

Metadata and MlxS* Checklists

***Minimal Information about any (x) Sequence**

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State of art: Working with molecular data: Is the contextual data acknowledged?

Very Minimum expectations

The contextual data can
and should be included in
the databases!

- Contextual data is not integrated to the molecular data inside taxonomic databases (*e.g.* NCBI).
- Non-standardized collection of contextual data.
- Public databases (such as the ISNDC) depend on author-submitted information.
- Establishment of standardized procedures is required.

Is the contextual data acknowledged?


Comment | [Open Access](#) | Published: 19 June 2020

COVID-19 pandemic reveals the peril of ignoring metadata standards

Lynn M. Schriml , Maria Chuvochina, Neil Davies, Emiley A. Eloë-Fadrosh, Robert D. Finn, Philip Hugenholtz, Christopher I. Hunter, Bonnie L. Hurwitz, Nikos C. Kyrpides, Folker Meyer, Ilene Karsch Mizrahi, Susanna-Assunta Sansone, Granger Sutton, Scott Tighe & Ramona Walls

Scientific Data **7**, Article number: 188 (2020) | [Cite this article](#)

7214 Accesses | **2** Citations | **216** Altmetric | [Metrics](#)

 This article has been updated

Efficient response to the pandemic through the mobilization of the larger scientific community is challenged by the limited reusability of the available primary genomic data. Here, the Genomic Standards Consortium board highlights the essential need for contextual genomic data FAIRness, for empowering key data-driven biological questions.

A research program at the University of Oxford, "Our World in Data", maintains a global database on testing for COVID-19. Asked whether there are 'low-hanging fruit' to improve the response to the pandemic, Program Director Max Roser had a very simple answer: "*for all those who publish original data, provide a clear description of your data*" (@MaxCRoser: 1:39am · 12 Apr 2020 · Twitter Web App), highlighting the importance of maximizing the reusability of data. In the age of COVID-19, we are seeing where value really lies. Describing the WHO, WHAT, HOW, WHERE, and WHEN of genomic data enables comparative analysis, informs

Is the contextual data acknowledged?

From: COVID-19 pandemic reveals the peril of ignoring metadata standards

a

Pathogen: clinical or host-associated sample from Severe acute respiratory syndrome coronavirus 2

Identifiers BioSample: SAMN14751340; Sample name: WA-UW-6185; SRA: SRS6545124

Organism [Severe acute respiratory syndrome coronavirus 2](#)
Viruses; Riboviria; Nidovirales; Comidovirineae; Coronaviridae; Orthocoronavirinae; Betacoronavirus; Sarbecovirus; Severe acute respiratory syndrome-related coronavirus

Package [Pathogen: clinical or host-associated; version 1.0](#)

Attributes

isolate	WA-UW-6185
collected by	University of Washington Virology Lab
collection date	missing
geographic location	USA
host	Homo sapiens
host disease	COVID-19
isolation source	missing
latitude and longitude	missing

Submission University of Washington, Pavitra Roychoudhury; 2020-04-27

b

Pathogen: clinical or host-associated sample from Severe acute respiratory syndrome coronavirus 2

Identifiers BioSample: SAMN14656632; Sample name: hCoV-19/USA/WI-176/2020; SRA: SRS6514341

Organism [Severe acute respiratory syndrome coronavirus 2](#)
Viruses; Riboviria; Nidovirales; Comidovirineae; Coronaviridae; Orthocoronavirinae; Betacoronavirus; Sarbecovirus; Severe acute respiratory syndrome-related coronavirus

Package [Pathogen: clinical or host-associated; version 1.0](#)

Attributes

strain	hCoV-19/USA/WI-176/2020
isolate	Homo sapien
collected by	Milwaukee Public Health Department
collection date	2020-03-20
geographic location	USA: Milwaukee, Wisconsin
host	Homo sapiens
host disease	COVID-19
isolation source	nasal swab
latitude and longitude	43.042180 N 87.908670 W
ARTIC barcode identifiers	NB23

Lost opportunities for data reuse, SARS-CoV-2 (txid2697049[Organism:noexp]) BioSample records, where (a) **collection date** = “missing”: 143; **latitude and longitude** = “missing”: 1375; (b) SARS-CoV-2 BioSample record with complete metadata.

Is the contextual data acknowledged?

From: COVID-19 pandemic reveals the peril of ignoring metadata standards

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Organism [Severe acute respiratory syndrome coronavirus 2](#)
Viruses; Riboviria; Nidovirales; Coronaviridae; Orthocoronavirinae; Betacoronavirus; Sarbecovirus; Severe acute respiratory syndrome-related coronavirus

Package [Pathogen: clinical or host-associated; version 1.0](#)

Attributes

strain	hCoV-19/USA/WI-176/2020
isolate	Homo sapien
collected by	Milwaukee Public Health Department
collection date	2020-03-20
geographic location	USA: Milwaukee, Wisconsin
host	Homo sapiens
host disease	COVID-19
isolation source	nasal swab
latitude and longitude	43.042180 N 87.908670 W
ARTIC barcode identifiers	NB23

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MiXS

Minimum Information about any (x) Sequence

developed by:



supported by:



Available in: <http://gensc.org/mixs/>

Published: 06 May 2011

Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MiXS) specifications

Pelin Yilmaz, Renzo Kottmann, [...] Frank Oliver Glöckner [✉](#)

Nature Biotechnology **29**, 415–420(2011) | [Cite this article](#)

2021 Accesses | **359** Citations | **35** Altmetric | [Metrics](#)

Abstract

Here we present a standard developed by the Genomic Standards Consortium (GSC) for reporting marker gene sequences—the minimum information about a marker gene sequence (MIMARKS). We also introduce a system for describing the environment from which a biological sample originates. The 'environmental packages' apply to any genome sequence of known origin and can be used in combination with MIMARKS and other GSC checklists. Finally, to establish a unified standard for describing sequence data and to provide a single point of entry for the scientific community to access and learn about GSC checklists, we present the minimum information about any (x) sequence (MiXS). Adoption of MiXS will enhance our ability to analyze natural genetic diversity documented by massive DNA sequencing efforts from myriad ecosystems in our ever-changing biosphere.

Specification projects	MIGS	MIMS	MIMARKS	New checklists
Checklists	EU BA PL VI ORG	metagenomes	survey specimen	e.g., pan-genomes
Shared descriptors	collection date, environmental package, environment (biome), environment (feature), environment (material), geographic location (country and/or sea, region), geographic location (latitude and longitude), investigation type, project name, sequencing method, submitted to INSDC			
Checklist-specific descriptors	assembly, estimated size, finishing strategy, isolation and growth condition, number of replicons, ploidy, propagation, reference for biomaterial		target gene	
Applicable environmental packages (measurements and observations)	Air Host-associated Human-associated Human-oral Human-gut Human-skin Human-vaginal		Microbial mat/biofilm Miscellaneous natural or artificial environment Plant-associated Sediment Soil Wastewater/sludge Water	

Download MlxS Checklist v5.0: [mixs_v5](#)

or from the MlxS GitHub [here](#)

Download MlxS Checklist v4.0 [here](#)

Specification projects	MIGS	MIMS	MIMARKS	New checklists
Checklists				
Shared descriptors	collection date, environmental package, environment (biome), environment (biotope), environment (material), geographic location (country and/or sea, region), geographic location (latitude and longitude), investigation type, project name, sequencing method, submitted to INSDC			
Checklist specific descriptors	assembly, estimated size, banking strategy, isolation and growth conditions, number of replicates, ploidy, propagation, reference for biomaterial		target gene	
Applicable environmental packages (measurements and observations)	Air Host-associated Human-associated Human-oral Human-gut Human-skin Human-vaginal	Microbial mat/biofilm Miscellaneous natural or artificial environment Plant-associated Sediment Soil Wastewater/sludge Water		

The core MlxS team developed the following environmental packages These packages are available as separate spreadsheets:

1. Air ([download MlxS-air only](#))
2. Built-environment ([download MlxS-built environment only](#))
3. Host-associated ([download MlxS-host associated only](#))
4. Human-associated ([download MlxS-human associated only](#))
5. Human-gut ([download MlxS-human gut only](#))
6. Human-oral ([download MlxS-human oral only](#))
7. Human-skin ([download MlxS-human skin only](#))
8. Human-vaginal ([download MlxS-human vaginal only](#))
9. Microbial mat/biofilm ([download MlxS-microbial mat/biofilm only](#))
10. Miscellaneous natural or artificial environment ([download MlxS-misc. natural or artificial environment only](#))
11. Plant-associated ([download MlxS-plant associated only](#))
12. Sediment ([download MlxS-sediment only](#))
13. Soil ([download MlxS-soil only](#))
14. Wastewater/sludge ([download MlxS-wastewater/sludge only](#))
15. Water ([download MlxS-water only](#))
16. Hydrocarbon resources-cores ([download from GitHub](#))
17. Hydrocarbon resources-fluids/swabs ([download from GitHub](#))

MixS - Water Checklist

Structured comment name	Item	Definition	Example	Expected value	Section	e	b	p	v	o	r	m	MIMAR KS Survey	MIMAR KS Specimen	Value syntax
1 4	project_name	project name	Name of the project within which the sequencing was organized		investigation	M	M	M	M	M	M	M	M	M	{text}
5	experimental_factor	experimental factor	Experimental factors are essentially the variable aspects of an experiment design which can be used to describe an experiment, or set of experiments, in an increasingly detailed manner. This field accepts ontology terms from Experimental Factor Ontology (EFO) and/or Ontology for Biomedical Investigations (OBI). For a browser of EFO (v 2.43) terms, please see http://purl.bioontology.org/ontology/EFO ; for a browser of OBI (v 2013-10-25) terms please see http://purl.bioontology.org/ontology/OBI	text or EFO and/or OBI	investigation	X	X	X	X	X	X	C	C	X	{term} {text}
6	lat_lon	geographic location (latitude and longitude)	The geographical origin of the sample as defined by latitude and longitude. The values should be reported in decimal degrees and in WGS84 system	decimal degrees	environment	M	M	M	M	M	M	M	M	M	{float} {float}
7	depth	geographic location (depth)	Please refer to the definitions of depth in the environmental packages	-	environment	E	E	E	E	E	E	E	E	E	-
8	alt_elev	geographic location (altitude/elevation)	Please refer to the definitions of either altitude or elevation in the environmental packages	-	environment	E	E	E	E	E	E	E	E	E	-
9	geo_loc_name	geographic location (country and/or sea,region)	The geographical origin of the sample as defined by the country or sea name followed by specific region name. Country or sea names should be chosen from the INSDC country list (http://insdc.org/country.html), or the GAZ ontology (v 1.512) (http://purl.bioontology.org/ontology/GAZ)	Germany:Sylt;Hausstrand	country or sea name (INSDC or GAZ):region(GAZ):specific location name	M	M	M	M	M	M	M	M	M	{term};{term};{text}
10	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, the date/time can be right truncated i.e. all of these are valid times: 2008-01-23T19:23:10+00:00; 2008-01-23T19:23:10; 2008-01-23; 2008-01; 2008; Except: 2008-01; 2008 all are ISO8601 compliant	date and time	environment	M	M	M	M	M	M	M	M	M	{timestamp}
11	env_biome	environment (biome)	Biomes are defined based on factors such as plant structures, leaf types, plant spacing, and other factors like climate. Biome should be treated as the descriptor of the broad ecological context of a sample. Examples include: desert, taiga, deciduous woodland, or coral reef. EnvO (v 2013-06-14) terms can be found via the link: www.environmentontology.org/Browse-EnvO	EnvO	environment	M	M	M	M	M	M	M	M	M	{term}
12	env_feature	environment (feature)	Environmental feature level includes geographic environmental features. Compared to biome, feature is a descriptor of the more local environment. Examples include: harbor, cliff, or lake. EnvO (v 2013-06-14) terms can be found via the link: www.environmentontology.org/Browse-EnvO	EnvO	environment	M	M	M	M	M	M	M	M	M	{term}
13	env_material	environment (material)	The environmental material level refers to the material that was displaced by the sample, or material in which a sample was embedded, prior to the sampling event. Environmental material terms are generally mass nouns. Examples include: air, soil, or water. EnvO (v 2013-06-14) terms can be found via the link: www.environmentontology.org/Browse-EnvO	EnvO	environment	M	M	M	M	M	M	M	M	M	{term}
			MIGS/MIMS/MIMARKS extension for reporting of measurements and observations obtained from one or more of the environments where the sample was obtained. All environmental packages listed here are further defined in												associated human-skin human-oral human-gut human-vaginal microbial mat biofilm mis environment plant-

EnvO – The Environment Ontology



The Environment
Ontology

About EnvO

Annotation guidelines

Browse EnvO

Downloads

Participate

Contact

The Environment Ontology

EnvO is a community ontology for the concise, controlled description of environments

ENVO is an expressive, community ontology which helps humans, machines, and semantic web applications understand environmental entities of all kinds, from microscopic to intergalactic scales. As a FAIR-compliant resource, it promotes interoperability through the concise, controlled description of all things environmental.

<https://sites.google.com/site/environmentontology/>

biome Search

Exact match Obsolete terms

Term type

Filter by type
class 195

Ontologies

× The Environment Ontology (ENVO)
ENVO 195

Clear all filters

Search results for biome

Previous Showing 11 to 20 of 195 results Next

desert biome ENVO:01000179

http://purl.obolibrary.org/obo/ENVO_01000179

A desert biome is a terrestrial biome which loses more liquid water by evapotranspiration than is supplied by precipitation and includes communities adapted to these conditions.

Ontology: [The Environment Ontology](#) ENVO

aquatic biome ENVO:00002030

http://purl.obolibrary.org/obo/ENVO_00002030

A biome which is determined by a water body and which has ecological climax communities adapted to life in or on water.

Ontology: [The Environment Ontology](#) ENVO

marine biome ENVO:00000447

http://purl.obolibrary.org/obo/ENVO_00000447

An aquatic biome which is determined by a marine water body.

Ontology: [The Environment Ontology](#) ENVO





ONTOLOGY SEARCH

OLS / The Environment Ontology ENVO / ENVO:00000447 Copy

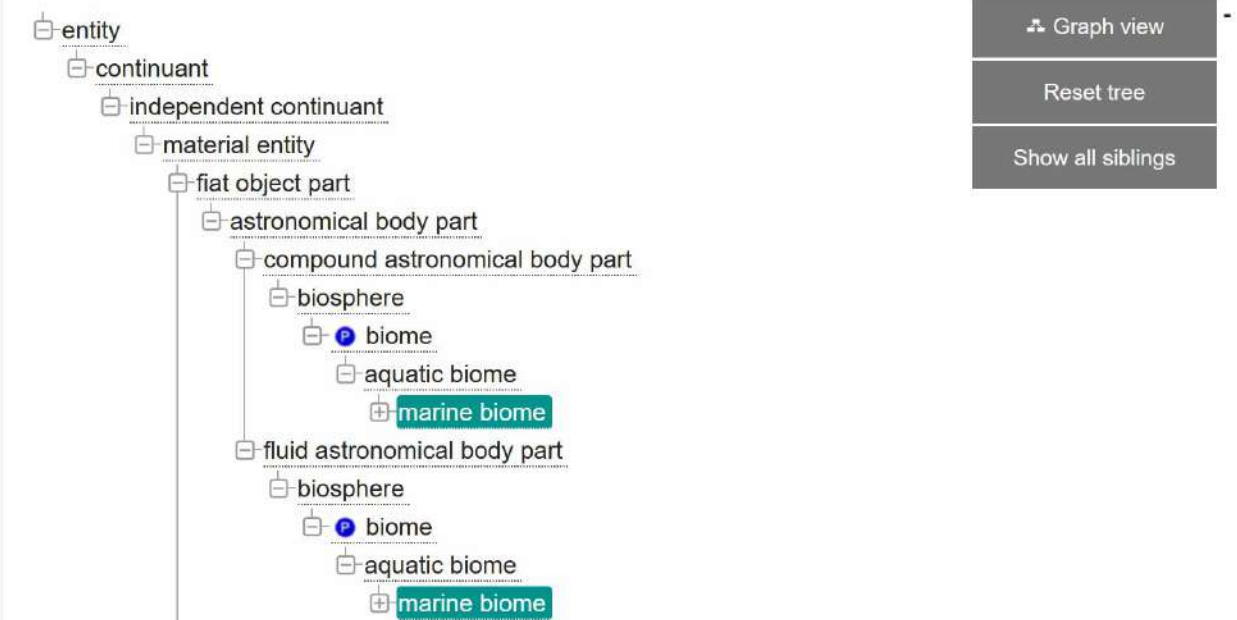
marine biome

Search ENVO Search

http://purl.obolibrary.org/obo/ENVO_00000447 Copy

An aquatic biome which is determined by a marine water body. [https://orcid.org/0000-0002-4366-3088 https://www.worldcat.org/search?q=bn%3A978-0-618-45504-1 http://www.informatics.jax.org/searches/AMA.cgi?id=MA:ma https://en.wikipedia.org/wiki/Ocean]

Tree view Term mappings Term history



Graph view Reset tree Show all siblings

Term information

database cross reference

- SPIRE:Marine

comment

This biome includes open-ocean and unprotected coastal ecosystems, characterized by exposure to wave action, tidal fluctuation, and ocean currents as well as systems that largely resemble these. Water in the marine biome is generally within the salinity range of seawater: 30 to 38 ppt.

has related synonym

marine realm

in subset

envoPolar

https://www.ebi.ac.uk/ols/ontologies/envo/terms?iri=http%3A%2F%2Fpurl.obolibrary.org%2Fobo%2FENVO_00000447

EnvO – The Environment Ontology



- **biome** - e.g. *concentration basin mediterranean sea biome*
- **environmental feature** - e.g. *circalitoral zone*
- **environmental material** - e.g. *coastal sea water*

Item	MIGS				MIMS		MIMARKS	
	EU	BA	PL	VI	ORG	ME	SU	SP
Project name	M	M	M	M	M	M	M	M
Collection date	M	M	M	M	M	M	M	M
Geographic location	M	M	M	M	M	M	M	M
Environment	M	M	M	M	M	M	M	M
Ploddy	M	-	-	-	-	-	-	-
Estimated size	M	X	X	X	X	-	-	-
Target gene	-	-	-	-	-	-	M	M



MIMARKS-Survey-Soil Checklist	
Item	SU
Project name	M
Collection date	M
Geographic location	M
Environment	M
Target gene	M
Elevation	M
Depth	M
Horizon	X
pH	X

Environmental Packages

Item	Environmental Packages		
	Human-gut	Soil	Water
Age	X	-	-
Body site	X	-	-
Elevation	-	M	C
Depth	-	M	M
Horizon	-	X	-
pH	-	X	X
Salinity	-	-	X



Yilmaz et al., 2011, Nature Biotechnology, 29, 5, 415-420



EMBL-EBI **BioSamples** Start your search
 Examples: leukaemia, virid

Home Search Submit Help About BioSamples

BioSamples > SAMEA104172529

Sample SAMEA104172529

Name	ERS1831547
Release date	2017-08-31
Last updated	2017-08-31
Submission title	121 marine metagenome samples from ENA SRA
Submission identifier	GEN-ERA979722
Organism	marine metagenome
Amount or size of sample collected	0.005-0.01 (L)
Collection date	2014-04-26T10:00:00/2014-05-01T15:30:00
Ena first public	2017-08-08
Ena last update	2017-08-30
Environment biome	concentration basin mediterranean sea biome [ENVO:01000004]
Environment feature	circalittoral zone [ENVO:01000412]coastal water body [ENVO:02000049]
Environment material	coastal sea water [ENVO:00002150]oligotrophic water [ENVO:00002223]
Geographic location-country and or sea	France
Geographic location depth	10-12 (m)
Investigation type	mimarks-survey
Latitude	43.402301 (DD)
Longitude	7.195801 (DD)
Observed biotic relationship	free living
Pcr primers	28F: 5'-GAGTTTGATCNTGGCTCAG-3', 519R: 5'-GTNTTACNGCGGCKGCTG-3'
Project name	IN-EX
Sample collection device or method	In situ Incubation
Sample material processing	filtering of seawater, DNA extraction
Sequencing method	Illumina MiSeq
Submitted to insdc	true
Synonym	1131:6d930886-7aaa-4eef-a260-6c6b426e4d50 130 Tf
Target gene	16S rRNA
Water environmental package	water
External references	ERS1831547 SAMEA104172529

MIXS standard in EBI-ENA

The screenshot shows the EBI-ENA website interface. At the top, there is a navigation bar with 'EMBL-EBI' on the left and 'Services', 'Research', 'Training', and 'About us' on the right. Below this is a teal header with the ENA logo and 'European Nucleotide Archive' text. A search bar is located on the right side of the header, with a 'Search' button and links for 'Advanced Sequence'. A secondary navigation bar contains 'Home', 'Search & Browse', 'Submit & Update' (highlighted), 'Software', 'About ENA', and 'Support'. The main content area is titled 'Submit and update' and features a section for 'Submitting and updating data' with a descriptive paragraph. Below this are two buttons: 'Submit to ENA' and 'Email ENA Helpdesk'. A 'Programmatic submissions' section is also visible. On the right side, a 'Submit & Update' sidebar lists various submission options such as 'Data formats', 'Taxon ID requests', 'Uploading data files', 'Reads', 'Sequences', 'Genome assembly submissions', 'Taxonomy', 'Sample checklists', 'Environmental', 'Epigenomic', 'Species BARCODE', 'Metadata model', 'Register submission account', and 'Programmatic XML submissions'.

<https://www.ebi.ac.uk/ena/submit>

Publish your sequences with metadata! | 26.04.2022

Please specify the release date of your study:
This is when your study will be made public.

11-Aug-2015

Please provide a short name for the study:

Please provide a short descriptive title for the study: (*)

Please provide an abstract to describe the study in detail: (*)

For genome assembly projects only: In this study, will you provide locus tags?
PLEASE ANSWER WITH YES IF YOU HAVE ANNOTATION: Locus tag p

Yes
 No

Please provide PubMed IDs of publications you want to associate with this study (numeric value)

PubMed IDs

Add

Please provide attributes to add a deeper description of the study

Tag	Value
-----	-------

Add

Please select the checklist attributes you would like to include with each sample. Recommended attributes can be unselected from within the corresponding attribute group on the left-hand side panel. You may also add custom attributes.

Filter attributes...
Add your own attribute + Add

- + internal environment
- + local environment conditions
- + non-sample term
- + sample collection
- + organism characteristics
- + concentration measurement
- + host details
- + other
- + host description
- + geography
- + User Attributes

12 of 78 attributes selected

+ Expand - Collapse Download Template

Please complete any fields that you would like to apply to all samples. This will act as a template for the rest of the samples.

Template Basic Details

Unique Name Prefix:
* Title:
Description:

Organism Details

If your organism is not found please go [here](#) and email datasubs@ebi.ac.uk with the required details listed on the page in order for us to request a taxon Id for your organism.

Search:
* Tax Id:
* Scientific Name:
Common Name:

non-sample term

* investigation type:
* project name:
* sequencing method:

sample collection

<< Previous Next >>

<< Previous

Submit



Demo

- **Submission template for sequence data**

Here: <https://gitlab.gwdg.de/gfbio/molecular-submission-templates/-/blob/master/Template-Description.md>

- **Available fields, defaults fields and suggested for FAIRness**
- **Walk through example**



Template Example

sample_title	taxon_id	sample_description	sequencing_platform	library_strategy	library_source	library_selection	library_layout	no	of	for	read	checksum	investigation_type	environmental	collection_date	geographic	geographic	geographic	geographic	environment (biome)
01_VP1c_Kstria	1300146	Kappaphycus striat	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.652	109.333	5	Vietnam	marine biome [ENVO:00000447]
03_VP1a_Kstria	1300146	Kappaphycus striat	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.652	109.333	5	Vietnam	marine biome [ENVO:00000447]
04_VP1b_Kstria	1300146	Kappaphycus striat	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.652	109.333	5	Vietnam	marine biome [ENVO:00000447]
07_VP2a_Eden	1300146	Euchema denticula	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.658	109.351	5	Vietnam	marine biome [ENVO:00000447]
09_VP5a_Eden	1300146	Euchema denticula	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.657	109.333	16	Vietnam	marine biome [ENVO:00000447]
12_VP4a_Eden	1300146	Euchema denticula	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.652	109.34	3	Vietnam	marine biome [ENVO:00000447]
14_VP4b_Eden	1300146	Euchema denticula	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.652	109.34	3	Vietnam	marine biome [ENVO:00000447]
15_CR4a_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.957	109.201	0.5	Vietnam	marine biome [ENVO:00000447]
16_CR4b_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.957	109.201	0.5	Vietnam	marine biome [ENVO:00000447]
17_CR5a_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.948	109.194	0.5	Vietnam	marine biome [ENVO:00000447]
18_CR5b_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.948	109.194	0.5	Vietnam	marine biome [ENVO:00000447]
19_CR1a_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.981	109.2	0.5	Vietnam	marine biome [ENVO:00000447]
20_CR1b_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.981	109.2	0.5	Vietnam	marine biome [ENVO:00000447]
21_CR2a_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.965	109.204	0.5	Vietnam	marine biome [ENVO:00000447]
22_CR2b_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.965	109.204	0.5	Vietnam	marine biome [ENVO:00000447]
23_CR3a_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.969	109.203	0.5	Vietnam	marine biome [ENVO:00000447]
24_CR3b_Kalva	1300146	Kappaphycus alvar	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	11.969	109.203	0.5	Vietnam	marine biome [ENVO:00000447]
43_VP1a_SPM	408172	Suspended_particul	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.652	109.333	0.3	Vietnam	marine biome [ENVO:00000447]
44_VP1b_SPM	408172	Suspended_particul	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.652	109.333	0.3	Vietnam	marine biome [ENVO:00000447]
45_VP2a_SPM	408172	Suspended_particul	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.658	109.351	0.3	Vietnam	marine biome [ENVO:00000447]
46_VP2b_SPM	408172	Suspended_particul	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.658	109.351	0.3	Vietnam	marine biome [ENVO:00000447]
47_VP3a_SPM	408172	Suspended_particul	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.655	109.346	0.3	Vietnam	marine biome [ENVO:00000447]
48_VP3b_SPM	408172	Suspended_particul	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.655	109.346	0.3	Vietnam	marine biome [ENVO:00000447]
49_VP4a_SPM	408172	Suspended_particul	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.652	109.34	0.3	Vietnam	marine biome [ENVO:00000447]
50_VP4b_SPM	408172	Suspended_particul	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.652	109.34	0.3	Vietnam	marine biome [ENVO:00000447]
51_VP5a_SPM	408172	Suspended_particul	Illumina MiSeq	AMPLICON	GENOMIC	PCR	paired	#	341F	341F	MD5		mimarks-survey	water	27/05/2017	12.657	109.333	0.3	Vietnam	marine biome [ENVO:00000447]

Example available in the GFBio Helpdesk (submission ID: DSUB-348)



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