and unambiguous identification for concepts and objects (Sansone *et al.*, 2019). In addition, ontologies can provide a hierarchical structure of the terms. Hierarchical ontologies are the most common used, they organize concepts into a hierarchy of parent-child semantic relationships which provide a richer context for understanding the relationships between concepts (**Figure 2**). For identifying and accessing concepts, terms, and relationships ontologies use URLs and IDs. Both URLs and IDs are important components of ontology design and usage. URLs provide access to additional information and context, while IDs provide efficient and unique references for ontology terms.

GO:0004713 (F) (m) (2/JSON)

protein tyrosine kinase activity	Ancestor Chart Child Terms
Molecular Function	Annotation Guid
Definition (GO:0004713 GONUTS page)	
Catalysis of the reaction: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.	Blacklist Cross-Reference
Secondary IDs	
GO:0004718	Protein Complex Replaces
99,433 annotations	Replaced By
Synonyms	Co-occurring Te GO Stims
Oynonyms	Change Log

Synonyms are alternative words or phrases closely related in meaning to the term name, with indication of the relationship between the name and synonym given by the synonym scope.

Synonym	Туре
JAK	narrow
protein-tyrosine kinase activity	exact
Janus kinase activity	narrow

Ancestor Chart 🐼



Figure 2. Snapshot of the protein tyrosine kinase entry in GO, showing the richness of an ontology and highlighting the terms and hierarchies that are used to populate controlled vocabularies.

In Fairsharing.org there are 63 entries for semantic standards dealing with genetic data for all species (Annex 1). These ontologies provide a common language to enhance data integration, interoperability, and automated reasoning in genomics research.

In the context of genetics and genomics, especially for plant genetic metadata, several semantic standards are commonly used (**Table 7**).

ACRONYM	NAME	NAME Used for	
GO	Gene Ontology	describing gene functions, biological processes, and cellular components in	
		a hierarchical model	
SO	Sequence Ontology	sequence features	
OBI	Ontology for Biomedical Investigations	biological investigations, experiments, and assays (including genetics)	
BAO	BioAssay Ontology	describing various types of assays	
EDAM	Sequence Types and Features Ontology	analysis, modelling, optimisation, and data life-cycle	
EFO	Experimental Factor Ontology	annotation, analysis and visualization of samples, phenotypes and studies	
	DDBJ/ENA/GenBank Feature Table	features and characteristics of genetic sequences	
	Definition		
ΡΑΤΟ	Phenotype And Trait Ontology	phenotypes	

Table 7. Common semantic standards used for annotating and standardizing genetic metadata

Overview

Synonyms

PO	Plant Ontology	plant anatomy, morphology and growth and development
то	Trait Ontology	phenotypic traits in plants
AgrO	Agronomy Ontology	agronomic practices, techniques, variables
СО	Crop Ontology	crop-specific agronomic, morphological, physiological, quality, and stress
		traits
PECO	Plant Experimental Condition Ontology	Abiotic treatments, growing conditions and study types
NCBI	NCBI Taxonomic Database	Species taxonomic classification and nomenclature
Taxonomy		
ChEBI	Chemical Entities of Biological Interest	chemical compounds

Some of them such as GO and SO are strictly used for genetic annotations, while others like OBI, BAO, EDAM, EFO are used to describe metadata associated to the samples and protocols used to generate the genetic data:

- GO: it provides a standardized vocabulary for describing more than 84.220 terms related to gene functions, biological processes, and cellular components associated with genes and gene products (The Gene Ontology Consortium, 2017). GO is one of the most widely used ontologies in genomics and implemented in major public databases. See more details in http://www.geneontology.org
- SO: The Sequence Ontology (Eilbeck *et al.*, 2005) defines 1,454 terms to describe sequence features, such as exons, introns, and regulatory elements. It's used to annotate genomic sequences and variants. While not exclusively for experimental features, SO includes terms related to experimental features, such as "assembly", "SNP," "SSR," and "AFLP," allowing genetic markers to be annotated within a genomic context. See http://www.sequenceontology.org/ for more details.
- OBI: While broader in scope, OBI is an ontology for investigations, materials, protocols and instrumentation used, the data generated and the types of analysis performed on it (Bandrowski *et al.*, 2016). It contains 4,887 terms, among them terms related to genomics research as well as terms for various biological and molecular entities as methods, which can be used to annotate genetic markers and their properties. This ontology is the foundry of new ontologies such as Next generation biobanking ontology (NGBO) (Alghamdi *et al.*, 2023). See https://obi-ontology.org/ for more detailed description and https://github.com/Dalalghamdi/NGBO.
- BAO: is a a semantic description of bioassays and high-throughput screening results (Visser *et al.*, 2011). It includes more than 8700 terms for describing various types of assays, which can include genetic assays and techniques used to analyze genetic material. See http://bioassayontology.org/
- EDAM: is domain ontology of data analysis and data management in bio- and other sciences, and science-based applications (Ison *et al.*, 2013). It comprises more around 3500 concepts related to analysis, modelling, optimisation, and data life-cycle including those used in genomics. EDAM is used in numerous resources, for example Bio.tools, Galaxy, Debian, or the ELIXIR Europe training portal TeSS. See http://edamontology.org/page# and https://edamontology.github.io/edam-browser/#topic_3175 for more details.
- EFO: provides a systematic description of more than 50.600 experimental variables available in EBI databases (Malone *et al.*, 2010), and for projects such as the EMBL-EBI GWAS catalogue. It combines parts of several biological ontologies such as OBI, GO, Cell ontology, Environment ontology (see https://agroportal.lirmm.fr/ontologies/EFO/?p=mappings) and aims to support the annotation, analysis and visualization of samples, phenotypes and studies. See https://www.ebi.ac.uk/efo/ for detailed info.
- DDBJ/ENA/GenBank Feature Table Definition: The Feature Table Definition provides a structured format for annotating and describing the features and characteristics of genetic sequences in a standardized manner in the frame of INSDC (Cochrane *et al.*, 2016). This format

allows to provide detailed information about various elements within a genetic sequence, such as genes, coding regions, promoters, introns, exons, and more. While not include the rich semantics and relationships seen in more complex semantic ontologies, it does establish a standardized way of representing and communicating important information about genetic features within a sequence. For detailed info see https://www.insdc.org/submitting-standards/feature-table/.

 Phenotypic Quality Ontology (PATO): PATO provides a standardized vocabulary for describing phenotypic qualities, such as color, size, shape, and behaviour (Gkoutos *et al.*, 2004). It's used to describe phenotypes associated to genetic data in a consistent and structured manner. See http://obofoundry.org/ontology/pato.html for more detail

In addition, there are several ontologies specifically designed for representing plant genetics and genomics concepts and relationships related to phenotype. While most common are generic, some of them are designed specifically for an organism (for specific ontologies see databases in **Table 6**). The most common are:

- PO: it is a structured vocabulary and database resource that links plant anatomy, morphology and growth and development to plant genomics data (Jaiswal *et al.*, 2005). It contains more that 200 terms used to annotate metadata for genetic studies, gene expression data, phenotypic traits, and other plant-related information. For detailed info see <u>https://github.com/Planteome/plant-ontology</u>
- TO: it provides more than 5000 standardized terms for describing phenotypic traits in plants, including morphological, physiological, and molecular traits (Jaiswal *et al.*, 2002; Arnaud *et al.*, 2012). It supports data integration and analysis across different plant species. See https://github.com/Planteome/plant-trait-ontology for more information.
- AgrO: is an ontology for representing agronomic practices, techniques, variables and related entities. AgrO provides more than 4000 terms provides terms from the agronomy domain such data on field management, soil, weather and crop phenotypes. For detailed info see https://bigdata.cgiar.org/resources/agronomy-ontology/ for more information.
- CO: provides crop-specific ontology descriptions of agronomic, morphological, physiological, quality, and stress traits along with a standard nomenclature for different plant species (Shrestha *et al.*, 2012). In August 2023 CO comprises 4,235 traits and 6,151 variables for 31 plant species. See https://cropontology.org/ for more detailed info.
- **PECO:** it describes the treatments, growing conditions, and/or study types used in plant biology experiments (Jaiswal *et al.*, 2002). Currently has more than 3000 entries. See https://github.com/Planteome/plant-experimental-conditions-ontology for more information.
- NCBI Taxonomy: is a comprehensive hierarchical classification system that organizes and categorizes all known living organisms. It provides a curated and standardized classification and nomenclature for all of the organisms in the public sequence databases. NCBI Taxonomy provides a unique taxonomic identifier (TaxID) for each species, allowing researchers to accurately identify and reference organisms in genetic studies and to integrate genetic data from different sources by providing a common framework for species classification. Currently represents about 10% of the described species of life on the planet. For more details see https://www.ncbi.nlm.nih.gov/taxonomy.
- **ChEBI:** is a dictionary of molecular entities focused on 'small' chemical compounds (Hastings *et al.*, 2016). It incorporates an ontological classification of 183,420 compounds, whereby the

relationships between molecular entities or classes of entities and their parents and/or children are specified. See <u>https://www.ebi.ac.uk/chebi/init.do</u>.

3.6 Review of existing Minimum reporting guidelines

Minimum reporting guidelines outline the necessary and sufficient information vital for contextualizing and understanding a digital object. They are conformed by rules, guidelines, or recommendations established by consensus and approved by a recognized body. They accurately describe the plurality of relevant attributes of experiments, protocols, and their results by harmonizing both the structure of the (meta)data and their descriptions using a controlled vocabulary. The ISA (Investigation/Study/Assay) model is often used as a framework for capturing and organizing experimental metadata to ensure compliance with Minimum Information Reporting Standards. Our survey has rendered 26 Minimum reporting guidelines for genetic data that can be used for all species (**Annex 1**).

3.6.1. Minimum reporting guidelines for sequences

The most accepted at this moment for genetic data are Minimum Information about any (x) Sequence (MIxS) developed (Field *et al.*, 2008; Yilmaz *et al.*, 2011) by the Genomic Standards Consortium (GSC) (<u>http://www.gensc.org/pages/standards/checklists.html</u>). They have been adopted by several public repositories for genetic data, including those appertaining to the INSDC and The Genomes Online Database (GOLD; <u>https://gold.igi.doe.gov/</u>). MixS initiative provides a set of standards and guidelines for reporting biological sequence data in a consistent and informative manner. These standards are designed to ensure that essential contextual information accompanies sequence data submissions to public databases, improving the quality and usability of the data for researchers and data users. The following checklists are under the MIxS umbrella:

- MIGS: Minimum information about a genome sequence
- MIMS: Minimum information about a metagenome sequence
- MIMARKS: Minimum information about a marker gene sequence
- MISAG: Minimum information about a single amplified genome sequence
- MIMAG: Minimum information about a metagenome-assembled genome sequence

MIGS and MIMARKS are further divided into additional subchecklists, based on the genome sequence in question, or the sequencing type.

- MIGS-EU: MIGS for eukaryotic genome sequences
- MIGS-BA: MIGS for bacterial and archaeal genome sequences
- MIGS-PL: MIGS for plasmid sequences
- MIGS-VI: MIGS for viral genome sequences
- MIGS-ORG: MIGS for organelle sequences
- MIMARKS-SP: MIMARKS-survey for marker gene sequences obtained directly from the environment
- MIMARKS-SU: MIMARKS-specimen for marker gene sequences from cultured or voucheridentifiable specimens

In general, all MIxS checklist covered the following concepts for describe and structure metadata:

Sample, Environmental Context and Investigation:

- **Project name**: Name of the project within which the sequencing was organized.
- **Biological Source:** Information about the biological origin of the sample, including taxonomic classification and ecological context.
- **Geographical Location:** Geographic coordinates and environmental context of the sampling site.

• Environmental Parameters: Relevant environmental conditions of the sampling site. Sequencing and Experimental Details:

- Sequencing Platform: Information about the sequencing instrument or platform used.
- **Sequencing Method:** Details about the sequencing method employed, such as shotgun or targeted sequencing.

• Library Preparation: Information about how the sequencing library was prepared.

Bioinformatics and Data Processing:

- Data Processing Steps: Description of the steps taken during data processing and analysis.
- Assembly and Annotation: Details about genome assembly and annotation methods used.
- Quality and Reliability:
- Quality Control: Information about quality control measures applied to the data.

• **Coverage and Read Statistics:** Data on read depth, coverage, and other relevant statistics. **Accession and Submission:**

- Accession Numbers: Any accession numbers associated with the data submission.
- **Database and Repository:** Information about the public database or repository where the data is being submitted.

The whole list of minimum information required for the current release (v6.0) for each MIxS checklist is in **Annex 5**. This file contains the complete list of core descriptors, which are shared by all MIxS checklists and, the checklist sequence type-specific descriptors. Users of MIxS should first determine the type of genome or marker gene sequence that they have, and then proceed to complement the core descriptors with the checklist specific mandatory descriptors to achieve MIxS compliant metadata. See <u>http://www.gensc.org/pages/standards/checklists.html</u> and <u>https://github.com/GenomicsStandardsConsortium/mixs/tree/main</u> for more detailed information. In addition, MIxS team have developed a series of environmental packages which expand on the basic set of mandatory terms to help flesh out metadata expectations for more specific environmental samples (**Annex 5**). These packages and the combination of MixS with environmental packages are described in more detail on <u>https://genomicsstandardsconsortium.github.io/mixs/</u>

One of the weaknesses of MIxS in relation to linkage with EURISCO is that MIxS Sample, Environmental Context and Investigation information is not fully compliant with other standards widely recognized for plants such as The FAO/Biodiversity Multicrop Passport Descriptors (MCPD; <u>https://alliancebioversityciat.org/publications-data/faoipgri-multi-crop-passport-descriptors-mcpd</u>) and Minimal Information About Plant Phenotyping Experiments (MIAPPE, <u>http://www.miappe.org/</u>). Despite this, MIxS enable to link plant genetic resources in EURISCO to sequences in INSDC repositories (such as BioSamples) through source materials identifiers (MIXS:0000026: source_mat_id), that can be used for PGR DOIs and (MIXS:0001107: samp_name) for BiosampleID.

3.6.1. Review of existing Minimum reporting guidelines for tracks metadata

A genetic data track refers to a visual representation of genetic or sequence-related information plotted along a linear or two-dimensional axis. These tracks are commonly used in genomics and bioinformatics to display various types of genetic and genomic data, such as DNA sequences, gene annotations, sequence variants, epigenetic modifications but they can also be queried by statistical analysis tools (Raney et al., 2011; Thorvaldsdóttir et al., 2013; Martin et al., 2023). The visualization of data in tracks allows researchers to explore and analyse complex genetic information in a comprehensible manner. Genetic data tracks are often displayed in genome browsers or visualization tools, where they are stacked vertically or horizontally to provide an overview of the genome or a specific region of interest. Each track may represent different types of data, with its own unique visual representation and annotations. File formats used to represent tracks were not designed with FAIR data principles https://f1000research.com/articles/10-268/v1(Wilkinson et al., 2016), in particular with respect to metadata (Gundersen et al., 2011). Thus, their potential impact through re-use is greatly limited. Recently a draft for genomic track metadata (FAIRtracks) has been proposed (Gundersen et al., 2021). Metadata are implemented as a set of JSON Schemas organized around four (meta)data models, namely studies, samples, experiments and track (see https://github.com/fairtracks/fairtracks_standard#overview-of-structure-of-the-fairtracks-standard and https://fairtracks.net/fair/#fair-02-metadata-models). The minimal set of attributes of each metadata model are:

- FAIRtracks document: Version id, version date, ontology versions, URL to original source
- Track Collection: Name, description, URL to original source, contact info
- Study: Name, publications, contact info
- Sample: Species, biospecimen class, sample type (e.g., specific cell type, cell line, tissue), phenotype
- Experiment: (Sample OR upstream experiment), technique, biological target (e.g., gene, motif, phenotype), lab/compute protocols
- Track: Assembly details, file URL, label, description, ID of source collection, IDs of raw files, file format, type of condensed data, genometric track type, checksum

Each metadata FAIRtrack model can be mapped to objects in other revelat metadata models (Table 8).

FAIRtrack	INSDC	ISA	Other	Comments
Track collection	SRA: Submission	Investigation	Track Hub Registry:	Can represent both original repository
	EGA: Dataset		Track Hub	submissions,
			GSuite: Track	as well as other sets of track files, e.g., as
			collection	analysed in a
				research paper.
Study	Study	Study		
Sample	Sample	Sample		
Experiment	Experiment &	Assay & Process		"aggregated_from" attribute allows
	Analysis			provenance
				through all experimental steps
Track	Analysis	Data	Track Hub Registry/	"raw_file_ids" can link to original data files in
			GSuite: Track	case a full
				experiment trace is not available
				"source_coll_ref" links to the source track
				collection if
				current collection is an <i>ad hoc</i> mix

Table 8. Mapping of FAIRtracks objects to objects in other metadata standards (Source (Gundersen et al., 2021)).

Metadata recomendations for FAIRtracks applied to Ensembl TrackHub tracks (<u>https://www.ensembl.org/info/website/trackhubs/index.html</u>) recommend to store track file in binary formats such as BigBed, BigWig or BCF, link experiments and studies to the European Genome-phenome Archive (EGA)https://f1000research.com/articles/10-268/v1 and Samples to as described in BioSamples. For more detail of FairTracks and tools see <u>https://fairtracks.net/</u>.

3.6.2 Review of existing standards for visual representation of genetic data

Visual representation of genetic data plays a crucial role in understanding the complexity and relationships within genomes, including the presentation of variants. There are some standards developed.

One of the most used standards for visual representation of genetic data is the Synthetic Biology Open Language Visual (SBOL Visual) (Baig *et al.*, 2021). This is a standard notation and visual representation system designed specifically to represent synthetic biology designs and genetic constructs in a standardized and intuitive way. It provides a graphical language for depicting biological parts, devices, and genetic circuits, making it easier for researchers to communicate complex synthetic biology concepts and designs. See more details in <u>https://sbolstandard.org/</u>. Key features of SBOL Visual include:

- **Standardized Symbols**: SBOL Visual provides a set of standardized symbols and glyphs that represent various biological components, such as promoters, coding sequences, terminators, and more. These symbols are designed to be easily recognizable and consistent across different design representations.
- **Hierarchy and Composition:** SBOL Visual allows for the hierarchical representation of genetic constructs. Complex designs, such as genetic circuits composed of multiple components, can be depicted in a way that shows the arrangement and connectivity of the different parts.
- **Visual Annotation:** Annotations can be added to the symbols to provide additional information, such as the name of the component, its sequence, and other relevant metadata.

Since this SBOL Visual aims to enhance the communication and sharing of synthetic biology designs is not directly applicable for the integration of genetic data into EURISCO, however it would be useful for illustrating future genetic engineered plants.

In addition, genome browsers offer powerful **visualization** tools for genetic data, an interactive interface that allows users to navigate, analyse, and interpret genomic information, including genes, regulatory elements, variants, and more **in the context of the genome** and gain insights into **their functional effects and relationships**, which is crucial for interpreting complex genomic information and making informed research decisions. Some of the most widely used genome browsers include:

UCSC Genome Browser (<u>https://genome.ucsc.edu/</u>: is one of the most widely used genome browsers. It provides a user-friendly interface to explore genomes of various species and offers a wide range of tracks for genes, transcripts, regulatory elements, genetic variants, epigenetic marks, and more, allowing multiple annotation tracks and data visualization options (Figure 3). UCSC Genome Browser allows users to upload and visualize their own data alongside the reference genome.



Figure 3. Snapshot of UCSC Genome Browser multiple track view

• Ensembl Genome Browser (http://www.ensembl.org, <u>https://plants.ensembl.org</u>) (Figure 4): it offers a comprehensive genome annotation for a wide range of species. Ensembl provides gene annotations, transcripts, regulatory elements, variation data, and more (Yates *et al.*, 2022). It allows users to visualize their data in the context of the Ensembl genome, supports advanced searching and filtering options and offers a REST API for programmatic access to data.



Figure 4. Snapshot of Ensembl Genome Browser

 NCBI Genome Data Viewer (<u>https://www.ncbi.nlm.nih.gov/genome/gdv/</u>) (Figure 5): developed by the National Center for Biotechnology Information (NCBI), it integrates data from GenBank, RefSeq, and other NCBI databases and provides interactive visualization of genomes with features such as genes, transcripts, and genetic variations. Also allows users to upload custom tracks.

NIH National Librar	tog In
	Have you explored our new Comparative Genome Viewer (CDV) yet?
Genome Data Viewer	Home Starte Thu page Result AI Move Today - Move ("Move Today - Move ("Move Today - Move ("Move Today - Move ("Mo
Homo sapiens (human)	Assembly: GRCh38_p14 (GCF_00001405.40) • Chr 1 (NC_000001.11) •
earch assembly Clocetion, gene or phenotype Examples P	
Assemblies	Exam Navigator: There are too many (330.1) genes in the region.
Ideogram View	Pileade namonia the region to enable even navigation.
wlaced/unlocalized scatfolds 155 t loci/patches 514	ja je koncentra dru dra jest je v jest je v jest jest jest jest jest jest jest jest
	Lave series, and bill bill v2 Lave series, appropries (filtered), NGE Emer escalar and a series
Tracks and User Data	
BLAST	20 20 20 20 20 20 20 20 20 20 20 20 20 2
Tracks by Accession	<u>1 pan pan pan pan pan pan pan pan pan pan</u>
Assembly Region Details	NC_200001.13: E_34M(34,554.42: r/l)
Making .	

Figure 5. Snapshot of NCBI Genome Data Viewer

In addition, genetic variants, such as single nucleotide polymorphisms (SNPs) and insertions/deletions (indels), can be visually represented in genome browsers. Besides visual representation, these browsers also often include the position of the variant on the genome, allele frequencies, functional annotations, linkage disequilibrium (LD) pattern and phenotypic associations (**Figures 6-7**)



Figure 6. Snapshot variant description in EnsemblPlants.

Common (1000 Genomes Phase 3 MAF >= 1%) Short Genetic Variants from dbSNP Release 155 (rs117018032)								
dbSNP: <u>rs117018032</u> Position: <u>chr11:71904432-71904432</u> Band: 11q13.4 Genomic Size: 1 View DNA for this feature (ho19/Human)								
Refere Alterna	nce allele: G ite allele: A							
Allele	1000Genomes	dbGaP_PopEreg	TOPMED	KOREAN	SGDP_PRJ	томмо	GnomAD	Korea1K
G	4949/5008 (0 988219)	14411/14420 (0 999376)	263922/264690 (0 997098)	2836/2922 (0 970568)	6/12 (0 500000)	16440/16758 (0.981024)	138612/138842 (0 998343)	1767/1832 (0.964520)
A	59/5008 (0.011781)	9/14420 (0.000624)	768/264690 (0.002902)	86/2922 (0.029432)	6/12 (0.500000)	318/16758 (0.018976)	230/138842 (0.001657)	65/1832 (0.035480)
Submi Variati Interest Va Va Va Va Va Va Va Va Va Va Va Va Va	Lossod (Scrint) [Interest (Boooder) [Intervence (Screener)] Lossod (Scrint) [Intervence (Screener)] Submitted by: 1000GENOMES, EVA, GNOMAD, GRE, HUMAN LONGEVITY, JMKIDD LAB, KHV HUMAN GENOMES, KOGIC, KRGDB, SGDP_PRJ, SSMP, TOMMO_GENOMICS, TOPMED Variation class/type: snv Interesting or anomalous conditions noted by UCSC: Variant is "common", i.e. has a Minor Allele Frequency of at least 1% in some, but not all, projects reporting frequencies. Variant is "rare", i.e. has a Minor Allele Frequency of less than 1% in some, but not all, projects reporting frequencies. Variant is "rare", i.e. has a Minor Allele Frequency of less than 1% in some, but not all, projects reporting frequencies. Variant is "rare", i.e. has a Minor Allele Frequency of less than 1% in some, but not all, projects reporting frequencies. Variant is "rare", i.e. has a Minor Allele Frequency of less than 1% in some, but not all, projects reporting frequencies. Variant is "rare", i.e. has a Minor Allele Frequency of less than 1% in some, but not all, projects reporting frequencies. Vis variant overlaps another variant with a different type/class. UCSC Spredicted function relative to selected gene tracks: UCSC Genes FOLR1 (uc001os 2) intron variant UCSC Genes FOLR1 (uc001os 2) intron variant UCSC Genes FOLR1 (uc001ors 2							
Data la	st updated at UCSC: 3	-						
Data last updated at UCSC: 2023-03-27 11:28:33 Description This track shows shot genetic variants (up to approximately 50 base pairs) from dbSNP build 155: single- nucleotide variants (SNVs), small insertions, deletions, and complex deletion/insertions (indels), relative to the reference genome assembly. Most variants in dbSNP are rare, not true polymorphisms, and some variants are known to be pathogenic. For hg38 (GRCh38), approximately 998 million distinct variants (RefSNP clusters with rs# ids) have been mapped to more than 1.06 billion genomic locations including alternate haplotype and fix patch sequences.								
dbSNP mapped all of wh	remapped variants from to more than 1.02 billio ich are included in UCS	hg38 to hg19 (GRCh37); on genomic locations inclu SC's hg19).	approximately 981 million di Iding alternate haplotype and	stinct variants were I fix patch sequences (r	not			
This tra	ck includes four subtrac	ks of variants:						

Figure 7. Snapshot variant description in UCSC Genome Browser

3.6.3 Review of existing standards and public repositories for linked genotype and phenotype data.

Characterization/sequencing of PGRFA is regularly performed on cultivars, landraces, farmer's breeds, or even crop wild relatives. This aims at linking phenotype and genotype (QTL and GWAS) and generally produces large amounts of (digital) data, but underlying genotype data and the associated sample and population metadata have not been routinely submitted to appropriate archives. Actually there are some standards for (meta)data of GWAs such as seqGWAS (McMahon *et al.*, 2021) and those used in GWAS Catalog (https://www.ebi.ac.uk/gwas/home) or in the database of Genotypes and Phenotypes (dbGaP) dbGAP (https://www.ncbi.nlm.nih.gov/gap/) that can handle with array-based genotyping and sequencing-based association studies, however they are only dedicated to human biomedical research.

Several other international initiatives are on-going to agree on data models that specify standards and for different types of data in relation to linking plant phenotype to genotype facilitating the exploration of genetic variations, QTLs, genetic markers, and phenotypic traits, enabling researchers to better understand the genetic basis of plant traits and develop improved crop varieties. Most of these initiatives to standardize QTL and GWAs studies and their results are private or organism-specific initiatives , such as Gramene (https://archive.gramene.org/qtl/; (Tello-Ruiz *et al.*, 2021)), SoyBase (https://www.soybase.org/search/qtllist by symbol.php, https://www.soybase.org/GWAS/list.php), MaizeGDB (https://curation.maizegdb.org/qtl.php), WheatIS (https://urgi.versailles.inrae.fr/wheatis/), CottonGen (https://www.cottongen.org/tripal_megasearch?datatype=tripal_megasearch_qtl) or Solgenomics (https://solgenomics.net/search/phenotypes/qtl)

Only a few initiatives aim to involve many species. The earliest one was **Minimum Information for QTLs and Association Studies (MIQAS). MIQAS** is a standard composed by a series of file formats designed to describe in a standardized way the results from a QTL or association study (Figure 8). They include

- **Experiment description file**: Contains meta-information and provides links to the rest of the data.
- **Population description file**: Describes the population used for the analysis.
- Pedigree file: Contains sex and pedigree for the individuals.
- **Trait description file:** Describes the trait(s) under investigation. More than one trait can be covered in a single file.
- Marker description file: Provides accession numbers and possible alleles for all markers.
- Map file: Provides the genetic map for the markers as generated on the study sample.
- Genotype data file: Contains the genotypes for all markers vs individuals.
- **Phenotype data file:** Contains the phenotypes for all traits vs individuals.

• **Results file:** Contains specifics for the analysis and location of qtls and associated markers. Despite the huge effort done for built MIQAS, it is not currently maintained and no widely implemented.



Figure 8. Overview of experiment design that is covered by the MIQAS_TAB specification (source <u>https://miqas.sourceforge.net/specification/MIQAS_TAB_specification.html</u>)

In addition, the French National Institute for Agricultural, Food and Environment (INRAE) initative GnpIS (Steinbach *et al.*, 2013)(<u>http://urgi.versailles.inra.fr/gnpis</u>) links phenomic, genetic, and genomic data and handles different types of data in the scope of genetics and genomics for plants including forest trees and fungi: genetic resources, polymorphisms and genotyping data, phenotyping data, association data, genetic maps and QTLs data.

GnpIS provides a series of complete and agreed FAIR compilant standards and ontologies for QTLs and GWAs (meta)data (**GnpisQTL, GnpisMetaQTL and GnpisAssso**) that are relevant for all species. See <u>https://urgi.versailles.inrae.fr/Data</u> for more details. See **Table 9** for a summary of main (meta)data to be submitted in these standards.

Table 9. Main information required for submission in GnpisQTL, GnpisMetaQTL and GnpisAssso standards

Sheet	Description	QTL	MetaQTL	Association
Contact	Professional information about persons involved in the project	Mandatory	Mandatory	Mandatory
Project	Information about projects	Mandatory	Mandatory	Mandatory

Institution	Information about institutions	-	-	Mandatory
Мар	Information about maps	Mandatory	Mandatory	
Plant material	Information about plant accessions studied	-	-	Mandatory
Population	Information about populations studied	Mandatory	Mandatory	
Experiment	Information on experimentations	Mandatory	Mandatory	Mandatory
Variable	List of variables observed in this trial. Ideally they are part of a			Mandatan
variable	well identified ontology.	-	-	wandatory
Measure	Measures for each experimentation	Mandatory	Mandatory	-
Marker	Description of the marker genomic location associated with the	Mandatan	Mandatan	Mandatan
Warker	data.	wandatory	wandatory	wandatory
Mapping	Localization of markers on a map	Mandatory	Optional	-
QTLDetection	Information on QTL detections	Mandatory	Mandatory	-
QTL	Localisation of QTLs on a map	Mandatory	Mandatory	-
QTL XREF	Description of the references for the QTL	Optional	-	-
MetaQTL	Information about metaQTLs	-	Mandatory	-
MetaAnalysis	Information about meta-analysis	-	Mandatory	-
MappingExperiment	Parameters needed for MetaQTL algorithm	-	Mandatory	-
Software	Software used	-	Mandatory	
Association analysis	associations analyses performed for this experiment	-	-	Mandatory
Linkage	Description of the Linkage Desequilibrium associated with the			Ontional
disequilibrium	data.	-	-	Optional
Kinship	Description of the kinship associated with the data.	-	-	Optional
Structure	Description of the structure associated with the data.	-	-	Mandatory
Association results	results of association associated with the data	-	-	Mandatory
Software	Software used	-	Mandatory	-
Publication	References of each publication	Optional	Optional	Optional

The last initiative for linking plant genetic data to phenotypic data comes from the ELIXIR Plant Community (https://elixir-europe.org/communities/plant-sciences). ELIXIR Plant Community has created **The plant genomics tool assembly** (https://rdmkit.elixireurope.org/plant genomics assembly), a Research Data Management Kit (RDMkit) for FAIR-ification of Plant Genotyping Data and its linking to Phenotyping (**Figure 9**). This online guide contains a set of instructions for managing plant genomics and genotyping data throughout their life cycle, with a particular focus on ensuring traceability of the biological material to enable interoperability with plant



phenotyping data.

Figure 9. The plant genomics tool assembly (source <u>https://rdmkit.elixir-</u> <u>europe.org/plant genomics assembly</u>). The roadmap of the Plant Genomics Tool Assembly recommends to submit samples to Biosamples, before submitting genomic data, with MIAPPE compliance validated using BioSamples' plantmiappe.json template. To ensure interoperability with plant phenotyping and genotyping data, the same PUIDs must be used in both the genotyping and phenotyping experiments as well in germplasm repository, preferably EURISCO. It is recommended that the biological plant material is accurately described using MCPD. Submission of sample descriptions to BioSamples can be done as early as the data collection stage, but at the latest, must accompany submission of the genomic data to the European Nucleotide Archive (ENA) or of genotyping data to the European Variation Archive (EVA). Reference genomes for genome assembly and annotation should be obtained from Ensembl Plants or PLAZA (https://bioinformatics.psb.ugent.be/plaza/), if available. Genetic variant data must be produced in the VCF format enriched with VCF metadata specifications (Beier et al., 2022). All sequencing data collected in plant genotyping experiments should be submitted to ENA together with metadata compliant to the GSC MIxS plant associated checklist. The final results of such studies in the form of VCF files should be submitted to EVA. Variant data and its associated phenotype can be visualized and reused from Ensembl Plants, PLAZA or FAIR Data-finder for Agronomic REsearch FAIDARE (https://urgi.versailles.inrae.fr/faidare/).

3.7 Quality control standards: how to QC data

Quality control (QC) thresholds are often used to assess the quality and reliability of genetic data, including data related to plant genetics. One point does not record in standards and file reviewed is quality control (QC) thresholds for submitting genetic data to public repositories. While there is no specific universal QC threshold standards that apply exclusively to plant genetics, many general QC practices and guidelines are commonly followed to ensure the quality of genetic data across various organisms, including plants. In fact, the responsibility to submit high quality sequence data to public repositories lies on the authors. Some common QC steps and considerations for plant genetics data might include:

- Sequence Quality:
 - Evaluating sequence quality scores and base-call accuracy.
 - Trimming low-quality bases and adapters from sequencing reads.
- Read Mapping:
 - Assessing the alignment quality of sequencing reads to the reference genome.
 - Filtering out poorly aligned or ambiguous reads.
- Variant Calling:
 - o Applying filters to variant calls to exclude low-quality or spurious variants.
 - o Considering variant depth and allele frequency thresholds.
- Duplicate Removal:
 - Identifying and removing PCR or sequencing duplicates that can affect downstream analyses.
- Coverage Analysis:
 - $\circ~$ Evaluating the coverage depth across the genome to ensure even and sufficient coverage.
- Contamination Detection:
 - Checking for potential sample cross-contamination or contamination with other species.
- Batch Effects:
 - o Identifying and addressing potential batch effects or technical variations in data.

- Replication and Validation:
 - Ensuring that results are reproducible and validated using independent methods or replicates.
- Genotype Concordance:
 - Comparing genotypes with known standards or replicate samples to assess concordance.
- Variant Annotation:
 - Annotating variants with functional information and considering the impact on genes and regulatory regions.

3.8 Recommendations for linkage of genetic data with EURISCO

Following the principle of requiring minimal changes to existing systems while maximizing advantages for users (standardization, long term storage, interoperability and funding), **one practical pathway of linking genetic data with germplasm sources, such as EURISCO, is to use repositories, knowledgebases and standards implemented by the International INSDC repositories** (Manzella *et al.*, 2023), especially those hosted in the EMBL-EBI.

For linking genetic metadata between INSDC and EURISCO, we must consider the following steps:

- **Data Identification and Linking:** Use shared identifiers or accession numbers to link genetic data in INSDC with corresponding metadata in EURISCO.
- **Use Common Standards:** both INSDC and EURISCO support common metadata standards, we recommend using those standards to ensure data consistency and exchangeability.
- **Custom Integration:** Develop custom integration methods or middleware that can bridge the gap between the two systems, translating and transferring data as needed.
- **Data Transformation:** Convert the data from the format used by one system to a format understood by the other, ensuring data integrity and consistency.
- Web Services and APIs: Explore the use of web services or APIs that are specific to the types of data you're exchanging. INSDC and EURISCO might offer APIs or services that facilitate data exchange.
- **Consult Experts:** It's advisable to involve experts in data integration, biodiversity informatics, and genomics to guide the integration process effectively.

Considering these steps, we recommend:

- Follow The plant genomics tool assembly (<u>https://rdmkit.elixir-europe.org/plant genomics assembly</u>) for genetic data submission to EMBL-EBI
- Use the standard file formats (or their compressed versions) described in **Table 3** and if possible to use for metadata on these file header the same identifier scheme and vocabulary proposed in minimal list of metadata fields for VCF (**Table 4**) (Beier *et al.*, 2022), specially for the equivalents of reference, contig and sample (BioSample, germplasm DOI). This will allow to link, through precise sample identifiers provided by BioSamples, raw and aligned sequences and variant data to other information recorded in the same sample (e.g. phenotypic, transcriptomic, metabolomic) but also to passport data in germplasm resources such as EURISCO.

- For Gene ID use the established nomenclature standards for the genome version of the organism you are studying (**Table 6**). In addition, it should ensure that gene IDs correspond exactly to the gene/gene products for a given assembly.
- Genetic marker data use as unique ID the EVA #SS and #RS codes.
- For tracks, we recommend following FAIRtracks metadata standards, use GTtrack files with rich metadata and submit them to the ENA or SRA and register in Track hub.
- Use preferentially ontologies reported in **Table 7**
- Redefine plants MixS standards to be MCPD and MIAPPE compliant.
- For GWAs and QTLs there is a need to agree standards for the plant community. A good solution would be the GnpisQTL, GnpisMetaQTL and GnpisAssso standards, however they need be MCPD and MIAPPE compliant.
- Create a centralized repository similar to those GWAS Catalog (<u>https://www.ebi.ac.uk/gwas/home</u>) or database of Genotypes and Phenotypes (dbGaP) dbGAP (<u>https://www.ncbi.nlm.nih.gov/gap/</u>) for submitting standardized QTL and GWAS data, including those that are published in the literature
- Use Ensembl plants as standard for genome, genes and variant visualization tool.
- Define QC thresholds standards for each type of sequence submitted to the EMBL-EBI repositories.
- Promote the use of BrAPI by developing APIs to exchange associated metadata or phenotypic data linked to genetic data between INSDC and EURISCO and between INSDC and EURISCO and other repositories
- Join PRO-GRACE to ELIXIR plant community

3.9. Discussion

To better describe and understand the genome and PGR genetic diversity stored in EURISCO, whether through genotyping/re-sequencing studies or de novo sequencing of new genotypes, it is essential to integrate passport, phenotypic, and genotypic (meta)data. Both data and metadata should also be formatted in standardized representations to enable automated processing and prevent errors arising from manual manipulations, particularly in the case of extensive datasets. This necessitates a community-wide consensus on annotation guidelines and tools for data preparation.

In this deliverable, we assess the strengths and weaknesses of the most common standards and databases to evaluate their suitability for linking genetic data with EURISCO. Additionally, we propose a set of recommendations that the PRO-GRACE community can follow in pursuing this objective.

The success of these standards resides on community adoption, influenced by factors such as publisher enforcement and the availability and user-friendliness of associated tools (Adam-Blondon et al., 2016; Pommier et al., 2019; Papoutsoglou et al., 2020). To foster universal adoption of the recommended standards and their future implementation, we propose the following steps:

- Develop detailed guides and tutorials
- Store them at the EURISCO central hub for direct download, along with comprehensive guides and tutorials
- Host them on GitHub for collaborative editing and versioning
- Include them in RDMKit and Fairsharing collections to achieve wider dissemination
- Conduct training courses in collaboration with WP1 partners to educate and encourage the PGR research community to embrace reporting standards from the outset of their research

 Advocate for journal adherence to PGR reporting standards to ensure consistency in published datasets

Deviations

No deviations

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Annex 1. Databases, public repositories and standards in FAIRsharing.org

related to genetic information

							FAIRorg	plant species	Applied to	o		
FAIRsharing URL	FAIRsharing DOI	Record Name	Record homepage URL	Resource Type	Manintenace	Ready-to-use	recommended	accepted	species	Туре	ELIXIR recommended	provider
										Model/formats or		
		BrAPI The Breeding API	https://brapi.org/	standard	maintained	ready-to-use	recommended	All plant species		syntax:models/syntax	recommended	
https://fairsbaring.org/93	10 25504/EAIRsharing hfgman	ACE format	format%20	- standard		ready-to-use			All species	svotax:Format		
https://fairsharing.org/2115	10.25504/FAIRsharing.anpa6	A Systematic Annotation Package	https://asap.ahabs.wisc.edu/asap/home.php	database	1	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/1494	10.25504/FAIRsharing.7tx4ac	Access to Biological Collection Data DNA extension	http://www.tdwg.org/standards/640/	standard		ready-to-use			All species	Minimum reporting guidelines		
https://fairsharing.org/1738	10.25504/FAIRsharing.8hcczk	Addgene	http://www.addgene.org/	database	maintained	ready-to-use	recommended		All species	Knowledgebase		
https://fairsharing.org/2584	10.25504/FAIRsharing.83wDfe	Ag Data Commons	https://data.nal.usda.gov/	database	maintained	ready-to-use	recommended		All species	Knowledgebase		
https://fairsharing.org/1742	10.25504/FAIRsharing.kn4ycg	AgBase	http://www.agbase.msstate.edu/	database	maintained			All plant species		Knowledgebase		
https://fairsnaring.org/2847	10.25504/FAIKsnaring.2PKttG	Agronomic Linked Data	http://www.agroid.org/	database	maintained	ready-to-use		All plant species		Knowledgebase		+
https://fairsharing.org/2673	10 25504/FAIRsharing ale954	Signaling database	http://allomans.hii.a-star.edu.sg	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/4894	N/A	AlphaFill	https://www.alphafill.eu	database	maintained	ready-to-use			All species	Knowledgebase		
			https://robertdavidstevens.wordpress.com/2010/08	3	1							
https://fairsharing.org/1050	10.25504/FAIRsharing.9zpcgj	Amino Acid Ontology	/09/an-ontology-of-amino-acids/	standard	maintained	ready-to-use			All species	Semantic standards		
https://fairsharing.org/1552	10.25504/FAIRsharing.s8vrb1	Apo and Holo structures DataBase	http://ahdb.ee.ncku.edu.tw/	database					All species	Knowledgebase		
hu												
https://fairsharing.org/2894	10.25504/FAIKsnaring.a308a0	DDBJ BioProject	https://www.ddbj.nig.ac.jp/bioproject/index-e.ntmi	database	maintained	ready-to-use	recommended		All species	Data repository		
https://fairsharing.org/3013	10.25504/FAIRsharing 23823e	DDBI Sequence Read Archive	https://www.ddbj.nig.ac.jp/ddbj https://www.ddbj.nig.ac.jp/ddbj	database	Inaintaineu	ready-to-use	recommended		All species	Data repository		DDBJ
https://fairsharing.org/3188	10.25504/FAIRsharing.b67925	DDBJ Trace Archive	https://www.ddbj.nig.ac.jp/dta/index-e.html	database		ready-to-use	licconnended		All species	Data repository		DDBJ
https://fairsharing.org/2743	10.25504/FAIRsharing.hESBcy	Genomic Expression Archive	https://www.ddbj.nig.ac.jp/gea	database	maintained	ready-to-use	recommended		All species	Data repository		DDBJ
		Evolutionary Genealogy of Genes: Non-supervised										
https://fairsharing.org/1577	10.25504/FAIRsharing.j1wj7d	Orthologous Groups	http://eggnog.embl.de	database		ready-to-use			All species	Knowledgebase		EMBL-EBI(EU)
										Model/formats or		
https://fairsharing.org/1645	10.25504/FAIRsharing.cp0f59	ARLEQUIN Project Format	http://cmpg.unibe.cn/software/ariequin35/	standard		ready-to-use			All species	syntax:Format		
https://fairsharing.org/1845	10.25504/FAIRsharing.sed5to	BAliBASE	http://www.lbgi.fr/balibase/	database		ready-to-use			All species	Knowledgebase		EIVIBL-EBI(EO)
	2012550 4 Printsharingiseastq			ducubuse	1	ready to use			, in species	Internedgebuse		
https://fairsharing.org/2380	10.25504/FAIRsharing.k4yzh	BCCM/GeneCorner Plasmid Collection	http://www.genecorner.ugent.be/	database	maintained	ready-to-use			All species	Knowledgebase		UGENT(Beligum)
https://fairsharing.org/1859	10.25504/FAIRsharing.hjybww	Ligand-Gated Ion Channel database	http://www.ebi.ac.uk/compneur-srv/LGICdb/	database	İ		1		All species	Knowledgebase		EMBL-EBI(EU)
https://fairsharing.org/2156	10.25504/FAIRsharing.txkh36	Database of Genomic Variants Archive	http://www.ebi.ac.uk/dgva/	database	maintained		recommended		All species	Knowledgebase		EMBL-EBI(EU)
		BCCM/MUCL Agro-food & Environmental Fungal										
https://fairsharing.org/2401	10.25504/FAIRsharing.4njvzy	Collection	http://bccm.belspo.be/about-us/bccm-mucl	database	maintained	ready-to-use		All plant species	All	Knowledgebase		
https://fairsharing.org/168	10.25504/FAIRsharing.krqvQ/	BCI-2 Database	https://www.bcioffils.org/#grammar	database	maintaineu	ready-to-use			All species	Knowledgebase		+
https://fairsharing.org/2240	10.25504/FAIRsharing.k5a3vt	Big Data Nucleic Acid Simulations Database	http://mmb.irbbarcelona.org/BIGNASim	database	maintained	ready-to-use			All species	Knowledgebase		
			8,							Model/formats or		
https://fairsharing.org/380	10.25504/FAIRsharing.b52795	вім	https://www.cog-genomics.org/plink2/formats#bim	standard		ready-to-use			All species	syntax:Format		
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https://fairsharing.org/4822	N/A	Binary Call Format	http://samtools.github.io/hts-specs/BCFv2_qref.pdf	standard		ready-to-use			All species	syntax:Format		
https://fairsharing.org/4475	10.25504/FAIRsharing.b2f583	BioData.pt Data Management Portal	https://dmportal.biodata.pt/	database	maintained	ready-to-use		All plant species		Knowledgebase		
https://foisehouing.oug/2502		BioInformatics Platform for Agroecosystem	had an 1/h-i	databasa						Kanudadanhara		
https://fairsharing.org/2592	10.25504/FAIRsharing.qqFIAF	Bioinformatics Web Service Ontology	https://bipad.genouest.org	standard	maintaineu	ready-to-use		All plant species	All species	Semantic standards		github
11(1)3.7/181318111g.01g/1240	10.23304/1 Altislianing.51 yavi	Biological and Chemical Oceanography Data	https://gittub.com/obi-webservice/obiws	Standard					All species	Semantic standards		Bitliub
https://fairsharing.org/2512	10.25504/FAIRsharing.pjj4gd	Management Office	https://www.bco-dmo.org/	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/1080	10.25504/FAIRsharing.8ktkqy	Biological Collections Ontology	https://github.com/BiodiversityOntologies/bco	standard	maintained	ready-to-use		1	All species	Semantic standards		github
https://fairsharing.org/2114	10.25504/FAIRsharing.p06nme	Biological Magnetic Resonance Data Bank	https://bmrb.io/	database	maintained	ready-to-use	recommended		All species	Data repository		
https://fairsharing.org/2212	10.25504/FAIRsharing.73reht	Bio-Mirror	http://www.bio-mirror.net/	database	maintained				All species	Knowledgebase		
https://fairsharing.org/467	N/A	Bioversity Molecular Markers Ontology	https://cropontology.org/term/CO_500:ROOT	standard		and the second		All plant species	Allenes	Semantic standards		
nttps://tairsnaring.org/3604	LU.25504/FAIKSnaring.0et9t5	bologna Annotation Resource	Intrps://dar.blocomp.unibo.it/bar3/	uatabase		ready-to-use			All species	INIUWIEdgebase		+
https://fairsharing.org/2856	10.25504/FAIRsharing.2cw3HU	BonaRes Repository	 https://datenzentrum.bonares.de/research-data.ph/	database	maintained	ready-to-use			All species	Data repository		
https://fairsharing.org/1850	10.25504/FAIRsharing.dj8nt8	European Nucleotide Archive	http://www.ebi.ac.uk/ena	database	maintained	ready-to-use	recommended		All species	Data repository	recommended	EMBL-EBI(EU)
https://fairsharing.org/1098	10.25504/FAIRsharing.Hbvvle	BpForms Grammar	https://www.bpforms.org/#grammar	standard	maintained	ready-to-use		1	All species	Semantic standards		1
https://fairsharing.org/3186	10.25504/FAIRsharing.ac95d5	Bridges	https://bridges.monash.edu/	database	maintained	ready-to-use			All species	Knowledgebase		
										Model/formats or		
https://fairsharing.org/3566	10.25504/FAIRsharing.313630	CABRI Guidelines for Catalogue Production	http://cabri.org/guidelines/catalogue/CPcover.html	standard	maintained	ready-to-use		All plant species		syntax:models/syntax		
https://fairsbaring.org/1332	10 25504/EAIRsharing 2h3at8	Biotechnology Checklist	http://www.ebiac.uk/epa/submit/microb2.chocklict	tstandard		ready-to-use			All species	Minimum reporting guidelines		EMBL-EBI/ELI
https://fairsharing.org/2155	10.25504/FAIRsharing 6824nv	European Variation Archive	http://www.ebi.ac.uk/ena/subinit/inicrobs-cireckis	database	maintained	ready-to-use	recommended		All species	Data renository	recommended	EMBL-EBI(EU)
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https://fairsharing.org/1560	10.25504/FAIRsharing.r3pbp3	motifs	http://www.bioinsilico.org/CAPSDB	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/1730	10.25504/FAIRsharing.dkbt9j	Carbohydrate Structure Database	http://csdb.glycoscience.ru/database/	database	maintained	ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/1852	10.25504/FAIRsharing.7zffgc	Gene Ontology Annotation Database	http://www.ebi.ac.uk/GOA	database	maintained	ready-to-use	recommended		All species	Knowledgebase		EMBL-EBI(EU)
https://fairsharing.org/1588	10.25504/FAIRsharing.f5zx00	Expression Atlas	http://www.ebi.ac.uk/gxa	database	maintained	ready-to-use	recommended		All species	Data repository		EMBL-EBI(EU)
https://tairsharing.org/2047	10.25504/FAIRsharing.2s4n8r	MERUPS	Inttp://www.ebi.ac.uk/merops/	database	-	ready-to-use	Irecommended	-	All species	Knowledgebase		EMBL-EBI(EU)
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https://fairsharing.org/227	10.25504/FAIRsharing.qz0rvm	Variant Effect Predictor data format	ormats.html	standard		ready-to-use			All species	syntax:Format		EMBL-EBI(EU)
https://fairsharing.org/2386	10.25504/FAIRsharing.923a0p	Ensembl Genomes	https://ensemblgenomes.org/	database	maintained	ready-to-use	1	All plant species		Knowledgebase	recommended	EMBL-EBI(EU)

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EAIRsharing LIPI	EAIRsharing DOI	Record Name	Record homenage LIRI	Resource Type	Manintenace	Ready-to-use	recommended	plant specie	s Applieu u	Type	ELIVIR recommended	provider
https://fairsbaring.org/2404	10.25504/EAIRsharing i8g2cv	Ensembl Plants	https://plants.ensembl.org/index.html	database	maintained	ready-to-use	recommended	All plant species	species	Knowledgebase	recommended	EMBL-EBI/EU)
https://fairsharing.org/1945	10.25504/FAIRsharing.jog20		https://plants.ensembl.org/index.ntmi	database	maintained	ready-to-use	racommondod	All plant species	All species	Data reportant	recommended	
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https://fairsharing.org/1280	10 25504/FAIRcharing #72a2w	Short Bood Archivo oYtoncible Morkun Longuage	1 E	ctandard		ready to use	recommended		All coording	cuntavimodols/cuntav		
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https://fairsharing.org/2691	10.25504/FAIRsharing.AU02Dj	Genome Properties	https://www.ebi.ac.uk/interpro/genomeproperties	database	maintained	ready-to-use			All species	Knowledgebase		EIVIBL-EBI(EU)
https://fairsnaring.org/2129	10.25504/FAIRsharing.dxj0/F	Nightiy	https://www.ebi.ac.uk/metagenomics/	ualabase	maintaineu	ready-to-use	recommended		All species	Knowledgebase		EIVIBL-EBI(EU)
https://fairsnaring.org/1851	10.25504/FAIRsnaring.p3n3th	Patent Data Resources	nttps://www.ebi.ac.uk/patentdata	database		ready-to-use			All species	Knowledgebase		EMBL-EBI(EU)
			http://geneontology.org/docs/download-									
https://fairsharing.org/378	10.25504/FAIRsharing.h4rs6h	GO-PLUS	ontology/#go_plus_owl	standard		ready-to-use			All species	Semantic standards		GBC(USA)
			http://geneontology.org/docs/gene-product-							Model/formats o		
https://fairsharing.org/1466	10.25504/FAIRsharing.rtm51	Gene Product Annotation Data	association-data-gpad-format/	standard	maintained	ready-to-use			All species	syntax:Format		GBC(USA)
			http://geneontology.org/docs/gene-product-							Model/formats o		
https://fairsharing.org/1468	10.25504/FAIRsharing.820ebm	Gene Product Information Format	information-gpi-format/	standard	maintained	ready-to-use			All species	syntax:Format		GBC(USA)
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		Gene Ontology (GO) Gene Association File Format	http://geneontology.org/docs/go-annotation-file-ga	f						Model/formats o		
https://fairsharing.org/766	10.25504/FAIRsharing.FGJ2T8	2.1	format-2.1/	standard	maintained	ready-to-use			All species	syntax:Format		GBC(USA)
		Gene Ontology (GO) Gene Association File Format	http://geneontology.org/docs/go-annotation-file-ga	f						Model/formats o		
https://fairsharing.org/1418	10.25504/FAIRsharing.77fbbf	2.2	format-2.2/	standard	maintained	ready-to-use			All species	syntax:Format		GBC(USA)
https://fairsharing.org/2077	10.25504/FAIRsharing.s1ne3g	UniProt Knowledgebase	https://www.uniprot.org	database	maintained	ready-to-use	recommended		All species	Knowledgebase		GBC(USA)
https://fairsharing.org/1237	10.25504/FAIRsharing.xhwrnr	Cell Cycle Ontology	https://www.biogateway.eu/tools/#CCO	standard	maintained	ready-to-use			All species	Semantic standards		1020(00.1)
https://fairsharing.org/2069	10 25504/FAIRsharing ntv8ne	Chemical Effects in Biological Systems	https://doi.org/10.22427/NTP-DATA-1	database	Indined	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2749	10.25504/FAIRsharing.httpp:/	China National ConePark DataPase	https://doi.org/10.2242//NTF-DATA-1	database	maintained	ready-to-use	racommondod		All species	Data repository		
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incps.//iansnaning.org/3500	10.25504/ PAIKShaning.052cce	CIRAD Dataverse	1111ps.//doi.org/10.1810//initastructure/00005	uatabase	maintaineu	reauy-to-use		All plant species		Madal/farmata		
Lun (11) - Lun (422										woder/formats 0		
https://fairsnaring.org/122	10.25504/FAIKsnaring.jx6ea0	CLUSTAL-W Alignment Format	nttp://www.clustal.org/clustal2/	standard	maintained	ready-to-use			All species	syntax:Format		
										Model/formats o		
https://fairsharing.org/1429	10.25504/FAIRsharing.8y5ayx	Common Workflow Language	http://www.commonwl.org	standard	maintained	ready-to-use			All species	syntax:models/syntax		
https://fairsharing.org/1155	10.25504/FAIRsharing.kay31r	Comparative Data Analysis Ontology	https://github.com/evoinfo/cdao	standard	maintained	ready-to-use			All species	Semantic standards		github
https://fairsharing.org/1902	10.25504/FAIRsharing.wyz5he	Conformation Angles Database	http://cluster.physics.iisc.ernet.in/cadb/	database		ready-to-use			All species	Knowledgebase		
			http://rna.urmc.rochester.edu/Text/File_Formats.ht	:						Model/formats o		
https://fairsharing.org/292	10.25504/FAIRsharing.695abb	Connectivity Table file format	ml#CT	standard		ready-to-use			All species	syntax:Format		
			https://cooler.readthedocs.io/en/latest/datamodel.	h						Model/formats o		
https://fairsharing.org/889	10.25504/FAIRsharing.VJDEtl	Cooler file format	tml	standard	maintained	ready-to-use			All species	syntax:Format		
https://fairsharing.org/2688	10.25504/FAIRsharing.02xjaW	CyVerse Data Common Repository	http://datacommons.cyverse.org/	database	maintained	ready-to-use			All species	Data repository		
			https://github.com/dagendresen/darwincore-			,						
https://fairsharing.org/841	10.25504/FAIRsharing.hgsFLe	Darwin Core Germplasm	germplasm	standard	maintained	ready-to-use			All species	Semantic standards		github
https://fairsharing.org/1566	10 25504/FAIRsharing eyfe2s	Database of Aligned Ribosomal Complexes	http://darcsite.genzentrum.lmu.de/darc/	database	Indiricance	incluy to use			All species	Knowledgebase		Brando
https://fairsharing.org/2385	10.25504/FAIRsharing.cvre23	Database Of Local Biomolecular Conformers	http://dalbico.org/	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2303	10.25504/FAIRsharing.ihipp0	Database of Local Dismolecular comorniers	http://dobico.org/	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2550	10.25504/FAIRsharing.jhjhpo	Database of Octoplaneous Prematers	http://ici.vscit.cz/projects/doice/viewnome	database	Inamaneu	reauy-to-use			All species	Knowledgebase		
https://fairsharing.org/1/45	10.25504/FAIRsharing.10miyi	Databases of Orthologous Fromoters	http://doop.abc.nu/	database	an elimeteria e al			All plant species	All en estes	Knowledgebase		
https://fairsnaring.org/3010	10.25504/FAIRsharing.Nmigg9	Datanator	https://www.datanator.inio	ualabase	maintained	ready-to-use			All species	Knowledgebase		
https://fairsnaring.org/2414	10.25504/FAIRsnaring.yyt78n	DataONE	nttps://www.dataone.org	database	maintained	ready-to-use	recommended	All plant species		Knowledgebase		
https://fairsharing.org/2040	10.25504/FAIRsharing.52qw6p	Description of Plant Viruses	http://www.dpvweb.net	database		ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/3314	10.25504/FAIRsharing.8d2e5c	DIGITAL.CSIC	https://digital.csic.es/	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2765	10.25504/FAIRsharing.23bdba	DISNOR	https://disnor.uniroma2.it/	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2526	10.25504/FAIRsharing.rt4gyp	Disordered Binding Sites Database	http://dibs.enzim.ttk.mta.hu	database	Imaintained	ready-to-use		-	All species	Knowledgebase		
				1	1				1	Model/formats o	1	
https://fairsharing.org/143	10.25504/FAIRsharing.mcgj5b	Distributed Sequence Annotation System	http://www.biodas.org/documents/spec-1.6.html	standard		ready-to-use			All species	syntax:models/syntax		<u> </u>
https://fairsharing.org/2860	10.25504/FAIRsharing.qgMKai	DNA Modification Database	https://dnamod.hoffmanlab.org/	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2865	10.25504/FAIRsharing.VXoFLf	Domain-centric GO	http://supfam.org/SUPERFAMILY/dcGO/index.html	database	maintained	ready-to-use			All species	Knowledgebase		
			https://www.tbi.univie.ac.at/RNA/ViennaRNA/doc/h	1								
			tml/rna structure notations.html#dot-bracket-							Model/formats o		
https://fairsharing.org/144	10.25504/FAIRsharing.4xrzw1	Dot Bracket Notation (DBN) - Vienna Format	notation	standard					All species	syntax:Format		
https://fairsharing.org/3015	10.25504/FAIRsharing.04fcf5	EMDataResource	http://www.emdataresource.org/	database	1	ready-to-use	recommended		All species	Knowledgebase		1
			https://ena-									
			docs readthedocs in /en /latest /submit /filepren /flat-							Model/formats		
https://fairsharing.org/1478	10 2EE04/EAIRcharing conh66	ENA Seguence Elet Eile Format	file example html	ctandard	maintained	roady to use			All choosing	current Sermat	recommended	
			https://epa-	Januaru	mannameu	- couy-co-use	1	1	p ai species	Syntax.i Ormat	- ccommended	1
	1		door roadthodoor in /on /latest /submit/and or	1	1				1	Madal/format-	.	
https://foimhosing.com/soco		FALA Commence VAL Colores	uucs.reautrieuucs.io/en/iatest/submit/general-	atomates 1	1				All	ividuel/lormats 0		
nttps://fairsharing.org/1061	10.25504/FAIRsharing.9ed958	ENA Sequence XML Schema	Iguide/programmatic.html	Istandard		ready-to-use			All species	isyntax:models/syntax	recommended	+
https://fairsharing.org/2683	10.25504/FAIRsharing.0VV4KB	Environmental Data Portal	https://www.envidat.ch/	database	maintained	ready-to-use			All species	Knowledgebase		+
https://fairsharing.org/511	10.25504/FAIRsharing.xmmsmr	Epigenome Ontology	https://github.com/EGO-ontology	Istandard	-	ready-to-use		-	All species	Semantic standards		github
https://fairsharing.org/4329	10.25504/FAIRsharing.1a0bbf	ERIC/open	https://opendata.eawag.ch/	database	maintained	ready-to-use		All plant species		Knowledgebase		
		Eukaryotic Pathogen, Host & Vector Genomics	https://github.com/VEuPathDB-									
https://fairsharing.org/1484	10.25504/FAIRsharing.9rhr9j	Resource Ontology	ontology/VEuPathDB-ontology	standard	maintained	ready-to-use			All species	Semantic standards		github
https://fairsharing.org/4715	10.25504/FAIRsharing.c3521d	EvolclustDB	http://evolclustdb.org/	database	maintained	ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/1757	10.25504/FAIRsharing.4eanvm	Evolutionary Trace	http://mammoth.bcm.tmc.edu/ETserver.html	database		ready-to-use			All species	Knowledgebase		1
https://fairsharing.org/1581	10.25504/FAIRsharing.2z0e8b	ExoCarta	http://www.exocarta.org	database	1	ready-to-use	1		All species	Knowledgebase		1
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							FAIRorg	plant specie	s Applied to			
FAIRsharing URL	FAIRsharing DOI	Record Name	Record homepage URL	Resource Type	Manintenace	Ready-to-use	recommended	accepted	species	Туре	ELIXIR recommended	provider
https://fairsharing.org/2262	10.25504/FAIRsharing.nnvcr9	FAIRDOMHub	https://fairdomhub.org/	database	maintained	ready-to-use			All species	Knowledgebase		
					1					Model/formats o	r	1
https://fairsharing.org/3640	10.25504/FAIRsharing.807b9d	FAIRtracks	https://fairtracks.net	standard	maintained	ready-to-use			All species	syntax:models/syntax	recommended	
https://fairsharing.org/985	10.25504/FAIRsharing.zc2tfa	Fanconi Anemia Ontology	http://lab.rockefeller.edu/smogorzewska/ifar/	standard		ready-to-use			All species	Semantic standards		
			http://news.open-bio.org/news/2009/12/nar-fastq-							Model/formats o	r	
https://fairsharing.org/114	10.25504/FAIRsharing.r2ts5t	FASTQ Sequence and Sequence Quality Format	format/	standard		ready-to-use			All species	syntax:Format		
https://fairsharing.org/478	10.25504/FAIRsharing.haxp7g	Feature Annotation Location Description Ontology	http://biohackathon.org/resource/faldo	standard	maintained	ready-to-use			All species	Semantic standards		
https://fairsharing.org/2516	10.25504/FAIRsharing./2tq1a	FlavorDB	http://cosylab.ilitd.edu.in/flavordb	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsnaring.org/3102	10.25504/FAIRsnaring.SIXD02	French Biodiversity (metajdata repository		Garabase	maintaineu	ready-to-use			All species			sourceforge/USA
https://fairsbaring.org/868	10 25504/FAIRsharing Specy7	FuGEFlow	http://flowcyt.sourceforge.net/fugeflow/	standard					All snecies	Minimum reporting guidelines)
intepsi//intersidentiglotig/000	zoizooo (i viitoita iligioxee) /			Standard					7 ur species	Model/formats	r	sourceforge(USA
https://fairsharing.org/1270	10.25504/FAIRsharing.namxfm	Functional Genomics Experiment Markup Language	http://fuge.sourceforge.net/dev/index.php	standard					All species	syntax:models/syntax)
		FunTree: A Resource For Exploring The Functional										
		Evolution Of Structurally Defined Enzyme										
https://fairsharing.org/1586	10.25504/FAIRsharing.556qpw	Superfamilies	http://www.funtree.info/FunTree/	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2163	10.25504/FAIRsharing.zv11j3	GBIF.org	https://www.gbif.org	database	maintained	ready-to-use	recommended		All species	Knowledgebase		
https://fairsharing.org/1660	10.25504/FAIRsharing.fyqk5z	Gene3D	http://gene3d.biochem.ucl.ac.uk	database					All species	Knowledgebase		
			http://software.broadinstitute.org/cancer/software/	1	1					Model/formats o	r	
https://fairsharing.org/414	10.25504/FAIRsharing.z057ar	GenePattern GeneSet Table Format	genepattern/file-formats-guide	standard	maintained	ready-to-use			All species	syntax:Format		
nttps://fairsharing.org/2136	10.25504/FAIRsharing.qmygaa	Generrot	Inttp://www.geneprof.org	database	Imaintained	-	-		All species	Knowledgebase	-	+
https://foischasing.org/1249	10 25504/54/Debesies deb0fc	Conside Foothers Foothers Manifest 2	nttps://gitnub.com/ine-Sequence-	-to a doub					All	Model/formats of	ſ	
https://fairsnaring.org/1548	10.23304/ FAIKSnaring.ankuro	Generic reature Format Version 5	ontology/specifications/blob/master/gff3.md	stafluaru	maintaineu	reauy-to-use			An species	syntax:P0fmdt		Igitinuu
		GeneSigDB: a manually curated database and										
https://fairsharing.org/1590	10.25504/FAIRsharing.1etv1h	resource for analysis of gene expression signatures	http://www.genesigdb.org	database					All species	Knowledgebase		
https://fairsharing.org/1062	10.25504/FAIRsharing.cizx96	Genetic Testing Ontology	http://gianzhu-lab.umbc.edu/	standard					All species	Semantic standards		-
									1	Model/formats o	r	
https://fairsharing.org/57	10.25504/FAIRsharing.sbbbf6	Genome Biology Ontology Language	http://gbol.life	standard	maintained				All species	syntax:models/syntax		
			https://github.com/The-Sequence-							Model/formats o	r	
https://fairsharing.org/379	10.25504/FAIRsharing.pkw5bj	Genome Variation Format	Ontology/Specifications/blob/master/gvf.md	standard	maintained	ready-to-use			All species	syntax:Format		github
			https://www.liebertpub.com/doi/10.1089/omi.2008	L.						Model/formats o	r	
https://fairsharing.org/69	10.25504/FAIRsharing.2hh7g7	Genomic Contextual Data Markup Language	0A10	standard	maintained	ready-to-use			All species	syntax:models/syntax		
https://fairsharing.org/279	10.25504/FAIRsharing.y1mmbv	Genomic Epidemiology Ontology	https://genepio.org/	standard	maintained	ready-to-use			All species	Semantic standards		
https://fairsharing.org/1328	10.25504/FAIRsharing.vbejb6	Genomic Feature and Variation Ontology	https://github.com/BioInterchange/Ontologies	standard		ready-to-use			All species	Semantic standards		github
https://fairsharing.org/3019	10.25504/FAIRsharing.wOcTaM	Genomic Observatories Meta-Database	https://geome-db.org/	database	maintained	ready-to-use			All species	Knowledgebase		aithuth
https://fairsnaring.org/3626	10.25504/FAIRSnaring.503560	Genomics Conorts Knowledge Ontology	https://github.com/monarch.initiative/GENO	stanuaru	maintaineu	ready-to-use			All species	Semantic standards		Igithub
https://fairsbaring.org/688	10 25504/FAIRsharing knhna7	Genotype Ontology	ontology/	standard		ready-to-use			All snecies	Semantic standards		github
https://fairsharing.org/2125	10.25504/FAIRsharing.rcbwsf	Giga Science Database	http://gigadb.org/	database	maintained	ready-to-use	recommended		All species	Knowledgebase		Bicitab
https://fairsharing.org/4445	10.25504/FAIRsharing.84b518	Gigwa	https://gigwa.southgreen.fr/	database	maintained	ready-to-use			All species	Knowledgebase		1
		Global Genome Biodiversity Network Data			1	1			<u> </u>			1
https://fairsharing.org/787	10.25504/FAIRsharing.eff3b2	Standard	https://wiki.ggbn.org/ggbn/GGBN_Data_Standard	standard		ready-to-use			All species	Minimum reporting guidelines		
https://fairsharing.org/632	10.25504/FAIRsharing.9ry4cz	GoMapMan	https://gomapman.nib.si/	database	maintained	ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/2086	10.25504/FAIRsharing.wfrsvq	gpDB	http://bioinformatics.biol.uoa.gr/gpDB	database		ready-to-use			All species	Knowledgebase		
			http://greenc.sequentiabiotech.com/wiki2/Main_Pa									
https://fairsharing.org/2235	10.25504/FAIRsharing.fe9kyy	Green Non-Coding Database	ge	database	maintained	ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/1947	10.25504/FAIRsharing.bpxgb6	Greengenes	http://greengenes.lbl.gov	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/1827	10 25504/EAIRsbaring 198570	comparative genomics	http://www.greenphyl.org	database	maintained	ready-to-use		All plant species		Knowledgebase		
inteps.//iairsnaring.org/182/	10.25504/ FAIKSHaring.j56570	Herbarium information standards and protocols for	http://www.greenphyl.org	uatabase	Inaintaineu	Teauy-to-use		All plant species		Kilowieugebase		
https://fairsharing.org/1084	10.25504/FAIRsharing.v49vi6	interchange of data	standards/tree/master/hispid3	standard		ready-to-use		All plant species		Minimum reporting guidelines		github
https://fairsharing.org/698	10.25504/FAIRsharing.gagfk4	HGeneCodonOntology	http://blog.51.ca/u-345129/	standard					All species	Semantic standards		8
					1				<u> </u>	Model/formats o	r	1
https://fairsharing.org/472	10.25504/FAIRsharing.n3rt95	HMMER Profile File Format	http://www.hmmer.org	standard		ready-to-use			All species	syntax:Format		
https://fairsharing.org/4454	10.25504/FAIRsharing.a945b0	HostDB	https://hostdb.org/hostdb/app	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/1595	10.25504/FAIRsharing.m4a6d3	HotRegion	http://prism.ccbb.ku.edu.tr/hotregion	database					All species	Knowledgebase		
										Model/formats o	r	
https://fairsharing.org/342	10.25504/FAIRsharing.8drfwh	ICM binary file Format	http://www.molsoft.com/icm/files.html	standard		ready-to-use			All species	syntax:Format		
https://fairsharing.org/4293	10.25504/FAIRsharing.bbd7df	IEEE 2/91-2020	Inttps://standards.ieee.org/ieee/2/91/7337/	standard	maintained	ready-to-use			All species	Invinimum reporting guidelines		
https://fairsharing.org/2///	10 25504/FAIRsharing Swf17w	Instein Registry of Standard Biological Parts	https://jdr.openmicroscopy.org	udidudse database	maintained	ready-to-use	recommended	All plant species	All species	Knowledgebase		+
https://fairsharing.org/1664	10.25504/FAIRsharing advhog	Indel Flanking Region Database	http://indel.bioinfo.sdu.edu.co	database	mannanneu	n cauy-to-use	recommended	An plant species	All species	Knowledgebase	1	
https://fairsharing.org/1600	10.25504/FAIRsharing.smgf7v	InterEvol database	http://biodev.cea.fr/interevol/	database		ready-to-use	-		All species	Knowledgebase		
https://fairsharing.org/2908	N/A	Internal Control Genes	http://icg.big.ac.cn/index.php/Main Page	database	1	,	1		All species	Knowledgebase	1	1
	1		https://isa-		1	1	İ	İ		Model/formats o	r	1
https://fairsharing.org/1501	10.25504/FAIRsharing.yhLgTV	Investigation Study Assay JSON	specs.readthedocs.io/en/latest/isajson.html	standard	maintained	ready-to-use			All species	syntax:models/syntax		
			https://isa-							Model/formats o	r	
https://fairsharing.org/1497	10.25504/FAIRsharing.53gp75	Investigation Study Assay Tabular	specs.readthedocs.io/en/latest/isatab.html	standard	maintained	ready-to-use	recommended		All species	syntax:models/syntax		
https://fairsharing.org/2750	N/A	ionomicHUB	https://www.ionomicshub.org/home/PiiMS	database				All plant species		Knowledgebase		<u> </u>
https://fairsharing.org/2492	10.25504/FAIRsharing.ekdqe5	iReceptor Public Archive	https://www.ireceptor.org/	database	Imaintained	ready-to-use			All species	Knowledgebase		<u> </u>

							FAIRorg	plant specie	s Applied 1	o		
FAIRsharing URL	FAIRsharing DOI	Record Name	Record homepage URL	Resource Type	Manintenace	Ready-to-use	recommended	accepted	species	Туре	ELIXIR recommended	provider
		IUPAC-IUB Commission on Biochemical										
		Nomenclature - Abbreviations and Symbols for	-									
		Nucleic Acids, Polynucleotides and their	https://www.qmul.ac.uk/sbcs/iupac/misc/naabb.ht									
https://fairsharing.org/950	10.25504/FAIRsharing.dee5fb	Constituents	ml	standard		ready-to-use			All species	Semantic standards		
		IUPAC-IUB Joint Commission on Biochemical									1	
		Nomenclature - Nomenclature and Symbolism for	https://www.qmul.ac.uk/sbcs/iupac/misc/naabb.ht									
https://fairsharing.org/959	10.25504/FAIRsharing.d5a210	Amino Acids and Peptides	ml	standard		ready-to-use			All species	Semantic standards		
https://fairsharing.org/1936	10.25504/FAIRsharing.vd25jp	J-GLOBAL	https://jglobal.jst.go.jp/en	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/1661	10.25504/FAIRsharing.5q1p14	Joint Genome Institute, Genomes OnLine Database	https://gold.jgi.doe.gov/	database	maintained	ready-to-use	recommended		All species	Knowledgebase		
https://fairsharing.org/3618	10.25504/FAIRsharing.826b4a	KnetMiner	https://knetminer.com	database	maintained	ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/4783	10.25504/FAIRsharing.d30a2a	KNOTTIN database	https://www.dsimb.inserm.fr/KNOTTIN/	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2189	10.25504/FAIRsharing.327nbg	Kyoto Encyclopedia of Genes and Genomes	http://www.genome.jp/kegg/	database		ready-to-use	recommended		All species	Knowledgebase		
https://fairsharing.org/2325	10.25504/FAIRsharing.dq46p7	Life Science Database Archive	http://dbarchive.biosciencedbc.jp/index-e.html	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2043	10.25504/FAIRsharing.2ma4gq	Ligand Expo	http://ligand-depot.rutgers.edu/	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2623	N/A	Longhorn Array Database	http://darwin.biochem.okstate.edu/lad/ilat/	database					All species	Knowledgebase		
			http://eebgroups.princeton.edu/lucapedia/index.ht									
https://fairsharing.org/3674	N/A	LUCApedia	mi	database					All species	Knowledgebase		
111.1111		Madagascar Biodiversity Information Facility IPT								with the desidence		
https://fairsnaring.org/2469	10.25504/FAIKsnaring.gdj215	GBIF France	nttp://ipt.madbit.mg/	database	maintained				All species	Knowledgebase		
https://foimharing.org/420	10 35504/FAIRsharing Fander									wodel/formats of		
https://fairsharing.org/450	10.25504/FAIRsharing.55edcc	mentha	http://www.cog-genomics.org/piinkz/formats#map	database	maintained	ready-to-use			All species	Knowledgebace		
https://lanshaning.org/2419	10.25504/ PARSharing.j1eyq2	Inentia		uatabase	maintaineu				All species	Model/formate		
https://fairsharing.org/115	10 25504/EAIRsharing windsc		http://gmod.org/wiki/Chado_XMI	standard	maintained	ready-to-use			All species	syntax:models/syntax		GMOD
	10.23304/TANSharing.wjwb3c		http://ginod.org/wiki/chado_xwe	standard	maintaineu	ready-to-use			Air species	Model/formats or		
https://fairsbaring.org/1347	10 25504/FAIRsharing bfodc8	Generic Feature Format Version 2	http://gmod.org/wiki/GEE2	standard					All species	syntax:Format		GMOD
https://fairsharing.org/2051	10 25504/FAIRsharing z1czxi	PeroviBase	http://peroxibase toulouse inra fr/	database		ready-to-use			All species	Knowledgebase	+	INRA(FRA)
https://fairsharing.org/2608	10 25504/FAIRsharing 178BmT	Portail Data INBAE	https://data.inrae.fr/	database	maintained	ready to use		All plant species	7 in species	Data repository	+	INRA(FRA)
		Open Data for Access and Mining Structural									1	
https://fairsharing.org/1499	10.25504/FAIRsharing.ld9wne	Metadata	https://inrae.github.io/ODAM/data-preparation/	standard	maintained	ready-to-use			All species	Minimum reporting guidelines	i l	INRA(FRA)
https://fairsharing.org/2263	10.25504/FAIRsharing.dw22y3	Genetic and Genomic Information System	https://urgi.versailles.inra.fr/gnpis	database	maintained	ready-to-use		All plant species		Data repository	1	INRA(FRA)
	1					1	1	1		Model/formats o	r	<u> </u>
https://fairsharing.org/1427	10.25504/FAIRsharing.4c7c1c	DDBJ/ENA/GenBank Feature Table	http://www.insdc.org/documents/feature-table	standard		ready-to-use			All species	syntax:models/syntax	recommended	INSDC
										Model/formats o	r	
https://fairsharing.org/438	10.25504/FAIRsharing.tn873z	INSD sequence record XML	http://www.insdc.org/documents/xml-status	standard		ready-to-use			All species	syntax:models/syntax		INSDC
		Metadata Schema for the Persistent Identification								Model/formats o	r	
https://fairsharing.org/4211	10.25504/FAIRsharing.209c8e	of Instruments (1.0)	https://doi.org/10.15497/RDA00070	standard		ready-to-use			All species	syntax:models/syntax		
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https://fairsharing.org/3337	10.25504/FAIRsharing./ad252	NCBI Genome Data Viewer	https://www.ncbi.nim.nin.gov/genome/gdv/	database		ready-to-use			All species	Knowledgebase		NCBI (USA)
https://fairsharing.org/1975	10.25504/FAIRsharing.5bc8vt	Gene Expression Omnibus	https://www.ncbi.nim.nin.gov/genome/gav/	database	maintained	ready-to-use	recommended		All species	Data repository		NCBI (USA)
https://fairsharing.org/1977	10.25504/FAIRsharing.mzc066	NCBI HomoloGene Database	https://www.ncbi.nim.nin.gov/geo/	database	mantaneu	ready-to-use	recommended		All species	Knowledgebase		NCBI (USA)
https://fairsharing.org/097	10.25504/FAIRsharing.inzcool	NGS ontology	https://www.ncon.nin.inn.gov/nonoiogene	standard		ready-to-use	recommended		All species	Semantic standards		github
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https://fairsharing.org/1981	10.25504/FAIRsharing.rgzvint	NCBI Structure	https://www.pcbi.plm.pib.gov/structure	database	maintained	ready-to-use	recommended		All species	Knowledgebase		NCBI (USA)
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https://fairsnaring.org/1621	10.25504/FAIRsharing.8ecbxx	NuclearDB	http://www.receptors.org/nucleardb	database					All species	Knowledgebase		
https://fairsnaring.org/2046	10.25504/FAIRsharing.bnuk/8	Nucleic Acid Database	http://hdbserver.rutgers.edu/	database	and a state to a st	and the second	recommended		All species	Knowledgebase		
https://fairsharing.org/1220	10.25504/FAIRsharing.fj07xj	NCBI Taxonomy	https://www.ncbi.nlm.nih.gov/taxonomy	standard	maintained	ready-to-use	recommended		All species	Semantic standards		NCBI (USA)
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https://fairsharing.org/1622	10.25504/FAIRsharing.hsy066	Online GEne Essentiality database	https://v3.ogee.info/#/home	database		ready-to-use			All species	Knowledgebase		
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https://fairsharing.org/2568	10.25504/FAIRsharing.9btkvp	Eukaryotes	http://bioinformatics.psb.ugent.be/orcae/	database	maintained	ready-to-use		All plant species		Knowledgebase		UGENT(Beligum)
https://fairsharing.org/1488	10.25504/FAIRsharing.284e1z	Ontology for Biomedical Investigations	http://obi-ontology.org/	standard	maintained	ready-to-use	recommended		All species	Semantic standards		L
			https://github.com/OpenSILEX/ontology-phis-oepo-									
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https://fairsharing.org/363	10.25504/FAIRsharing.zmx7nn	Ontology of Genes and Genomes	https://bitbucket.org/hegroup/ogg	standard	maintained	ready-to-use			All species	Semantic standards		bitbucket
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https://fairsharing.org/1790	10.25504/FAIRsharing.8dak0r	Open Regulatory Annotation	http://www.oreganno.org/	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2393	10.25504/FAIRsharing.g3j5qj	Orthologous MAtrix	http://omabrowser.org/oma/about/	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/77	10.25504/FAIRsharing.4877h0	Orthology Ontology	https://github.com/qfo/OrthologyOntology	standard		ready-to-use			All species	Semantic standards		github
		Pacific Northwest National Laboratory DataHub										
https://fairsharing.org/3692	10.25504/FAIRsharing.45bf5b	Scientific Data Repository	https://data.pnnl.gov/	database	maintained	ready-to-use	recommended		All species	Data repository		
https://fairsharing.org/3306	10.25504/FAIRsharing.9289d4	Paired Omics Data Platform	https://pairedomicsdata.bioinformatics.nl/	database		ready-to-use			All species	Knowledgebase		
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https://fairsharing.org/1014	10.25504/FAIRsharing.zsnv69	Multiple alignment	http://bioportal.bioontology.org/ontologies/1026	standard					All species	Semantic standards		NCBO(USA)
https://fairsharing.org/3301	10.25504/FAIRsharing.d02054	PDB-REDO	https://pdb-redo.eu	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/1839	10.25504/FAIRsharing.k4sp7m	PDB-REPRDB	http://mbs.cbrc.jp/pdbreprdb-cgi/reprdb_menu.pl	database					All species	Knowledgebase		
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https://fairsharing.org/1925	10.25504/FAIRsharing.rxe7z2	PDZBase	http://abc.med.cornell.edu/pdzbase	database					All species	Data repository		University
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https://fairsharing.org/930	10.25504/FAIRsharing.23th83	GeoSpecies Ontology	http://bioportal.bioontology.org/ontologies/1247	standard		ready-to-use			All species	Semantic standards		NCBO(USA)
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https://fairsharing.org/1303	10.25504/FAIRsharing.bnx9cf	Molecular Connections Cell Line Ontology	https://bioportal.bioontology.org/ontologies/MCCL	standard					All species	Semantic standards		NCBO(USA)
https://fairsharing.org/263	10.25504/FAIRsharing.4qyf0f	Regulation of Transcription Ontolology	https://bioportal.bioontology.org/ontologies/RETO	standard	maintained	ready-to-use			All species	Semantic standards		NCBO(USA)
https://fairsharing.org/2415	10.25504/FAIRsharing.tdhkc6	Genome Sequence Archive	https://bigd.big.ac.cn/gsa/	database	maintained	ready-to-use	recommended		All species	Data repository		NGDC (China)
https://fairsharing.org/2905	10.25504/FAIRsharing.910279	Genome Waration Map	https://bigd.big.ac.cn/gvm/	database	maintained	ready-to-use		All plant species	All spasios	Data repository		NGDC (China)
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https://fairsharing.org/2913	10.25504/FAIRsharing.4ef690	Plant Editosome Database	https://bigd.big.ac.cn/ped	database		ready-to-use		All plant species		Knowledgebase		NGDC (China)
https://fairsharing.org/2763	10.25504/FAIRsharing.52da68	National Genomics Data Center Repository	https://ngdc.cncb.ac.cn/	database		ready-to-use		in plane species	All species	Data repository		NGDC (China)
https://fairsharing.org/2911	10.25504/FAIRsharing.d1a9bd	MethBank	https://ngdc.cncb.ac.cn/methbank/	database	1	ready-to-use			All species	Data repository		NGDC (China)
https://fairsharing.org/4333	10.25504/FAIRsharing.45990b	Open Archive for Miscellaneous Data	https://ngdc.cncb.ac.cn/omix/	database	maintained	ready-to-use			All species	Knowledgebase		NGDC (China)
https://fairsharing.org/1417	10.25504/FAIRsharing.6xq0ee	Gene Ontology	http://www.geneontology.org	standard	maintained	ready-to-use	recommended	1	All species	Semantic standards		NHGRI(USA)
https://fairsharing.org/554	10.25504/FAIRsharing.7y955w	Gene Ontology Extension	http://www.geneontology.org	standard		ready-to-use		1	All species	Semantic standards		NHGRI(USA)
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https://fairsharing.org/42/	10.25504/FAIRsharing.820et3	Generix Results Format	ePix-File-Formats#gpr	standard		ready-to-use			All species	syntax:Format		SIB(SSWISS)
https://fairsnaring.org/311	10.25504/FAIRsnaring.rbpdg	PGXO	https://pgx0.iona.in	stanuaru		ready-to-use			All species	Model/formate		
https://fairsbaring.org/1273	10 25504/EAIRsharing 9ysgcr	Phenotyne eXchange Format	format	standard		ready-to-use	recommended		All species	syntax:Format		github
https://fairsharing.org/12/5	10.25504/FAIRsharing 73codk	PHI-hase	http://www.phi-base.org/	database	maintained	ready-to-use	recommended	All plant species	All species	Knowledgebase		Bittion
https://fairsharing.org/3297	10.25504/FAIRsharing.625fde	Phylogenes	http://www.philogenes.org/	database	maincaineu	ready-to-use		All plant species		Knowledgebase		1
https://fairsharing.org/1838	10.25504/FAIRsharing.7hxxc4	PhylomeDB	http://phylomedb.org	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2727	10.25504/FAIRsharing.w7Yuyx	PhytoMine	https://phytozome.jgi.doe.gov/phytomine/	database	maintained	ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/2734	10.25504/FAIRsharing.83d06b	Phytozome	https://phytozome.jgi.doe.gov/pz/portal.html	database	1	ready-to-use	1	All plant species		Knowledgebase		1
https://fairsharing.org/1288	10.25504/FAIRsharing.tghhc4	Pipeline Patterns Ontology	https://bitbucket.org/PlantExpAssay/ontology	standard		ready-to-use			All species	Semantic standards		bitbucket
			https://proteininformationresource.org/pirwww/db	i								
https://fairsharing.org/2035	10.25504/FAIRsharing.vssch2	PIR SuperFamily	nfo/pirsf.shtml	database		ready-to-use			All species	Knowledgebase		
https://fairsharing.org/1025	10.25504/FAIRsharing.nft558	Plant Diversity Ontology	http://gooa.las.ac.cn/external/index.jsp	standard				All plant species		Semantic standards		
https://fairsharing.org/2141	10.25504/FAIRsharing.7qexb2	Plant DNA C-values database	http://data.kew.org/cvalues/	database	maintained	ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/1314	10.25504/FAIRsharing.fgmzk8	Plant Experimental Assay Ontology	https://bitbucket.org/PlantExpAssay/ontology	standard		ready-to-use		All plant species		Semantic standards		bitbucket
			https://github.com/Planteome/plant-experimental-									
https://fairsharing.org/1184	10.25504/FAIRsharing.6yNXYK	Plant Experimental Condition Ontology	conditions-ontology	standard	maintained	ready-to-use		All plant species		Semantic standards		github
https://fairsharing.org/2867	10.25504/FAIRsharing.BnLUyq	Plant Genome Integrative Explorer	https://plantgenie.org	database	maintained	ready-to-use		All plant species		Knowledgebase		
https://foimhoning.org/1840	10 35504/54/Babasing 2016-	Direct Commune Nationali		databasa						Data seconditary		Cornell
https://fairsnaring.org/1840	10.25504/FAIRsnaring.591trx	Plant Genomics and Phonomics Research Date	http://pgn.comeii.edu/	uatabase				All plant species				
https://fairsbaring.org/2195	10 25504/EAIRsharing rf3m4g	Repository	http://edal-pgp.ink-gatersleben.de	database	maintained	ready-to-use		All plant species		Data repository		
https://fairsharing.org/1629	10 25504/FAIRsharing rn1nxg	Plant Natural Antisense Transcrints Database	http://bis.ziu.edu.cn/nnatdb/	database	Indincu	ready to use		All plant species		Knowledgebase		1
https://fairsharing.org/237	10.25504/FAIRsharing.3ngg40	Plant Ontology	http://plantontology.org/	standard	maintained	ready-to-use		All plant species		Semantic standards		1
https://fairsharing.org/2133	10.25504/FAIRsharing.7k8zh0	Plant Promoter Database	http://ppdb.agr.gifu-u.ac.ip	database		ready-to-use		All plant species	1	Knowledgebase		
https://fairsharing.org/1721	10.25504/FAIRsharing.ysp7ke	Plant Resistance Gene Database	http://prgdb.org/prgdb4/	database		ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/1807	10.25504/FAIRsharing.ex3fqk	Plant Transcription Factor Database	http://planttfdb.cbi.pku.edu.cn	database	maintained	ready-to-use	1	All plant species		Knowledgebase		1
https://fairsharing.org/2528	10.25504/FAIRsharing.k0kcjw	Planteome	http://www.planteome.org	database	maintained	ready-to-use		All plant species		Knowledgebase		1
https://fairsharing.org/1713	10.25504/FAIRsharing.fy2ebk	PlantRNA	http://plantrna.ibmp.cnrs.fr/	database		ready-to-use		All plant species		Knowledgebase		
https://fairsharing.org/2766	10.25504/FAIRsharing.wBOua0	PLAZA	https://bioinformatics.psb.ugent.be/plaza/	database	maintained	ready-to-use		All plant species		Knowledgebase	recommended	UGENT(Beligum)
https://fairsharing.org/3814	10.25504/FAIRsharing.23ac74	PlutoF	https://plutof.ut.ee/	database	maintained	ready-to-use			All species	Knowledgebase		1
https://fairsharing.org/1671	10.25504/FAIRsharing.etqbej	Pocket Similarity Search using Multiple-Sketches	http://possum.cbrc.jp/PoSSuM/	database	maintained	ready-to-use			All species	Knowledgebase		
		Pocketome: an encyclopedia of small-molecule										
https://fairsharing.org/1631	10.25504/FAIRsharing.tc6df8	binding sites in 4D	http://pocketome.org	database					All species	Knowledgebase		
https://fairsharing.org/1632	10.25504/FAIRsharing.s9ztmd	Polbase	https://polbase.neb.com/	database		ready-to-use			All species	Knowledgebase		
111-111-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-			Inttps://github.com/PopulationAndCommunityOntol	Lucia -						Contraction of the state		
https://fairsharing.org/1053	10.25504/FAIRsharing.vq28qp	Population and Community Ontology	ogy/pco	standard	maintained	ready-to-use			All species	Semantic standards		github
https://fairsharing.org/1684	10.25504/FAIRsharing.22s2bs	Predictive Networks	http://predictivenetworks.org/	database		and the same			All species	Knowledgebase		
mups.//tairsnaring.org/2/90	10.23304/ FAIKSnaring.22e3be	Franceton University MicroArray database	http://www.bioinf.manchester.ac.uk/dbbrowser/PP		+	ready-to-use	+		An species			+
https://fairsharing.org/2099	10.25504/FAIRsharing h8r843	PRINTS	NTS/PRINTS.html	database		ready-to-use	recommended		All species	Knowledgebase		
https://fairsharing.org/2232	10.25504/FAIRsharing.t6win7	probeBase	http://www.probebase.net	database	maintained	ready-to-use			All species	Knowledgebase		1
		P					1			Model/formats		1
https://fairsharing.org/1143	10.25504/FAIRsharing.v033mi	proBed	http://www.psidev.info/probed	standard	maintained				All species	syntax:Format		
https://fairsharing.org/1532	10.25504/FAIRsharing.zve9cc	Proteasix Ontology	https://dx.doi.org/10.1186%2Fs13326-016-0078-9	standard		İ	İ	İ	All species	Semantic standards	i	1
https://fairsharing.org/1637	10.25504/FAIRsharing.wv5q9d	ProtoNet	http://www.protonet.cs.huji.ac.il/	database		1	1		All species	Knowledgebase		1
	1 .									Model/formats or		1
https://fairsharing.org/1244	10.25504/FAIRsharing.dmhjcg	Quality Control Markup Language	http://www.psidev.info/groups/quality-control	standard	maintained	<u> </u>	recommended		All species	syntax:models/syntax		
https://fairsharing.org/2327	10.25504/FAIRsharing.txcn6k	RDF Portal	https://rdfportal.org	database	maintained	ready-to-use			All species	Knowledgebase		

							FAIRorg	plant specie	s Applied	to		4
FAIRsharing URL	FAIRsharing DOI	Record Name	Record homepage URL	Resource Type	Manintenace	Ready-to-use	recommended	accepted	species	Туре	ELIXIR recommended	provider
										Model/formats or		
https://fairsharing.org/1269	10.25504/FAIRsharing.a4wgws	Real-time PCR Data Markup Language	http://rdml.org/	standard	maintained	ready-to-use			All species	syntax:models/syntax		
https://fairsharing.org/2177	10.25504/FAIRsharing.pxnqyt	RepeatsDB	http://repeatsdb.bio.unipd.it/	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/4548	10.25504/FAIRsharing.ta2ct3	Resource Identification Portal	https://scicrunch.org/resources	database	and at start and	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2009	10.25504/FAIRsharing.9sb9qh	Restriction enzymes and methylases database	http://rebase.neb.com/rebase/rebase.ntml	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2396	10.25504/FAIRsharing.tex4c8	KTam	http://rram.xram.org/	database	maintained	ready-to-use		Ambidancia	All species	Knowledgebase		
https://fairsharing.org/2009	10.25504/FAIRsharing.th11nh	RIKEN Bioresource Research Center	http://web.brc.nken.jp/en/	database	maintained	ready-to-use	recommended	Arabidopsis /rico	All species	Knowledgebase		+
https://lansharing.org/3200	10.25504/ PAikSharing.h5pwqc	RNA Atlas of Structure Frobing	http://rasp.znangiab.net	uatabase	Indintaliteu	ready-to-use		Arabidopsis/fice	All species	Kilowieugebase		
https://fairsbaring.org/1640	10 25504/FAIRsharing vehide	Motifs	https://www.rpacossmos.com/index.php	database		ready-to-use			All species	Knowledgebase		
incepsi// initialianingiolog/ 2040	20120504/174itistianingreesjee			dutubuse			1		7 in species	Model/formats or		<u> </u>
https://fairsharing.org/308	10.25504/FAIRsharing.e729c4	RNA Markup Language	http://www-lbit.iro.umontreal.ca/rnaml/	standard		ready-to-use			All species	syntax:models/syntax		
https://fairsharing.org/65	10.25504/FAIRsharing.kgt2h2	RNA Ontology	https://github.com/bgsu-rna/rnao	standard	maintained	ready-to-use			All species	Semantic standards		github
https://fairsharing.org/2891	10.25504/FAIRsharing.KcCjL7	RNAcentral	https://rnacentral.org	database	maintained	ready-to-use	1		All species	Knowledgebase		1
https://fairsharing.org/1739	10.25504/FAIRsharing.zzgvrv	RNAJunction	https://rnajunction.ncifcrf.gov/	database	1	ready-to-use	1		All species	Knowledgebase		1
https://fairsharing.org/2853	10.25504/FAIRsharing.6mMhZp	rPredictor	http://rpredictordb.elixir-czech.cz/	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/1810	10.25504/FAIRsharing.x16th8	RTPrimerDB	http://medgen.ugent.be/rtprimerdb/	database					All species	Knowledgebase		UGENT(Beligum
https://fairsharing.org/2231	10.25504/FAIRsharing.bb5rna	Sea scientific open data publication	https://www.seanoe.org/	database	maintained	ready-to-use	recommended		All species	Knowledgebase		
										Model/formats or		
https://fairsharing.org/138	10.25504/FAIRsharing.k97xzh	Sequence Alignment Map	https://github.com/samtools/samtools	standard		ready-to-use			All species	syntax:Format		github
https://fairsharing.org/238	10.25504/FAIRsharing.6bc7h9	Sequence Ontology	http://www.sequenceontology.org/	standard	maintained	ready-to-use			All species	Semantic standards		
			https://members.loria.fr/ACoulet/files/snpontology	1								
https://fairsharing.org/22	10.25504/FAIRsharing.cnbjkn	Single Nucleotide Polymorphism Ontology	.6_description.html	standard	maintained	ready-to-use			All species	Semantic standards		
https://fairsharing.org/1673	10.25504/FAIRsharing.kq47fy	SpliceDisease	http://cmbi.bjmu.edu.cn/Sdisease	database					All species	Knowledgebase		
Lu (11. L. L. L. (22.22)												
https://fairsharing.org/2283	10.25504/FAIRsharing.ekj9zx	Standards for Reporting Enzymology Data Database	https://www.beilstein-strenda-db.org/strenda/	standard	maintained	ready-to-use	recommended		All species	Minimum reporting guidelines		
https://tairsnaring.org/2057	10.25504/FAIKsnaring.x93ckv	Stanford Microarray Database	http://sma.princeton.edu/	database					All species	Data repository		
https://foischasing.org/1877		STINC	http://www.abi.eastic.east	databasa						Kanudadaabaaa		
https://fairsharing.org/1877	10.25504/FAIRsharing.q7bkqr	STING	http://sms.col.cnptia.embrapa.br/swis/index_s.ntm	uatabase					All species	Model/formate		
https://fairsbaring.org/139	10 25504/EAIRsharing dogo6t	Stockholm Multiple Alignment Format	http://sonnhammer.shc.su.se/Stockholm.html	standard		ready-to-use			All species	syntax:Format		
https://fairsharing.org/155		Stress Knowledge Man	https://skm.nih.si/	database	maintained	ready-to-use		All plant species	Air species	Knowledgebase		
https://fairsharing.org/1875	10 25504/FAIRsharing 9h7wyk	STRING	https://skining.db.org/	database	Indined	ready-to-use		rui plane species	All snecies	Knowledgebase		
https://fairsharing.org/2239	10.25504/FAIRsharing.bya6z	Super-Enhancer Archive	http://sea.edbc.org/	database	maintained	ready-to-use			All species	Knowledgebase		1
			http://genome.ucsc.edu/FAQ/FAQformat.html#forn	1						Model/formats or		1
https://fairsharing.org/116	10.25504/FAIRsharing.mwmbpg	Browser Extensible Data Format	at1	standard	maintained	ready-to-use			All species	syntax:Format		UCSC(USA)
https://fairsharing.org/1952	10.25504/FAIRsharing.frryvx	SUPERFAMILY	http://supfam.org	database	maintained	ready-to-use			All species	Knowledgebase		1
			http://genome.ucsc.edu/FAQ/FAQformat.html#forn	1					1 1 1 1 1	Model/formats or		1
https://fairsharing.org/132	10.25504/FAIRsharing.gnga3t	Personal Genome SNP Format	at10	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/FAQ/FAQformat.html#forn	1	1					Model/formats or		
https://fairsharing.org/32	10.25504/FAIRsharing.20df5w	ENCODE peak information Format	at13	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/FAQ/FAQformat.html#forn	1						Model/formats or		
https://fairsharing.org/901	10.25504/FAIRsharing.9sdcx8	Multiple Alignment Format	at5	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/FAQ/FAQformat.html#forn	1						Model/formats or		
https://fairsharing.org/98	10.25504/FAIRsharing.ckjmt3	Binary sequence information Format	at7	standard	maintained	ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/FAQ/FAQformat.html#forn	1						Model/formats or		
https://fairsharing.org/131	10.25504/FAIRsharing.wkh9j2	nucleotide inFormation binary Format	at8	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/FAQ/FAQformat.html#forn	1						Model/formats or	·	
https://fairsharing.org/148	10.25504/FAIRsharing.fe4pja	Gene Prediction File Format	at9	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
https://fairsharing.org/1691	10.25504/FAIRsharing.se4zhk	SuperTarget	http://bioinformatics.charite.de/supertarget	database					All species	Knowledgebase		
				1	1				l	Model/formats or		
nttps://fairsharing.org/1087	10.25504/FAIRsharing.cwt4py	Synthetic Biology Open Language	Inttps://spoistandard.org/	standard	maintained	ready-to-use	-	-	All species	syntax:models/syntax		+
https://fairsharing.org/2	10 25504/FAIRsharing dg76vs	Sunthatic Biology Open Language Visual	https://cholstandard.org/wicual.about/	standard	maintained	ready to use			All spacios	iviodei/formats oi		1
https://fairsharing.org/3	10.25504/FAIKsharing.dg/6vs	Synthetic Biology Open Language Visual	https://sboistandard.org/visual-about/	standard	maintained	ready-to-use			All species	syntax:models/syntax		
https://fairsharing.org/1772	10.25504/FAIRsharing.onOppp	The Parcede of Life Data Systems	http://unuen.bulds/stops.org/	database		ready-to-use			All species	Knowledgebase		+
https://lansharing.org/1775	10.25504/ PARSilaring.en5ilpit	The Department of Energy Systems Biology	Inteps.//www.boldsystems.org/	uatabase		ready-to-use			All species	Kilowieugebase		+
https://fairsbaring.org/2381	10 25504/EAIRcharing isyark	Knowledgebase	https://www.kbase.us	database	maintained	ready-to-use	recommended	All plant species		Knowledgebase		
https://fairsharing.org/1889	10.25504/FAIRsharing.aftff2	The Gene Index Project	http://compbio.dfci.harvard.edu/tei/	database	maintainea	- cauy-to-use	recommended	, plant species	All species	Knowledgebase		+
https://fairsharing.org/2533	10.25504/FAIRsharing.8ng9t6	The Network Data Exchange	https://www.ndexbio.org	database	maintained	ready-to-use	recommended	1	All species	Knowledgebase		1
https://fairsharing.org/4907	N/A	The Nucleic Acid Knowledgebase	http://nakb.org/	database		ready-to-use		1	All species	Knowledgebase		1
https://fairsharing.org/1643	10.25504/FAIRsharing.6648ht	The SEQanswers wiki	https://www.seganswers.com/	database	maintained		1	1	All species	Knowledgebase	i	1
https://fairsharing.org/2736	10.25504/FAIRsharing.a1de61	The Track Hub Registry	https://www.trackhubregistry.org/	database	1	ready-to-use	1	1	All species	Knowledgebase	i	1
						1	1	1		Model/formats or		1
https://fairsharing.org/482	10.25504/FAIRsharing.3pxg2f	Axt Alignment Format	http://genome.ucsc.edu/goldenPath/help/axt.html	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
				1		1	1		1	Model/formats or		1
https://fairsharing.org/78	10.25504/FAIRsharing.hza1ec	Binary Alignment Map Format	http://genome.ucsc.edu/goldenPath/help/bam.htm	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/goldenPath/help/bedgraph							Model/formats or		
https://fairsharing.org/525	10.25504/FAIRsharing.vttygv	BEDgraph	html	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/goldenPath/help/bigChain.							Model/formats or		
https://fairsharing.org/666	10.25504/FAIRsharing.wzp79x	Big Chain	html	standard	maintained	ready-to-use			All species	syntax:Format		UCSC(USA)

							EAIRorg	nlant specie	c Applied t			4
FAIRsharing URL	FAIRsharing DOI	Record Name	Record homepage URL	Resource Type	Manintenace	Ready-to-use	recommended	accepted	species	Type	ELIXIR recommended	provider
			http://genome.ucsc.edu/goldenPath/help/bigGeneF							Model/formats d	r	
https://fairsharing.org/660	10.25504/FAIRsharing.6eg9a3	Big Gene Prediction	red.html	standard	maintained	ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/goldenPath/help/bigMaf.h	t	1		1			Model/formats c	r	1
https://fairsharing.org/615	10.25504/FAIRsharing.78make	Big Multiple Alignment Format	ml	standard	maintained	ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/goldenPath/help/bigPsl.ht							Model/formats c	r	
https://fairsharing.org/517	10.25504/FAIRsharing.c9fakh	Big Pattern Space Layout	ml	standard	maintained	ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/goldenPath/help/bigWig.ht	:						Model/formats d	r	
https://fairsharing.org/518	10.25504/FAIRsharing.x9k6a1	bigWig Track Format	ml	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/goldenPath/help/chain.htm	n						Model/formats c	r	
https://fairsharing.org/110	10.25504/FAIRsharing.72e4we	Chain Format for pairwise alignment	1	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
										Model/formats c	r	
https://fairsharing.org/128	10.25504/FAIRsharing.evxcfb	net alignment annotation Format	http://genome.ucsc.edu/goldenPath/help/net.html	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
			http://genome.ucsc.edu/goldenPath/help/wiggle.ht							Model/formats c	r	
https://fairsharing.org/864	10.25504/FAIRsharing.2nrf9f	Wiggle Track Format	ml	standard		ready-to-use			All species	syntax:Format		UCSC(USA)
https://fairsharing.org/405	10.25504/FAIRsharing.9y3gv0	Enzyme Structure Function Ontology	http://sfld.rbvi.ucsf.edu/	standard		ready-to-use			All species	Semantic standards		UCSF(USA)
https://fairsharing.org/2641	N/A	Structure Function Linkage Database Archive	http://sfld.rbvi.ucsf.edu/	database					All species	Knowledgebase		UCSF(USA)
https://fairsharing.org/2873	10.25504/FAIRsharing.83jovl	T-psi-C	http://tpsic.igcz.poznan.pl/	database	maintained	ready-to-use			All species	Knowledgebase		
			http://www.edgar-									
https://fairsharing.org/1360	10.25504/FAIRsharing.ylYItV	Transcription Factor Class Schema	wingender.de/TFClass_schema.html	standard	maintained	ready-to-use			All species	Semantic standards		
https://fairsharing.org/3655	10.25504/FAIRsharing.de533c	Translational Data Catalog	https://datacatalog.elixir-luxembourg.org/	database	maintained	ready-to-use			All species	Knowledgebase		L
https://fairsharing.org/1903	10.25504/FAIRsharing.1nwy41	Transmembrane Helices in Genome Sequences	http://pranag.physics.iisc.ernet.in/thgs/	database					All species	Knowledgebase		
https://fairsharing.org/2022	10.25504/FAIRsharing.p3bzqb	Transporter Classification Database	https://tcdb.org/	database	maintained	ready-to-use			All species	Knowledgebase		
https://fairsharing.org/2072	10.25504/FAIRsharing.zcn4w4	TreeBase	https://www.treebase.org	database		ready-to-use	recommended		All species	Knowledgebase		
https://fairsharing.org/2338	10.25504/FAIRsharing.x6nr7d	Tropical Data Hub	https://tropicaldatahub.org/	database					All species	Knowledgebase		
https://fairsharing.org/935	10.25504/FAIRsharing.wf28wm	UniProt Taxonomy	http://www.uniprot.org/taxonomy/	standard	maintained	ready-to-use			All species	Semantic standards		
https://fairsharing.org/2264	10.25504/FAIRsharing.j97pjn	Validated Antibody Database	http://www.labome.com	database	maintained	ready-to-use			All species	Knowledgebase		
https://foischaring.org/125		Variant Call Farmet	incups://www.ga4gn.org/product/genetic-variation-							iviouei/iormats d	"	
https://fairsharing.org/125	10.25504/FAIRsharing.cizzon	Variation Ontology	Iormats-vcr/	standard	an alastala a d	ready-to-use			All species	Syntax:Pormat		
https://fairsharing.org/2910	10.25504/FAIRSharing.05XKDS		http://waltadb.cwitchlab.org	database	maintaineu	ready-to-use			All species	Knowledgebase		+
https://fairsharing.org/2819	10.25504/FAIRsharing.EGn1ut	WALIZ-DB 2.0	http://wait200.switchiab.org	ualabase	maintaineu	ready-to-use			All species	Knowledgebase		+
https://iansnaning.org//10	10.25504/ FAIKSHAITING.J4ERCD	XML for evolutionary biology	http://xeo.couepiex.com/	stanuaru					All species	Model/formate	-	+
https://foircharing.org/17	10 2EE04/EAIBsharing 2mprr8	comparative	http://www.phyloyml.org/	standard		roady to use			All coording	cuntavimodols (suntav	'	
nups.//iansnainig.org/1/	10.20004/ FAINSHalling.5mprr8	genomics.	Intth://www.hukioxiii.org/	Istanuaru	1	peauy-co-use	1	1	I'm species	syntax.mouels/Syntax	1	1

Annex 2. Examples of file format standards

FASTA

FASTQ

Instrument ID lane tile X Y barcode read#	
	Header lines sequence quality scores
8HWI-EAS209_0006_FC706VJ:5:58:5894:21141#ATCACG/1 TTAATTGGTAAATAAATCTCCTAATAGCTTAGAINTTACCTINNNNNNNNNNNNN HWI-EAS209_0006_FC706VJ:5:58:5894:21141#ATCACG/1	ITTCTTGAGATTTGTTGGGGGGAGACATTTTTGTGATTGCCTTGAT

EMBL Format

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ΧХ
AC X64011; S78972;
ΧХ
SV X64011.1
ΧХ
DT 28-APR-1992 (Rel. 31, Created)
DT 30-JUN-1993 (Rel. 36, Last updated, Version 6)
ΧХ
DE Listeria ivanovii sod gene for superoxide dismutase
ΧХ
KW sod gene; superoxide dismutase.
ΧХ
OS Listeria ivanovii
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
ΧХ
RN [1]
RX MEDLINE; 92140371.
RA Haas A., Goebel W.;
RT "Cloning of a superoxide dismutase gene from Listeria ivanovii by
RT functional complementation in Escherichia coli and characterization of the
RT gene product.";
RL Mol. Gen. Genet. 231:313-322(1992).
ΧХ
RN [2]
RP 1-756
RA Kreft J.;
RT ;
RL Submitted (21-APR-1992) to the EMBL/GenBank/DDBJ databases.
RL J. Kreft, Institut f. Mikrobiologie, Universitaet Wuerzburg, Biozentrum Am
RL Hubland, 8700 Wuerzburg, FRG
ΧХ
              Location/Qualifiers
FH Key
FH
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FT
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ХΧ	
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120

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GenBank Format
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gtaatttctt

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LOCUS LISOD 756 bp DNA linear BCT 30-JUN-1993 DEFINITION Listeria ivanovii sod gene for superoxide dismutase. ACCESSION X64011 S78972 VERSION X64011.1 GI:44010 KEYWORDS sod gene; superoxide dismutase. SOURCE Listeria ivanovii ORGANISM Listeria ivanovii Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria. REFERENCE 1 (bases 1 to 756) AUTHORS Haas, A. and Goebel, W. TITLE Cloning of a superoxide dismutase gene from Listeria ivanovii by functional complementation in Escherichia coli and characterization of the gene product JOURNAL Mol. Gen. Genet. 231 (2), 313-322 (1992) MEDLINE 92140371 REFERENCE 2 (bases 1 to 756) AUTHORS Kreft,J. TITLE Direct Submission JOURNAL Submitted (21-APR-1992) J. Kreft, Institut f. Mikrobiologie, Universitaet Wuerzburg, Biozentrum Am Hubland, 8700 Wuerzburg, FRG FEATURES Location/Qualifiers source 1..756 /organism="Listeria ivanovii" /strain="ATCC 19119" /db_xref="taxon:1638" /mol_type="genomic DNA" regulatory 95..100 /gene="sod" /regulatory_class="ribosome_binding_site"

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61 gtaatttctt

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DDBJ flat file format

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                         756 bp DNA linear BCT 30-JUN-1993
DEFINITION Listeria ivanovii sod gene for superoxide dismutase.
ACCESSION X64011 S78972
VERSION X64011.1 GI:44010
KEYWORDS sod gene; superoxide dismutase.
SOURCE Listeria ivanovii
 ORGANISM Listeria ivanovii
      Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE 1 (bases 1 to 756)
 AUTHORS Haas, A. and Goebel, W.
 TITLE Cloning of a superoxide dismutase gene from Listeria ivanovii by
      functional complementation in Escherichia coli and characterization
      of the gene product
 JOURNAL Mol. Gen. Genet. 231 (2), 313-322 (1992)
 MEDLINE 92140371
REFERENCE 2 (bases 1 to 756)
 AUTHORS Kreft,J.
 TITLE Direct Submission
 JOURNAL Submitted (21-APR-1992) J. Kreft, Institut f. Mikrobiologie,
      Universitaet Wuerzburg, Biozentrum Am Hubland, 8700 Wuerzburg, FRG
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ORIGIN
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   61 gtaatttctt .....
//
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SAM (from https://www.samformat.info/sam-format-flag)



QNAME: query template name, aka. read ID

VCF format (from https://davetang.github.io/learning_vcf_file/)



BED format

Track line

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chr7	127472363	127473530	Pos2 0 +	127472363	127473530	255,0,0
chr7	127473530	127474697	Pos3 0 +	127473530	127474697	255,0,0
chr7	127474697	127475864	Pos4 0 +	127474697	127475864	255,0,0
chr7	127475864	127477031	Neg1 0 -	127475864	127477031	0,0,255
chr7	127477031	127478198	Neg2 0 -	127477031	127478198	0,0,255
chr7	127478198	127479365	Neg3 0 -	127478198	127479365	0,0,255
chr7	127479365	127480532	Pos5 0 +	127479365	127480532	255,0,0
chr7	127480532	127481699	Neg4 0 -	127480532	127481699	0,0,255

Mandatory columns

Optional columns

BedGraph format

browser position chr19:49302001-49304701

browser hide all

browser pack refGene encodeRegions

browser full altGraph

- # 300 base wide bar graph, autoScale is on by default == graphing
- # limits will dynamically change to always show full range of data
- # in viewing window, priority = 20 positions this as the second graph
- # Note, zero-relative, half-open coordinate system in use for bedGraph format

track type=bedGraph name="BedGraph Format" description="BedGraph format" visibility=full color=200,100,0 altColor=0,100,200 priority=20

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GFF3/GTF format (from https://bioinfogp.cnb.csic.es/tools/seqnjoy/help/)

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1	five prime utr	3631	3759		+	gene name=NAC001:ID=five prime utr 1:Parent=AT1G01010.
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1 .	exon 5174	5 Pai	irs tag-va	alue hav	e (gene name=NAC001;exon number=5;exon id=AT1G01010.1.exon5;ID=exon 5;Parent=AT1G01010.1
1	CDS 5174	5:sligh	tly differ	rent aspe	ct	gene name=NAC001;exon number=5;protein id=AT1G01010.1;ID=CDS 5;Parent=AT1G01010.1
Columns	exon 5439	5895			. \	gene name=NAC001;exon number=6;exon id=AT1G01010.1.exon6;ID=exon 6;Parent=AT1G01010.1
Columns	CDS 5439	5627		÷	0	gene name=NAC001;exon number=6;protein id=AT1G01010.1;ID=CDS 6;Pare
1 to 8 are	stop_codon	5628	5630	- C	+	o gene_name=NAC001;exon_number=6;ID=stop_codon_1;Parent=AT10 HierarChy is expressed differently.
1 10 0 00 0	three_prime_utr	5631	5899	2	+	. gene_name=NAC001;ID=three_prime_utr_1;Parent=AT1G01010.1 In GTF "gene_id" and "transcript_id"
- Identical	-					are compulsory from trasnscript level
#Igonomo build TA	P10		10.000			in GFF3, the use of Patent
#Igenome build ac	RIU GCA 0000	01725 1	GT	F		allows more flexibility to
#Igenohuild last up	dated 2010.00	01735.1	01	1		represent dependence relationships
1	dene 3631	5900		2		nene id "ATIG01010": gene name "NAC001", gene Antyne "protein codina":
1 .	transcrint 3631	5800		1	*	gene_a antochologi, (gene_name traccor), gene_active procen_coung ,
1 .	exon 3631	3013	÷	1	*	gene a "Allocitor", Ranschiel a "Allocitor", gene name victor, ansche dotte victore processioner de anti-
1 .	CDS 3760	3013	Č.	1	0	gene_id "ATIGOTIOD", Rahschipt_id "ATIGOTIOD.1", exon number 1", gene name "NACOOT", protein id "ATIGOTIOD.1.Exon1",
1 .	start codon	3760	3762	T	+	gene a Artooloto, Ranschich a Artooloto, exon number 1, gene name "NACOOL"
1	evon 3006	4276	5102	1		ane if attission in transmint if attission in the aven number "?", gene name "NACOOI", evon if "Attission".
1	CDS 3006	4276	1	-	2	gene d "ATIGO1010", transcrint d "ATIGO10101", evon number "2", gene name "NACO01", protein d "ATIGO10101"
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Annex3. <u>Identinfier.org</u> ID schemes related to genetic data or their annotation

ы	n		Domain	pattern	definition	prefix	url p	eficed resources									มางกรุสาน
								id eccessURL	mfo	Institution	location c	official n	resourcePrefix	localld	testString	resourceURL	
					Ensembl is a joint project between EMBL			MR:00100011 https://www.ensembi.org/id/(Sid)	Ensembl at Sanger/EMBL-EBI	Sanger Institute and European Bioinformatics Institute Hisaton Cambridge	uk t	nue e	ebi	EN5G00000139618	Homo sapiens	https://www.ensembi.org/	
MIR-000	00003 Ense	mbl	All species	^((ENS[FFTG]\\d[11](\.\\d+)?)(FB\\ w(2)\\d[7])((FA-2)(2)\\d[3][a-zA- 20)((a-2))(2)(a-z-a-	EBI and the Sanger Institute to develop software system which produces an maintains automatic annotation o	a d n ensembl	http://identifiers.org/ersembl 0	MIR:00200561 http://uswest.ensembl.org/id/(\$id)	Ensembl US West mirror		USA f	alse		EN5G00000139618	Homo sapiens	http://uswest.ensembl.org/	
				9]+(_3?(t)?(\\d+)?[[a-z]]?]]\$	selected eukaryotic genomes. Thi collections also references outgroup organisms.	p		MR:00100562 http://useast.ensembl.org/id/(5id)	Ensembl US East mirror		USA f	alse		EN5G00000139618	Homo saplens	http://useast.ensembl.org/	1
								MR 00100563 http://asia.emembi.org/id//Sid)	Ensembl Asia mirror		Sineapore f	alse		EN5600000139618	Homo sapiens	http://www.ensembl.org/	-
	_							id arread III	info	Institution	official	could be	test String	reserved IBI	Invation	resourceDealty	In Contra
								N PROFESSION	Internet Protein Researce color Resident 1981 colors	Instruction	tour P			http://www.unionst.em/	(Calcon)	TELEVISION CONTRACTOR	La Pool
					The UniProt Knowledgebase (UniProtKII) a comprehensive resource for protein	is n		Her washing a state of the stat	contention products and pressions. One sports			00723		inder) www.unproc.org/			
MR-000	00005 Uni#	rot Knowledgebase	All species	^([A-N,R-Z][D-9][A-Z][A-Z, D-9][A-Z, D 9][D-9][(1,2])]([D,P,0]]D-9[[A-Z, D- 9][A-Z, D-9][A-Z, D-9][D-9][(\.\d+)]5	extensive cross-references to more that 220 external databases. Besides amin	n ouniprot	http://identifiers.org/uniprot D	Mikroszusza intps://www.ncsi.nim.nin.gov/protein/1540)	Childree through NLB	National Center for addectinology information (NCar)	tine .	00/23	Camoduin	mpc//www.ncol.nem.net.gov/protein/	054	100	Procein Anowiedgebase
					acid sequence and a description, it als provides taxonomic data and citation information.	o n											UniProt-TrEMBL
																	UniProt/TrEMBL
												1		1	1		UniProtKB/Swiss-Prot
MIR-000	00010 IntA	t	All species	^EBI\-[0-9]+\$	IntAct provides a freely available, ope source database system and analysis tool	n Is intact	http://identifiers.org/intact 0	id accessURL	info	Institution	location	official n	resourcePrefix	localid	testString	resourceURL	_
					for protein interaction data.			MR:0010017 https://www.ebi.ac.uk/intact/interaction/(\$id)	IntAct at EBI	European Bioinformatics Institute, Hinston, Cambridge	uk t	nue e	ebi	EBI-2307691	ATP hydrolysis by RADS1 inhibition by BRCA2	https://www.ebi.ac.uk/intact/	
					InterPro is a database of protein families			id accessURL	info	Institution	location c	official n	resourcePrefix	localid	testString	resourceURL	
MIR-000	00011 Inte	Pro	All species	MPR\d(6)\$	domains and functional sites in whic identifiable features found in know proteins can be applied to unknow	n interpro n	http://identifiers.org/interpro D	MR:00100018 https://www.ebi.ac.uk/interpro/entry/[\$id]	Intel®ro	European Bioinformatics Institute, Hirston, Cambridge	uk t	nue e	ebi	199000100	Ribonuclease P	https://www.ebi.ac.uk/interpro/	
					probein sequences.			NER:00100697 df.org/trespro:{5id}	Bio2RDF	Bio28DF.org	f	istae		179300100	Ribonuclease P	http://interpro.bio2rdf.org/fct/	
					REGG PATHWAY is a collection o manually drawn pathway map	sé n		id accessURL	info	Institution	location c	official lo	localid	testString	resourceURL		KEGG
MIR-000	00012 KEG	Pathway	All species	~(w[2,4]\d[3]\$	representing our knowledge on th molecular interaction and reaction networks.	e kegg pathway n	http://identitiers.org/kegg.pathway 0	NER:00100020 https://www.kegg.jp/entry/(\$id)	KEGG PATHWAY Dutabase	Ryoto University Bioinformatics Center	Japan t	nue h	hsa00520	Pyruvate metabolism	https://www.genome.jp/kegg/ pathway.html		
					EIGG reaction contains our knowledge o			id eccessURL	info	institution	location c	official lo	localld	testString	resourceURL		REGG
MIR.000	00014 KEG	Reaction	All species	^R\d+\$	the universe of reactions that are relevan to life.	t kegg reaction	http://identifiers.org/kegg.reaction 0	MIR:00100022 https://www.kegg.jp/entry/(\$id)	KEGG Reaction Database	Kyoto University Bioinformatics Center	Japan t	nue R	800100	NADH ferricytochrome-b5 oxidoreductase	https://www.genome.jp/kegg/ eaction/	r	
								id accessURL	info	Institution	location of	official lo	localid	testString	resourceURL		Online Mendelian Inheritance in Man
					Calma Mandalian Inhasimana in Man in			MR:00100024 https://ornim.org/entry/[\$id]	OMIM at John Hopkins	Johns Hopkins University, Baltimore, Maryland	USA t	nue 6	603903	SICKLE CELL ANEMIA	https://omim.org/		Mendelian Inheritance in Man
MIR.000	00016 OM		Human	~[*#+35~]3/Q[0]\$	catalog of human genes and geneti disorders.	a ic mim	http://identifiers.org/mim 0	MR: 00100694 http://omim.bio2rdf.org/describe/?turl=http://bio2rdf.	BuzRDF	Bio28DF.org		alue 6	603903	Scriver and Wasath	http://omim.bio2rdf.ore/fct		MM
								http://mirms.com/m.con/entro/Mirki	CIMIM mirror at John Honkins	Inhra Hankim University Beltimore Maryland	1154	inter 6	503903	SCOLF CTLL ANTMIA	hites //mirror amim are/		
					The PIR SuperFamily concept is being use	d		Ad execution		antibulina	territori			ter finite			Restain Information Researce
MIR-000	00017 PIRS		All species	^PIRSE\dj6)\$	comprehensive and non-overlapping clustering of UniProtXB sequences into	e pinsf	http://identifiers.org/pirsf 0										
	_				evolutionary relationships.			Microsoftanza Intelación de Contractor de Contractor (Contractor de Contractor		Georgetown University Medical Center	USA P	2158		uniomate s-denydrogenase	rntps://pir.georgetown.eou/		
MIR-000	00018 Rea	tome	Human	(^R-[A-Z](3]-\d+(- \d+)?\(_\d+)?\$) (^REACT_\d+(_\d+) ?5)	The Reactome project is a collaboration to develop a curated resource of cor pathways and reactions in human biology.	ereactome	http://identifiers.org/reactome D	id accessURL	into Beartrome a runated knowledgebase of biologica	Institution Ontario Institute for Cancer Research, NYU Medica	location c	official lo	locald	testString	resourceURL		Reactorne Stable ID
								MR:00100026 https://reactome.org/content/detail/(\$id)	pathways	School, Cold Spring Harbor Laboratory and European Bioinformatics Institute	Canada / USA / UK f	alse R	R-HSA-201451	TGF-beta/BMP	https://www.reactome.org/		
MIR-000	00019 DOI		all species	^(dol/\;)?\d[2]\.\d[4].*\$	The Digital Object Identifier System is fo identifying content objects in the digita	er al doi	http://identifiers.org/doi 0	ld accessURL	info	Institution	location c	official lo	localid	testString	resourceURL		Digital Object Identifier
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MIR-000	00020 Prot	in Data Bank	All species	^[0-9][A-Za-zD-9][3]\$	The Protein Data Bank is the singl worldwide archive of structural data o	e of pdb	http://identifiers.org/pdb 0	MR:00100037 http://www.pdbe.org/(\$id)	Protein Databank in Europe (PDBe)	European Bioinformatics Institute, Hirston, Cambridge	uk f	alse p	pdbe	2gc4	Methylamine dehydrogenasi heavy chain	http://www.pdbe.org/	
					biological macromolecules.			MR:00100096 http://proteopedia.org/wki/index.php/(\$id)	Proteopedia	Weizmann Institute of Science	brael f	iatse		2gc4	Paracoccus denitrificans	http://www.proteopedia.org/	
								MR:00100165 http://pdbj.org/mine/summary/[5id]	Protein Data Bank Japan (PDBj)	Institute for Protein Research, Osaka University	Japan f	iatse p	pdbj	2gc4	methylamine dehydrogenase	http://www.pdbj.org/	
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					erganism.			MR:00100237 http://purl.bioontology.org/ontology/GO/GO:(\$id)	GO through BioPortal	National Center for Biomedical Ontology, Stanford	USA f	iatse b	bpti	6915	apoptosis	http://bioportal.bioontology.org/ontologies/GD	
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MIR-0000008	HGNC	Human	^(()HGNC hgnc):)?\d[1,5]\$	abbreviation) for each known human gene. All approved symbols are stored in the HGNC database, and each symbol is	hgnc	http://identifiers.org/hgnc 0	0 MR	00100111	https://www.gerenames.org/cg- bin/gene_vymbol_report?hgnc_id=(\$id)	HUGO Genome Nomenclature Committee	European Bioinformatics Institute, Hinston, Cambridge	шк	true	ebi	2674	CCD543842	https://www.genenames.org	
				unique. HGNC identifiers refer to records in the HGNC symbol database.			MR	00100698	http://hgnc.bio2rdf.org/describe/?url=http://bio2rdf. org/[\$id]	Bio2808	Bio28DF.org		false		hgnc:2674	Gene Symbol for DAPK1	http://hgnc.bio2ndf.org/fct	
							id		accessURL	info	institution	location	official	localid	testString	resourceURL	resourcePrefix	so
				The Sequence Ontology (SO) is a			_		http://www.sequencegntploev.org/misp/current_rele		Department of Molecular and Cellular Biology, Universit	br .				http://www.vequenceontology		
MIR-0000008	Sequence Ontology	All species	^50:\d{7}\$	parts of a genomic annotation. It provides a common set of terms and definitions to	10	http://identifiers.org/so	1	0100112	ase/term/SO:{\$id}	sequence Cristology	of California, Berkeley	USA	Tatse	704	Necessary to encode a functional transcript.	.org/		pequence types and reacures
				facilitate the exchange, analysis and management of genomic data.			MR	00100241	http://purl.bioontology.org/ontology/SO/SO:(\$id) 5	Sequence Ontology through BioPortal	National Center for Biomedical Ontology, Stanford	USA	false	704	necessary to encode a functional transcript.	http://bioportal.bioontology.o tg/ontologies/50	bpti	
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	1			UniPathway is a manually curated resource of metabolic pathways for the			ы		accessURL	info	Institution	location	official	localid	testString	resourceURL		
MIR-0000008	Unipathway	All species	^UPA\d(5)\$	UnProtKE/Swiss-Prot knowledgebase. It provides a structured controlled	unipathway	http://identifiers.org/unipathway	•		http://www.grenoble.prabi.fr/obiwarehouse/unioath		Swiss Institute of Bioinformatics (SIB) and French Nationa					http://www.grenoble.prabi.fr/		-
				protein in a metabolic pathway.			MR	w100114	way)\upa ?upid+(\$id)	our sum Tf	Institute for Research in Computer Science and Control	seltzerund	. 2130	ur-400200	evanual termencecon	oblwarehouse/unipathway		
MIR-0007018	PharmGKE Pathway*	Human	1PA\d+S	and cellular phenotype data and clinical information about people who have	pharmekb.pathwa~	http://identifiers.one/pharmekb.path-www	ы 0	•	accessURL	info	Institution	location	official	localid	testString	resourceURL		
				participated in pharmacogenomics research studies. The data includes, but is			MR	00100120	http://www.pharmgkb.org/pathway/{\$id}	PharmGKB at Stanford	Department of Genetics, School of Medicine, Stanfor University, Stanford, California	usa	false	PA146123006	Codeine and Morphine	http://www.pharmgkb.org/		
				The NCBI BioSystems database centralizes and cross-links existing biological systems			ы		accessURL	info	Institution	location	official	resourcePrefix	localid	textString	resourceURL	
MIR-0000009	BioSystems	All species	^\d+\$	databases, increasing their utility and target audience by integrating their	biosystems	http://identifiers.org/biosystems	•									Aspartate undergoes a		1
				resources.			MR	00100128	https://www.ncbi.nim.nih.gov/biosystems/(Sid)	BioSystems database at NCBI	National Center for Biotechnology Information (NCBI)	USA	talse	ncbi	1	number of reactions that an not in any linear order.	https://www.ncbi.nim.nih.gov/biosystems/	
MBOOOT	CTD Gene	Human	Mitas	Database (CTD) presents scientifically reviewed and curated information on chemicals relevant	rtd same	http://idantifians.com/ntd	, id		accessURL	info	Institution	location	official	localid	testString	resourceURL		
				and their interactions in vertebrates and invertebrates. It integrates sequence,			- MR	00100131	http://ctdbase.org/detail.go?type=gene&acc=(\$id)	Comparative Toxicogenomics Database (Gene)	The Mount Desert Island Biological Laboratory	USA	false	101	ADAM metallopeptidase domain	http://ctdbase.org/		
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MIR-0000010	GeneDB	human patogen	^[\w\d_]*\$	provides a portal through which data generated by the "Pathogen Genomics" atous at the Wellcome Trust Senser	genedb	http://identifiers.org/genedb	•	[Pathopen Genomics Senser Institute and Former		-		-			4
				institute and other collaborating			MR	00100139	http://www.genedb.org/gene/(Sid)	GeneDG at Sanger Institute	Bioinformatics institute	uk	false	Q1536c	Q1536c - GeneDB	http://www.genedb.org/		
	Molecular Interact	om		forms a structured controlled vocabulary for the annotation of experiments			id		accessURL a	info	Institution	location	official	resourcePrefix	localid	testString	nesourceURL	м
MIR-0000010	Ontology	All species	-wei:\d[4]5	concerned with protein-protein interactions. MI is developed by the HUPO	psimi	nttp://dentifiers.org/psimi	MR	00100142	https://www.ebi.ac.uk/ols/ontologies/mi/terms?obo_ id=MI:Sidi	Molecular Interactions Ontology through OLS	European Bioinformatics Institute, Hirston, Cambridge	uk	fatse	ols	303	permeabilising cell	https://www.ebi.ac.uk/ok/ontologies/mi	
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MR-0000011	i smart	All species	rsm(d(s)\$	The Simple Modular Architecture Research Tool (SMART) is an online tool for the identification and annotation of probein domains, and the analysis of domain architectures.	smart	http://identifiers.org/umart t	0 HR	00100151	accessURL http://wmart.embl- heldelbarg.do/wmart/do_annotation.pl?DOMAIN+(5kd)	info SMART (Simple Modular Architecture Research Tool)	Indyo, Jokyo Indotution EMBL, Heidelberg	location Germany	official false	localid SM00015	testString Calmodulin-binding motif.	resourceURL http://smart.embi- heidelberg.de/		-

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 | http://weinene.org/cou | MRO | 00100152 B
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s?uid=(Sid) | Conserved Domain Database at NCE
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an integrated ontology for the description
of biological and clinical investigations.
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ations | Human | (^OBI:\d(7)\$) (^OBI_\d(7)\$) | The ontology will represent the design of
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| MR-0000159 | ibiST | All species | ^([A-Z]+)?\d+(\.\d+)?\$ | The dbEST contains sequence data and
other information on "single-pass" cDNA
sequences, or "Expressed Sequence Tags", dbest | http://identifiers.org/dbest | MIR-00100

 | Https://www.ncbi.nim.nih.gov/nucest/(\$id)
 | dbEST at NCBI | National Center for Biotechnology Information (NCBI) US | SA I
 | alse ncbi | BP100000
 | 8P100000 Chaetomium cDNA https://www.ncbi.nim.nih.gov/nucest | NCBI EST |
| | | | | from a number of organisms. | | MIR:00100

 | 31 https://www.ebi.ac.uk/ena/data/view/(\$id}
 | dbEST through European Nucleotide Archive (ENA) | European Bioinformatics Institute, Hirston, Cambridge UR | к
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 | Chaetomium globosum https://www.ebi.ac.uk/ena | |
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 | 51 http://getentry.ddbj.nig.ac.jp/getentry/na/(\$id)
 | dbEST through DNA Data Bank of Japan (DDBJ) | DNA Data Bank of Japan, Mishima, Shizuoka Jap | apan f
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| | | | | registry of nucleic acid reagents designed
for use in a wide variety of biomedical | | ы

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| MIR-00000160 | dbProbe | Human | ~\d+\$ | research applications, together with dbprobe
information on reagent distributors,
probe effectiveness and computed | http://identifiers.org/dbprobe 0 | MIR:00100

 | 25 https://www.ncbi.nim.nih.gov/probe/?term=(\$id)
 | dbProbe at NCBI | National Center for Biotechnology Information (NCBI) US | ISA I
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| MIR:00000161 | ildanp | Human | ^rs\d+\$ | both single base nucleotide substitutions
and short deletion and insertion | http://identifiers.org/dasnp 0 | ~

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| MR-00000162 | UniSTS | human and mouse | ~\d+S | sequence tagged sites (STSs) derived from
STS-based maps and other experiments.
STSs are defined by PCR primer pairs and unists | http://identifiers.one/unists | id

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information such as genomic position, | | MIR:00100

 | https://www.ncbi.nim.nih.gov/genome/sts/sts.cgi?uid
+{Sid}
 | UniSTS at NCBI | National Center for Biotechnology Information (NCBI) | ISA I
 | alse ncbi | 456789
 | voltage-gated channel https://www.ncbi.nim.nih.gov/sites/entrez?db=unists | |
| | | | | The EcoGene database contains updated
information about the E. coli K-12 genome | | ы

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| MIR-0000263 | tcoGene | E.coli | ~EG\d+S | extensive gene bibliographies. A major
EcoGene focus has been the re-evaluation | http://identifiers.org/ecogene 0 | MIR-00100

 | 16 http://www.ecogene.org/gene/(\$id)
 | EcoGene at University of Miami | Miller School of Medicine, University of Mami | 5A I
 | rue EG10173 | Cytochrome d
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| MIR-00000164 | SABI | Plant species | ^*(m+\$ | constitutes a repository for a wide array
of heterogeneous data from high-gabi
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 | http://www.gabipd.org/database/cgi-
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| | | | | species. These data (i.e. genomics, | | MIR-00100

 | 10 bin/GreenCards pl.cgi?BioObjectid=(Sid)&Mode=Show
BioObject
 | GABI at Max Planck | Max Planck Institute of Molecular Plant Physiology, Berlin Ge | lermany 1
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 | http://www.gabipd.org/ | |
| MR-00000165 | StrenGenes | All species | ~\d+S | A 165 rRNA gene database which provides
chimera screening, standard alignment, preespenses | http://identifiers.org/greengenes | id

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| | | | | and taxonomic classification using multiple published taxonomies. | | MIR-00100

 | http://greengenes.bl.gov/cgi-
bin/show_one_record_v2.pl?prokMSA_id=(\$id)
 | GreenGenes at Lawrence Berkeley | Center for Environmental Biotechnology, Lawrence
Berkeley National Laboratory, California | ISA I
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 | http://greengenes.ibi.gov/ | |
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| MIR-00000167 | H-InvOb Locus | Human | ^HEX\d(7)[\.\d+]?\$ | annotations of human genes and hinv.locus
transcripts including gene structures,
characterized informe services | http://identifiers.org/hinv.locus | MIR-00100

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| MR-0000258 | H-InvOb Transcript | Human | ~eat\d(9)(\\d+)?\$ | transcripts. It provides curated
annotations of human genes and himctranscript | http://identifiers.org/hinv.transcript 0 |

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| MR-00000169 | 1-InvOb Protein | Human | mm/d/3i/\\d+175 | Integrated database of human genes and
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| MIR:00000170 | Metainformation | Human | ^SEQF\d+\$ | than 600 prokaryote species that are hornd.seq
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16 me=GenomeList&file=indes&link=detallinfo&seqid=(\$
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The Forsyth Institute, Boston US | ISA I
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| MIR-00000172 | RD Segment Sequence | Influenza | ^/m+(/_)?/d+(/./d+)?\$ | virus, including genomic sequence, strain,
protein, epitope and bibliographic ind segment
information. The Segment Details page | http://identifiers.org/ird.segment 0 |

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| MR-00000173 | 57 inder | bacteria | ^(5)w+(\-\d)?\$ | Grinder is a catactese of bacteriae
insertion sequences (5). It assigns IS
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Ss. Each IS is annotated with information infinder | http://identifiers.org/isfinder 0 | id

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insertion supervices (6). It suggest 15
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MIR-00000185	EDAM Ontology	All species	^(data topic operation format)_\ d[4]\$	vocabulary for the description, in semantic terms, of things such as: web	edam	http://identifiers.org/edam	0 MIR:001	0536 http://purl.bioontology.org/ontology/EDAM/(\$id)	EDAM through BioPortal	National Center for Biomedical Ontology, Stanford	USA	false	bpti	data_1664	Minimal Information Requested in the Annotation of Biochemical Models	n http://bioportal.bioontology.org/ontologies/EDAM	
				tool collections and packages, work- benches and workflow software,			MIR:001	0762 https://www.ebi.ac.uk/ols/ontologies/edam/terms? ort_form=(\$id)	tDAM through OLS	European Bioinformatics Institute, Hinston, Cambridge	ик	false	pls	data_1664	Minimal Information Requested in the Annotation of Biochemical Models	n https://www.ebi.ac.uk/ols/ontologies/edam	
				a manually curated database providing information on the sequence, structure			ы	accessURL	iefo	Institution	location	official	localid	testString	resourceURL		
MIR-0000193	ArachnoServer	Spider	^AS\d(6)\$	and biological activity of protein toxins from spider venoms. It include a molecular target ontology designed	arachrioserver	http://identifiens.org/arachnoserver	0 MIR:001	0250 http://www.arachnoserver.org/tosincard.html?id+[5	id ArachnoServer at Brisbane	Institute for Molecular Bioscience, The University Overniland, Brisbane	of Australia	false	A5000050	Latrotoxin-Lt1a	http://www.arachnoserver.org /		
				BioCyc is a collection of Pathway/Genome			ы	accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR.00000194	BioCyc	All species	^[A-Z-0-9]+(\;)?[A-Za-z0-9+%-]+\$	electronic reference source on the genomes and metabolic pathways of	biocyc	http://identifiers.org/biocyc	0 MIR-001	0251 http://bjocyc.org/entid/id=(Sid)	BioSyc at SRI International	Bioinformatics Research Group, SRI Internation	al, USA	false	ECOU:CYT-D-UBIOK-CPLX	3 cytochrome axidase enzymes	http://biocyc.ore		-
				database is a resource specialized in			d	accessURL	afo.	intitution	location	official	localid	tentString	resourceURL		Carbohydrate-Active enzYmes
MIR-00000195	CAZy	All species	^(GT GH PL CE CBM /d+(_/d+)?\$	enzymes that build and breakdown complex carbohydrates and glycoconjugates. These enzymes are	cazy	http://identifiers.org/cazy 0	0	1977 http://www.com.en.iffed.html	Caller of Children	Architecture et Fonction des Macromolécules Biologique	h	false.	0710	6	han the second		
				classified into families based on structural inter otox (uene ontorogy Annotation) project provides high-quality Gene				and with have raised by the same		CNIS, Marselle	1.00				(100-) www.caryorgy		
MIR-0000196	GDA	All species	^()]A-N,R-2][D-9][A-2][A-2, D-9][A-2, 9][D-9]](([D,P,Q]]D-9][A-2, D-9][A-2, 9][A-2, D-9][D-9]))(UR5]D-97	Octology (GD) annotations to proteins in the UniProt Knowledgebase (UniProtKB) and International Protein Index (IDI) This	g04	http://identifiers.org/goa	D Id	accessURL	into	institution	location	official	resourcePrefix	localid	testString	resourceURL	Gene Ontology Annotation
			F[[10][_0-9]+][0,1]][[EBI-[0-9]+]5	involves electronic annotation and the trie Wanofoldy offscase VERs to			MIR-001	0253 https://www.ebi.ac.uk/QuickGO/GProtein?ac+(\$id)	SOA through QuickGD	European Bioinformatics Institute, Hirston, Cambridge	UK	talse	dnicklo	P12345	Oryctolagus cuniculus	https://www.ebi.ac.uk/GOA/	UniProtKB-GDA
MIR-00000197	PaleoDS	Animal	~\ _{id+\$}	information about the entire fossil record. It stores global, collection-based	paleodb	http://identifiers.org/paleodb	o id	accessURL	info	institution	location	official	localid	testString	resourceURL		Paleobiology database
				eccurrence and taxonomic data for marine and terrestrial animals and plants eccuastacing of the statement occupies or			MR:001	0254 http://fossilworks.org/?a+tasoninfo&taxon_no+(\$id)	PaleoDB at Macquarie University	Macquarie University, Sydney	Australia	false	83088	ground dwelling omnivore	http://paleodb.org/		
MIR-0000200	EchoBASE	E.coli	^cs),d+\$	contain and manipulate information from post-genomic experiments using the model bacterium Escherichia coli X-12.	echobase	http://identifiers.org/echobase C	ld D	accessURL	info	institution	location	official	localid	testString	resourceURL		
				The database is built on an enhanced annotation of the updated genome assured additionally assured or sense.			MR:001	0259 http://www.york.ac.uk/res/thomas/Gene.cfm?recor D+{\$id}	di EchoBASE at the University of York	Department of Biology (Area 10), University of York, York	: UK	false	880170	Electron acceptor	http://www.york.ac.uk/		
MIR-0000201	ant NOG	All smeries	Almark.	Non-supervised Orthologous Groups) is a database of orthologous groups of genes. The orthologrup groups are appreciated		http://dentifian.org/genog	ld n	accessURL	iefo	institution	location	official	localld	testString	resourceURL		
				with functional description lines (derived by identifying a common denominator for			MR:001	0260 http://eggnog.embi.de/version_3.0/cgi/search.py?se ch_term_0=(\$id)	ar eggNOG Version 3 at European Molecular Biolo Laboratory	pgy European Molecular Biology Laboratory, Heidelberg	Germany	false	veNOG12876	MAGI family member	http://eggnog.embil.de/version _3.0/	5	
				Ensembl Genomes consists of five sub- portals (for bacteria, protists, fungi, plants and invertebrate metazoa) designed to			d	accessURL	info	institution	location	official	resourcePrefix	localid	testString	resourceURL	Ensembl Genomes Bacteria
MIR-0000203	Ensembl Bacteria	bacteria	^((EB/w+))([A-20-9]+_[A-20-9]+)]5	complement the availability of vertebrate genomes in Ensembl. This collection is concerned with bacterial announces	ensembl.bacteria	http://identifiers.org/ensembilibacteria	0 MIR:001	0261 https://bacteria.ensembl.org/id/{Sid}	Ensembl Bacteria at EBI	European Bioinformatics Institute, Hinston, Cambridge	ик	false	ebi	MU9_3181	Cysteinyl-tRNA synthetase	https://bacteria.ensembl.org/	
				Ensembl Genomes consists of five sub- portals (for bacteria, protists, fungi, plants			ы	accessURL	iefo	institution	location	official	resourcePrefix	localid	testString	resourceURL	Ensembl Genomes Protists
MIR:0000203	Ensembl Protists	protists	~\u=\$	and invertebrate metazoa) designed to complement the availability of vertebrate genomes in Ensembl. This collection is	ensembl.protist	http://identifiers.org/ensembl.protist	0 MIR:001	0262 https://protists.ensembl.org/id/(\$id)	Ensembl Protists at EBI	European Bioinformatics Institute, Hirviton, Cambridge	uĸ	false	ebi	PTC0120w	Cytoadherence linked asexual	https://protists.ensembl.org	
				concerned with protist genomes. Ensembl Genomes consists of five sub- portals (for bacteria, protists, fungi, plants			ы	accessURL	info	institution	location	official	resourcePrefix	localid	testString	resourceURL	Ensembl Genomes Metazoa
MIR-0000204	Ensembl Metazoa	Metazoa	^(m+()))d+\$	and invertebrate metazoa) designed to complement the availability of vertebrate genomes in Ensembl. This collection is	ensembl metazoa	http://identifiers.org/ensembl.metazoa	0 MIR-003	0263 https://metacos.ensembl.org/id//Sid)	Enzembi Metazoa at EBI	European Bioinformatics Institute, Hirston, Cambridge	UK	false	ebi	FBr/0084214	Pyruvate kinase	https://metapoa.ensembl.org/	
				concerned with metazoa genomes. Ensembl Genomes consists of five sub-				and the second s	a fa	lastitutine .	handler	attend		handed	terifficies.		Farrandol Concerner Mania
MIR-0000205	Ensembl Plants	Plant species	^\w+(\d+)?(\d+)?\$	and invertebrate metazoa) designed to complement the availability of vertebrate anomalies in Energies.	ensembl.plant	http://identifiers.org/ensembl.plant	0	miles of the second second field	Encomental Principants and P.F.F.	Formers Richformatics Institute Minster Combusies		felse		AT107304F	CLAVATA3/ESR (CLE)-relates	d bites (fetente encombi encl	Allocities des Alloc Planta
				concerned with plant genomes. Ensembl Genomes consists of five sub-				and with the second s		corpean arean and a month, mixed, camering	un.				protein	mpr./pans.manu.org	
MIR-0000208	Ensembl Fungi	Fungi	^[A-Z-8-20-9]+\$	portals (for bacteria, protists, fungi, plants and invertebrate metazoa) designed to complement the availability of vertebrate	ensembl fungi	http://identifiers.org/ensembil.fungi	D Id	accessURL	into	institution	location	official	resourcePrefix	localid	testString	resourceURL	Ensembl Genomes Fungi
				genomes in Ensembl. This collection is concerned with fungal genomes.			MR:001	0265 https://fungi.ensembl.org/id/(Sid)	Enzembl Fungi at EBI	European Bioinformatics Institute, Hirviton, Cambridge	ик	false	ebi	CADAFLATD0006211	RING finger protein	https://fungi.ensembil.org/	
MIR-0000207	HCVDB	Human	^w/d[s]\$	collection of computer-annotated sequences based on reference	hevdb	http://identifiers.org/hcvdb	ы 0	accessURL	iefo .	institution	location	official	localld	testString	resourceURL		euHCVDB
				genomes mainly dedicated to HCV protein sequences, 3D structures and functional mathematications			MIR:001	0266 https://euhcvdb.ibcp.fr/euHCVdb/do/displayHCVEnt primaryAC+(\$id)	Y HOVER IN CARS	Institut de Biologie et Chimie des Protéines, CN University of Lyon , Lyon-Gerland	RS, France	false	M58335	Hepatilis C virus	http://euhcvdb.ibcp.fr/euHCVc b/	1	
MIR-0000208	Genetias	Human	Aur-S	GenAtlas is a database containing	erutia	http://identifiers.com/een.atias	d o	accessURL	Info	Institution	location	official	localld	testString	resourceURL		
				and phenotypes.			MR-001	0267 http://genatlas.medecine.univ- paris5.fr/fiche.php?tymbol+(\$id)	Genatias at Paris Descartes University	Paris Descartes University, Paris	France	false	наз	Heinz body anemia	http://genatias.medecine.univ paris5.fr/	-	
1410.00000.100	CATH - mademin	All seconds		domain classification of protein structures in the Protein Data Bank. Protein	and a second second	http://doubles.com/outbourgets	ld .	accessURL	info	institution	location	official	localld	testString	resourceURL		
	contrappinantly	ALL SPECIFIC	. (pall (pall (pall (pall))))))	combination of automated and manual procedures. There are four major levels in	Calcon Support Internety	http://www.initia.com/carticoperiativy	MR-001	0268 http://www.cathdb.info/cathnode/[\$id}	CATH superfamily at UCL	Institute of Structural and Molecular Biology, Univers College London	united Kingdom	false	1 10 10 200	1mw7A01	http://www.cathdb.info/		
				domain classification of protein structures in the Protein Data Bank. Protein			ы	accessURL	info	institution	location	official	localld	testString	resourceURL		
MIR-00000210	CATH domain	All species	~(m+2	structures are classified using a combination of automated and manual procedures. There are four major levels in	cath.domain	http://identifiers.ong/cath.domain C	0 MIR:001	0269 http://www.cathdb.info/domain/(Sid)	CATH domain at UCL	Institute of Structural and Molecular Biology, Univers College London	ity uK	false	lcukA01	Nucleic acid-binding proteins	http://www.cathdbinfo/		
				GeneFarm is a database whose purpose is			ы	accessURL	iefo	institution	location	official	localld	testString	resourceURL		
MIR-00000211	GeneFarm	Arabidopsis	M(d+\$	Arabidopsis nuclear genes and gene products.	genefarm	http://identifiers.org/genefarm 0	MR 001	0270 https://urgi.versailles.inra.fr/Genefarm/Gene/display	- GeneFarm at Unité de Recherche en Génomique Végétal	e Unité de Recherche en Génomique Végétale, Evry	France	false	4892	Gene 'ALDO1'	http://urgi.versailles.inra.fr/Ge nefacm/	1	1
			1	penes from fully sequenced organisms			ы	accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-00000213	HOGENOM	All species	~(m+\$	collection references phylogenetic trees which can be retrieved using either linited eccession products	hogenom	http://identifiers.org/hogenom C	MR-001	0272 http://pbil.univ-lyon1.fr/cgi-bin/view-	HOGENOM at CNRS	Laboratoire de Biométrie et Biologie Evolutive, CN	RS, France	false	HBG284870	Chlamydiales	http://pbil.univ-		1
				Genetros accession numbers, or HOGENOM Genetros displays the maximum likelihood phylogenetic (protein) trave			ы	ecessing	info	Institution	location	official	localid	testString	resourceURL		Ensembl GeneTree
MIR:00000214	GeneTree	All species	rensgt\d+\$	representing the evolutionary history of the genes. These are constructed using the canonical popters for many and the	genetree	http://identifiers.org/genetree		nzza http://www.ensembl.org/Multi/GeneTree/Image?db	" GeneTree at Frourish	Sanger Institute and European Bioinformatics Institu	te,	false	1956/100550000774747	101	hitter //www.aucounted.auco."		
				Ensembl. both in silico generated and manually				core;gt+(Sid)		Hinaton, Cambridge	un .				(http://www.enterna.org/		
MIR-00000216	Mycolinowser tuberculosis	Mycobacterium	^Ru\d[4]{A B c}?\$	reviewed information within databases dedicated to the complete genomes of Memberterism holescolosis	myco.tuber	http://identifiers.org/myco.tuber	0 Id	accessURL	eto	institution	location	official	localid	testString	resourceURL		TubercuList
				Mycobacterium leprae, Mycobacterium Mycobacterium in a hestorium mar providen			MIR:001	e=(Sid)	Mycollrowser tuberculosis at Global Health Institute	Global Health Institute, Lausanne	Switzerland	false	Rv1908c	both a catalase	http://tuberculist.epfl.ch/		
MIR-00000211	Mycolicowser leprae	Mycobacterium	*ML\u+S	both in silico generated and manually reviewed information within databases dedicated to the complete genomes of	myco.Jepra	http://identifiers.org/myco.lepra	ы 0	accessURL	iefo .	institution	location	official	localld	testString	resourceURL		Leproma
		-	L	Nycobacterium tuberculosis, Mycobacterium leprae, Mycobacterium mycoborownel M schestorium nasc protilicer			MIR:001	0276 http://mycobrowser.epfl.ch/leprosysearch.php?gens name=(\$id)	¹⁺ Mycollrowser leprae at Global Health Institute	Global Health Institute, Lausanne	Switzerland	false	ML0224	dihydrofolate biosynthesis	rmp://mycobrowser.epfl.ch/le prosy.html		
MIR-00000218	Mycolicowser marinum	Mycobacterium	"MMAR_\d+S	both in silico generated and manually reviewed information within databases dedicated to the complete genomes of	myco.matinum	http://identifiers.org/myco.marinum	ld D	accessURL	lefa	Institution	location	official	localld	testString	resourceURL		marinolist
			-	Mycobacterium tuberculosis, Mycobacterium leprae, Mycobacterium matiocroanel 18 schoolcour con matio			MIR:001	0277 http://mycobrowser.epfl.ch/marinosearch.php?gene name=(\$id)	* MycoBrowser marinum at Global Health Institute	Global Health Institute, Lausanne	Switzerland	false	MMAR_2462	arginine biosynthesis	http://mycobrowser.epfl.ch/m arinolist.html		
Millionoon	Mycolicogram and and	Mycobacterium	rmsmeg/w+S	both in silico generated and manually reviewed information within databases dedicated to the committee manual	myco amer	http://identifiers.ong/myro.ung	ы	accessURL	info	institution	location	official	localld	testString	resourceURL		smegmalist
	, surgestis			Mycobacterium epise, Mycobacterium interculosis, Mycobacterium lepise, Mycobacterium		and a second sec	MR-001	0278 http://mycobrowser.epfl.ch/smegmasearch.php?ger +name=(Sid)	Mycollowier smegmatis at Global Health Institute	Global Health Institute, Lausanne	Switzerland	false	MSMEG_3769	HMM TIGROOB38	http://mycobrowser.epfl.ch/s megmalist.html		
		vertebrates,		orthologous protein-coding genes across vertebrates, arthropods, and fungi,			ы	accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-00000223	OrthoD5	arthropods, and fungi	~(=+\$	Orthology refers to the last common	orthodb	http://identifiers.org/orthodb 0	•				1	1			1	1	1
				ancestor of the species under consideration, and thus OrthoD8 explicitly			MIR:001	0280 http://cegg.unige.ch/orthodb/results?searchtext+[\$i	d) OrthoDB at Swiss Institute of Bioinformatics	Department of Genetic Medicine and Development, Sv Institute of Bioinformatics, Geneva	^{dss} Switzerland	false	C(SPOK)S	Transcription factor, fork head	http://cegg.unige.ch/orthodb4		
				ancestor of the species under consideration, and thus OrthoD8 explicitly feterates and the species of the Perceibase provides access to percoidase sequences from all kingdoms of life, and			MIR:003	228D http://cegg.unige.ch/orthodb/results?searchitext={\$i accessURL	d) OnhoD8 at Swiss Institute of Bioinformatics	Department of Genetic Medicine and Development, Sv Institute of Bioinformatics, Geneva Institution	fiss Switzerland	false official	C/3PDKB localid	Transcription factor, fork head	http://cegg.unige.ch/orthodb4 resourceUBL		

mm.0000022	P III UAANANI	Per species		and facilities suitable for analysing these	per concentre la	and the second second has seen as	MI	R-00100281	http://perceduse.toulouse.inna.fr/browse/process/vi	Percoxbase at University of Geneva	Department of Plant Biology, University of Geneva,	Switzerland	false	5282	CatA_Human	http://peroxibase.toulouse.inr		
				PhylomeC6 is a database of complete phylomes derived for different genomes			id		accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-00000221	Phylome06	All species	~t==\$	within a specific taxonomic range. It provides alignments, phylogentic trees and tree-based orthology predictions for	phylomedb	http://identifiers.org/phylomedb 0	0	P-00100282	htter//eholomarth.org/Danido/Cirl)	PholomeDB at Centro de Investigación Principe Belline	Bioinformatics Department,Centro de Investigación	Snain	false	Physics M BAT	Discontrars HIMAN	http://whichengedh.org/		
				all encoded proteins. ProtClustDB is a collection of related					undrit/brikerinen officiende-fore)		Principe Felipe, Valencia	apam.		-	ripponauto_nomen	map.)/preparation.org/		
MIR-00000226	ProtClustDB	All species	~\u=\$	Reference Sequence proteins encoded by complete genomes. This database	protclustdb	http://identifiers.org/protclustdb	0		accessum	810	Instation	location	omciai	resourcerrenx	localito	teststring	PRODUCTION.	Prosein Clusters Database
				contains both curated and non-curated clusters.			MI	R-00100285	nclusters&Cmd=DetailsSearch&Term=(\$id)	ProtClustDB at NCBI	National Center for Biotechnology Information (NCBI)	USA	talse	ncbi	080725	P-glycoprotein 21	https://www.ncbi.nim.nih.gov/proteinclusters?db+proteinclusters	Entrez ProtClustOB
MIR-0000221	рмр	All species	^([A-N,R-Z][D-9][A-Z][A-Z, D-9][A-Z, D 9][0-9][(([D,P,Q]]0-9][A-Z, 0-9][A-Z, D protein structures. Homology (or Comparative) modeling methods make use	pmp	http://identifiers.org/pmp	0 Id		accessURL	info	institution	location	official	localid	testString	resourceURL		Protein Model Portal	
			alws, e alle alle	build models for evolutionary related			MI	R-00100286	nttp://www.proteinmodelportal.org/query/uniprot/(s id)	PMP at University of Basel	Biozentrum, University of Basel, Basel	Switzerland	false	QUVCA6	158	al.org/		
MIR-0000228	ProtoNet ProteinCard	All species	~ld+S	classification of protein sequences in the UniProt database, partitioning the protein space, into clusters, of similar proteins	protonet.proteincard	http://identifiers.org/protonet.proteincard	o id		accessURL	Info	institution	location	official	localid	testString	resourceURL		
				This collection references protein information.			MI	R-00100287	http://www.protorvet.cs.huji.ac.il/requested/protein_ card.php?protein_id={\$id}	ProtoNet at Hebrew University	Hebrew University, Jerusalem	tsrael	false	16941567	Colicin	http://www.protonet.cs.huji.ac .l/		
MIR-00000225	ProtoNet Cimber	All species	Middle .	ProtoNet provides automatic hierarchical classification of protein sequences in the UniProt database, partitioning the protein	erologat cluster	http://dentifians.com/nontroast.cluster	n Id		accessURL	info	institution	location	official	localld	testString	resourceURL		
				space into clusters of similar proteins. This collection references cluster information.			MI	R-00100288	http://www.protoriet.cs.huji.ac.il/requested/cluster_c ard.php?cluster={\$id}	ProtoNet at Hebrew University	Hebrew University, Jerusalem	tsrael	false	4349895	Cyclotide	http://www.protonet.cs.huji.ac .ll/		
		_		Information about restriction enzymes, DNA methyltransferases and related			id		accessURL	info	institution	location	official	localid	testString	resourceURL		Restriction Enzyme Database
MIR-00000230	REBASE	All species	~td+5	proteins involved in the biological process of restriction-modification (R-M). It contains fully referenced information	rebase	http://identifiens.org/rebase 0	MI	R 00100289	http://rebase.neb.com/rebase/enz/(\$id).html	REDASE at New England Biolabs	New England Biolabs, Ipswich, Massachusetts	USA	false	101	Asp14H	http://rebase.neb.com/rebase /		
				Electrometric Resource Center focused on Invertebrate vectors of human pathogens.			id		accessURL	iefa	Institution	location	official	resourcePrefix	localid	testString	resourceURL	
MIR-0000233	VectorBase	invertebrate	^\D(4(\d(6))(\-\D(2))?\$	VectorBase annotates and curates vector genomes providing a web accessible integrated resource for the research	vectorbase	http://identifiers.org/vectorbase	D MI	R-00100291	https://www.vectorbase.org/search/site/{\$id]?&site+" Generate"	Vectorbase at EMBL-EBI	European Bioinformatics Institute, Hinston, Cambridge	ик	true	ebi	ISCW007415	hypothetical protein	https://www.vectorbase.org/	
				and the Control Vertex are			id		accessURL	info	institution	location	official	resourcePrefix	localid	testString	resourceURL	00
				The Disease Ontology has been developed as a standardized ontology for human disease with the purpose of providing the			MI	R 00100292	http://purl.bioantalary.one/antalary/DOID/DOID-(\$id)	Human Disease Ontology through BioPortal	National Center for Biomedical Ontology, Stanford	usa	false	boti	11337	commensal bacterial	http://bioportal.bioportplany.org/ontologies/DOID	
MIR-00000233	Human Disease Ontology	Human	^DCIID\;\\d+\$	biomedical community with consistent, reusable and sustainable descriptions of human disease terms observations	doid	http://identifiers.org/doid	1		https://www.ebi.ac.uk/ols/ontologies/doid/terms?ob	Numero Disease Castellano Mananak (215	University		failer.			common of basebasial	hillion (Amura aki an ah lak fantalantar (da id	
				characteristics and related medical vocabulary disease concepts.					o_id+DOID:(\$id)	name been bring strong of	University of Maryland (Maryland) and Northwestern							
							M	KUD100297	http://disease-ontology.org/term/UCIU:(348)	numan Disease Ontology at Northwestern University	University (filinois)	USA	ratse		1187	commensal dacterial	nttp://disease-ontology.org/	
MIR:00000234	Cell Cycle Ontology	All species	^CC0/;/w+\$	The Cell Cycle Ontology is an application ontology that captures and integrates detailed knowledge on the cell cycle	CCD	http://identifiers.org/cco	1		accessURL	info	Institution	location	official	resourcePrefix	localId	testString	resourceURL	
				process.			MI	R-00100294	lookup/?termid=CCO:(\$id)	Cell Cycle Ontology through OLS	European Bioinformatics Institute, Hinston, Cambridge	шк	false	ols	P0000023	last of the stages of mitosis	https://www.ebi.ac.uk/ontology-lookup/browse.do?ontName=DCD	
MIR-0000235	miRBase mature sequence	All species	MIMAT\d{7}	The miRBase Sequence Database is a searchable database of published miRNA sequences and annotation. This collection	mirbase.mature	http://identifiers.org/mirbase.mature	o id		accessURL	info	institution	location	official	localid	testString	resourceURL		
				refers specifically to the mature miRNA sequence.			MI	R 00100296	http://www.mirbase.org/cgi- bin/mature.pl?mature_acc={\$id}	rri Rilase	Faculty of Life Sciences, University of Manchester	ик	false	MIMAT000001	cel·let-7-5p	http://www.mirbase.org/		
MIR-0000236	nestProt	Muman	THE I WH	neXXProt is a resource on human proteins, and includes information such as proteins' function, subcellular location.	rextprot	http://identifiers.one/nextprot	d o		accessURL	info	Institution	location	official	localid	testString	resourceURL		
				expression, interactions and role in diseases.			MI	R 00100300	https://www.restprot.org/db/entry/[\$id}	nextProt at Swiss Institute of Bioinformatics	Swiss Institute of Bioinformatics, Geneva	Switzerland	false	NX_000165	Promotes cell survival	https://www.nextprot.org/		
				KEGG Genome is a collection of organisms			id		accessURL	info	Institution	location	official	localid	testString	resourceURL		KEGG Organism
MIR 00000238	to da Genome	All species	-(10(0+) (W(3,5))5	whose genomes have been completely sequenced.	cegg genome	http://denomen.org/kegg.genome	MI	R 00100303	http://www.kegg.jp/entry/(\$id)	KEGG Genome Database	Kyoto University Bioinformatics Center, Kyoto	Japan	true	eco	MG1655	http://www.genome.jp/kegg/c atalog/org_list.html		ress
				The KEGG Metagenome Database			id		accessURL	info	institution	location	official	localid	testString	resourceURL		xtos
MIR:00000235	KEGG Metagenome	All species	^T3\d+S	samples (ecosystems) of genome sequences for multiple species.	kegg metagenome	http://identifiers.org/kegg.metagenome	D MI	R 00100304	http://www.kegg.jp/entry/(\$id)	KEGG Metagenome Database	Kyoto University Bioinformatics Center, Kyoto	Japan	true	130002	microbial communities	http://www.genome.jp/kegg/c atalog/ore_list3.html		
							id		accessURL	info	institution	location	official	localid	testString	resourceURL	resourcePrefix	
				information on biological networks, the relationships between networks and the			MI	R-00100309	http://rgd.mcw.edu/rgdweb/ontology/annot.html?acc	Pathway Ontology at Rat Genome Database	Medical College of Wisconsin, Wisconsin	USA	false	208	Diabetes mellitus	http://rgd.mcw.edu/rgdweb/o		
MIR-0000243	Pathway Ontology	Human	197W:\d(7)\$	networks within a hierarchical structure. The five main branches of the ontology	pw	http://identifiers.org/pw	1	P-00100310	_id=PW3;540) https://www.ebi.ac.uk/ols/ontologies/pw/terms?obo_	Pathway Ontriney through OIS	Funnasa Bininformatica Institute Minuton Cambridge	I.K.	false	208	Diabates multitus	https://www.ebi.ac.uk/oh/ont	rin	
				are: classic metabolic pathways, regulatory, signaling, drug, and disease pathwaysfor complex human conditions.					id=PW:(Sid)	Raibura Ostalam ikanak BisBadal	National Center for Biomedical Ontology, Stanford,		fature .	107	Dislates melling	ologies/pw http://bioportal.bioontology.o	had	
				The Semanne Bead Archite (SBA) stores					urd://par.monitor@f.m@ruror@fi/w/rwi/wi		California	uun .				rg/ontologies/PW	alan	
				raw sequencing data from the next generation of sequencing platforms Data			id		accessURL	into	Institution	location	official	resourcePrefix	localid	testString	resourceURL	
MIR-0000243	Sequence Read Archive	All species	^[SED]#[AP#SXZ]\d+\$	metadata model consisting of six objects: study, sample, experiment, run, analysis	insdc.sra	http://identifiers.org/insdc.sra	D	R-00100312	https://www.ncbi.nlm.nlh.gov/sra/[\$id]?&report+full	Sequence Read Archive at NCBI	National Center for Biotechnology Information (NCBI)	USA	false	ncbi	\$80000007	5102748	https://www.ncbi.nlm.nlh.gov/sra	
				high-level information including goals of the study and literature references, and			MI	R-00100313	https://www.ebi.ac.uk/ena/data/view/(\$id}	European Nucleotide Archive (ENA)	European Bioinformatics Institute, Hinston, Cambridge	UK	false	ebi	580000007	SID2748	https://www.ebi.ac.uk/ena	
				may be linked to the INSDC BioProject database.			MI	R 00100314	http://trace.ddbj.nig.ac.jp/DRASearch/experiment?acc +[\$id}	DDBJ Sequence Read Archive (DRA)	DNA Data Bank of Japan, Mishima, Shizuoka	Japan	false		\$80000007	502748	http://trace.ddbj.nig.ac.jp/dra/	
MIR-00000244	Scer 17	yeast	^\u=+\$	matrices (PWMs) for transcription factors in Saccharomyces species. It identifies a single matrix for each TF that best	scrett	http://identifiers.org/scretf	b d		accessURL	info	Institution	location	official	localid	testString	resourceURL		
				predicts in vivo data, providing metrics related to the performance of that matrix			MI	R 00100315	http://stormo.wusti.edu/Scer17/details/[\$id]/	ScerTF at Washington University	Department of Genetics, Washington University Medical School, St Louis, Missouri	USA	false	RSC3	RSC chromatin remodeling	http://stormo.wustl.edu/ScerT F/		
MIR-01007144	PharmGKB Gene	Human	19A\w+5	repository for genetic, genomic, molecular and cellular phenotype data and clinical information about reworks why here	phurmekb.erre	http://identifiers.ong/pharmakh.ason	ы		accessURL	Info	institution	location	official	localid	testString	resourceURL		
				participated in pharmacogenomics research studies. The data includes, but is orthing the adiational and house			MI	R 00100316	http://www.pharmgib.org/gene/[\$id}	PharmGKB Gene at Stanford	Department of Genetics, School of Medicine, Stanford University, Stanford, California	USA	false	PA131	CYPIAS	http://www.pharmgkb.org/		
				miRNEST is a database of animal, plant and virus microRNAs, containing miRNA			id		accessURL	info	institution	location	official	localld	testString	resourceURL		
MIR-00000246	mRNEST	All species	^MNEST\d+\$	predictions conducted on Expressed Sequence Tags of animal and plant species.	minnest	http://identifiers.org/mimest	D MI	R 00100317	http://rhesus.amu.edu.pl/mirnest/copy/details.php?i d+(Sid)	miRNEST at Adam Mickiewicz University	Institute of Molecular Biology, Adam Mickiewicz University, Poznan	Poland	false	MNEST029358	hsa-mir-3190	http://rhesus.amu.edu.pl/mim est/copy/		
				is a clustering method based on conserved proceeding PNA (rcPNA)			id		accessURL	info	institution	location	official	localid	testString	resourceURL		Nucleic Acid Phylogenetic Profiling
MIR:00000243	NADP	bacteria	~\d+5	elements in a bacterial genomes. Short intergenic regions from a reference	napp	http://identifiers.org/napp	D MI	R-00100318	http://maigmon.u-	NARP at CNRS	Institut de Génétique et Microbiologie, UMR 8521, CNR5,	France	false	151	CP000247	http://napp.u-psud.fr/		
				sensine are compared with other nonecode tria defaulte or hap-tence are functional incRNA (long noncoding RNA)			и		accessURL	nfo	institution	location	official	localid	textString	resourceURL		
MIR-0000248	NONCODE v3		^\ _{[d+\$}	data obtained from microarray studies. IndRNAs have been shown to play key roles in various biological processes such	noncodev3	http://identifiers.org/noncodev3		P-001007330	- http://www.noncode.org/NONCODERv3/ncma.php?nc	NONCODE at Chinese Analass of Friends	Bioinformatics Research Group, Chinese Academy of	China	false	177550	Human Jan BA	http://www.epressite.eve/		
-				as imprinting control, circuitry controlling The VIRsIRNA database contains datalis of			- NI		id=(\$id}	A REAL PROPERTY OF SCIENCES	Sciences, Beijing							
MIR-00000245	VIRNIRNA	virus	∿inilid+\$	serve/shENA which target viral genome regions. It provides efficacy information where available, as well as the siRNA	virsima	http://identifiers.org/virsinna	о d		accessure.		Institute of Microbial Technology Council of Accession	location	official	rocald	unishing	heter//mid.audit.ext/www.		vrus urmA database
		+		sequence, viral target and subtype, as well as the target genomic region. Linear motifs are short, evolutionarily			MI	R-00100320	etailu=(Sid)	VIRsIBNA at Institute of Microbial Technology	and Industrial Research (CSR), Chandigarh, India	India	false	vini 1909	ganguaacucgaucugcu	insimadb		VIRuRNAdb
MIR-0000250		All species	1A-Ze-2 0-91+5	plastic components of regulatory proteins. Mainly focused on the eukaryotic	eim	http://idantifians.com/alm	o Id		accessURL	info	Institution	location	official	localid	testString	resourceURL		Eukaryotic Linear Motifs
	- Lon			sequences,the cukaryooc Linear Motin							and a set of the second second							
				resource (ELM) is a database of curated motif classes and instances.			MI	R-00100321	http://elm.eu.org/ekm/elmPages/[\$id].html	ELM at EMBL (Germany)	Structural and Computational Biology, European Molecular Biology Laboratory, Heidelberg	Germany	false	CLV_MEL_PAP_1	Melanisation activation	http://elm.eu.org/		

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 | kinases, providing structural and
functional information. | | | MR:001
 | 0324 https://bykdb.ibcp.fr/data/html/annotated/(\$id).html
 | BYRdb at CNRS | Unité Bases Moléculaires et Structurales des Système
Infectieux; CNRS - Université Claude Bernard, Lyon
 | France | false | A0A010039 | is a bacterial tyrosine kinase
 | http://bykdb.ibcp.fr/WMKdb/ | | |
| | | human, mouse, year | ^[[A-N,R-Z][D-9][A-Z][A-Z, D-9][A-Z, D
 | TopFIND is a database of protein termini,
terminus modifications and their
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| MIR:0000025 | TopFind | and E.coli | 9][0-9][((0,P,Q]]0-9][A-Z, 0-9][A-Z, 0
9][A-Z, 0-9][0-9][\$
 | Homo sapiens, Mus musculus, Arabidopsis
thaliana, Saccharomyces cerevisiae and | topfind | http://identifiers.org/topfind 0 | 0
MIR:001
 | 0326 http://clipserve.clip.ubc.ca/topfind/proteins/(\$id)
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| MIR.0000026 | CABRI | All species | ^([A-Za-z]+)?(_)?[A-Za-z-]+)\:([A-Za
z0-9]+)\$
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lists the availability of a particular | cabri | http://identifiers.org/cabri D | 0 MR-001
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 | CABRI Cell Lines catalogue in Genova (SRS) | National Cancer Research Institute of Genova, Genova
 | Italy | true | dsmz_mutz-id:ACC 291 | human glioblastoma
 | http://www.cabri.org/ | | |
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 | the set of technical specifications and
procedures which should be used to | | | MR:001
 | 0335 http://www.be.cabri.org/CABRI/srs-bin/wgetz?-e+-
page+EntryPage+[[Sid]]
 | CABRI Cell Lines catalogue in Brussels (SRS) | BCCM, Brussels
 | Belgium | false | dsmz_mutz-id-ACC 291 | human glioblastoma
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Database (CYGD) provides information on | | | вł
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budding yeast, Saccharomyces cerevisiae, | cygd | http://identifiers.org/cygd D | 0
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 | large (>4 kb) cDNAs identified in the
Kazusa cDNA sequencing project. | | | MR:001
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 | HUGE at Kazusa DNA Research Institute | Kazusa DNA Research Institute, Chiba
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 | interacting Genes/Proteins) is a database
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 | resourceURL | | Search Tool for Retrieval of Interacting Genes/Proteins |
| MIR:0000026 | STRING | All species | ^(]A-N,R-Z][D-9][A-Z][A-Z, D-9][A-Z, D
9][0-9][(([O,P,Q]]0-9][A-Z, 0-9][A-Z, 0
9][A-Z, 0-9][0-9])(([0-9][A-Za-d0
 | interactions. The interactions include
direct (physical) and indirect (functional)
associations; they are derived from four | string | http://identifiers.org/string | 0 MR:001
 | 0341 http://string.embl.de/interactions/[\$id}
 | STRING at Heidelberg | European Molecular Biology Laboratory, Heidelberg
 | Germany | false | P53350 | polo-like kinase 1
 | http://string.embl.de/ | | |
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 | sources:Genomic Context, High-
throughput Experiments,(Conserved) | | | MR:001
 | 0342 http://string-db.org/interactions/[\$id]
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 | clinical information such as diseases,
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 | 0405 http://www.snomedbrowser.com/Codes/Details/{Sid}
 | SNOMED-CT at The National Pathology Eschange | The Health Informatics Service, NHS, West Yorkshire
 | UK | false | 284196006 | Burn of skin (disorder)
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| MIR-0000027 | MaSH 2012 | human | 14.74.40.044
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terms namine descriptors in a bierarchical | mash 2012 | http://identifiers.com/mash.2012 | ld
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various levels of specificity. This thesaurus | | | MR:001
 | 10349 http://www.nim.nih.gov/cgi/mesh/2012/MB_cgi?mod
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 | genes that have been manually curated
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| MIR:000028 | IOPNAK receptor | mamatan | ~(0+>
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cyclic nucleotide-modulated ion channels | iupnar receptor | http://idensitiens.org/upnat/receptor | MR:001
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splayForward?objectId+(Sid)
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 | http://www.guidetopharmacol
ogy.org/targets.jsp | | IUPHAR-DB |
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| MIR-0000028 | Aceview Worm | worm | ^[a=20-0-]+\$
 | RefSeq, and single pass cDNA sequences
from dbEST and Trace). These are aligned | aceview.worm | http://identifiers.org/aceview.worm D | 0
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				The Plant Ontology is a structured vocabulary and database resource that				MR:00100389 http://www.plantontology.org/amigo/go.cgi?view=det alh&query=PO:{Sid}	Plant Ontology through Amigo	Cold Spring Marbor Laboratory, Cold Spring Marbor, N York	ew USA	fatse	amigo	5089	endosperm	http://www.plantoritology.org/	
MIR-00000307	Plant Ontology	Plant species	^PD:\d+5	links plant anatomy, morphology and growth and development to plant genomics data.	i po	http://identitiers.org/po	1	MR:00100390 http://puri.bicontology.org/ontology/PO/PO:(\$id)	Plant Ontology through BioPortal	National Center for Biomedical Ontology, Stanford	USA	fatse	bpti	5089	endosperm	http://bioportal.bioontology.org/ontologies/PO	
								MIR:00100676 https://www.ebi.ac.uk/ols/ontologies/po/terms?obo_ id=PO:{\$id}	Plant Ontology through OLS	European Bioinformatics Institute, Hinston, Cambridge	UK	fatse	ols	5089	endosperm	https://www.ebi.ac.uk/obi/ontologies/po	
				a comprehensive listing of post- transcriptionally modified nucleosides				id accessURL	info	institution	location	official	localid	testString	resourceURL		RNAmods
MIR-00000308	RNA Modification Database	All species	*\d[3]\$	from RNA. The database consists of all RNA-derived ribonucleosides of known structure, including those from	l mamods	http://identifiers.org/mamods	0	MIR:00100391 http://mods.ma.albany.edu/mods/modifications/vie w/(Sid)	RNA Modification Database at University of Utah	Department of Medicinal Chemistry and Department Biochemistry, University of Utah, Salt Lake City, Utah	ofUSA	false	101	lsowyosine	http://ma- mdb.cas.albany.edu/RNAmods		
				designed to manage and explore information on phylosenetic				id accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-00000312	TreeBASE	All species	^TB[1,2]?:[A-2][a-2]?\d+\$	relationships. It includes phylogenetic trees and data matrices, together with information about the relevant	treebase	http://identifiers.org/treebase	0	http://purl.org/phylo/treebase/phylows/study/(\$id)%	TreeBASE (hosted at National Evolutionary Synthesi Genter)	Phyloinformatics Research Foundation, Durham, Nor Catolina	th	false	TE2:51000	Out of Anatolia: Longitudina	http://treebase.org/		
				(TGD) Wiki is a database of information about the Tetrahamena thermobile				id accessURL	Info	institution	location	official	localid	testString	resourceURL		TCD
MIR-00000313	Tetrahymena Genom Database	¹⁰ Tetrahymena	^TTHERM(_\d+\$	genome sequence. It provides information curated from the literature about each rehibited area including a standardized	tgd	http://identifiers.org/tgd	0	MR:00100396 http://ciliate.org/index.php/feature/details/(Sid)	TGD at Stanford University	Department of Genetics, School of Medicine, Stanfo	rd USA	false	TTHERM_00648910	Intraflagellar transport 52	http://cliate.org/index.php/		
				curated multiple sequence alignments,				id accessURL	lefa	institution	location	official	localid	testString	resourceURL		
MIR-00000315	TIGRFAMS	All species	^TIGR\d+\$	protein sequence classification, and associated information designed to	tigrfam	http://identifiers.org/tigrfam	o	MIR:00100398 http://www.jcvi.org/cgi-	TGREAM at JCVI	The Institute for Genomic Research, Rockville, Maryland	USA	false	TIGR00010	starting with a unease alpha subunit	http://www.jcvi.org/cgi-		
				(AnimalTFDB) classifies TFs in sequenced				di accesuURL	info	institution	location	official	localid	textStrine	binyogmamiy Listing, cgi resource/URL		Animal Transcription Factor Database
MIR-00000316	Animal TFDB Family	animal	^/(m+\$	animal genomes, as well as collecting the transcription co-factors and chromatin remodeling factors of those genomes. This	atfdb.family	http://identifiers.org/atfdb.family	0	http://www.bioguo.org/AnimaiTTDB/family.php?fam-	Animal TTDB at Hubei Bioinformatics & Molecular Imaging	Hubei Bioinformatics and Molecular Imaging H	ley China	false	OUT.	Alleronoda melanolaura	http://www.bioguo.org/Anima		
				collections refers to transcription factor	r			H arrestill	Key Laboratory	Laboratory, Wuhan	location	reffectual	localid	test Grine	ITFDB/family_index.php		Database for Barbarial Govern II Introns
MIR-00000318	DBG2 Introns	bacteria	^\\w[1,2]{\w[1,2]}}[A-ZB-zD-9]+\$	Introns provides a catalogue of full-length, non-redundant group II introns present in basissing DML group II introns	dbg2introns	http://identifiers.org/dbg2introns	0	http://webapps2.ucalgary.ca/*groupii/cgi-		Department of Biological Sciences, University of Calga	76				http://webapps2.ucalgary.ca/~		
				actin a provide provide in demand.				bin/intron.cg/hame=[\$id]	activital Group II Introne at University of Calgary	Calgary, Alberta	Cartada	tatse .	Cumen	c gagengen	BLOTDII/		
MIR-0000320	Vbase2	human and mouse	^*(w+\$	The database VBASE2 provides germ-line sequences of human and mouse immunoriobulin variable (V) erres.	vbase2	http://identifiers.org/vbase2	0	IS RECENSIONS		Department of Experimental Immunology, Germ	an .	omciai	localio	teststring	resourceux. http://www.ybase2.org/ybase2		-
				Environment of the second seco			_	MIR:00100403 http://www.vbase2.org/vgene.php?id=(5id)	Vbase2 at German Research Centre for Biotechnology	Research Centre for Biotechnology, Braunschweig	Germany	talse	humiGHV025	GAGGTGCAGCTOG	php		
MIR-00000321	SPIKE Map	human	^spike\d[5]\$	store, organise and allow retrieval of pathway information in a way that will be useful for the research commonly. The	spike.map	http://identifiers.org/spike.map	0	id accessURL	info	Institution School of Computer Sciences and School of Medicine 1	location	official	localid	testString	resourceURL		Signaling Pathways Integrated Knowledge Engine
				database currently focuses primarily on net-constantion of the current of the cur				MIR:00100404 http://www.cs.tau.ac.i/~spike/maps/[\$id].html	SPIKE database at Tel Aviv University	Aviv University	Israel	false	spice00001	Cdk4-Cyclin D complex	http://www.cs.tau.ac.il/*spike/		
MIR-00000323	GeneCards	human	^(A-Za-z-0-9_]+(\@)?\$	genetic, proteomic, functional and disease information. It uses standard	genecards	http://identifiers.org/genecards	o	id accessURL	Info	institution	location	official	localid	testString	resourceURL		
				symbols. GeneCards presents a complete				MIR:00100407 http://www.genecardio.org/cgi- bin/carddisp.pl?gene=(\$id}	GeneCards at Weizmann Institute	Science, Rehavat	f Israel	true	ABLI	protooncogene	http://www.genecards.org/		
MIR-00000329	mirtX	Arabidopsis	25(+u/)+b/*	expression data, storing RT-qPCR-based gene expression profile over seven	n minex	http://identifiers.org/minex	0	id accessURL	efo	institution	location	official	localid	testString	resourceURL		-
				provides RNA structural models, publicly englishingdate statutistic provides total or			_	MR:00100423 http://compen.ps/mirex1/?page=results/record&name =[54]&eoref=pp2a&Imit=yes	mirtX at Adam Mickiewicz University	University, Poznan	** Poland	false	165a	CUGCUAAGAUC	+home		
MIR-00000330	Dictybase EST	Dictyostelium	roodi,d+S	the model organism Dictyostelium discoldeum and related species. It contains the complete genome sequence,	t dictybase.est	http://identifiers.org/dictybase.est	0	id accessURL	nfo	Institution	location	official	localid	textString	resourceURL		
				ESTs, gene models and functional annotations. This collection references serue, one extension of Thiodison inter-				MR:00100424 http://dictybase.org/db/cgr- bin/feature_page.pl/primary_id+(\$id)	Dictybase Gene at Northwestern University	Northwestern University Biomedical Informatics Cerr and Center for Genetic Medicine, Chicago, Illinois	USA	fatse	0080016567	CATTAATCAA	http://dictybase.org/		
MIR-00000331	IMGT HLA	Dictyostelium	^[A-ZD-9*:]+\$	project, is a collection of high-quality integrated databases specialising in immunoglobulins, T cell receptors and the	ingthia	http://identifiers.org/imgt.hla	0	id accessURL	Info	institution	location	official	resourcePrefix	localid	testString	resourceURL	IPD IMST/HLA
				Major Histocompatibility Complex (MHC) of all vertebrate species. IMGT/HLA is a Fotnbase for similation of glimhin-tratacase			_	MIR:00100425 bin/imgt/hia/get_allele.cgi?(\$id)	IMGT HLA at EBI	European Bioinformatics Institute, Hirston, Cambridge	UK	fatse	ebi	A*01-01-01-01	Caucasold, Oriental	https://www.ebi.ac.uk/imgt/hia/aliele.html	
MIR-00000335	Pomilase	Yeast	^5\m+()?\m+()?5	established to provide access to molecular data and biological information for the fission yeast Schizosaccharomyces pombe.	pombase	http://identifiers.org/pombase	0	id accessURL	info	institution	location	official	localid	testString	resourceURL		
				It encompasses annotation of genomic sequence and features, comprehensive the rightan process Apath Inpan is a				MIR:00100430 http://www.pombase.org/spombe/result/(Sid)	PomBase at University of Cambridge	Cambridge Systems Biology Centre, Department Biochemistry, University of Cambridge	ofuk	false	SPCC13811.01	alcohol dehydrogenase	http://www.pombase.org/		
MIR.00002114	194	human	^ENSG\d[11]\$	publicly available database with high- resolution images showing the spatial distribution of proteins in different	hpa	http://identifiers.org/hoa	0	id accessURL	info	institution	location	official	localid	testString	resourceURL		Numan Protein Atlas
				normal and cancer human cell lines. Primary access to this collection is through				MR 00100431 http://www.proteinatias.org/{\$id}	Numan Protein Atlas at AlbaNova University	Department of Proteomics, School of Biotechnolog AlbaNova University Center, Stockholm	^{IV,} Sweden	false	EN5G0000026508	Blood group antigen proteins	http://www.proteinatlas.org/		
MR-0002111	IAX Mire		Midas	IAX Mice is a catalogue of mouse strains	isomire	http://dentifiers.com/sources		id accessURL	iefo	institution	location	official	localid	testString	resourceURL		
				supplied by the Jackson Laboratory.		and a second second second second second second second second second second second second second second second		MIR 00100432 http://jawnice.jax.org/strain/(Sid).html	AXX Mice at Jackson Laboratory	The Jackson Laboratory, Sacremento, California	USA	false	5012	Chemically induced Mutation	http://jaamice.jax.org/		
140.000		Verent	A	The Yeast Transcription Factor Specificity Compendium (YeTFasCO) is a database of transcription factor specificities for the		han the second second		id accessURL	Info	institution	location	official	localid	testString	resourceURL		Yeast Transcription Factor Specificity Compendium
MIC0000339	rerrat.0	renit	./m+/"/D+(//D+)/\$	yeast Saccharomyces cerevisiae in Position Frequency Matrix (PFM) or Position Weight Matrix (PWM) formats.	PROSED	http://wentitiens.org/yettasco	0	MIR:00100434 http://yetfasco.ccbr.utoronto.ca/show9FM.php?mot=[Sid]	YeTFasCo at University of Toronto	Department of Molecular Genetics, Terrence Donne Centre for Cellular and Biomolecular Research, Univers of Toronto, Toronto	By By Canada	false	YOR172W_571.0	Motif 571 for YOR172W	http://yetfasco.ccbr.utoronto.c a/		
			^[a-2][3]\-[mir]let]lin]\-\w+(\-\w+\-	TarBase stores microRNA (miRNA) information for miRNA-gene interactions, as well as miRNA- and gene-related facts				id accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-00000340	TarBase	All species	(pr+)?	to information specific to the interaction and the experimental validation methodologies used.	tarbase	http://identifiers.org/tarbase	0	http://diana.imis.athena- MIR:00100713 innovation.gr/DianaTools/Index.php?r=tarbase/index Banimas=/Sidi	TarBase v7 at University of Thessaly	DIANA-Lab, Department of Electrical & Comput Engineering, University of Thessaly	er Greece	fatse	hsa-let-7a-2-3p	IGF8P3	http://diana.imis.athena- innovation.gr/DianaToob/inde x.oho?r=tarbase.f=vdev		1
				that identifies orthologs among publicly available, complete genome sequences. It	r u			id accessURL	info	institution	location	official	localid	textString	resourceURL		Orthologous MAtrix
			the set of the barries of the barrie	And the second sec	· · · · · · · · · · · · · · · · · · ·	terms with the section of the section of the	in in										

				can be accessed either group-wise, where all group members are orthologous to all			N	IR 00100437	http://omabrowser.org/cgi- bin/gateway.pl?f=DisplayEntry&p1=(\$id)	OMA Protein through OMA browser at ETH Zurich	ETH Zurich, Computer Science, Zurich	Switzerland	false	HUMAN16963	colled-coil domain	http://omabrowser.org/cgi- bin/gateway.pl		
		_		that identifies orthologs among publicly available, complete genome sequences. It			id		accessURL	info	Institution	location	official	localid	testString	resourceURL		
MR-00000343	OMA Group	All species	~(A-2]+S	identifies orthologous relationships which can be accessed either group-wise, where all group members are orthologous to all	oma.grp	http://identifiers.org/oma.grp	0 N	IR 00100438	http://omabrowser.org/cgi- bin/gateway.pl?f=DisplayGroup&p1=(\$id)	OMA Group through OMA browser at ETH Zurich	ETH Zurich, Computer Science, Zurich	Switzerland	false	LESCEPN	SA8HA02316	http://omabrowser.org/cgi- bin/gateway.pl		
				The Protein database is a collection of sequences from several sources, including	6		d		accessURL	info	Institution	location	official	resourcePrefix	localid	testString	resourceURL	
MIR.00000344	NCBI Protein	All species	~//w+\d+(\.\d+)?) (NP_\\d+)\$	regions in GenBank, RefSeq and TPA, as well as records from SwissProt, PIR, PRF,	ncbiprotein	http://identifiers.org/ncbipratein	0 N	IR:00100439	https://www.ncbi.nim.nih.gov/protein/(\$id)	NCBI Protein at NCBI	National Center for Biotechnology Information (NCBI)	USA	false	ncbi	CAA71118.1	Klebsiella preumoniae	https://www.ncbi.nim.nih.gov/protein	
				and PDB.			id		accessURL	info	institution	location	official	resourcePrefix	localid	testString	resourceURL	protein genbank identifier
MIR-00000345	GenPept	All species	~1]\d[5](\d+)?5	sequences based on translations from annotated coding regions in GenBank.	geripept	http://identifiers.org/genpept	0	IP-00100440	https://www.ncbi.nim.nih.gov/protein/[\$id]?report+g	GenDerit at NCB	National Center for Bisterboolney Information (NCB)	154	false	nchi	C44711181	Elabelella non-moniae	hites //aquae echi elee elle anu/ocetain	
				sequences that appear to come from the					enpept			lanation.	uttered					
MIR-00000346	UniGene	All species	~\d+\$	same transcription locus (gene or expressed pseudogene), together with information on protein similarities, sene	unigene	http://identifiers.org/unigene	0		accession. http://www.orbi.olm.olb.env/UniGena/cbst.cei/NGDD		ansotution .	location	omciai	ICC800	tentstrong	http://www.ochi.olm.oih.anu/		-
				expression, cDNA clone reagents, and proprioriated in one or the catabases that			N	IR:00100441	=(\$id)	UniGene at NCBI	National Center for Biotechnology , Maryland	USA	talse	4900	Arabidopsis thaliana	unigene		
MIR-0000353	PiroplasmaDB	Eukaryotic pathogens	^TA\d+S	(http://LuPathDB.org; formerly ApIDB) portal, covering eukaryotic pathogens of	f piroplasma	http://identifiers.org/piroplasma	0	1	accessURL	info	institution	location	official	localid	testString	resourceURL		
				the genera Cryptosporidium, Glardia, Leishmania, Neospora, Plasmodium, Dents ¹ m Talihungan tofee meenar			N	IR:00100448	http://piroplasmadb.org/piro/showRecord.do?name+ GeneRecordClasses.GeneRecordClass&source_id+(\$id)	ProplasmaBD at EuPathDB	Center for Tropical & Emerging Global Diseases University of Georgia, Georgia	USA	false	TA14985	topolsomerase IV subunit A	http://piroplasmadb.org/		
MIR-00000353	Unite	fungus	~uD#)d(6)5	transcribed spacer (ITS) sequence database. It focuses on high-quality ITS sequences generated from fruiting bodies.	s surite	http://identifiers.org/unite	ы 0		accessURL	info	institution	location	official	localid	testString	resourceURL		
				collected and identified by experts and deposited in public herbaria. Entries may	5		N	IR:00100449	http://unite.ut.ee/bl_forw.php?nimi+(\$id)	Unite at University of Tartu	Institute of Botany, University of Tartu, Tartu	Estonia	false	UD8020691	albatrelizs	http://unite.ut.ee/		
				repository of bacterial and archaeal glycoproteins with at least one			d		accessURL	info	Institution	location	official	localid	testString	resourceURL		
MIR0000154	Prougente	bacteria and arches	-JA-10/8(1,3(5	(glycosylated residue). Each entry in the database is fully cross-referenced and	i progyc	nttp://dentmen.org/progyc	N	IR 00100451	http://www.proglycprot.org/detail.aspx?ProId=(\$id)	ProGlycProt at IMT	Institute of Microbial Technology, Council of Scientifi and Industrial Research (CSIR), Chandigarh	India	false	AC119	Staphylothermus marinus F1	http://www.proglycprot.org/		
				SUPERIAMLY provides structural, functional and evolutionary information			id		accessURL	info	institution	location	official	localid	testString	resourceURL		SUPERFAMILY
MIR-00000357	SUPTAM	All species	~\u+5	for proteins from all completely sequenced genomes, and large sequence rollections such as UniProt	supfam	http://identifiers.org/supfam	0 N	IR:00100454	http://supfam.org/SUPERFAMILY/cgi- hin/scon.ce/2mitis/Sufl	SUPFAM at MRC and University of Bristol	MRC Laboratory of Molecular Biology, Cambridge	ик	false	55/57625	cellulose binding domain	http://supfam.org/SUPERFAMI		
				high quality annotation for the rice			id		accessURL	Info	Institution	location	official	localid	testString	resourceURL		
MIR-00000358	Rice Genome Annotati Project	rice	~LOC_Os/d(1,2)g/d(5)\$	Npponbare. All genes are annotated with functional annotation including	ricegap I	http://identifiers.org/ricegap	0 N	IR 00100455	http://rice.plantbiology.msu.edu/cgi-	Rice Genome Annotation Project at TIGR	The Institute for Genomic Research, Rockville, Marvland	usa	false	LOC 0x02r13300	mitochondrial carrier protein	http://rice.plantbiology.msu.e du/annotation_pseudo_curren		
				PinA platform is an integrated platform					bin/ORF_intopage.cgi7&ort={Sid}		instance.		attend		test Fision	Lahtmi		Readeric Internation Westman's Associate
MIR-00000355	PINA	human	^([A-N,R-Z][D-9][A-Z][A-Z, D-9][A-Z, 9][D-9]](([D,P,Q]]D-9][A-Z, D-9][A-Z 9][A-Z, D-9][D-9][\$	0-for protein interaction network , 0-construction, fiftering, analysis, visualization and management. It	c pina t	http://identifiers.org/pina	0		http://cbg.garvar.unsw.edu.au/pina/interactome.one	Protein Interaction Network Analysis (PINA) at Gary	an		Chine.tan	ALCON .	unitering.	http://cbg.garvan.uraw.edu.au		Product in the account recovery company
				integrates protein-protein interaction data-faptic air eliborant, Editabore anni of follo sensenced harterial records in			N	IR:00100456	P.do?ac+(Sid)&showExtend+null	Institute	Garvan Institute of Medical Research, Sydney	Australia	talse	013485	SMAD4	/pina/		
MIR-0000363	BacMap Biography	bacteria	~\d+\$	contains labeled, zoomable and searchable chromosome maps for	bacmap blog	http://identifiers.org/bacmap.biog	0 H		accessURL	info	institution	location	official	localid	testString	resourceURL		-
				and eubacterial) species. Each map can be memeride. the loop of under the loop of the			N	IR:00100459	http://bacmap.wishartlab.com/organisms/(\$id)	BacMap Biography at University of Alberta	Department of Computing Science, Food and Nutritional Science, University of Alberta, Edmonton	Canada	false	1050	thermoacidophilic, anaerobic	hitp://bacmap.wishartlab.com /		
MIR-00000363	HGNC Symbol	buman	1A-Ze-2-0-9]+(\#)/5	Committee) provides an approved gene name and symbol (short-form abbreviation) for each known human	henc.symbol	http://identifiem.one/henc.symbol	o id	1	accessURL	info	Institution	location	official	resourcePrefix	localid	testString	resourceURL	NUGO Gene Nomenclature Committee Symbol
				gene. All approved symbols are stored in the HGNC database, and each symbol is prime. This selection many to sense			N	IR 00100460	https://www.genenames.org/cgi- bin/gene_symbol_report?match+(\$id)	MGNC Symbol at MUGO Genome Nomenclatu Committee	are European Bioinformatics Institute, Hirston, Cambridge	ик	false	ebi	DAPKI	000543842	https://www.genenames.org/	
				Evolutionary Relationships) Classification System is a resource that classifies genes			d		accessURL	info	Institution	location	official	localid	testString	resourceURL		
MIL DOCUME.		AL QUELOS		scientific experimental evidence and evolutionary relationships to predict	s t	THE PERSON AND A PERSON AND A PERSON AND A PERSON AND A PERSON AND A PERSON AND A PERSON AND A PERSON AND A PE	υ N	IR:00100461	http://www.paritherdb.org/pathway/pathwayDiagram .jsp?catAccession+(\$id)	PANTHER Pathway at USC (Los Angeles)	Keck School of Medicine, University of Southern California	usa	false	P00024	Głyczłysis	http://www.pantherdb.org/		
				genomes. It contains contains genome sequence and annotation from several			id		accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-00000365	FungiDS	fungi	^(A-Za-z_0-9)+\$	fungal classes, including the Ascomycota classes, Eurotiomycetes, Sordariomycetes, Saccharomycetes and the Basicliomycota	fungida	http://identifiers.org/fungidb	0 N	IR:00100464	http://fungidb.org/gene/(Sid)	FungIDS at University of California	Department of Plant Pathology & Microbiology, University of California, Riverside, California	USA	false	CN86_0001	2,143 to 5,911	http://FungiDB.org		
				Centel tracks both production of reagents			id		accessURL	info	Institution	location	official	localid	testString	resourceURL		пулла
MIR-0000367	DRSC	Drosophila	ronsc\d+\$	br kisk interference (kiska) screening in Drosophila cells and RNAi screen results. It maintains a list of Drosophila gene	drsc	http://identifiers.org/drsc	0 N	IR 00100466	http://www.flyrnai.org/cgi-	DRSC at Harvard Medical School	Department of Genetics, Marvard Medical School, Boston	USA	false	D#5C05221	Loneitudinah lackine	http://flymai.org/		Drosophila FNAI Screening Cente
				names, identifiers, symbols and synonyms onder m'd caldioana for Countil genom- wide mapping studies of confirmed and					bin/RNALgene_lookup_public.pl/gname+(Sid)		Massachusetts		attend		test fining			
MIR-0000368	OriD& Schizosaccharomyces	Yeast	~\d+5	predicted replication origin sites in Saccharomyces cerevisiae and the fission yeast Schizosaccharomyces pombe. This	oridb.schizo	http://identifiers.org/oridb.schizo	0				Centre for Genetics and Genomics, The University of	(Chine and			http://pombe.oridb.org/index.		-
				collection references Schizosaccharomyces onobins a catacase or constant generation			N	IR:00100467	http://pombe.oridb.org/details.php?id=(\$id)	OriDB Schizosaccharomyces at University of Nottingham	Nottingham, Queen's Medical Centre, Nottingham	uk	talse	1	tandem intergenic	php		
MIR-0000365	OriDB Saccharomyces	Yeast	~\d+\$	predicted replication origin sites in Saccharomyces cerevisiae and the fission	eridb.sacch	http://identifiers.org/oridb.sacch	0 H		accessURL	info	institution	location	official	localid	testString	resourceURL		-
				collection references Saccharomyces			N	IR:00100468	http://cerevisiae.oridb.org/details.php?hd+(\$id)	OnDB Saccharomyces at University of Nottingham	Centre for Genetics and Genomics, The University o Nottingham, Queen's Medical Centre, Nottingham	^t uk	false	1	not chromosomally active	http://cerevisiae.oridb.org/ind ex.php		
				Protein) database is a comprehensive ordering of all proteins of known			ed.		accessURL	info	institution	location	official	localid	testString	resourceURL		Structural Classification of Proteins
MIR-00000371	SCOP	All species	^\td+\$	functional and structural relationships. The basic classification unit is the protein	scop	http://identifiers.org/scop	0 N	IR:00100470	http://scop.mrc- Imb.cam.ac.uk/scop/search.cgi?sunid=(\$id)	SCOP at MRC	MRC Laboratory of Molecular Biology, Centre for Protein Engineering, Hills Road, Cambridge	ик	false	47419	HTH repressors	http://scop.mrc- Imb.cam.ac.uk/scop/		
				classified into species, proteins, families, superfamilies, folds, and classes.	-		N	IR:00100471	http://scop.berkeley.edu/sunid=(\$id)	SCOP at Berkeley	University of California, Berkeley	USA	false	47429	HTH repressors	http://scop.berkeley.edu/		
				captures and presents information relating to experimental workflows that			id		accessURL	iefa	institution	location	official	resourcePrefix	localid	testString	resourceURL	European Nucleotide Archive
MIR-00000372	ENA	All species	^[A-Z]+[0-9]+(\d+)?\$	are based around nucleotide sequencing. ENA is made up of a number of distinct databases that includes EMBL-Bank, the	ena.embl	http://identifiers.org/ena.embl	0 N	IR 00100473	https://www.ebi.ac.uk/ena/data/view/(\$id}	ENA at European Bioinformatics Institute	European Bioinformatics Institute, Hiroton, Cambridge	ик	false	ebi	BN000085	Homo sapiens SMP1 gene	https://www.ebi.ac.uk/ena/	Embl-Bank
				Sequence Read Archive (SRA) and the Trace Archive each with their own data formats and standards. This collection			N	IR-00100889	https://www.ncbi.nim.nih.gov/nuccore/(Sid)	ENA through Genllank	National Center for Biotechnology Information (NCBI)	USA	false		EN00005		https://www.ncbi.nim.nih.gov/Genbank/	
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				iner consensus 'cos' (ccos, 'project a a collaborative effort to identify a core set	5 5		4		e(\$id)	info	Inditution	Institut	official	resourceDrafty	brald	testOrine	resourced IRI	CEDS.
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				Locus Reference Genomic (LRG) provides			N	IR:00100478	ftp://ftp.ebi.ac.uk/pub/databases/irges/[\$id].xml	Locus Reference Genomic at University of Leicester	Department of Genetics, University of Leicester, Leicester	ик	false	LRG_1	Osteogenesis Imperfecta	http://www.irg-sequence.org/		
MIR:00000376	Locus Reference Genomic	human	~LRG_\d+\$	sequences for regions of the human genome, providing a recognized reference-	Ing	http://identifiers.org/irg	0	IR:00100627	http://www.ensembl.org/Nomo_sapiens/LRG/Summa y?irg=(\$id)	⁷ Locus Reference Genomic through Ensembl	EnSembl, Sanger Institute and European Bioinformatics Institute, Hinaton, Cambridge	ик	false	186_1	Chromosome 17: 50,182,096-50,206,639	http://www.ensembi.org/		
				waters, estandard for reporting sequence variants. LRG is maintained by the NCBI and the European Bioinformatics institute			N	IR 00100529	http://asia.ensembi.org/Homo_sapiens/LRG/Summary Yrg=(\$id)	⁷ Locus Reference Genomic through Ensembl mirror (asia)		Singapore	false	LRG_1	Chromosome 17: 50,182,096-50,206,639	http://asia.ensembi.org/		
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and their interacting (phospho)-proteins. | hosphopoint.kinase
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 | Faculty of Engineering, Maebashi Institute of Technology,
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				nonprotein substrates. Reliability scores are provided for dephosphorylation		MR:001	http://www.koehnlab.de/depod/showp.php?gene=(S d}	DEPOD at EMBL	European Molecular Biology Laboratory EMBL, Heidelberg	Germany	fatse	PTPN1	Tyrosine-protein phosphatase	http://www.koehnlab.de/depo d/	
				enytozome is a project to facestate comparative genomic studies amongst green plants. Familes of orthologous and		ы	accessURL	info	institution	location	official	localid	testString	resourceURL	
MIR-00000	12 Phytozome Locus	Plant species	^(A-Za-20-9]+\$	paralogous genes that represent the phytozome.locus modern descendents of ancestral gene such are constructed at low micloseretic	http://identifiers.org/phytocome.locus	0 MR:001	http://www.phytozome.net/genePage.php?crown&m 20556 ethod=0&search=1&detail=1&searchText=focusname	1 -{ Phytozome Locus at Joint Genome Institute	Joint Genome Institute, California, and the Center fo	USA and Switzerland	false	Glyma0021x00410	Histories H3 and H4	http://www.phytozome.net/	-
				various aspects of the genomic		d	Sid) accessURL	nfo	institution	location	official	localid	testStrine	resourceURL	
MIR-00000	13 SubtiList	bacillus subtilis	naci)d+S	information from B. subtilis, the paradigm of sporulating Gram-positive bacteria subtilist SubtiList provides a complete dataset of	http://identifiers.org/subtilist	•	http://genolist.pasteur.fr/SubtiList/genome.cgi?esten							http://genolist.pasteur.fr/Subt	-
				DNA and protein sequences derived from Westernisms 's 'collaporative'' & bakedge		MIKUUS	al_query+(\$id)	Subbluit at Patieur Intistuse	Vanteur Institute, Vans	France	Tatse	0511523	nangenn-chacone	Eist/	
MIR-00000	17 WikiGenes	All species	~\d+\$	based on the general wiki idea but employs specifically developed technology wikigenes	http://identifiens.org/wikigenes	0 Id	accessURL	info	Connector Science and Artificial Intelligence Laboration	location	official	localid	testString	resourceURL	4
				to serve as a rigorous scientific tool. The rationale behind WikiGenes is to provide addriagonum "enanci: this cases advention		MIR:001	00567 http://www.wikigenes.org/e/gene/e/(\$id).html	WikiGenes at Massachusetts Institute of Technology	Massachusetts Institute of Technology, Cambridg Massachusetts	USA	false	3771877	Alcohol dehydrogenase	http://www.wikigenes.org/	
110.0000	Broad Fungal Genor	e (ant due	rice blast disease, is one of the most devasting threats to food security	http://doubles.com/brand	ы	accessURL	info	Institution	location	official	localid	testString	resourceURL	Magnaporthe comparative genomics database
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				EcoliWki is a wiki-based resource to store information related to non-oathozenic E.		ы	accessURL	info	Institution	location	official	localid	testString	resourceURL	
MIR-00000	12 EcoliWiki	E.coli	^[A-Za-20-9-]+\$	coli, its phages, plasmids, and mobile ecolwiki genetic elements. This collection	http://identifiers.org/ecoliwiki	0 MIR:001	00573 http://ecoliwiki.net/colipedia/index.php/[\$id]:Gene	Ecol/Wiki at Texas Agrilife Research	Texas Agrilife Research, Texas A&M Universit	USA	false	aanA	Aromatic (carboxylic) acid efflux	http://ecoliwiki.net/colipedia/	
				resources to support scientific research		н	errent (0)	nin	Inditution	Institut	official	localid	faulGrine	response and 101	Viral Bininformatics Bencures Canter
MIR-00000	IS VERC	virus	~\d+S	directed at viruses belonging to the Arenaviridae, Burryaviridae, Filoviridae, vbrc Flaviviridae, Paramysoviridae, Poxviridae,	http://identifiers.org/vbrc	•			University of Alabama, Birmingham and the University						
				and Togaviridae families. The Center matching's statistical triagenergistication		MIKUUS	Actar http://vorc.org/gene_becar.ap/gene_br(540)	Valid, at oniversity of Alabama	Victoria, British Columbia	USA Ind Canada	Tatse	25/42	mp_NS3	http://warc.org/	
MIR-00000	19 ViralZone	virus	Md+S	endexindge with genomic and proteomic sequences. It provides fact sheets on all known virus families/genera with easy viralzone	http://identifiers.org/viralcorve	ы 0	accessURL	info	institution	location	official	localld	testString	resourceURL	-
				access to sequence data. A selection of reference strains (RefStrain) provides		MR:001	00583 http://viralzone.expasy.org/all_by_protein/(\$id).html	ViralZone at SIB	Swiss Institute of Bioinformatics, Centre Médic Universitaire, Geneva	^d Switzerland	fatse	992	virus membrane	http://www.expany.org/viralzo ne/	
				abstracts that can be cited in the GO protologies (e.g. as doxrefs for term		ы	accessURL	info	Institution	location	official	localid	testString	resourceURL	GO reference collection
MICOLOD	o Gene Ontology Reference	Atspecies	-00_KE1-18(/)5	definitions) and annotation rules (in the gover Reference column). It provides two types of reference; It can be used to provide	http://dentmen.org/go.ren	MR:001	00584 http://www.geneontology.org/cgi- bin/references.cgi#(\$id)	Gene Ontology Reference at The Gene Ontols Consortium	787 The Gene Ontology Consortium	USA	false	GO_RIF:0000041	Gene Ontology annotation based UniPathway vocabulary mapping	on http://www.geneontology.org/ cgi-bin/references.cgi	
				dat Gunlude consolidate, and integrate rat genomic and energic data with curated functional		ы	accessURL	info	institution	location	official	localid	testString	resourceURL	
MIR-00000	51 Rat Genome Database qTL	rat	^\d+\$	and physiological data and make these rgd.qtl data widely available to the scientific	http://identifiers.org/rgd.qtl 0	0 MIR:001	http://rgd.mcw.edu/rgdweb/report/qd/main.html?id	Rat Genome Database qTL at Medical College	of Medical College of Wisconsin, Milwaukee, Wisconsin	USA	false	1354581	Blood pressure QTL 247	http://ngd.mcw.edu/	
				DOOR (Database for prOkaryotic OpeRons)		н	arrent (B)	nin	Inditution	Institut	official	localid	faulGrine	response and 101	Database for reflicerentic Gradiens
MIR-00000	53 DOOR	procariotes	~\d+S	contains computationally predicted operons of all the sequenced prokaryotic door genomes. It includes operons for RNA	http://identifiers.org/door	•	http://csbi1.bmb.uga.edu/OperonDB/genedetail.php	2	Computational Systems Biology Laboratory, Department	t			MTARETLMPVLLEKVIQUQDKLELAQQPLVTQLGG	QH http://csbl1.bmb.uga.edu/Ope	
				genes. Ine Degradoria Cacadate Contains		MR:001	20588 (d-(\$id)	DODR v1 at University of Georgia	of Biochemistry and Molecular Biology, University of Georgia, Athens, Georgia	f USA	false	60202	LFSNISQDDLVERNESDLYGAVLSLWHHINEKK	ronD8/DOOR.php	
MIR-00000	14 Degradome Database	mamalian	^[AMCST][0-9x][0-9]\$	predicted proteases present in a a variety of mammalian species that have been degradome	http://identifiers.org/degradome	ы 0	accessURL	info	Institution	location	official	localld	testString	resourceURL	-
				subjected to whole genome sequencing. Each protease sequence is curated and, when parameters closed and sequenced		MIR:001	00589 http://degradome.uniovi.es/cgi-bin/protease/{\$id}	Degradome Database at	Biología Molecular, Facultad e Medicina, Universidad de Oviedo	r e Spain	false	Ax1	seminal vesicle antigen-like 1	http://degradome.uniovi.es/	
				provides genome-wide transcription factor predictions for organisms across		ы	accessURL	info	institution	location	official	localid	testString	resourceURL	Transcription Factor Database
MR-00000	15 080	All species	~1d+5	the tree of life. The prediction method dbd identifies sequence-specific DNA-binding transcription factors through homology	http://identifiers.org/dbd C	0 MR:003	http://www.transcriptionfactor.org/index.cgi?Search/ Domain+domain(\$id)+cat.00D	08D at MRC Laboratory of Molecular Biology	MRC Laboratory of Molecular Biology, Cambridge	ик	fatse	45320	0016_009111	http://www.transcriptionfacto r.org/	
				core - collockid-action - and - gleances Arabidopsis transcription factors (1827 annes in 55 femilies) with the unique		в	accessURL	nfo	Institution	location	official	localid	testString	resourceURL	Database of Arabidopsis transcription factors
MIR-00000	16 DATE	Arabidopsis	^AT[2-5]G\d[5](\.\d+)?\$	information of 1177 cloned sequences datf and many other features including 3D	http://identifiers.org/datf	0 MR:001	http://planttfdb.cbi.pku.edu.cn/tf.php?sp=Ath&did={	DATF through PlantTFDB	Center for Bioinformatics, Peking	Peoples Republic of China.	false	AT1G01030.1	NGA3	http://datf.cbi.pku.edu.cn/	
				Information Service Service Action Repository (YRC PDR) serves as a single			500		laster a		attend	hunded	fact Fining		Name Research Control Buildin Data Researchers
MIR-00000	19 YRC PDR	Yeast	~\d+\$	point of access for the experimental data produced from many collaborations yrcpdr typically studying Saccharomyces	http://identifiers.org/yrcpdr	•	a cassone		Department of Biochamistry University of Washington	ACCESSION 1	Chine an	incare.	analog .	TELCOOK.	reast needer or center Pacin, considerations
				cerevisiae (baker's yeast). The mar vessel infition 'outlinism' (version' s)		MR:001	20594 http://yeastrc.org/pdr/viewProtein.do?id=(\$id}	YRC PDR at University of Washington	Seattle	USA	false	2673500	PKHD-type hydroxylase	http://www.yeastrc.org/pdr/	
MIR-00000	50 Yeast Intron Database v3	Yeast	^(A-2D-9]+\$	contains information on the spliceosomal introns of the yeast Saccharomyces cerevisiae. It includes expression data that yid	http://identifiers.org/yid	ы 0	accessURL	info	Institution	location	official	localld	testString	resourceURL	-
				relates to the efficiency of splicing relative to other processes in strains of yeast		MR:001	00595 http://metarray.ucsc.edu/cgi- bin/intron/yirintrondb?orfName+(\$id)	Yeast Intron Database version 3 at Baskin School Engineering	of Biology of RNA, University of California, Santa Cru California	, USA	false	SNR17A	U3A snoRNA	http://compbio.soe.ucsc.edu/y east_introns.html	
				can serve to focus experimental resources on high-priority experimental tasks.		ы	accessURL	info	institution	location	official	localid	testString	resourceURL	
MICOLOD	st Functione Hy	Drosophila	~1 0+ 5	quantitative machine learning-based gene function annotations. Quantitative	http://denthers.org/functase.ny	MR:001	http://func.mshri.on.ca/fby/genes/list_functional_scores/{Sid}	r FuncBase Fly at Harvard Medical School	Harvard Medical School, Boston, Massachusetts	USA	false	10194	Wet5	http://func.mshri.on.ca/fly	
				compotences gene induction in predicuous can serve to focus experimental resources on high-grightly experimental tasks.		ы	accessURL	info	institution	location	official	localid	testString	resourceURL	
MIR-00000	52 FuncBase Human	human	^\d+\$	functiase is a web resource for viewing funcbase.human quantitative machine learning-based gene	http://identifiers.org/funcbase.human	0 MR-001	http://func.mshri.on.ca/human/genes/list_functional	FuncBase Human at Harvard Medical School	Harvard Medical School, Boston, Massachusetts	USA	false	119514	GALNT12	http://func.mshri.on.ca/huma	-
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MIR-00000	33 FuncBase Mouse	mouse	^ld+\$	on high-priority experimental tasks. FuncBase is a web resource for viewing funcbase.mouse quantitative machine learning-based gene	http://identifiers.org/funcbase.mouse	•	http://func.mshri.on.ca/mouse/serves/list_functional							http://func.mshri.on.ca/marcia	 -
-				function annotations. Quantitative competiers of regime induction (predicular		MIR:001	ADVB scores/(\$id)	Functase Mouse at Harvard Medical School	narvard Medical School, Boston, Massachusetts	usA	talse	1.01141	ысти	/	
MIR-00000	54 FuncBase Yeast	Yeast	~\d+\$	on high-priority experimental testus. functions is a web resource for viewing functions-yeast	http://identifiers.org/funcbase.yeast	o d	accessURL	info	institution	location	official	localid	testString	resourceURL	4
				quantitative machine learning-based gene function annotations. Quantitative memberus/asser anive/int fuscols		MR 001	20599 http://tunc.mshri.on.ca/yeast/genes/list_functional_s cores/(Sid)	FuncBase Yeast at Harvard Medical School	Harvard Medical School, Boston, Massachusetts	USA	fatse	2701	55D1	http://func.mshri.on.ca/yeast	
MP0007	S YDPM	Yeast	mie zlizij delowie	Teast Deletion and the Mitochondrial Proteomics Project. The project aims to promate the understanding of adverse	http://identifiers.pne/yvines	ы 0	accessURL	nfo	institution	location	official	localid	testString	resourceURL	Yeast Deletion Project and Proteomics of Mitochondri Database
			·*··************	mitochondrial function and biogenesis in the context of the cell. In the Deletion	Contraction of the State of Contraction of Contract	- MR:001	http://www-deletion.stanford.edu/cgi- bin/YDPM/YDPM_search.cgi?thelist={Sid}	YDPM at Stanford University School of Medicine	Stanford University School of Medicine, Stanford California	USA	false	YAL001C	TTIIC (transcription initiation factor)	http://www- deletion.stanford.edu/YDPM/	
				database of the biology and genome of the model organism Caenorhabditis		ы	accessURL	info	institution	location	official	localid	testString	resourceURL	
MIR-00000	55 WormBase RNAi	worm	~wurnA/(d)s)\$	elegans and related nematodes. It is used wb.mai by the C. elegans research community both as an information resource and as a	http://identifiers.org/wb.rnai	0 MR:003	https://www.wormbase.org/species/c_elegans/mai/	5 WormBase RNAi	European Bioinformatics Institute, Hinston, Cambridge	UK	false	WERNA/00086878	C. elegans	https://www.wormbase.org/	-
				metholocoldali calalogole (robolec) a a hierarchically structured, organism-		d	accessURL	nfo	institution	location	official	localid	testStrine	resourceURL	MIPS Functional Catalonue Database
MIR-00000	57 FunCat	All species	^\d[2] \d[2]\.\d[2] \d[2]\.\d[2]\.\d[2] \d[2]\.\d[2]\.\d[2]\.\d[2]\.\d[2]\.\d[independent, flexible and scalable controlled classification system enabling funcat the functional description of proteins	http://identifiers.org/funcat	0	http://mips.helmholtz-muenchen.de/funcatDB/cei-		Institute for Bioinformatics (MIPS), GSF National Researc	h	1		-	http://mips.helmholtz-	
-				from any organism. It has been applied locking motigraphic frank comparison		MIR:001	bin/search_advanced.pl?action=2&wert+(Sid)	runuat at MIPS (Neuherberg)	Center for Environment and Health, Neuherberg	Germany	talse	az 01.01	coopative stress response	muenchen.de/funcatDB/	
MIR-00000	59 ICEberg element	bacteria	~\d+\$	conjugative elements (ICEs) found in bacteria. ICEs are conjugative self-iceberg.element	http://identifiers.org/iceberg.element	o 4	accessURL http://db-	info	Institution State Key Laboratory of Microbial Matabalam and Febr	location	official	localid	testString	resourceURL	4
				transmissible elements that can integrate into and excise from a host chromosome,		MR:001	00504 mmi.sjtu.edu.cn/)CIberg/feature_page.php?ice_id+(5 d}	CEEberg element at Shanghai Jiaotong University	of Life Sciences & Biotechnolog Shanghai Jaotong University, Shanghai	, China	false	100	Tn5383	http://db- mmi.sjtu.edu.cn/ICEberg/	
MPONO	D Ciberr fami-	hartania	Minut	elements) is a database of integrative and conjugative elements (ICEs) found in barteria ICEs are conjugative and	http://www.factofilers.com/a-thorastic	ы	accessURL	info	institution	location	official	localid	testString	resourceURL	
	- terrer must			transmissible elements that can integrate into and excise from a host chromosome,	and a second second second second	- MR:001	http://db- mml.ijtu.edu.cn/ICIberg/browse_result.php?type+fa m&fam.id=/Sidi	CEberg family at Shanghai Jiaotong University	State Key Laboratory of Microbial Metabolism and Scho of Life Sciences & Biotechnology, Shangh Jactone University, Shanghai	China	false	1	5x7/8391	http://db- mml.sjtu.edu.cn/ICEberg/	
				WTDB is a repository of virulence factors		ы	accessURL	info	institution	location	official	localid	testString	resourceURL	
MR-00000	72 VTDB Gene	bacteria	~\u+\$	(VTs) of pathogenic bacteria. This vfdb.gene collection references VT genes.	http://identifiers.org/vfdb.gene 0	0 MR:001	20507 http://www.mgc.ac.cn/cgi- bin/VFi/eene.cei?Gene/Ini/Gen	VTDB Gene at Institute of Pathogen Biology	Engineering, Institute of Pathogen Biology, Chines Academy Medical Sciences and Dationa University	China	false	V7G2154	Chlamydia trachomatis	http://www.mgc.ac.cn/VFs/	1
		1		National Library of Medicine's controlled		и	accessURL	nfo	Callers Balles	location	official	localid	textStrine	resourceURL	
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					various levels of specificity. This thesaurus Itzog ⁻¹ Indiada ¹ indiada ¹ internativy ¹ Setting			MIR-00100608	e=&index=(\$id)&view+expanded	MeSH 2013 at National Library of Medicine	Health, Maryland	USA	talse	17165	Codon, Terminator	/		
			and the second se	NT- JUB FL VIRE JUB F	functional units used in the annotation and biological interpretation of	hite. (Identifiers on Dean module		id	accessURL	info	institution	location	official	localid	testString	resourceURL		KEGG
	7174 ALGO MOS	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	a species	(0+40+1) m (451)	corresponds to a set of 'KEGG Orthology' (MIR:00000116) entries. KEGG Modules	http://weithinic.org/wigg.needer		MR-00100605	http://www.kegg.jp/entry/(Sid)	KEGG Module at Kyoto University Bioinformatics Center	Department of Computational Biology, University of Tokyo, Tokyo	af Japan	true	M00002	Glycolysis	http://www.kegg.jp/kegg/mod ule.html		
					School			id	accessURL	info	institution	location	official	localid	testString	resourceURL		Japan Consortium for Glycobiology and Glycotechnolog
MIR:00000	3479 JCGGD8		inimal	^3CGG-STR\d]6]\$	integrate all glycan-related data held in jcggdb various repositories in Japan. This	http://identifiers.org/jcggdb	o		Note: (Accords to Adv Accords (1974)	PP/PPE at Subsecond Entering Institute (Insue)	Advanced Science Institute(ASI), Chemical Biolog	N	false	1000 17000000	Children Care	hite (locath infeder or hire)		
					includes databases for large-quantity wollcolocificit unspass of eliptets or and			MICUDIO0514	uttr://jc88as/b/se//c88as/2+a)	accube at Advanced science institute (Japan)	Saltama	o, sepen	tatse	ICura-si Robillogo	Gyldocan	http://jcggod.jp/index_en.nom		
MIR-00000	1480 NONCODE	v4 Gene A	All species	NONHSAG\dj5}\$	data obtained from microarnay studies. LocRNAs have been shown to play keynoncodev-Lge	e http://identifiers.org/nancodev4.gene	0	id	accessURL	info	institution	location	official	localld	testString	resourceURL		
					roles in various biological processes such as imprinting control, circuitry controlling chalantaneous and differentiation improves			MIR:00100616	http://www.bioinfo.org/NONCODEv4/show_gene.php hd=(\$id)	NONCODE v4 Gene at Chinese Academy of Sciences	Bioinformatics Research Group, Chinese Academy o Sciences, Beijing	China	false	NONHSAG00001	11869	http://www.bioinfo.org/NONC CDEv4/		
					functional IncRNA (long noncoding RNA) data obtained from microarray studies.			id .	accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-00000	3481 NONCODE	v4 Transcript A	All species	NONHSAT\d[6]\$	EncRNAs have been shown to play key noncodev&ma roles in various biological processes such as imprinting control circuitry controlling	http://identifiers.org/noncodev4.rna	0	MIR 00100617	http://www.bioinfo.org/NONCODEv4/show_rna.php?i	NONCODE v4 Transcript at Chinese Academy of Sciences	Bioinformatics Research Group, Chinese Academy of	of China	false	NONHSAT000001	11858	http://www.bioinfo.org/NONC		
					chystadase provides a view or rice (crysta sativa) as a model monocot plant by				8+(340)		sciences, beging					ODEWy		
MIR-0000	3482 Oryzabase	Gene	ice	~\d+\$	integrating biological data with molecular genomic information. It contains oryzabase.gen	http://identifiers.org/oryzabase.gene	o	10	accessure.		Instructor	location	omciai	ECC #10	teststring	resourceux.		
					anatomy, rice mutants, and genetic orysesses provide for while or inter (of pra-			MIR-00100618	etal/(Sid)	(Japan)	Genetics, Mishima, Shizuoka	"Japan	false	117	frizzy panicle, BRANCHED SILKLESS	e/oryzabaseV4/		
	MET Creations			ah u . e	sativa) as a model monocot plant by integrating biological data with molecular	at http://doutifium.am/anashers.au/ant		id	accessURL	info	Institution	location	official	localid	testString	resourceURL		
	res organism				information about rice development and anatomy, rice mutants, and genetic	in http://window.com/organization		MR-00100615	http://www.shigen.nig.ac.jp/rice/oryzabaseV4/strain/l nducedMutationLine/detail/(\$id)	Oryzabase v4 Mutant at National Institute of Geneti (Japan)	cs Genetic Strains Research Center, National Institute Genetics, Mishima, Shizuoka	af Japan	false	21393	GM1	http://www.shigen.nig.ac.jp/ric e/oryzabaseV4/		
					provide detailed information on human			id	accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-00000	3487 Gene Wiki	A	All species	^\d+\$	an automated manner, with further genewiki information added by the community.	http://identifiers.org/genewiki	o						<i>a.</i>			http://en.wikipedia.org/wiki/G		-
_	_				Gene Wiki can be accessed in wikipedia valabili in "a "fetbolice" "Selicased to		_	MIK 00100623	auth/brillur.pollbr.pull.dl-ou/wb.dl.up+(hg)	Gene wiki tirougn BioGro	wikimedia Foundation, san Francisco, California	USA	1254	1017	protein in G1-5 transition	ene_Wiki		
MIR-00000	3489 PaxDb Prot	tein A	All species	~\d+\$	protein abundance levels across different organisms. Publicly available experimental pasdb.protein	http://identifiers.org/paxdb.protein	0	d	accessURL	efo	Institution	location	official	localid	testString	resourceURL		1
					data are mapped onto a common namespace and, in the case of tandem			MIR 00100525	5 http://pax-db.org/#iprotein/{\$id}	PaxDb v3 at University of Zurich	Institute of Molecular Life Sciences, University of Zurich Zurich	^{1,} Switzerland	false	977869	apolipoprotein C-I	http://pas-db.org/		
					collection of sequence, structure, interaction, genomic and functional			id	accessURL	info	Institution	location	official	localid	testString	resourceURL		
MIR-00000	3497 Homeodor	main Research h	nemen	~\d+\$	Information on the homeodomain family, hdr It contains sets of curated homeodomain sequences from folly sequence	http://identifiers.org/hdr	o	MIR 00100638	http://research.nhgri.nih.gov/apps/homeodomain/we 5 0/index.cgi?mode=view&view=proteins&id=	Nomeodomain Research at National Human Genom	Genome Technology Branch, National Human Genom Research Institute, National Institutes of Health	e 1, USA	false	63	Protein coding	http://research.nhgri.nih.gos/a res/bremandometa/umb/		1
-					novelaises som tally sequenced genomes, Normforser af "unticked" undersom to normforsomal peptides (NRPs) in bacteria				(\$id)	nesee on and table (Nim)	Bethesda, Maryland	hereiting		handle	territories.	Med - round on and mark meb/		
MIR-00000	1498 NORINE	b	pacteria and fungi	"NOR'(d+\$	and fungi, in addition to the traditional ribosomal proteic biosynthesis, an norine	http://identifiers.org/norine	o	10	m.tessiHL		Computer Science Laboratory of Lille. INRIA an	d d	omcial	10.400	manif	ereidürceum.		4
					pathway called NRP synthesis allows net'disactory Vaccable Tolcaular (oncor)			MIR:00100535	9 http://bioinfo.lift.fr/norine/result.jsp?ID+(\$id)	NORINE at Computer Science Laboratory of Lille	ProBioGEM, University of Sciences and Technologies Lille, Lille	of France	false	NORDOSE1	Vancomycin is a glycopeptide antibiotic	http://bioinfoJifi.fr/norine/		
			inimal , fungi and		is a repository of genomics and proteomics information of olfactory			id	accessURL	info	institution	location	official	localid	testString	resourceURL		oros
MIRCOULD	MVV Unactory V	heceptor Database bi	sacteria	~18+5	of chemosensory genes and proteins, that includes in addition to ORs the taste	http://identifiers.org/ordb	0	MR-00100540	http://senselab.med.yale.edu/ORDB/Data/{\$id}	Olfactory Receptor Database at Yale University School Medicine	of Center for Medical Informatics, Yale University School (Medicine, New Haven, Connecticut	^{af} USA	false	8497	ATGAGGGGGGAG	http://senselab.med.yale.edu/ OrD0/		
					PIDD) is a database that provides			id.	accessURL	la fa	institution	location	official	localid	textStrine	respurceURL		
MIR-00000	2501 P3D8 Prote	ein Pl	Nant species	^\d+\$	information on experimentally determined phosphorylation sites in the p3db.protein proteins of various plant species. This	http://identifiers.org/p3db.protein	٥		http://www.p3db.org/protein.php?id=(\$id)&ref=		Department of Computer Science, University of Missour	v		_				
	_				collection references plant proteins that math's robust' prioritation: concerns			MIR-00100643	0	P3DB Protein at University of Missouri	Columbia, Missouri	USA	talse	70	receptor-like kinase 2	http://www.p3db.org/		
MIR-0000	2502 P3D8 Site	P	Plant species	Md+S	(P3DB) is a database that provides information on experimentally determined phosoborvlation sites in the p3db.site	http://identifiers.one/p3db.site	0	id	accessURL	info	Institution	location	official	localid	testString	resourceURL		
					proteins of various plant species. This collection references phosphorylation			MIR 00100643	http://www.p3db.org/phosphosite.php?id=(\$id)&ref= 0	P3D8 Site at University of Missouri	Department of Computer Science, University of Missour Columbia, Missouri	^L USA	false	65	somatic embryogenesis	http://www.p3db.org/		
					Transmembrane Proteins (TOPDB) is a collection of transmembrane protein			id	accessURL	Info	institution	location	official	localid	testString	resourceURL		
MIR-00000	2503 TOPDS	~	All species	^[A-2D-9]+\$	datasets containing experimentally topdb derived topology information. It contains	http://identifiers.org/topdb	o	MIR 00100644	http://topdb.engim.hu/?m=show&id=(Sid)	TOPD8 at Hunsarian Academy of Sciences	Institute of Enzymology, Hungarian Academy of Science	^N Hunsary	false	AP00378	MVGLTTLPWL	http://topdb.enzim.hu/		
-					Information gathered from the literature Intel Annual Codintitioner Trait Cost (Urc) Hatabase (Annual OTIdb) is designed to						Budapest							
MIR:0000	2504 Animal Ger	nome Cattle QTL ca	attle	^\cd+\$	house publicly all available QTL and single- nucleotide polymorphism/gene cattleqtidb	http://identifiers.org/cattleqtidb	0	id	accessURL	into	institution	location	official	localid	testString	resourceURL		
					association data on livestock animal species. This collection references cattle			MIR 00100545	bin/QTLdb/BT/qdetails?QTL_ID+(Sid)	Animal QTL Cattle at Iowa State University	Department of Animal Science and Center for Integrate Animal Genomics, Iowa State University, Iowa	d USA	false	4685	Holstein-Friesian cattle	http://www.animalgenome.org /cgi-bin/QTLdb/BT/index		
					database (Animal QTLdb) is designed to house publicly all available QTL and single-			id	accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-00000	1505 Animal Ger	nome Chicken QTL cf	chicken	~\d+\$	nucleotide polymorphism/gene chickenqtidb association data on livestock animal species. This collection references chicken	http://identitiens.org/chickenqtidb	0	MR-00100546	http://www.animalgenome.org/cgi- bin/QTLdb/GG/qdetails/QTL_ID=(\$id}	Animal QTL Chicken at Iowa State University	Department of Animal Science and Center for Integrate Animal Genomics, Iowa State University, Iowa	d USA	false	14362	cross between Xinghua and White Recess Rock	ive http://www.animalgenome.org /cgi-bin/QTLdb/GG/index		
					database (Animal QTLdb) is designed to			ы	accessURL	lefo	institution	location	official	localid	testString	resourceURL		
MIR.00000	2505 Animal Ger	nome Pig QTL Pi	¹ 8	~\d+\$	nucleotide polymorphism/gene pigqtidb association data on livestock animal	http://identifiers.org/pigqtidb	o		http://www.animalgenome.org/cgi-	Andread OTE Rise at Jacob Firsts	Department of Animal Science and Center for Integrate	d	fatu.	14	hash even of Matching	http://www.animalgenome.org		-
-					species. This collection references pig		_	MR 00100543	bin/QTLdb/SS/qdetails?QTL_ID=(\$id)	whimai Qirc Pig at fowa State University	Animal Genomics, Iowa State University, Iowa	USA	raise	14	pack-cross of Meishan x White composite	/cgi-bin/QTLdb/SS/Index		
MIR-00000	2507 Animal Ger	nome Sheep QTL SI	iheep	Md+\$	batabase (Animal QTLdb) is designed to house publicly all available QTL and single- nucleotide polymorphism/gene sheepotidb	http://identifiers.org/sheepqtidb	0	d	accessURL	Info	Institution	location	official	localid	testString	resourceURL		
					association data on livestock animal species. This collection references sheep			MIR:00100648	http://www.animalgenome.org/cgi- bin/QTLdb/OA/qdetails?QTL_ID=(\$id)	Animal QTL Sheep at lowa State University	Department of Animal Science and Center for Integrate Animal Genomics, Iowa State University, Iowa	^d USA	false	19803	Red Maasal and Dorper	http://www.animalgenome.org /cgi-bin/QTLdb/OA/index		
					archiving and sharing of all types of personally identifiable genetic and			ы	accessURL	info	Institution	location	official	resourcePrefix	localid	testString	resourceURL	tGA Dataset
MIR:00000	2512 European	Genome-phenome	uman	^0GAD(d(11)\$	phenotypic data resulting from biomedical research projects. The EGA ega.dataset	http://identifiers.org/ega.dataset	0	MIR 00100558	https://www.ebi.ac.uk/ega/datasets/(Sid)	EGA Dataset at European Bioinformatics Institute	European Bioinformatics Institute, Hirxton, Cambridge	UK	true	ebi	EGAD0000000001	WTCCC case-control study for	https://www.ebi.ac.uk/ega/dataset	
	chive Da				individuals whose consent agreements authorize data release only for specific				tates for an interaction of the second second second second second second second second second second second s	17.5 Dataset Manuals Cardin Di	Formania Materia and a Martin a		fature	- total	FC 479702702702	-point crosself	and a start of the start	
-	_				research use or to bona fide researchers.			MIR: U0100853		www.usdater.through.umicsDI	survyvan exemprimetics institute, Hinkton, Cambridge	un	raise	w++C101	10-0-00000001	+	mps.//www.omcadi.org/	
					The PRIDE PRoteomics IDEntifications database is a contralized, standards			id	accessURL	Info	Institution	location	official	resourcePrefix	localId	testString	resourceURL	
MIR-00000	2515 PRIDE Proj	ject		^P(K R D\d+(6)\$	provides protein and peptide project identifications together with supporting	http://identifiers.org/pride.project	o	MIR:00100663	thtps://www.ebi.ac.uk/pride/archive/projects/(\$id}	PRIDE Project at EE	European Bioinformatics Institute, Hirxton, Cambridge	UK	true	ebi	PXD000440	Qualitatively Different T Cel Phenotypic Responses	https://www.ebi.ac.uk/pride/	
					evidence. This collection references projects.			MIR:00100858	5 https://www.omicsdi.org/dataset/pride/[\$id}	PRIDE Project through OmicsDI	European Bioinformatics Institute, Hinston, Cambridge	uĸ	false	omicidi	PXD000440		https://www.omicsdi.org/	
					Committee) provides an approved gene			ы	accessURL	info	Institution	location	official	localid	testString	resourceURL		
MIR-00000	2520 HGNC Fam	siy b	nemun	^[A-ZD-9-]+(#[A-ZD-9-]+)?\$	name and symbol (short-form abbreviation) for each known human hgnc.family gene. All approved symbols are stored in	http://identifiers.org/hgnc.family	٥											
-					the MGNC database, and each symbol is min-rule officer MCMCaster periodin way		_	wiik 00100671	nups.//www.genenames.org/generamises/(Sid)	ename raising at mouse control nomenciature Committee	 www.peeee.exdemormatics.institute, ministori, Cambridge 	wn.	ane	r man	reporte a grane deminases	maps://www.generames.org/		
MIR-00000	3521 Yeast Intro	on Database v4.3 Yo	feast	^[A-2D-9]+\$	contains information on the spliceosomal introns of the yeast Saccharomyces cerevisiae. It includes expression data that yeastintron	http://identifiers.org/yeastintron	0	id .	accessURL	Info	Institution	location	official	localid	testString	resourceURL		
					relates to the efficiency of splicing relative to other processes in strains of yeast		Ĩ	MIR:00100673	http://ittron.ucsc.eou/cgi- bin/yeast4.3/intronreports.pl?outputformat=full&am p;orfName=(\$id}	Yeast Intron Database version 4.3 at Baskin School Engineering	of Biology of RNA, University of California, Santa Cru California	z, USA	false	SNR17A	Oct 12, 1998	http://intron.ucsc.edu/yeast4. 3/		
		-			(ARDB) is a manually curated database which characterises genes involved in			ы	accessURL	info	Institution	location	official	localid	testString	resourceURL		ARDS
MIR.00000	Database	weaturce Genes	nemun	^[A-Z_][3]]D-9][4,]S	antibiotic resistance. Each gene and ardb resistance type is annotated with	http://identifiers.org/ardb	o	MIR:00100578	http://ardb.cbcb.umd.edu/cgi/search.cgi?db=L&fi	ARDS at University of Maryland	Center for Bioinformatics and Computational Biolog	^{r,} USA	false	CAE46076	Ribosomal protection	http://ardb.cbcb.umd.edu/		
-					Protection of the identification of the human				energi (10)		www.atty.or.nearyuano, nearyland	hereiting		handle	ter Ficine			
MIR-00000	2524 Proteomic	aD6 Protein h	naman	^\ _{id+\$}	proteome and its use across the scientific community. This human proteome data is proteomicsdb.	rotein http://identifiers.org/proteomicsdb.protein	n 0		hiter former meteories de seclide en a	Restaurates DB Restate at Caster for her set		and the later	un no di			hiter //managedage		-
					from liquid chromatography tandem-mass- tronicemetour is Mr. Miller restriction to			MIR 00100680	h/[\$id]/iummary	Science	Center for Integrated Protein Science, Manich,	Germany	false	53504	Calmodulin-binding	/whoman		
1					expedite the identification of the human proteome and its use across the scientific			ыd	accessURL	info	institution	location	official	localld	testString	resourceURL		1

		annable Peprine		-1947 A	assembled primarily using information	protection and advised	united to an an an all the second second second	ĭ.	IP-00100581	https://www.proteomicsdb.org/#human/proteinDetai	Proteomics DB Peptide at Center for Integrated Protein	Cantar for Integrated Distain Science, Munich	Germany	false	5,1504	Neurorendialin	https://www.proteomicsdb.org		
					from liquid chromatography tandem-mass- ine-incentry ViGabina Vice (violat) porta- integrates the centitie sensemine result					ls/(Sid)/peptides/	Science						/#peptideSearch		
MIR:000	000526 Prote	n Proteome Map in	human	~\d+\$	from the draft map of the human proteome project. The project was based	hpm.protein	http://identifiers.org/hpm.protein	0		accessURL	into	Institution	location	official	localid	testString	resourceURL		HPM.
					on LC-MS/MS by utilizing of high resolution and high accuracy Fourier			5	IR:00100582	http://www.humanproteomemap.org/protein.php?hp m_id={\$id}	Human Proteome Map Protein at Institute o Bioinformatics (Bangalore)	finstitute of Bioinformatics, International Tech Par Bangalore	¹ India	false	1958	Eukaryotic translation initiation	http://www.humanproteome map.org/index.php		
	Num	n Proteome Map			integrates the peptide sequencing result from the draft map of the human			k		accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR-000	Pepti	de	human	~\d+S	proteome project. The project was based on LC-MS/MS by utilizing of high resolution and high accuracy Fourier	l hpm.peptide	http://identifiers.org/hpm.peptide	0	IR:00100683	http://www.humanproteomemap.org/spectrum.php? pep_id+(Sid)	Human Proteome Map Peptide at Institute o Bioinformatics (Bangalore)	f Institute of Bioinformatics, International Tech Par Bangalore	⁶ India	false	9606117	AGGE	http://www.humanproteome map.org/index.php		
					bioinformatics and chemoinformatics			k		accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR:000	000528 Drug	iank Target v4	human	^@E\d(7)\$	chemical, pharmacological and pharmaceutical) data with comprehensive	drugbankv-Ltarget	http://identifiers.org/drugbankv4.target	•				Departments of Computing Science, Biological Science					http://www.drugbank.ca/targe	1	
					drug target (i.e. sequence, structure, and anti-ceptoiner-stare "recention-worgs	1			IR:00100687	http://www.drugbank.ca/biodb/bio_entities/[\$id}	DrugBank Target information version 4	University of Alberta	Canada	talse	810000048	Prothrombin	ts		
MIR:000	000532 Orph	net Rare Disease	All species	^Orphanet(_]:)C?(d+\$	diseases, capturing relationships between diseases, genes and other relevant	orphanet.ordo	http://identifiers.org/orphanet.ordo	0		accessURL	info	institution	location	official	resourcePrefix	localid	testString	resourceURL	000
		-67			features which will form a useful resource for the computational analysis of rare			5	IR:00100705	https://www.ebi.ac.uk/ols/ontologies/ordo/terms?sh art_farm=(\$id)	ORDO via OLS	European Bioinformatics Institute, Hinston, Cambridge	UK	true	ols	Orphanet_C023	age of onset	https://www.ebi.ac.uk/ok/ontologies/ordo	
					among medically important variants and phenotypes. It records human variation,			×		accessURL	info	Institution	location	official	resourcePrefix	localld	testString	resourceURL	
MIR:000	000534 ClinV	ir Record	human	^RCV\d+(_\d+)?\$	interpretations of the relationship specific variations to human health, and supporting evidence for each	c clinvar.record	http://identifiers.org/clinwar.record	0 1	IR-00100710	http://www.ncbi.nlm.nlh.gov/clinvar/[\$id]/	ClinVar Record at NCB	National Center for Biotechnology Information (NCB) NIH, Maryland	l. USA	fatse	ncbi	RCV000033555-3	protein tyrosine phosphatase	http://www.ncbi.nlm.nih.gov/clinvet/	
					(ExAC) is a coalition of investigators					accessURL	nfo	institution	ocation	official	localid	testStrine	resourceURL		
MIR:000	000541 ExAC	Variant	human	^\d[1,2]\-\d+\-{GATC]\-{GATC]\$	seeking to aggregate and harmonize exome sequencing data from a variety of large-scale sequencing projects, and to	f exac variant	http://identifiers.org/exac.variant	0				Exome Agregation Consortium (ExAC). Cambridge							
_					make summary data available for the overco-certifia - greecolos7 - orient numari				IR-00100718	http://exac.broadinstitute.org/variant/(Sid)	ExAC Variant at Exome Aggregation Consortium	Massachusetts	USA	talse	22-46615880-T-C	1209806.67	http://exac.broadinstitute.org/		
MIR:000	000542 GWA	Central Marker	human	1995/W/jd+\$	Genome Variation database of Genotype- to-Phenotype information) is a database of summary level findings from genetic	gwascentral.marker	http://identifiers.org/gwascentral.marker	e 1		accessURL	nfo	Institution	location	official	localld	testString	resourceURL		
					association studies, both large and small. It gathers datasets from public domain			2	IR:00100719	http://www.gwascentral.org/marker/{\$id}	GWAS Central Marker at University of Leicester	Department of Genetics, University of Leicester, Leicester	UK	false	HGVM15354	n#580	http://www.gwascentral.org/m arkers/	h	
					contains information on experimental reagents (small molecule perturbagens,			8		accessURL	info	Institution	location	official	localld	testString	resourceURL		
MIR:000	000545 LINC	Protein	animal	~\d+\$	cells, and proteins). It aims to collect and disseminate information relating to the fundamental principles of calible	lincs.protein	http://identifiers.org/lincs.protein	0 3	IR:00100722	http://lincs.hms.harvard.edu/db/proteins/(\$id)/	LINCS Protein at Harvard Medical School	Harvard Medical School, Boston, Massachusetts	USA	false	200282	Myasin IIIA	http://lincs.hms.harvard.edu/d		
					Signatures (LINCS) Program aims to create					errend (B)	nto	Institution	Incation	official	brald	feet Grine	representation in the		
MIR:000	000546 LINC	Small Molecule	animal	^LSM-\d+(4)\$	a network-based understanding of biology by cataloging changes in gene expression and other cellular processes that occur	lincs.smallmolecule	http://identifiers.org/lincs.smailmolecule	0		http://lincsportal.ccs.miami.edu/SmallMolecules/Wvi							http://incsportal.ccs.miami.ed		
_					when cells are exposed to a variety of met transmission segments of the second				IR:00100723	ew/(\$id)	UNCS Portal	University of Miami, BD2K-LINCS DCIC, USA	USA	talse	LSM-6306	Diraciclib	u/SmallMolecules/		
MIR:000	000547 ExAC	Transcript	human	^ENST\d[11]\$	(ExAC) is a coalition of investigators seeking to aggregate and harmonize exome sequencing data from a variety of	f exac transcript	http://identifiers.org/exac.transcript	e 1		accessURL	nfo	Institution	location	official	localld	testString	resourceURL		
					large-scale sequencing projects, and to make summary data available for the			2	IR:00100724	http://exac.broadinstitute.org/transcript/(\$id)	ExAC Transcript at Exome Aggregation Consortium	Exome Aggregation Consortium (ExAC), Cambridge Massachusetts	USA	false	ENST00000407236	PPARA	http://exac.broadinstitute.org/		
					(ExAC) is a coalition of investigators seeking to aggregate and harmonize			8		accessURL	info	Institution	location	official	localld	testString	resourceURL		
MIR:000	000548 ExAC	Gene	human	~ENSG\d[11]\$	exome sequencing data from a variety of large-scale sequencing projects, and to make summary data available for the	f exac.gene	http://identifiers.org/exac.gene	0 1	IR:00100725	http://exac.broadinstitute.org/gene/{\$id}	ExAC Gene at Exome Aggregation Consortium	Exome Aggregation Consortium (ExAC), Cambridge	USA	false	EN5G00000169174	proprotein convertase	http://exac.broadinstitute.org/		
					elder objetlik community. The data open					1.00		institution	and the second se	efficient	handled	fant Finlan			
MIR:000	000552 5880	Subsystem	Microbial organisms	^/(m+5	(FIG), Argonne National Laboratory, and the University of Chicago, focuses on the development of the comparative	seed	http://identifiers.org/seed	•		http://seed-		Armone National Laboratory University of Chicago	bullout .	Crincian	0.112	ana ang	http://seed-		
					genomics environment called the SEED. It			5	IR:00100729	viewer.theseed.org/seedviewer.cgi?page=Subsystems &subsystem={Sid}	SEED Subsystem at Argonne National Laboratory	Argonne, Illinois	USA	false	Biotin_biosynthesis	salvage	viewer.theseed.org/seedviewe r.cgi		
MIR-000	000553 5880	Corrected	Microbial preanisms	^cod/d+S	Fellowship for Interpretation of Genomes (FIG), Argonne National Laboratory, and the University of Chicago, focuses on the	seed.compound	http://dentifiers.one/seed.compound	×		accessURL	info	institution	location	official	localid	testString	resourceURL		
					development of the comparative genomics environment called the SEED. It				IR:00100730	http://modelseed.org/blochem/compounds/{\$id}	SEED Compound at Argonne National Laboratory	Argonne National Laboratory, University of Chicago Argonne, Illinois	^U USA	false	cpd15380	5'-deoxyribose	http://modelseed.org/		
					Genetically and Genomically structured eenome-scale metabolic network			k		accessURL	info	institution	location	official	localid	testString	resourceURL		
MIR:000	000554 BIGG	Model	All species	^(a-z_A-2D-9]+\$	reconstructions. It more published genome-scale metabolic networks into a	bigg.model	http://identifiers.org/bigg.model	0	IR:00100731	http://bies.ucid.edu/models/(Sid)	BIGG Model at University of California	Systems Biology Research Group at the University	f USA	false	ECABU <1320	Escherichia coli	http://bies.ucsd.edu/models		
	_				the United interest of the set of standard the United interest interest of biomedical vocabularies.							California, San Diego							
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					Interactions (MTIs), collected manually from relevant literature, following Natural			k		accessURL	info	institution	location	official	localid	testString	resourceURL		
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					resource of enzyme-catalyzed and spontaneous chemical reactions. It	5		k		accessURL	info	institution	location	official	localid	testString	resourceURL		
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Annex4 List of plant genomes stored in Ensembl Plants

Name	Classification	Taxon ID	Assembly	Accession	Variation database	Regulation database	Whole genome alignments	Other alignments	In pentide compara	In nan-taxonomic compara
Actinidia chinensis	eudicotyledons	1590841	Red5 PS1 1 69 0	GCA_003024255_1	vullation autubase		whole genome angliments	other ungrintents	in peptide compara	
Aegilops tauschii	Lilionsida	200361	Aet v4 0	GCA_002575655.1						-
Amborella trichopoda	Amborellales	1333	AMTR1.0	GCA 000471905.1	-	-				
Ananas comosus	Liliopsida	4615	F153	GCA 902162155.1	-	-		-		-
Arabidopsis halleri	eudicotyledons	63677	/ Ahal2.2	GCA 900078215.1	-					-
Arabidopsis Ivrata	eudicotyledons	81972	v.1.0	GCA 000004255.1	-	-				-
Arabidopsis thaliana	eudicotyledons	3702	TAIR10	GCA 000001735.1						
Arabis alpina	eudicotyledons	50452	A alpina V4	GCA 000733195.1	-	-		-		-
Asparagus officinalis	Liliopsida	4686	Aspof.V1	GCA 001876935.1	-	-		-		-
Avena sativa OT3098	Liliopsida	4498	Oat_OT3098_v2	GCA_022788535.1	-	-		-		-
Avena sativa Sang	Liliopsida	4498	Asativa_sang.v1.1	GCA_910574605.1	-	-		-		-
Beta vulgaris	eudicotyledons	3555	RefBeet-1.2.2	GCA_000511025.2	-	-				-
Brachypodium distachyon	Liliopsida	15368	Brachypodium_distachyon_v3.0	GCA_000005505.4		-				
Brassica juncea	eudicotyledons	3707	ASM1870372v1	GCA_018703725.1	-	-		-		-
Brassica napus	eudicotyledons	3708	AST_PRJEB5043_v1	GCA_000751015.1	-					-
Brassica oleracea	eudicotyledons	109376	BOL	GCA_000695525.1	-					-
Brassica rapa	eudicotyledons	3711	Brapa_1.0	GCA_000309985.1	-		-		-	-
Brassica rapa R-o-18	eudicotyledons	1813537	SCU_BraROA_2.3	GCA_017639395.1	-	-		-		-
Cajanus cajan (pigeon pea) - GCA_000340665.1	eudicotyledons	3821	C.cajan_V1.0	GCA_000340665.1	-	-		-		-
Camelina sativa	eudicotyledons	90675	Cs	GCA_000633955.1	-	-		-		-
Cannabis sativa female	eudicotyledons	3483	cs10	GCA_900626175.1	-	-		-		-
Capsicum annuum	eudicotyledons	4072	ASM51225v2	GCA_000512255.2	-	-		-		-
Chara braunii	Streptophyta	69332	2 Cbr_1.0	GCA_003427395.1	-	-	-	-		-
Chenopodium quinoa	eudicotyledons	63459	ASM168347v1	GCA_001683475.1	-	-		-		-
Chlamydomonas reinhardtii	Chlorophyta	3055	Chlamydomonas_reinhardtii_v5.5	GCA_000002595.3	-	-				
Chondrus crispus	Rhodophyta	2769	ASM35022v2	GCA_000350225.2	-	-		-		-
Citrullus lanatus	eudicotyledons	3654	Cla97_v1	GCA_000238415.2	-	-		-		-
Citrus clementina	eudicotyledons	85681	Citrus_clementina_v1.0	GCA_000493195.1	-	-		-		-
Coffea canephora	eudicotyledons	49390	AUK_PRJEB4211_v1	GCA_900059795.1	-	-		-		-
Corchorus capsularis	eudicotyledons	210143	CCACVL1_1.0	GCA_001974805.1	-	-				-
Corylus avellana	eudicotyledons	13451	CavTom2PMs-1.0	GCA_901000735.2	-	-		-		-
Corymbia citriodora	eudicotyledons	360336	Ccitriodora_v2_1	GCA_014858505.1	-	-		-		-
Cucumis melo	eudicotyledons	3656	Melonv4	GCA_902497455.1	-	-		-		-
Cucumis sativus	eudicotyledons	3659	ASM407v2	GCA_000004075.2		-				-
Cyanidioschyzon merolae	Rhodophyta	280699	ASM9120v1	GCA_000091205.1	-	-		-		
Cynara cardunculus	eudicotyledons	59895	CcrdV1	GCA_001531365.1	-	-		-		
Daucus carota	eudicotyledons	79200	ASM162521v1	GCA_001625215.1	-	-				-
Digitaria exilis	Liliopsida	1010633	Fonio_CM05836	GCA_902859565.1	-	-		-		
Dioscorea rotundata	Liliopsida	55577	TDr96_F1_v2_PseudoChromosome	GCA_009730915.1	-	-		-		-
	Liliopsida	90397		GCA_020466025.1	-	-		-		-
Eragrostis curvula	Liliopsida	38414	CERZOS_E.curvula1.0	GCA_007726485.1	-	-		-		-
Eragrostis ter	Liliopsida	11083	Saik_ten_dabbi_3.0	GCA_024500355.1	-	-		-		-
Eucalyptus grandis	eudicotyledons	71135	Egrandis1_0	GCA_000612305.1	-	-		-		
	eudicotyledons	72664	Eutsaigi_U	GCA_000478725.1	-	-				-
	eudicotyledons	20072		GCA_009761775.1	-	-		-		
Caldiaria autoburaria	Bhadaphuta	120091	ACM24129-4	GCA_900149125.1		-		-		
	audicatuladana	13008	Chucino may v2 1	GCA_00004E1285.1	-	-		-		
Gossynium raimondii	eudicotyledons	384	Graimondii2 0 v6	GCA 000227265 1	-					
Helianthus annuus	eudicotyledons	129/30	HanXROr2 0-SLINRISE	GCA 002127225 2	-					-
	Lilionsida	112500	Morey/3 nseudomolecules accombly	GCA 00/8/0725 1		-		-		-
Hordeum vulgare GoldenPromise	Lilionsida	112505	GPv1	GCA 902500625 1	-		_			-
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	eudicotyledons	3288	ΔSM357664v1	GCA_903613005.1	-	-	-	-	-	-
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Name	Classification	Taxon ID	Assembly	Accession	Variation database	Regulation database	Whole genome alignments	Other alignments	In peptide compara	In pan-taxonomic compara
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Kalanchoe fedtschenkoj	eudicotyledons	63787	K fedtschenkoj M2 v1	GCA_002312845_1			Whole genome angliments	other ungrintents		
Lactura sativa	eudicotyledons	4236	Isat Salinas v7	GCA_002870075.2				-		-
Leersia perrieri	Liliopsida	77586	Lperr V1.4	GCA_000325765.3	-	-				-
Lolium perenne	Liliopsida	4522	MPB Lper Kyuss 1697	GCA 019359855.1	-	-		-		-
Lupinus angustifolius	eudicotyledons	3871	LupAngTaniil v1.0	GCA 001865875.1	-	-				-
Malus domestica Golden	eudicotyledons	3750	ASM211411v1	GCA 002114115.1		-		-		-
Manihot esculenta	eudicotyledons	3983	Manihot esculenta v6	GCA 001659605.1	-	-				-
Marchantia polymorpha	Embryophyta	3197	Marchanta polymorpha v1	GCA 003032435.1	-	-		-		
Medicago truncatula	eudicotyledons	3880	MedtrA17 4.0	GCA 000219495.2	-					-
Musa acuminata	Liliopsida	214687	Musa_acuminata_v2	GCA_904845865.1	-	-				-
Nicotiana attenuata	eudicotyledons	49451	NIATTr2	GCA_001879085.1	-					-
Nymphaea colorata	Embryophyta	210225	ASM883128v1	GCA_008831285.1	-	-		-		-
Olea europaea	eudicotyledons	158383	OLEA9	GCA_902713445.1	-	-		-		-
Olea europaea var. sylvestris	eudicotyledons	158386	O_europaea_v1	GCA_002742605.1	-	-	-	-	-	-
Oryza barthii	Liliopsida	65489	O.barthii_v1	GCA_000182155.2	-					-
Oryza brachyantha	Liliopsida	4533	Oryza_brachyantha.v1.4b	GCA_000231095.2	-	-				-
Oryza glaberrima	Liliopsida	4538	Oryza_glaberrima_V1	GCA_000147395.1						-
Oryza glumipatula	Liliopsida	40148	Oryza_glumaepatula_v1.5	GCA_000576495.1						-
Oryza longistaminata	Liliopsida	4528	O_longistaminata_v1.0	GCA_000789195.1	-					-
Oryza meridionalis	Liliopsida	40149	Oryza_meridionalis_v1.3	GCA_000338895.2	-					-
Oryza nivara	Liliopsida	4536	Oryza_nivara_v1.0	GCA_000576065.1	-					-
Oryza punctata	Liliopsida	4537	Oryza_punctata_v1.2	GCA_000573905.1	-					-
Oryza rufipogon	Liliopsida	4529	OR_W1943	GCA_000817225.1	-					-
Oryza sativa (Geng/Japonica-sbtrp var. Chao Meo)	Liliopsida	1736656	Os132278RS1	GCA_009831315.1	-	-	-	-	-	-
Oryza sativa (Geng/Japonica-trop1 var. Azucena)	Liliopsida	1736656	AzucenaRS1	GCA_009830595.1	-	-	· ·	-	-	-
Oryza sativa (Geng/Japonica-trop2 var. Ketan Nangka)	Liliopsida	1736656	Os128077RS1	GCA_009831275.1	-	-	· ·	-	-	-
Oryza sativa (Xian/Indica-1A var. Zhenshan 97)	Liliopsida	39946	ZS97RS3	GCA_001618795.1	-	-	-	-	-	-
Oryza sativa (Xian/Indica-1B1 var. IR64)	Liliopsida	39946	OsIR64RS1	GCA_009914875.1	-	-	-	-	-	-
Oryza sativa (Xian/Indica-1B2 var. PR106)	Liliopsida	39946	Os127742RS1	GCA_009831045.1	-	-	-	-	-	-
Oryza sativa (Xian/Indica-2A var. Gobol Sail)	Liliopsida	39946	Os132424RS1	GCA_009831025.1	-	-	-	-	-	-
Oryza sativa (Xian/Indica-2B var. Larha Mugad)	Liliopsida	39946	Os125619RS1	GCA_009831355.1	-	-	-	-	-	-
Oryza sativa (Xian/Indica-3A Var. Lima)	Liliopsida	39946	05127564R51	GCA_009829395.1	-	-	-	-	-	-
Oryza sativa (Xian/Indica-3B1 var. Khao Yai Guang)	Liliopsida	39946	05127518851	GCA_009831295.1	-	-	•	-	-	-
Oryza sativa (Xian/Indica-362 Var. Liu Xu)	Liliopsida	39940	05125627851	GCA_009829375.1	-	-		-		-
Oriza sativa (kian/mulca-adm val. winghul 05)	Liliopsida	1726650	000022852	GCA_0010E226E 2	-	-	-	-	-	-
Oryza sativa (circum-Ausz var. Natel Boro)	Liliopsida	1736650	0:127652851	GCA_001932303.2	-	-		-		-
Oryza sativa (circum-Ausz var. Nater Boro)	Liliopsida	1736659	0:117/052851	GCA_009831355.1						-
Oryza sativa (circum-basinati val. ARC 10457)	Liliopsida	39946	ASM465v1	GCA_000004655.2	-	-	-	-	-	
Oryza sativa Japonica Group	Liliopsida	39947	IBGSP-1.0	GCA_001433935.1						
Ostreococcus lucimarinus	Chlorophyta	436017	ASM9206v1	GCA 000092065.1	-	-	-			-
Panicum hallii FIL2	Liliopsida	206008	PHallii v3.1	GCA_002211085.2	-	-	-	-	-	-
Panicum hallii HAL2	Liliopsida	1504633	PhalliiHAL v2.1	GCA_003061485.1	-	-		-		-
Papaver somniferum	Embryophyta	3469	ASM357369v1	GCA 003573695.1	-	-		-		-
Phaseolus vulgaris	eudicotyledons	3885	PhaVulg1 0	GCA 000499845.1						-
Physcomitrium patens	Embryophyta	3218	Phypa V3	GCA 000002425.2	-	-				
Pistacia vera	eudicotyledons	55513	PisVer v2	GCA 008641045.1	-	-		-		-
Pisum sativum	eudicotyledons	3888	Pisum_sativum_v1a	GCA_900700895.2	-	-		-		-
Populus trichocarpa	eudicotyledons	3694	Pop_tri_v4	GCA_000002775.4	-	-		-		-
Prunus avium	eudicotyledons	42229	PAV_r1.0	GCA_002207925.1	-	-		-		-
Prunus dulcis	eudicotyledons	3755	ALMONDv2	GCA_902201215.1	-	-		-		-
Prunus persica	eudicotyledons	3760	Prunus_persica_NCBIv2	GCA_000346465.2	-	-				-
Quercus lobata	eudicotyledons	97700	ValleyOak3.0	GCA_001633185.2	-	-		-		-
Quercus suber	eudicotyledons	58331	CorkOak1.0	GCA_002906115.4	-	-		-		-
Rosa chinensis	eudicotyledons	74649	RchiOBHm-V2	GCA_002994745.2	-	-		-		-

Name	Classification	Taxon ID	Assembly	Accession	Variation database	Regulation database	Whole genome alignments	Other alignments	In peptide compara	In pan-taxonomic compara
Saccharum spontaneum	Liliopsida	62335	Sspon.HiC chr asm	GCA 003544955.1	-	-		-		-
Secale cereale	Liliopsida	4550	Rye_Lo7_2018_v1p1p1	GCA_902687465.1	-	-		-		-
Selaginella moellendorffii	Embryophyta	88036	v1.0	GCA_000143415.1	-	-				
Sesamum indicum	eudicotyledons	4182	S_indicum_v1.0	GCA_000512975.1	-	-		-		-
Setaria italica	Liliopsida	4555	Setaria_italica_v2.0	GCA_000263155.2	-	-				-
Setaria viridis	Liliopsida	4556	Setaria_viridis_v2.0	GCA_005286985.1	-	-		-		-
Solanum lycopersicum	eudicotyledons	4081	SL3.0	GCA_000188115.3						
Solanum tuberosum	eudicotyledons	4113	SolTub_3.0	GCA_000226075.1	-	-				-
Solanum tuberosum RH89-039-16	eudicotyledons	4113	ASM1418947v1	GCA_014189475.1	-	-	-	-	-	-
Sorghum bicolor	Liliopsida	4558	Sorghum_bicolor_NCBIv3	GCA_000003195.3		-				-
Theobroma cacao Belizian Criollo B97-61/B2	eudicotyledons	3641	Criollo_cocoa_genome_V2	GCA_000208745.2	-	-	-	-	-	-
Theobroma cacao Matina 1-6	eudicotyledons	3641	Theobroma_cacao_20110822	GCA_000403535.1		-				-
Trifolium pratense	eudicotyledons	57577	Trpr	GCA_900079335.1	-	-				-
Triticum aestivum	Liliopsida	4565	IWGSC	GCA_900519105.1						-
Triticum aestivum Arinalrfor	Liliopsida	4565	PGSBv2.1	GCA_903993985.1	-	-		-		-
Triticum aestivum Cadenza	Liliopsida	4565	Elv1.1	GCA_902810645.1	-	-	-	-	-	-
Triticum aestivum Claire	Liliopsida	4565	Elv1.1	GCA_902810655.1	-	-	-	-	-	-
Triticum aestivum Jagger	Liliopsida	4565	PGSBv2.1	GCA_903993795.1	-	-		-		-
Triticum aestivum Julius	Liliopsida	4565	PGSBv2.1	GCA_903994195.1	-	-		-		-
Triticum aestivum Kariega	Liliopsida	4565	Tae_Kariega_v1	GCA_910594105.1	-	-	-	-	-	-
Triticum aestivum Lancer	Liliopsida	4565	PGSBv2.1	GCA_903993975.1	-	-		-		-
Triticum aestivum Landmark	Liliopsida	4565	PGSBv2.1	GCA_903995565.1	-	-		-		-
Triticum aestivum Mace	Liliopsida	4565	PGSBv2.1	GCA_903994175.1	-	-		-		-
Triticum aestivum Norin61	Liliopsida	4565	PGSBv2.1	GCA_904066035.1	-	-		-		-
Triticum aestivum Paragon	Liliopsida	4565	Elv1.1	GCA_902810665.1	-	-	-	-	-	-
Triticum aestivum Refseqv2	Liliopsida	4565	IWGSC_RefSeq_v2.1	GCA_018294505.1	-	-	-	-	-	-
Triticum aestivum Renan	Liliopsida	4565	Triticum_aestivum_Renan_v2.1	GCA_937894285.1	-	-	-	-	-	-
Triticum aestivum Robigus	Liliopsida	4565	Elv1.1	GCA_902810685.1	-	-	-	-	-	-
Triticum aestivum Stanley	Liliopsida	4565	PGSBv2.2	GCA_903994155.1	-	-		-		-
Triticum aestivum Sy Mattis	Liliopsida	4565	PGSBv2.1	GCA_903994185.1	-	-	-	-	-	-
Triticum aestivum Weebill	Liliopsida	4565	WeebilV1	GCA_902810675.1	-	-	-	-	-	-
Triticum dicoccoides	Liliopsida	85692	WEWSeq_v.1.0	GCA_002162155.1	-					-
Triticum spelta	Liliopsida	58933	PGSBv2.0	GCA_903994165.1	-	-	-	-	-	-
Triticum turgidum	Liliopsida	4567	Svevo.v1	GCA_900231445.1		-		-		-
Triticum urartu	Liliopsida	4572	IGDB	GCA_003073215.1	-	-				-
Vigna angularis	eudicotyledons	3914	Vigan1.1	GCA_001190045.1	-					-
Vigna radiata	eudicotyledons	3916	Vradiata_ver6	GCA_000741045.2	-					-
Vigna unguiculata	eudicotyledons	3917	ASM411807v1	GCA_004118075.1	-	-		-		-
Vitis vinifera	eudicotyledons	29760	PN40024.v4	GCA_910591555.1				-		
Zea mays	Liliopsida	4577	Zm-B73-REFERENCE-NAM-5.0	GCA_902167145.1				-		-

Annex5 Minimum information required for each each MIxS v6.0 checklist

TYPE OF INFORMATION						DESCRIPTOR DEFINITION AND SYNTAX						CHECKLIST	REQUIREME	NT (M:manda	atory; C: con	ditional mand	latory;X:option	al; E:Enviror	ment depend	ent; (-): not ap	llicable)	
Туре	Section	sub-section	MIXS ID	Structured comme	nt Item (rdfs:label)	Definition	Expected	Value syntax	Example	Preferred	Occurence	migs_eu	migs_ba	migs_pl	migs_vi	migs_org	mims	mimarks_	s mimarks_	c misag	mimag	miuvig
Sample, Environmental Context	investigation	Project name	MIXS:0000092	project name	project name	Name of the project within which the sequencing was organized		(text)	Forest so	iil	1	м	м	м	м	м	м	м	м	м	м	м
and investigation Sample, Environmental Context and investigation	investigation	Biological Source	MIXS:0001107	samp_name	sample name	A local dentifier or name that for the material sample used for extracting nucleic acids, and subsequent sequencing. It refer either to the original material collected or to any derived sub-samples. It can have any format, but we suggest to you make it concerving unique and consistent within your lack and a simomative as possible. NSDC requires every sam name from a single Submitter to be unique. Use of a globally unique identifier for the field source_nat_id is recomment addition to sample name.	an lat ed	{text}	ISDsoil1		1	м	м	м	м	м	м	м	м	м	м	м
Sample, Environmental Context and investigation	investigation	Biological Source	MIXS:0001320	samp_taxon_id	taxonomy ID of DN sample	NCBI taxon id of the sample. Maybe be a single taxon or mixed taxa sample. Use 'synthetic metagenome' for mo community/positive controls, or 'blank sample' for negative controls.	ck Taxonomy ID	{text} [NCBI:txid]	Metagenome [NCBI:txid749 06]	9	1	м	м	м	м	м	м	м	м	м	м	м
Sample, Environmental Context and investigation	investigation	Environmental Parameters	MIXS:000008	experimental_factor	experimental factor	Experimental factors are essentiably the variable sapects of an experiment design which can be used to describe experiment, or set of experiments, in a increasingly detail manner. This feld accepts ontology terms from Experiment Factor Ontology (EFO) and/or Ontology for Biomedical Investigations (OBI). For a browser of EFO (v 2.55) terms, plea see http://purt.bioontology.org/ontology/EFO, for a browser of OBI (v 2018-02-12) terms please a http://purt.bioontology.org/ontology/EFO.	an tal se and/or OBI	O {termLabel} {[termID]} {tex	time serie design [EFO:EFO_00 01779]	s	1	x	x	x	x	x	с	С	x	с	С	с
Sample, Environmental Context and investigation	environment	Geographical Location	MIXS:0000009	lat_ion	geographic locatic (latitude and longitude)	The geographical origin of the sample as defined by latitude and longitude. The values should be reported in decir degrees and in WGS84 system	to 8 decimal to 8 decim points	nit al {float} {float}	50.586825 6.408977		1	м	м	М	м	м	м	м	м	м	м	м
Sample, Environmental Context and investigation	environment	Geographical Location	MIXS:0000018	depth	depth	The vertical distance below local surface, e.g. for sediment or soil samples depth is measured from sediment or s surface, respectively. Depth can be reported as an interval for subsurface samples.	oil measurement value	t {float} {unit}	10 meter		1	E	E	Е	Е	Е	Е	E	E	E	Е	Е
Sample, Environmental Context and investigation	environment	Geographical Location	MIXS:0000094	alt	altitude	Altitude is a term used to identify heights of objects such as airplanes, space shuttles, rockets, atmospheric balloons a heights of places such as atmospheric layers and clouds. It is used to measure the height of an object which is above is earth's surface. In this context, the altitude measurement is the vertical distance between the earth's surface above s level and the sampled position in the air.	nd he measurement ea value	t {float} {unit}	100 meter		1	E	E	E	E	E	E	E	E	E	E	E
Sample, Environmental Context and investigation	environment	Geographical Location	MIXS:0000093	elev	elevation	Elevation of the sampling site is its height above a fuxed reference point, most commonly the mean sea level. Elevation mainly used when referring to points on the earth's surface, while altitude is used for points above the surface, such as aircraft in flight or a spacecraft in orbit.	an value	t {float} {unit}	100 meter		1	E	E	E	Е	E	E	E	E	E	Е	E
sample, Environmental Context and investigation	environment	Environmental Parameters	MIXS:0000113	temp	temperature	Temperature of the sample at the time of sampling.	measurement value	t {float} {unit}	25 degre Celsius	e degree Celsius	1	E	E	E	E	E	E	Е	Е	E	E	E
Sample, Environmental Context and investigation	environment	Geographical Location	MIXS:0000010	geo_loc_name	geographic locatio (country and/ sea,region)	The geographical origin of the sample as defined by the country or sea name followed by specific region name. Country sea names should be chosen from the INBDC country list (http://insid.org/country.html), or the GA2 ontoid (http://put.beomtil.org/.org/ontology.GA2)	or GAZ gy region(GAZ), specific location name	ea IC {term}: {term {text}	I), USA: Maryland, Bethesda		1	м	м	м	м	м	м	м	м	м	м	м
Sample, Environmental Context and investigation	environment	Biological Source	MIXS:0000011	collection_date	collection date	The time of sampling, either as an instance (single point in time) or interval. In case no exact time is available, date/time can be right truncated i.e. all of these are valid times: 2008-01-23719-23-10+00-00; 2008-01-23719-23-10; 201 01-23; 2008-01; 2008. Except; 2008-01; 2008 all are ISO8601 compliant	he I8- date and time	timestamp}	2018-05- 11T10:00:00+ 1:00; 2018-05 11	0	1	м	м	м	м	м	м	м	м	м	м	м
Sample, Environmental Context and investigation	investigation	Biological Source	MIXS.0001321	neg_cont_type	negative control type	The substance or equipment used as a negative control in an investigation	enumeration text	[distilled water[phosph te buffer]emp collection device]empty collection tube[DNA-fre PCR mix[sterile swab [steri syringe]	a ty le		1	c	c	с	с	с	с	с	с	с	с	c
Sample, Environmental Context and investigation	investigation	Biological Source	MIXS:0001322	pos_cont_type	positive control type	The substance, mixture, product, or apparatus used to verify that a process which is part of an investigation delivers a ti positive.	ue	{term} or {text	9		1	с	с	с	с	с	с	с	с	с	С	С
Sample, Environmental Context and investigation	environment	Environmental Parameters	MIXS:0000012	env_broad_scale	broad-scale environmental context	Report the major environmental system the sample or specimen came from. The system(s) identified should have coarse spatial grain, to provide the general environmental context of where the sampling was done (e.g. in the desert coarse (e.g. in the desert of the same set of the same coarse (fill) and the same set of	The maj environment type(s) whet the samp was collecte a Recommend subclasses biome ENVO.00000 28]. Multip terms can b separated to one or moo pipes.	or re le d. d. (termLabel) {[termID]} 14 le De De Dy re	oceanic epipelagic zone biom [ENVO:01000 33] fc annotating " water sampi from the photi zone in middl of the Atlanti Ocean	e 0 Yr a e c c	1	м	м	М	М	М	М	м	м	м	м	м
Sample, Environmental Context and investigation	environment	Environmental Parameters	MIXS.0000013	env_local_scale	local environment	Report the entity or entities which are in the sample or specimen's local vicinity and which you believe have signific causal influences on your sample or specimen. We recommend using EnvO terms which are of smaller spatial grain th your entry for emy Jonad scale. Terms, such as anatomical states, from other GBO Library ontelogies which intercept whit. EmO (e.g. UBERON) are ascepted in this floct. EmO occumentation about how to use the fer through the combination about how to use the fer	Environmenta Int entities havin an causal Ide influences Id: upon the entit at time sampling.	il ig (termLabel) ity (termID)) of	Ifter laye [ENVO-01000 38]; Annotafin a poole sample take from variou layers in in forest canopy [ENVO-01000 37][Itter laye [ENVO-01000 38][understor] (p1000335][Itol 101003536] (p1000356] (p100	x x 3 9 9 4 1 5 8 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	1	м	M	Μ	М	М	М	м	м	М	м	м

TYPE OF INFORMATION						DESCRIPTOR DEFINITION AND SYNTAX						CHECKLIST	REQUIREME	INT (M:mano	datory; C: co	onditional man	datory;X:optic	onal; E:Enviro	nment depende	ent; (-): not ap	llicable)	
Туре	Section	sub-section	MIXS ID	Structured com	ment Item (rdfs:label)	Definition	Expected	Value syntax	x Example	Preferred	Occurence	migs_eu	migs_ba	migs_pl	migs_vi	migs_org	g mims	mimarks	_s mimarks_	c misag	mimag	miuvig
Sample, Environmental Context and Investigation	environment	Environmental Parameters	MIXS-0000014	env_medium	environmental medium	Report the environmental material(a) immediately surrounding the sample or specimen at the time of sampling, recommedi using subclasses of "environmental material" (http://put.dobitary.org/b05EWU_0001443). Terms tom other COGD enabligies are permissible as long as they reference mass/volume nouns (e.g. ar, water, bi and not discrete, counsable entities (e.g. a vree, a lead, a table top).	The mater displaced the entity We lime WO sampling. S. Recommendo subclasses environment Terrial (ENVC:0001 83].	rial by of of ([termLabe]} of ([termID]) al 04	soil [ENVC-00011 98]; Annotating a fisi swimming in the upper 10 m of th Atlantic Ocean, consider [ENVC-00002 51]. Example Annotating a duck on a pond consider pond ovsite [ENVC-00002 28]air [ENVC_00002	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	1	м	м	М	М	М	М	м	м	М	М	м
Sample, Environmental Context and investigation	nucleic acii sequence source	1 Biological Source	MIXS:0000020	subspecf_gen_lin	subspecific gene lineage	Information about the genetic distinctness of the sequenced organism below the subspecies level, e.g., service, service to lockpe, cor any relevant genetic byping softemes like Group I plasmid. Subspecies should not be recorded in term, but in the KCBI taxonomy. Supply both the lineage name and the lineage rank separated by a colon, e biovar.abc123.	Genetic lineage bell lowest rank NCBI rpe, taxonomy, this which e.g., subspecies, e.g. serov biotype, ecotype, variety, cultivar.	ow of is {rank name}:{text}	serovar:Newpo rt	5	1	с	с	с	С	с			с			
Sample, Environmental Context and investigation	nucleic aci sequence source	Biological Source	MIXS:0000021	ploidy	ploidy	The pixity level of the genome (e.g. altopolypixit, haptoid, cipixid, tripixid, tetrapixid). It has implications for downstream study of duplicated gene and regions of the genomes (and perhaps for diffuculties in assembly). For tet please select terms listed under class pixid (PATO.001374) of Phenotypic Quality Ontology (PATO), and for a brows PATO (v 2016)-227 please refer to the thip/juxit blochtogy orgonitology/PATO	the ms, r of	{termLabel} {[termID]}	allopolyploidy [PATO:000137 9]	r	1	x	-	-	-	-	-	-	-	-	-	-
Sample, Environmental Context and investigation	nucleic acii sequence source	l Biological Source	MIXS:0000022	num_replicons	number of replicons	Reports the number of replicons in a nuclear genome of eukaryotes, in the genome of a bacterium or archaes or number of segments in a segmented virus. Always applied to the haploid chromosome count of a eukaryote	the chromosome (haploid count); viruses: segments	tes ria: ts {integer} for	2		1	x	м		с							
Sample, Environmental Contex and investigation	nucleic aci sequence source	Biological Source	MIXS:0000023	extrachrom_elements	s extrachromosomal elements	Do plasmids exist of significant phenotypic consequence (e.g. ones that determine virulence or antibiotic resistan Megapiasmids? Other plasmids (borrelia has 15+ plasmids)	ce). number extrachromo mal elements	of s {integer} s	5		1	x	с			с			x		-	
Sample, Environmental Contex and investigation	nucleic aci sequence source	Biological Source	MIXS:0000024	estimated_size	estimated size	The estimated size of the genome prior to sequencing. Of particular importance in the sequencing of (eukaryotic) gen which could remain in draft form for a long or unspecified period.	ome number base pairs	of {integer} bp	300000 bp		1	x	x	x	x	x	-	-	-	-	-	x
Sample, Environmental Contex and investigation	nucleic aci sequence source	Biological Source	MIXS:0000025	ref_biomaterial	reference for biomateria	Primary publication if isolated before genome publication; otherwise, primary genome report.	PMID, DOI URL	or {PMID} {DOI} URL}	doi:10.1016/j.s yapm.2018.01 009		1	x	м	x	x	x	x			x	x	x
Sample, Environmental Context and investigation	nucleic acii sequence source	1 Biological Source	MIXS:0000026	source_mat_id	source material identifie	A unique identifier assigned to a material sample (as defined by <u>lice)</u> is then <u>condition/ammetrial/sampleD</u> , an opposed to a particular digati record or a material sample under or extracting nucleica dost, and subsequent sequent. The identifier can refer either to the original material collected or to any derived sub-samples. The INSDC quality appearines, voucher, ibo, material or, collutar collector may the material collected or to any derived sub-samples. The INSDC quality periodic subsection of the same subsection of the same values as the source, mail of for instance, the ripectimen voucher qualifier and source, mail of may toth contain UAM.Heips,14 ^o , referring to both periodic subsection of the source instance. Here, H	a sfor cultures microorganis ing. s: identifie for two cultu- collections; the o a a uniq arbitrary identifer	of ens are for {text} rial	MPI012345		m	с	с	с	с	с	с	с	с	с	с	с
Sample, Environmental Context and investigation	nucleic aci sequence source	i Biological Source	MIXS:0000027	pathogenicity	known pathogenicity	To what is the entity pathogenic	names organisms th the entity pathogenic to	of hat is o	human, animal, plant fungi, bacteria	-	1	с	с		с							x
Sample, Environmental Context and investigation	nucleic aci sequence source	Biological Source	MIXS:0000028	biotic_relationship	observed bio relationship	Description of relationship(s) between the subject organism and other organism(s) it is associated with. E.g., parasities $S_{\rm constraint}(s)$ is parallely a subject of the relationship, and the other organism(s) is object.	on the enumeration	[free living parasiti m[commensa sm[symbiotic mutualism]	is ali free living		1	x	с		x	-			с			x
Sample, Environmental Context and investigation	sequence source	Biological Source	MIXS:0000029	specific_host	host scientific name	Report the host's taxonomic name and/or NCBI taxonomy ID.	nost scient name, taxonomy ID	taxid}	Homo sapien: and/or 9606	8	1	x	с	с	с			-			-	x
Sample, Environmental Contex and investigation	sequence source	Biological Source	MIXS:0000030	host_spec_range	host specificity or range	The range and diversity of host species that an organism is capable of infecting, defined by NCBI taxonomy identifier.	NCBI taxid	{integer}	9606		m	x	x	x	с			-	-		-	x
Sample, Environmental Contex and investigation	sequence source	Biological Source	MIXS:0000031	host_disease_stat	host disease status	Liss or usecases war which the host has been alignosed; can include multiple alignoses. The Value of the field depe on host, for humans the terms should be chosen from the DO (Human Disease Ontology) at https://www.dise. ontology.org.non-human host diseases are free text	or Disea Ontology ten	(termLabel) (termID]}	rabies xt} [DOID:11260]		m	х	с		с							С

TYPE OF INFORMATION						DESCRIPTOR DEFINITION AND SYNTAX						CHECKLIST	REQUIREM	ENT (M:mand	latory; C: con	ditional man	datory;X:optio	nal; E:Enviror	ment depender	nt; (-): not ap	llicable)	
Туре	Section	sub-section	MIXS ID	Structured commen	t Item (rdfs:label)	Definition	Expected	Value syntax	Example	Preferred	Occurence	migs_eu	migs_ba	migs_pl	migs_vi	migs_org	mims	mimarks	s mimarks_c	misag	mimag	miuvig
Sample, Environmental Contex and investigation	nucleic aci sequence source	d Biological Source	MIX5.0000032	trophic_level	trophic level	Trophic levels are the feeding position in a food chain. Microbes can be a range of producers (e.g. chemolithotroph)	enumeration	(autory ream sayddrophic emsautoroph) chemobileter aphic bernalith aphic bernalith aphic bernalith aphic bernalith aphic bernalith hemosynthetic chemotrophic chemotrophic chemotrophic chemotrophic abriotrophic abriotrophic phimethyddi ophimethyddi abriotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo phimethyddi chemotrophic bigata(chemo chemotrophic chemotrophic bigata(chemo chemotrophic ch	0 0 0 0 0 0 0 0 0 0 0 0 0 0		1	с	с						c			
Sample, Environmental Contex and investigation	t nucleic aci sequence source	d Biological Source	MIXS-0000033	propagation	propagation	The type of reproduction from the parent stock. Values for this field is specific to different taxa. For phage or v lyticlysogenic/temperate/obligately lytic. For plasmids: incompatibility group. For eukaryotes: sexual/aserual.	for virus: lyti lysogenic, temperate, obligately lyti for plasmi incompatibility group; fr asexual, sexual, oth more specifi values (e.g. incompatibility group) at allowed	locialebooteree ic; d: voor {text} er ic; d: voor {text} er ic; y y re	lytic		1	с	-	м	м	-		-		-	-	
Sample, Environmental Contex and investigation	t nucleic aci sequence source	d Biological Source	MIXS:0000034	encoded_traits	encoded traits	Should include key traits like antibiotic resistance or xenobiotic degradation phenotypes for plasmids, converting gene phage	for plasmi antibiotic s for resistance; fo phage: converting genes	d: or {text}	beta- lactamase class A		1	-	x	с	с							-
Sample, Environmental Contex and investigation	t nucleic aci sequence source	d Biological Source	MIXS:0000015	rel_to_oxygen	relationship to oxygen	is this organism an aerobe, anaerobe? Please note that aerobic and anaerobic are valid descriptors for mice environments	obial enumeration	[aerobe anaero be facultative microaerophilli [microanaerob e obligate aerobe obligat e anaerobe]	o aerobe		1	-	с	-		-	x	x	с	x	x	
Sample, Environmental Contex and investigation	t nucleic aci sequence source	d Biological Source	MIXS:000003	isol_growth_condt	isolation and growth condition	Publication reference in the form of pubmed ID (pmid), digital object identifier (doi) or urt for isolation and growth cond specifications of the organism/material	ition PMID,DOI o	or {PMID} {DOI} { URL}	doi: 10.1016/j.syap m.2018.01.009	9	1	м	м	м	М	м			м			
Sample, Environmental Contex and investigation	t nucleic aci sequence source	d Biological Source	MIXS:000002	samp_collec_device	sample collection device	The device used to collect an environmental sample. This field accepts terms listed under environmental sampling de (http://put.db.olitinary.org/cbo/ENVO). This field also accepts terms listed under specimen collection de (http://put.db.olitinary.org/cbo/GENEPIO_0002094).	vice vice device name	{termLabel} {[termID]} {text	swab, biopsy niskin bottle push core t} drag swal [GENEPIO:00 02713]	/, t, b	1	x	x	x	x	x	С	с	x	с	с	С
Sample, Environmental Contex and investigation	t nucleic aci sequence source	d Biological Source	MIXS:0001225	samp_collec_method	sample collection method	The method employed for collecting the sample.	PMID,DOI,url or text	. {PMID} {DOI} { URL} {text}	{ swabbing		1	x	x	x	x	x	с	С	х	С	С	С
Sample, Environmental Contex and investigation	t nucleic aci sequence source	d Biological Source	MIXS:0000016	samp_mat_process	sample material processing	A brief description of any processing applied to the sample during or after retrieving the sample from environment, or a to the relevant protocol(s) performed.	link text	{text}	filtering o seawater, storing samples in ethanol	n	1	x	x	x	x	x	с	с	с	с	с	с
Sample, Environmental Contex and investigation	t sequence source	Biological Source	MIXS:0000017	size_frac	size fraction selected	Filtering pore size used in sample preparation	filter size valu range	ue {float}-{float} {unit}	0-0.22 micrometer		1	-	-	-	-	-	x	x	-	x	x	с
Sample, Environmental Contex and investigation	t nucleic aci sequence source	d Biological Source	MIXS:0000001	samp_size	amount or size of sample collected	The total amount or size (volume (ml), mass (g) or area (m2)) of sample collected.	measurement value	t {float} {unit}	5 liter	milliter, gram, milligram, liter	1	x	x	x	x	x	с	с	x	С	С	с
Sample, Environmental Contex and investigation	t nucleic aci sequence source	d Biological Source	MIXS:0000111	samp_vol_we_dna_ext	sample volume or weight for DNA extraction	Volume (mi) or mass (g) of total collected sample processed for DNA extraction. Note: total sample collected shoul entered under the term Sample Size (MIXS:000001).	d be measurement value	t {float} {unit}	1500 milliliter	milligram, square centimeter	1	x	×	x	x	x	x	x	x	x	x	x

TYPE OF INFORMATION						DESCRIPTOR DEFINITION AND SYNTAX						CHECKL	ST REQUIREM	ENT (M:mand	iatory; C: con	ditional man	datory;X:option	nal; E:Enviro	nment depend	lent; (-): not a	ollicable)	
Туре	Section	sub-section	MIXS ID	Structured commen	t Item (rdfs:label)	Definition	Expected	Value synta	x Example	Preferred	Occurence	migs_eu	migs_ba	migs_pl	migs_vi	migs_org	mims	mimarks_	s mimarks_	c misag	mimag	miuvig
Sample, Environmental Contex and Investigation	nucielo aci sequence source	Biological Source	MIXS:000035	source_u/g	source of UV/Gs	Type of dataset from which the UV/G was obtained	enumeration	[Intelagenceric] (Intel viii targeted)(viii fraction metagenome (viirome)iseen metagenome metagenome metagenome metagenome metagenome metagenome metagenome (SAC)(viirome)iseen viirome)iseen metagenome (SAC)(viirome)iseen single amplified genome (SAC)(viirome)iseen single amplified genome (VSAC)[isota) single single	e e ise ise is ise ise ise ise ise (viral fractione (viral fractione (viral) fractio	n	1	-	-	-		-		-				М
Sample, Environmental Contex and investigation	nucleic acii sequence source	Biological Source	MIXS:0000036	virus_enrich_appr	virus enrichme approach	^N List of approaches used to enrich the sample for viruses, if any	enumeration	[filtration]ultra tration]eentrit gation]utract trifugation]PF Precipitation] eCI Precipitation] sCI dens gradient[DNJ e RNAse]targ ted sequen capture]other one]	afil u u F F filtration + FeC Precipitation + ultracentrifugat ion + DNAse e ce fin	51 + + t	1	-	-	-	с							м
Sequencing and Experimenta Details	sequencing	Library Preparation	MIXS:0000037	nucl_acid_ext	nucleic acid extraction	A link to a literature reference, electronic resource or a standard operating procedure (SOP), that describes the mate separation to recover the nucleic acid fraction from a sample	rial PMID, DOI URL	or {PMID} {DOI] URL}	https://mobio.c om/media/wysi wyg/pdfs/proto cols/12888.pdf		1	с	c	С	с	С	с	с	С	С	с	с
Sequencing and Experimenta Details	sequencing	Library Preparation	MIXS:0000038	nucl_acid_amp	nucleic acid amplification	A link to a literature reference, electronic resource or a standard operating procedure (SOP), that describes the enzyma amplification (PCR, TMA, NASBA) of specific nucleic acids	atic PMID, DOI URL	or {PMID} {DOI] URL}	https://phyloge nomics.me/pro tocols/16s-pcr- protocol/		1	с	с	с	С	с	с	С	с	с	с	с
Sequencing and Experimenta Details	sequencing	Library Preparation	MIXS:0000039	lib_size	library size	Total number of clones in the library prepared for the project	dones	of {integer}	50		1	х	х	х	х	х	С	С	-	с	С	С
Sequencing and Experimenta Details	sequencing	Library Preparation	MIXS:0000040	lib_reads_seqd	library reads sequenced	Total number of clones sequenced from the library	number reads sequenced	of {integer}	20		1	x	x	x	x	x	с	С	-	С	С	с
Sequencing and Experimenta Details	sequencing	Library Preparation	MIXS:0000041	lib_layout	library layout	Specify whether to expect single, paired, or other configuration of reads	enumeration	[paired single ector other]	paired		1	х	х	х	х	х	с	С	-	с	С	С
Sequencing and Experimenta Details	sequencing	Library Preparation	MIXS:0000042	lib_vector	library vector	Cloning vector type(s) used in construction of libraries	vector	{text}	Bacteriophage P1		1	х	x	х	х	х	с	С	-	с	с	с
Sequencing and Experimenta Details	sequencing	Library Preparation	MIXS:0000043	lib_screen	library screening strategy	Specific enrichment or screening methods applied before and/or after creating libraries	screening strategy nan	ne {text}	enriched, screened,		1	x	x	x	x	x	с	с		с	С	с
Sequencing and Experimenta Details	sequencing	sequencing	MIXS:0000044	target_gene	target gene	Targeted gene or locus name for marker gene studies	gene name	{text}	16S rRNA 18S rRNA, nif	L. F.	1	-	-					м	м			
Sequencing and Experimenta	sequencing	sequencing	MIXS:0000045	target_subfragment	target subfragment	Name of subfragment of a gene or locus. Important to e.g. identify special regions on marker genes like V6 on 16S rRN/	gene fragm	ent {text}	V6, V9, ITS		1		-					с	с			
Sequencing and Experimenta Details	sequencing	sequencing	MIXS:0000046	pcr_primers	por primers	PCR primers that were used to amplify the sequence of the targeted gene, locus or subfragment. This field should cont all the primers used for a single PCR reaction if multiple forward or reverse primers are present in a single PCR read The primer sequence should be reported in uppercase littlers	FWD: forw ain primer on. sequence;R :reverse prir sequence	ard EV FWD:{dna};F ner V:{dna}	FWD:GTGCC AGCMGCCGC GGTAA;REV: GGACTACHV GGGTWTCTA AT	с	1							с	с			
Sequencing and Experimenta Details	sequencing	sequencing	MIXS:0000047	mid	multiplex identifiers	Molecular barcodes, called Multiplex Identifiers (MIDs), that are used to specifically tag unique samples in a sequence run. Sequence should be reported in uppercase letters	ing multiplex identifier	{dna}	GTGAATAT		1	-	-				с	с		с	с	с
Sequencing and Experimenta Details	sequencing	sequencing	MIXS:0000048	adapters	adapters	Adapters provide priming sequences for both amplification and sequencing of the sample-library fragments. Both adapt about be reported, in uppercase letters	ers adapter A a B sequence	and {dna};{dna}	AATGATACG GCGACCACC GAGATCTAC ACGCT;CAAG CAGAAGACG GCATACGAG AT	5	1	с	с	с	с	с	с	с		с	с	с
Sequencing and Experimenta Details	sequencing	sequencing	MIXS:0000049	per_cond	pcr conditions	Description of reaction conditions and components of PCR in the form of 'initial denaturation:94degC_1.5m annealing=_:*	initial denaturation egrees_minu s;annealing: grees_minut ;elongation: grees_minut ifinal elongation: rees_minute otal cycles	initial initial denaturation: te egrees_minut es grees_minute grees_minute initial grees_minute initial eg elongation:de it rees_minute: otal cycles	d te initial de denaturation:9 es 4_3;annealing; e 50_1;elongatio n:72_1.5;final elongation:72_ eg 10;35 ;;t	-	1	-	-		-			с	с	-	-	
Sequencing and Experimenta Details	sequencing	sequencing	MIXS:0000050	seq_meth	sequencing method	Sequencing machine used. Where possible the term should be taken from the OBI list of DNA sequenc (http://purt.obolibrary.org/cbo/OBI_0400103).	ers Text or OBI	{termLabel} {[termID]} {te	454 Genome Sequencer FLX [OBI:0000702]		1	м	м	м	м	м	м	м	м	м	м	м
Bioinformatics and Data Processing	sequencing	sequencing	MIXS:0000051	seq_quality_check	sequence quality check	Indicate if the sequence has been called by automatic systems (none) or undergone a manual editing procedure (e.g. inspecting the raw data or chromatograms). Applied only for sequences that are not submitted to SRA.ENA or DRA	by none manually	or [none]manua edited]	^{illy} none		1	-	-					с	с			
Bioinformatics and Data Processing	sequencing	sequencing	MIXS:0000052	chimera_check	chimera check software	Tool(s) used for chimera checking, including version number and parameters, to discover and remove chime sequences. A chimeric sequence is comprised of two or more phylogenetically distinct parent sequences.	edited name a version software, parameters used	of {software};{v sion};{param ers}	er uchime;v4.1;d efault parameters		1	-	-				-	с	с			

TYPE OF INFO	MATION							DESCRIPTOR DEFINITION AND SYNTAX					CHECK	LIST REQUIR	EMENT (M:mar	datory; C: co	nditional man	datory;X:optic	nal; E:Enviro	onment depend	lent; (-): not aj	ollicable)	
Туре		5	Section	sub-section	MIXS ID	Structured comme	nt Item (rdfs:label)	Definition	Expected	Value syntax	Example	Preferred	Occurence migs_e	u migs_t	a migs_pl	migs_vi	migs_org	g mims	mimarks	_s mimarks_	c misag	mimag	miuvig
Bioinformatics Processing	and	Data	sequencing	sequencing	MIXS:0000053	tax_ident	taxonomic identity marker	The phylogenetic marker(s) used to assign an organism name to the SAG or MAG	enumeration	[16S rRNA gene multi- marker approach other 1	other: rpoB r ^{gene}	unix	1 C	с	с	с	с	-			м	м	x
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000056	assembly_qual	assembly quality	The security quality category is batted on sets of orbits outlined for each security quality category. To INSR-00MIMS, Finaled Single and contexpose secures per region willing apper or regional security and the security of	t enumeration	[Finished genome High- quality draft genome Mediu m-quality draft genome Low- quality draft genome Geno me fragment(s)]	t t High-quality draft genome t		1 M	м	x	x	x	C			М	м	м
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000057	assembly_name	assembly name	Name/version of the assembly provided by the submitter that is used in the genome browsers and in the community	name a version assembly	nd of {text} {text}	HuRef, JCVI_ISG_i3_ 1.0		1 C	с	с	с	с	с	-	-	с	с	с
Bioinformatics Processing	and	Datas	sequencing	data processing	MIXS:0000058	assembly_software	assembly software	Tool(s) used for assembly, including version number and parameters	name a version software, parameters used	nd of {software};{ver sion};{paramet ers}	metaSPAdes;3 .11.0;kmer set 21,33,55,77,99 ,121, default parameters otherwise		1 M	м	м	м	м	с	с	-	м	м	м
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000059	annot	annotation	Tool used for annotation, or for cases where annotation was provided by a community jamboree or model organism distabase rather than by a specific submitter	name of tool pipeline use or annotati source description	or d, n {text}	prokka		1 C	с	с	с	с	с			x	x	x
Bioinformatics	and	Data	sequencing	data processing	MIXS:0000060	number_contig	number of contigs	Total number of contigs in the cleaned/submitted assembly that makes up a given genome, SAG, MAG, or UVIG	value	{integer}	40		1 M	м	х	х	х	С	-		х	х	м
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000061	feat_pred	feature prediction	Method used to predict UV/Gs features such as ORFs, integration sile, etc.	names a versions software(s), parameters used	nd of {software};{ver sion};{paramet ers}	Prodigal;2.6.3; default parameters		1 X	x	x	x	x	x		-	x	x	с
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000062	ref_db	reference database(s)	List of database(s) used for ORF annotation, along with version number and reference to website or publication	names, versions, ai references databases	nd (database);{ve of rsion);{referen ce}	pVOGs;5;http:/ /dmk- brain.ecn.uiow a.edu/pVOGs/ Grazziotin et al. 2017 doi:10.1093/na r/gkw975		1 X	x	x	x	x	x			x	x	С
Bioinformatics Processing	and	Data s	sequencing	data processing	MIXS:0000063	sim_search_meth	similarity search method	Tool used to compare ORFs with database, along with version and cutoffs used	names ai versions software(s), parameters used	nd of {software};{ver sion};{paramet ers}	HMMER3;3.1b 2;hmmsearch, cutoff of 50 on score		1 X	x	x	x	x	x		-	x	x	с
Bioinformatics Processing	and	Data _S	sequencing	data processing	MIXS:0000064	tax_class	taxonomic classification	Method used for taxonomic classification, along with reference database used, classification rank, and thresholds used to classify new genomes	classification method, database name, ai other parameters	nd ^{text}	vConTACT vContact2 (references from NCBI RefSeq v83, genus rank classification, default parameters)		1 X	x	x	x	x	x			x	x	С
Bioinformatics	and	Data	equencing	data processing	MIXS:0000065	16e recover	16S recovered	Can a 16S name he recovered from the submitted S&G or M&G?	hoolean	(hoolean)	Vee		1 .								Y	Y	
Processing Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000066	16s_recover_software	16S recovery software	Tools used for 16S rRNA gene extraction	names ai versions software(s), parameters used	of {software};{ver sion};{paramet ers}	rambl;v2;defau It parameters		1 -	-							x	x	
Bioinformatics	and	Data	seauencina	data processing	MIXS:0000067	tmas	number of standard	The total number of tRNAs identified from the SAG or MAG	value from	0-	18		1 -	-							x	x	x
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000068	trna_ext_software	tRNA extraction software	Tools used for IRNA identification	names ai versions software(s), parameters used	of {software};{ver sion};{paramet ers}	infernal;v2;def ault parameters		1 -	-	-					-	x	x	x
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000069	compl_score	completeness score	Completeness score is typically based on either the fraction of markers found as compared to a database or the percent or a genome found as compared to a closely related reference genome. High Quality Draft >90%, Medium Quality Draft >50%, and Low Quality Draft < 50% should have the indicated completeness accres	f quality;perce completenes	nt [high med low]; s {percentage}	med;60%		1 X	x	x	x	x		-		м	м	с
Bioinformatics Processing	and	Data s	sequencing	data processing	MIXS:0000070	compl_software	completeness software	Tools used for completion estimate, i.e. checkm, anvi'o, busco	names ai versions software(s)	nd of {software};{ver sion}	checkm		1 X	x	x	x	x				м	м	x
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000071	compl_appr	completeness approach	The approach used to determine the completeness of a given genomic assembly, which would typically make use of a set of conserved marker genes or a closely related reference genome. For UVIG completeness, include reference genome o group used, and contig feature suggesting a complete genome.	t	[marker gene[reference based other]	other: UVIG length compared to the average length of reference genomes from the P22virus genus (NCBI RefSeq v83)		1 -	-							x	x	с
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000072	contam_score	contamination score	The contamination score is based on the fraction of single-copy genes that are observed more than once in a quen- genome. The following scores are acceptable for; High Quality Draft < 5%, Medium Quality Draft < 10%, Low Quality Draft < 10%. Contamination must be below 5% for a SAG or MAG to be deposited into any of the public databases	/ value	{float} percentage	1%		1 -	-							м	м	
Bioinformatics	and	Data	sequencing	data processing	MIXS:0000005	contam_screen_input	contamination screening	The type of sequence data used as input	enumeration	[reads contigs]] contigs		1 -	-	-	-	-		-	-	x	x	
Bioinformatics Processing	and	Data	sequencing	data processing	MIXS:0000073	contam_screen_param	contamination screening parameters	Specific parameters used in the decontamination software, such as reference database, coverage, and kmers Combinations of these parameters may also be used, i.e. kmer and coverage, or reference database and kmer	. enumeration; alue or name	[ref db]kmer[cover age]combinatio n];{text[integer]	o kmer }		1 -	-							x	x	-
Bioinformatics Processing	and	Data s	sequencing	data processing	MIXS:0000074	decontam_software	decontamination software	Tool(s) used in contamination screening	enumeration	jcneckm/refine m[anvi'o]prode ge[bbtools:dec ontaminate.sh] acdc[combinati on]	anvi'o		1 -	-	-					-	x	x	

TYPE OF INFORMATION						DESCRIPTOR DEFINITION AND SYNTAX						CHECKLIST	REQUIREME	NT (M:mand	atory; C: con	ditional manda	atory;X:optio	nal; E:Enviro	nment depend	ient; (-): not ap	llicable)	
Туре	Section	sub-section	MIXS ID	Structured commen	t Item (rdfs:label)	Definition	Expected	Value syntax	Example	Preferred	Occurence	migs_eu	migs_ba	migs_pl	migs_vi	migs_org	mims	mimarks_	s mimarks	c misag	mimag	miuvig
Bioinformatics and Dat Processing	^a sequencing	data processing	MIXS:0000075	sort_tech	sorting technology	Method used to sort/isolate cells or particles of interest	enumeration	[flow cytometric cel sorting microflu idics lazer- tweezing optic al manipulation m icromanipulatio n other	optical manipulation		1	-	-							м		с
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000076	single_cell_lysis_appr	single cell or viral particle lysis approach	Method used to free DNA from interior of the cell(s) or particle(s)	enumeration	[chemical enzy matic physical combination]	enzymatic		1	-	-	-				-		м		с
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000054	single_cell_lysis_prot	single cell or viral particle lysis kit protocol	Name of the kit or standard protocol used for cell(s) or particle(s) lysis	kit, protoci name	ol {text}	ambion single cell lysis kit	e	1	-	-	-						х		С
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000055	wga_amp_appr	WGA amplification approach	Method used to amplify genomic DNA in preparation for sequencing	enumeration	[pcr based mda based]	mda based		1	-	-		-	-	-	-	-	м	-	с
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000006	wga_amp_kit	WGA amplification kit	Kit used to amplify genomic DNA in preparation for sequencing	kit name	{text}	qiagen repli-g		1	-	-	-	-	-		-		х	-	С
Bioinformatics and Dat Processing	^a sequencing	data processing	MIXS:0000077	bin_param	binning parameters	The parameters that have been applied during the extraction of genomes from metagenomic datasets	enumeration	[homology search kmer c overage codon usage combina tion]	coverage and kmer	d	1	-	-	-	-		-	-	-	-	м	с
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000078	bin_software	binning software	Tool(s) used for the extraction of genomes from metagenomic datasets, where possible include a product ID (PID) of the tool(s) used.	names an versions o software(s) used	nd of {software};{ver sion}{PID}	MetaCluster- TA (RRID:SCR_0 04599), MaxBin (biotools:maxb n)	bő	1	-	-				-	-	-		м	с
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000079	reassembly_bin	reassembly post binning	Has an assembly been performed on a genome bin extracted from a metagenomic assembly?	boolean	{boolean}	no		1	-	-	-							х	с
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000080	mag_cov_software	MAG coverage software	Tool(s) used to determine the genome coverage if coverage is used as a binning parameter in the extraction of genome from metanenomic datasets.	enumeration	[bwa bbmap b	bbmap		1	-	-	-	-	-	-	-		-	х	х
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000081	vir_ident_software	viral identification software	Toc/(s) used for the identification of UV/G as a viral genome, software or protocol name including version numbe parameters, and cutoffs used	software r, name, versio and relevan parameters	on sion};{paramet ers}	VirSorter; 1.0.4; Virome database, category 2	e	1	-	-									м
Bioinformatics and Dat Processing	^a sequencing	data processing	MIXS:0000082	pred_genome_type	predicted genome type	Type of genome predicted for the UVIG	enumeration	[DNA dsDNA s sDNA RNA ds RNA ssRNA ss RNA (+) ssRNA (-) mixed unchar acterized]	dsDNA		1	-	-	-					-		-	м
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000083	pred_genome_struc	predicted genome structure	Expected structure of the viral genome	enumeration	[segmented]no n- segmented[un determined]	non- segmented		1	-	-	-				-				м
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000084	detec_type	detection type	Type of UVIG detection	enumeration	[independent sequence (UViG)[proviru s (UpViG)]	independent sequence (UVIG)		1	-	-									м
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000085	otu_class_appr	OTU classification approach	Catoffs and approach used when clustering "species-level" OTUs. Note that results from standard 95% ANI / 85% A clustering should be provided alongiate OTUS defined from another set of thresholds, even if the latter are the one primarity used during the analysis	F cutoffs an method used	{ANI cutoff};{AF cutoff};{clusteri ng method}	95% ANI;85% AF; greedy incremental clustering	у У	1	-	-									с
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000086	otu_seq_comp_appr	OTU sequence comparison approach	Tool and thresholds used to compare sequences when computing "species-level" OTUs	and relevant parameters	on sion};{paramet ers}	blastn;2.6.0+;e value cutoff 0.001	e- f:	1	-	-									с
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:0000087	otu_db	OTU database	Reference database (i.e. sequences not generated as part of the current study) used to duster new genomes in "specie level" OTUs, if any	 database an version 	rsion}	NCBI Vira RefSeq;83	bl.	1	-	-	-	-	-	-	-	-	-	-	с
Bioinformatics and Dat Processing	^a sequencing	data processing	MIXS:0000088	host_pred_appr	host prediction approach	Tool or approach used for host prediction	enumeration	[provirus]host sequence similarity[CRIS PR space match[kmer similarity[co- occurrence]co mbination[othe r]	r CRISPR spacer match		1	-	-									С
Bioinformatics and Dat Processing	a sequencing	data processing	MIXS:000089	host_pred_est_acc	host prediction estimated accuracy	For each tool or approach used for host prediction, estimated failse discovery rates should be included, either computed on novo or from the literature	le false discover rate	ry {text}	CRISPR spacer match 0 or 11 mismatches, estimated 8% FDR at the host genus rank (Edwards et al. 2016 doi:10.1093/fe msre/fuv048)	2 6 8 8 6	1	-	-			-	-	-	-	-	-	с
Accession and Submission	sequencing	Accession an Submission	d MIXS:0000091	associated resource	relevant electronic resources	A related resource that is referenced, cited, or otherwise associated to the sequence.	reference f resource	to {PMID} {DOI] {URL}	http://www.earl hmicrobiome.o	1	m	с	с	с	с	с	с	с	с	с	с	с
Accession and Submission	sequencing	Accession an Submission	d MIXS:0000090	sop	relevant standard operating procedures	Standard operating procedures used in assembly and/or annotation of genomes, metagenomes or environment sequences	al reference 1 SOP	to {PMID} {DOI} { URL}	b.anl.gov/earth microbiome/pr otocols-and- etandarde/ite/	<u>1</u>	m	с	с	с	с	с	с	с	с	с	с	с