



BLUEPRINT proposed data submission schemas

Draft v0.3.0.1

*(model SHA1 fc5784608f407a120787f6fc5efdd3ee7d82b8e9)
(schema model SHA1 513101aab46ea8490646f1a8706491d7811aa43)
(external controlled vocabulary SHA1 f3d12b04843388c067cd70fe67aaa2bdcd286a05)*

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January 20, 2014

(Contents of this page should not going to be printed)

This PDF contains a file attachment named 'BLUEPRINT-data_model-0.3.0.1-20140120.bpmmodel', which is the version 0.3.0.1 of BLUEPRINT DCC data model.

*(model SHA1 fc5784608f407a120787f6fc5efdd3ee7d82b8e9)
(schema model SHA1 513101aabe46ea8490646f1a8706491d7811aa43)
(external controlled vocabulary SHA1 f3d12b04843388c067cd70fe67aaa2bdcd286a05)*

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Chapter 1

Data Submission

1.1 Overview of Data Submission Process

There are four major steps in the data submission process:

1. Submit raw sequence data to the European Genome-phenome Archive
2. Prepare the BLUEPRINT submission files according to DCC data format specifications
3. Verify conformity of the submission files
4. Submit files to the DCC Secure FTP server

All submitted data must be based on **Human reference genome assembly GRCh37** and **GENCODE 15** (which uses **EnsEMBL gene set version 70**)

When submitting experimental data, please make sure you've already deposited your raw data to the appropriate public data repositories (eg: sequencing reads to EBI EGA) and then populate in your submission files the data elements **raw_data_repository** and **raw_data_accession** with the correct repository and accession number respectively.

1.2 Preparing Sample Tracking Data and Analyzed Contents for their submission

Submitted experimental data files must be from any one of these categories:

- [Sample Tracking](#)
- [Gene Expression](#)
- [Exon Junctions](#)
- [DNA *-lation \(Methylation, Hydroxy-Methylation, Formylation, etc...\)](#)
- [Protein-DNA interactions](#)
- [Regulatory regions](#)

BLUEPRINT DCC is hosting both sample tracking data and analyzed contents. Contents must be sent following the textual tabular formats defined below. Files with those contents must also follow the BLUEPRINT DCC file naming convention.

Each submitter must have a unique signing key, provided by DACO and DCC. Each file in a submitted archive must be accompanied by its SHA1 **uncompressed** content digest file, digitally signed with the submitter's signing key.

Signed digest generation and verification using OpenSSL

```
# Signed digest of uncompressed contents, will be dlat-p--001-20120920--mycode.txt.sha1
openssl dgst -sha1 -sign subKey.pem -out dlat-p--001-20120920--mycode.txt.sha1 \
dlat-p--001-20120920--mycode.txt

# Signed digest of already compressed contents
bunzip2 -c dlat-p--001-20120920--mycode.txt.bz2 | openssl dgst -sha1 -sign subKey.pem \
-out dlat-p--001-20120920--mycode.txt.sha1

# Verification of uncompressed contents using
# signed digest dlat-p--001-20120920--mycode.txt.sha1
openssl dgst -sha1 -verify subKey.pem.pub -signature dlat-p--001-20120920--mycode.txt.sha1 \
dlat-p--001-20120920--mycode.txt

# Verification of compressed contents
bunzip2 -c dlat-p--001-20120920--mycode.txt.bz2 | openssl dgst -sha1 -verify subKey.pem.pub \
-signature dlat-p--001-20120920--mycode.txt.sha1
```

The procedure to submit analyzed contents to BLUEPRINT DCC also involves first having the raw data used for the analysis in the [European Genome-phenome Archive \(EGA\)](#), as all the metadata entries from the analyzed contents to be stored in BLUEPRINT DCC **must point** to the original raw data.

1.2.1 File Naming Conventions

Submitted files, containing either sample tracking data or analyzed experiment contents, must follow next file naming convention

```
featureType-fileType--institutionCode-dateFileCreated--freeField.txt
```

```
featureType-fileType--institutionCode-dateFileCreated--freeField.txt.sha1
```

The file name components are mapped in the next way:

Components	Description	Key
<i>featureType</i>	Sample Tracking data Gene Expression Exon Junctions DNA *-lation (Methylation, Hydroxy-Methylation, Formylation, etc...) Protein-DNA interactions Regulatory regions	sdata exp jcn dlat pdna rreg
<i>fileType</i>	Metadata file Primary data file Secondary data file Gene expression file Donor file Specimen file Sample file Donor's Family file	m p s g donor specimen sample family
<i>institutionCode</i>	Institution submitting data	CV Table A.5.1
<i>dateFileCreated</i>	The date on which the file is created	YYYYMMDD (ISO-8601)
<i>freeField</i>	An alphanumeric field (max length of 16 characters) where submitters can put internal codes, file sequence numbers, etc...	e.g.: mysample, 0B1845

Different file types of the same feature type are interrelated, because the data they are storing is intertwined. Specific relations are defined on the documentation of each feature type and their file types. For instance, information stored in a primary data file is related and depends on the data from its corresponding metadata file, and the same happens to secondary data files and primary data files. Metadata file contents are related to sample tracking data sample files.

1.2.2 Tabular File Structure

The submitted analyzed contents are kept in tab-delimited text files. General comments may be added to the beginning of the file with a hash ('#') prefixed at beginning of each comment line. The first non-comment line is the header containing the names of the columns. Each column corresponds to a data element defined in DCC Submission Tabular Formats specification ([Chapter 2](#)).

There is a subset of comment lines used to attach data labels to the text files. These data labels follow the form '##labelName value [value ...]'. Currently acknowledged data labels are:

- **format:** This label is **required**, and its value defines the BLUEPRINT data formatting schema used on the file.
- **depends:** Although this label is not always required, it is important to validate the data coherence of the whole data set, because it ensures related data is not corrupted. The values of this label are the file on the same submission this file is related to (for instance, the name of a metadata file), and the SHA1 digest value (in its hexadecimal representation) of that file's contents.

There are several ways to generate the SHA1 digest of a file, like libraries in most of the programming languages and command-line tools:

SHA1 digest generation

```
# Getting the SHA1 digest value of uncompressed contents using OpenSSL
openssl dgst -sha1 dlat-p--001-20120920--mycode.txt

SHA1(dlat-p--001-20120920--mycode.txt)= 81ae49a7014d2d0260625d3535fa6e2a4a0bc06f

# Getting the SHA1 digest value of uncompressed contents using sha1sum
sha1sum dlat-p--001-20120920--mycode.txt

81ae49a7014d2d0260625d3535fa6e2a4a0bc06f  dlat-p--001-20120920--mycode.txt
```

An example file is shown below (note that parts of the lines are omitted for readability):

```
dlat-p--001-20120920--mycode.txt
# This is an example of a primary analysis file for simple somatic mutations.
# File name: dlat-p--001-20120920--mycode.txt
#
# And it has its labels
##format 0.3.0.1
##depends dlat-m--001-20120920--mycode.txt 03366af5145107cc818f4827e86b61dcf998ff29
analysis_id  ↗analyzed_sample_id  ↗d_lated_fragment_id  ↗chromosome  ↗...  ↗note
an:001:000124  ↗sample:001:000035  ↗dlat:001:1234ff33  ↗1  ↗...  ↗#FF#
an:001:000124  ↗sample:001:000035  ↗dlat:001:00019878  ↗1  ↗...  ↗#FF#
an:001:000124  ↗sample:001:000092  ↗dlat:001:a712838  ↗21  ↗...  ↗#FF#
an:001:000124  ↗sample:001:000092  ↗dlat:001:abebdZZZZZ  ↗4  ↗...  ↗#FF#
```

All the declared columns for each file type must be set. Data columns are labeled as identifier or reference (**I**), required (**R**), desirable (**D**) or optional (**O**). Data providers (i.e. submitters) must put all the efforts in order to provide values for the idref and required data columns. The exception for this rule are the desirable fields, required fields which can be unknown on the first submissions, but in that case the fields these exceptions are properly documented.

There are several possible reasons why a column value (either desirable or optional) has not been provided. Next reserved codes must be used to describe the reason:

Code	Meaning
#FFF#	Data not supplied at this time (<i>for future fill</i>)
#NAA#	Not applicable for the context of the surrounding knowledge
#VO#	Data verified to be unknown (void, undef, null)
#DEF#	Data derived from a required or idref field

Some data columns described in this submission manual contain values used as identifiers on BLUEPRINT DCC (e.g. `analysis_id`, `regulatory_region_id`, ...). As such, these identifiers should uniquely identify the entity they are referring (an analysis, a regulatory region, ...), and the identifier's value should be globally unique within a center's data submission. Also, these identifiers should be consistent along the different data submissions and releases. If you have to generate your own identifiers, there are some general recommendations, like using the same prefix for the identifiers of the same kind.

When you are submitting string values for columns which can contain URLs or multiple values delimited by commas, each separate value string, before being joined, should be [URI encoded](#).

1.3 File Submission Procedure

Files with the contents to be submitted, along with their corresponding signed digest, must be sent in a single [tar](#) archive. Either the tar archive or its embedded contents should be submitted compressed, using [gzip](#), [bzip2](#) or [xz](#) formats.

To be finished/defined

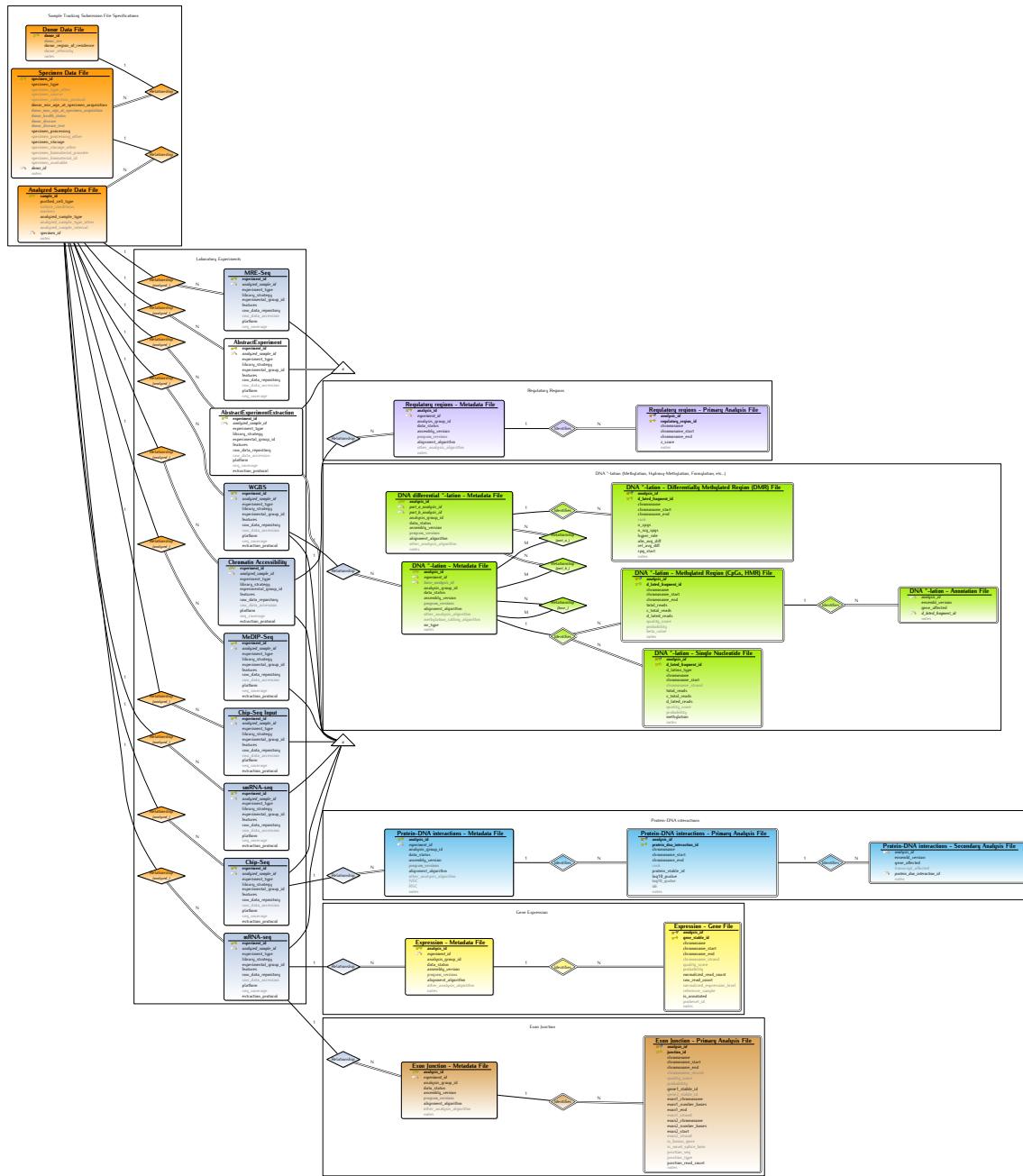


Figure 1.1: Overview of BLUEPRINT 0.3.0.1 data model

Chapter 2

DCC Submission Tabular Formats

2.1 Sample Tracking Submission File Specifications

Overview

There are three **required** sample and tissue annotation submission files, and one **optional** template file.

Core Sample Tracking Data Files

1. *Donor Data File (donor)*

Mandatory information about the donor's age, gender and vital status.

2. *Specimen Data File (specimen)*

Mandatory information about a specimen that was obtained from a donor. There may be several specimens per donor that were obtained concurrently or at different times.

3. *Analyzed Sample Data File (sample)*

Mandatory information about an analyzed sample that was subjected to molecular analysis. There may be several analyzed samples per specimen, for example, blood samples at different ages.

All data submissions to the DCC **must include the three core sample tracking data files**.

Optional Template Files

1. *Donor Family History (family)*

Optional details about family history of the donor

Coding of donor IDs

The three mandatory data files contain donor, specimen and analyzed sample IDs, respectively. These IDs are to be coded specifically for BLUEPRINT purposes and only the submitting group will keep the key that will permit to link back the data to the individual donors. The key must not be communicated to the data users. It should not be derived from other IDs such as biobank or hospital identifiers. These IDs are to be coded in such a way that they cannot be tracked back to the individual donors, except by the submitting group. IDs are assigned by each submitting group, and must be unique within all the data submitted by that group (i.e. no duplicate IDs allowed). The DCC will prevent collisions between similar IDs submitted by different groups by including the project source column by default in all BioMart queries.

Mapping with IHEC metadata As BLUEPRINT is integrated into IHEC ([International Human Epigenome Consortium](#)), many of the fields from the sample related concepts have been mapped to IHEC metadata fields. The fields which have not been (yet) mapped from Level 0 SAMPLES Data are:

- MOLECULE

- BIOMATERIAL_TYPE

The fields from Level 0 Data which are not going to be mapped, because they are not applicable to BLUEPRINT (project is not working with cellular lines) are:

- LINE

- LINEAGE
- DIFFERENTIATION_STAGE
- DIFFERENTIATION_METHOD
- PASSAGE and PASSAGE_IF_EXPANDED
- MEDIUM
- BATCH

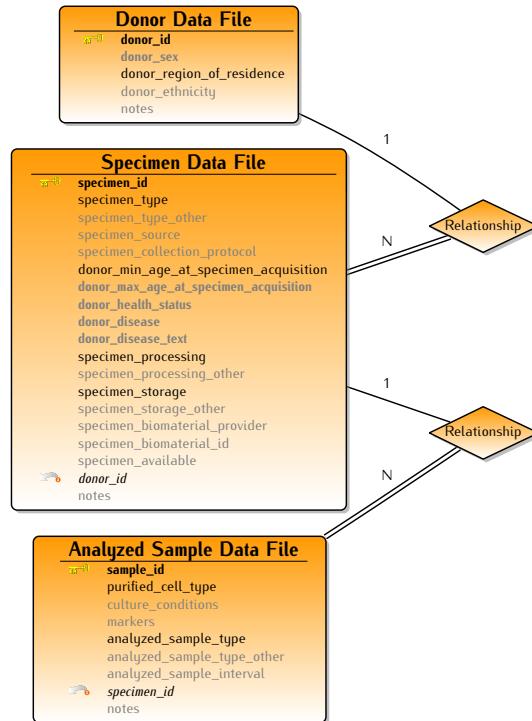


Figure 2.1: Sample Tracking Submission File Specifications Sub-Schema

2.1.1 Donor Data File

Donor Data File [donor] (required)

This submission file describes a donor from which one or more specimens were obtained.

Table 2.1.1: Donor Data File

Name	Type	Need	Description / Values
<code>donor_id</code>	<code>string</code>	I	<i>Unique identifier for the donor; assigned by data provider.</i> <i>It corresponds with IHEC Level 0 DONOR_ID (Primary Cell, Primary Cell Culture & Primary Tissue)</i>
<code>donor_sex</code>	<code>string</code>	D	Donor biological sex. <i>It corresponds with IHEC Level 0 SEX (Cell Line) and DONOR_SEX (Primary Cell, Primary Cell Culture & Primary Tissue)</i> $m \mapsto$ male $f \mapsto$ female

Continued on next page

Table 2.1.1 – continued from previous page

Name	Type	Need	Description / Values
donor_region_of_residence	string[] (array seps ,)	R	Country, and optionally state or province code, but not city. <i>ISO3166-1-alpha-2 or ISO3166-2 codes, eg: "CA" or "CA-ON" (See external CV description A.4)</i>
donor_ethnicity	string	0	Donor ethnicity, from LOINC (subset ethnicity) <i>It corresponds with IHEC Level 0 DONOR_ETHNICITY (Primary Cell, Primary Cell Culture & Primary Tissue)</i>
notes	text	0	Any additional non-identifying information can be included here.

2.1.2 Specimen Data File

Specimen Data File [specimen] (required)

This submission file describes a specimen from which one or more samples were derived. Use additional rows for more than one specimen from the same patient. If more than one specimen was extracted during the same procedure, each gets a distinct ID.

Table 2.1.2: Specimen Data File

Name	Type	Need	Description / Values
specimen_id	string	I	Unique identifier for the specimen assigned by data provider.
specimen_type	string	R	Controlled vocabulary description of specimen type. <i>It more or less corresponds to IHEC Level 0 TISSUE_TYPE (Primary Tissue)</i> 1 ↳ primary tumour 2 ↳ tumour local recurrence 3 ↳ tumour metastasis to local lymph node 4 ↳ tumour metastasis to distant location per_blood ↳ peripheral blood 6 ↳ bone marrow 7 ↳ lymph node c_tissue ↳ normal control (tissue adjacent to primary) c_blood ↳ normal control (blood) c_other ↳ normal control (other) d_tissue ↳ disease tissue (other) cord_blood ↳ cord blood
specimen_type_other	string	0	Free text description of site of specimen if "normal control (other)" or "disease tissue (other)" was specified in specimen_type field. <i>It more or less corresponds to IHEC Level 0 TISSUE_TYPE (Primary Tissue)</i>
specimen_source	string	0	Details about the anatomical location from which the specimen was collected <i>It more or less corresponds to IHEC Level 0 TISSUE_DEPOT (Primary Tissue)</i>
specimen_collection_protocol	text	0	The protocol followed to collect the specimen <i>It more or less corresponds to IHEC Level 0 COLLECTION_METHOD (Primary Tissue)</i>

Continued on next page

Table 2.1.2 – continued from previous page

Name	Type	Need	Description / Values
donor_min_age_at_specimen_acquisition	duration	R	Donor minimal age when the specimen was acquired, in ISO-8601 duration (basic format) <i>It corresponds with IHEC Level 0 DONOR_AGE (Primary Cell, Primary Cell Culture & Primary Tissue), which contains the minimal age</i>
donor_max_age_at_specimen_acquisition	duration	D	Donor max age when the specimen was acquired. If it is set to #DE#, the default value for this column is from donor_min_age_at_specimen_acquisition <i>It corresponds with IHEC Level 0 DONOR_AGE (Primary Cell, Primary Cell Culture & Primary Tissue), which contains the maximal age</i>
donor_health_status	boolean	D	The donor health status at specimen acquisition (when available) <i>It corresponds with IHEC Level 0 DONOR_HEALTH_STATUS (Primary Cell, Primary Cell Culture & Primary Tissue)</i>
donor_disease	string	D	If the donor was ill, the EFO code (browsable here) or SNOMED-CT code (from Disease branch) of the disease at acquisition time. Use code EFO_0000761 when the donor was healthy <i>This value can come from EGA Phenotype field. When this field and donor_disease_text are set, the description of the term in this field should be used</i>
donor_disease_text	string	D	If the donor was ill, the disease name at acquisition time. <i>It corresponds to IHEC Level 0 DISEASE (Cell Line, Primary Cell, Primary Cell Culture & Primary Tissue). When it is possible, use donor_disease field</i>
specimen_processing	string	R	Description of technique used to process specimen 1 ↳ cryopreservation in liquid nitrogen (dead tissue) 2 ↳ cryopreservation in dry ice (dead tissue) 3 ↳ cryopreservation of live cells in liquid nitrogen 4 ↳ cryopreservation, other 5 ↳ formalin fixed, unbuffered 6 ↳ formalin fixed, buffered 7 ↳ formalin fixed & paraffin embedded 8 ↳ fresh 9 ↳ other technique
specimen_processing_other	string	O	If "other" specified for specimen_processing, may indicate technique here.
specimen_storage	string	R	Description of how specimen was stored. For specimens that were extracted freshly or immediately cultured, answer (1) "NA". 1 ↳ frozen, liquid nitrogen 2 ↳ frozen, -70 freezer 3 ↳ frozen, vapor phase 4 ↳ RNA later frozen 5 ↳ paraffin block 6 ↳ cut slide 7 ↳ other

Continued on next page

Table 2.1.2 – continued from previous page

Name	Type	Need	Description / Values
specimen_storage_other	string	0	If "other" specified for specimen_storage, may indicate technique here.
specimen_biomaterial_provider	string	0	If the specimen was obtained from a biobank, provide the biobank name here <i>It corresponds with IHEC Level 0 BIOMATERIAL_PROVIDER (Cell Line, Primary Cell, Primary Cell Culture & Primary Tissue)</i>
specimen_biomaterial_id	string	0	If the specimen was obtained from a biobank, provide the biobank accession number here.
specimen_available	boolean	0	Whether additional tissue is available for followup studies.
donor_id	string	R	<i>Unique identifier</i> for the donor; assigned by data provider. Relates to Donor Data File (donor_id) <i>It corresponds with IHEC Level 0 DONOR_ID (Primary Cell, Primary Cell Culture & Primary Tissue)</i>
notes	text	0	Any additional non-identifying information can be included here.

2.1.3 Analyzed Sample Data File

Analyzed Sample Data File [sample] (required)

This submission file describes an analyzed sample on which molecular characterization was performed. It includes both control samples (from healthy people) and samples from ill people.

Table 2.1.3: Analyzed Sample Data File

Name	Type	Need	Description / Values
sample_id	string	I	<i>Unique identifier</i> for the sample assigned by data provider
purified_cell_type	string	R	Purified cell type for the sample <i>It corresponds more or less with IHEC Level 0 CELL_TYPE (Primary Cell & Primary Cell Culture) (See external CV description A.3)</i>
culture_conditions	string	0	The conditions under which the primary cell was cultured <i>It corresponds with IHEC Level 0 CULTURE_CONDITIONS (Primary Cell Culture)</i>
markers	string	0	Markers used to isolate and identify the cell type <i>It corresponds with IHEC Level 0 MARKERS (Primary Cell & Primary Cell Culture)</i>

Continued on next page

Table 2.1.3 – continued from previous page

Name	Type	Need	Description / Values
analyzed_sample_type	string	R	Controlled vocabulary description of sample type n_blood ↪ Normal blood l_blood ↪ Leukemic blood 3 ↪ Normal control adjacent to primary 4 ↪ Normal control from non-tumour site 5 ↪ Control from cell line derived from normal tissue 6 ↪ Normal mouse host 7 ↪ Primary tumour 8 ↪ Mouse xenograft derived from tumour 9 ↪ Cell line derived from tumour 10 ↪ Cell line derived from xenograft 11 ↪ Other (specify)
analyzed_sample_type_other	string	O	Free text description of site of sample if "other" was specified in <i>analyzed_sample_type</i> field
analyzed_sample_interval	integer	O	Interval from specimen acquisition to sample use in an analytic procedure (e.g. DNA extraction), in days
specimen_id	string	R	Unique identifier for the specimen assigned by data provider. Relates to <i>Specimen Data File (specimen_id)</i>
notes	text	O	Any additional non-identifying information can be included here.

2.2 Laboratory Experiments

These concepts are based on Version 1.1 of IHEC Metadata (July 3rd, 2013)

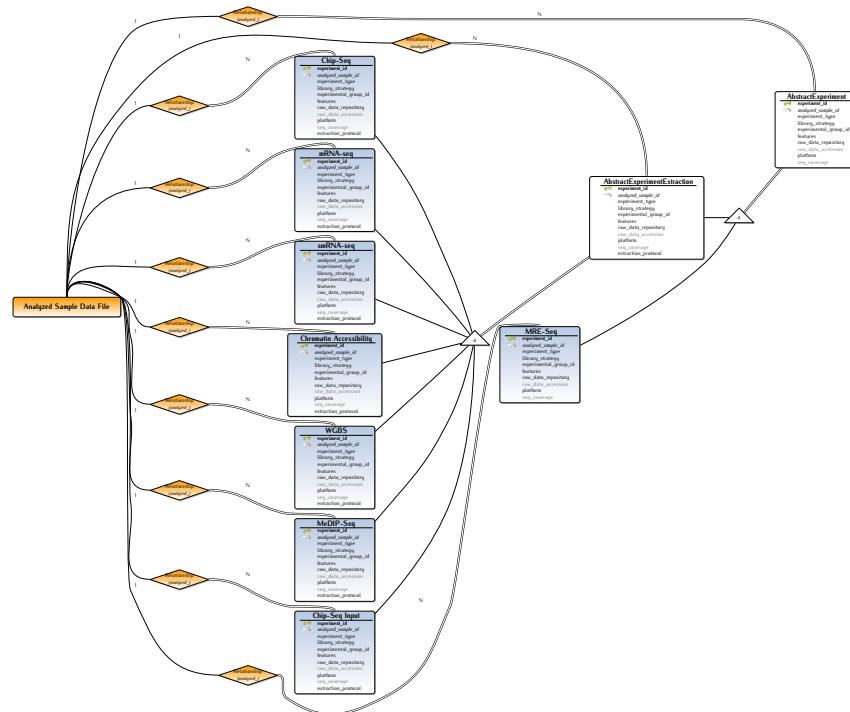


Figure 2.2: Laboratory Experiments Sub-Schema

2.2.1 AbstractExperiment

Table 2.2.1: AbstractExperiment

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> Relates to Analyzed Sample Data File (sample_id)
experiment_type	string	R	The type of experiment, from the point of view of IHEC (it is later subclassified) <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (Chromatin Accessibility, WGBS, MeDIP-Seq, MRE-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq)</i>
library_strategy	string	R	The type of experiment, from the point of view of EGA/SRA (it is later subclassified) <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata (See CV A.17)</i>
experimental_group_id	string	R	Identifier of the experimental group who did the experiment (See CV A.5)
features	compound[] <i>feature=value*units (array seps ;)</i>	R	The known features/experimental conditions about the experiment
raw_data_repository	integer	R	Public repository where raw data is submitted (#) (See CV A.9)
raw_data_accession	compound <i>accession;url</i>	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase (See CV A.6)
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms

2.2.2 AbstractExperimentExtraction

This concept extends [AbstractExperiment](#)

Table 2.2.2: AbstractExperimentExtraction

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> Relates to Analyzed Sample Data File (sample_id)
experiment_type	string	R	The type of experiment, from the point of view of IHEC (it is later subclassified) <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (Chromatin Accessibility, WGBS, MeDIP-Seq, MRE-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq)</i>

Continued on next page

Table 2.2.2 – continued from previous page

Name	Type	Need	Description / Values
library_strategy	string	R	The type of experiment, from the point of view of EGA/SRA (it is later subclassified) <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata (See CV A.17)</i>
experimental_group_id	string	R	Identifier of the experimental group who did the experiment <i>(See CV A.5)</i>
features	compound[] feature=value*units (array seps ;)	R	The known features/experimental conditions about the experiment
raw_data_repository	integer	R	Public repository where raw data is submitted (#) <i>(See CV A.9)</i>
raw_data_accession	compound accession;url	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase <i>(See CV A.6)</i>
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms
extraction_protocol	text	R	The protocol used to isolate the extracted material <i>It corresponds with IHEC Level 0 EXTRACTION_PROTOCOL (Chromatin Accessibility, WGBS, MeDIP-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq)</i>

2.2.3 Chromatin Accessibility

This concept extends [AbstractExperimentExtraction](#)

Table 2.2.3: Chromatin Accessibility

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> <i>Relates to Analyzed Sample Data File (sample_id)</i>
experiment_type	string	R	Type of experiment: Chromatin Accessibility <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (Chromatin Accessibility)</i>
library_strategy	string	R	The library strategy, from the point of view of EGA/SRA <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata</i>
experimental_group_id	string	R	Identifier of the experimental group who did the experiment <i>(See CV A.5)</i>

Continued on next page

Table 2.2.3 – continued from previous page

Name	Type	Need	Description / Values
features	compound[] <i>feature=value*units (array seps ;)</i>	R	The known features/experimental conditions about the Chromatin Accessibility experiment feature <i>DNASE_PROTOCOL</i> ↪ Protocol used for DNase treatment
raw_data_repository	integer	R	Public repository where raw data is submitted (#) (See CV A.9)
raw_data_accession	compound <i>accession;url</i>	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase (See CV A.6)
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms
extraction_protocol	text	R	The protocol used to isolate the extracted material <i>It corresponds with IHEC Level 0</i> EXTRACTION_PROTOCOL (<i>Chromatin Accessibility, WGBS, MeDIP-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq</i>)

2.2.4 WGBS

This concept extends [AbstractExperimentExtraction](#)

Table 2.2.4: WGBS

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> Relates to Analyzed Sample Data File (sample_id)
experiment_type	string	R	Type of experiment: DNA Methylation <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (WGBS)</i>
library_strategy	string	R	The library strategy, from the point of view of EGA/SRA <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata</i>
experimental_group_id	string	R	Identifier of the experimental group who did the experiment (See CV A.5)
features	compound[] <i>feature=value*units (array seps ;)</i>	R	The known features/experimental conditions about the WGBS experiment feature ↪ (See CV A.10)
raw_data_repository	integer	R	Public repository where raw data is submitted (#) (See CV A.9)
raw_data_accession	compound <i>accession;url</i>	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase (See CV A.6)

Continued on next page

Table 2.2.4 – continued from previous page

Name	Type	Need	Description / Values
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms
extraction_protocol	text	R	The protocol used to isolate the extracted material <i>It corresponds with IHEC Level 0</i> EXTRACTION_PROTOCOL (<i>Chromatin Accessibility, WGBS, MeDIP-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq</i>)

2.2.5 MeDIP-Seq

This concept extends AbstractExperimentExtraction

Table 2.2.5: MeDIP-Seq

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> Relates to Analyzed Sample Data File (sample_id)
experiment_type	string	R	Type of experiment: DNA Methylation <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (MeDIP-Seq)</i>
library_strategy	string	R	The library strategy, from the point of view of EGA/SRA <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata</i>
experimental_group_id	string	R	Identifier of the experimental group who did the experiment (See CV A.5)
features	compound[] <i>feature=value*units</i> (array seps ;)	R	The known features/experimental conditions about the MeDIP-Seq experiment feature → (See CV A.11)
raw_data_repository	integer	R	Public repository where raw data is submitted (#) (See CV A.9)
raw_data_accession	compound <i>accession;url</i>	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase (See CV A.6)
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms
extraction_protocol	text	R	The protocol used to isolate the extracted material <i>It corresponds with IHEC Level 0</i> EXTRACTION_PROTOCOL (<i>Chromatin Accessibility, WGBS, MeDIP-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq</i>)

2.2.6 MRE-Seq

This concept extends AbstractExperiment

Table 2.2.6: MRE-Seq

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> Relates to Analyzed Sample Data File (sample_id)
experiment_type	string	R	Type of experiment: DNA Methylation <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (MRE-Seq)</i>
library_strategy	string	R	The library strategy, from the point of view of EGA/SRA <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata</i>
experimental_group_id	string	R	Identifier of the experimental group who did the experiment (See CV A.5)
features	compound[] <i>feature=value*units</i> (array sep ;)	R	The known features/experimental conditions about the MRE-Seq experiment feature ↔ (See CV A.12)
raw_data_repository	integer	R	Public repository where raw data is submitted (#) (See CV A.9)
raw_data_accession	compound <i>accession;url</i>	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase (See CV A.6)
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms

2.2.7 Chip-Seq Input

This concept extends [AbstractExperimentExtraction](#)

Table 2.2.7: Chip-Seq Input

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> Relates to Analyzed Sample Data File (sample_id)
experiment_type	string	R	Type of experiment: ChIP-Seq Input <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (Chip-Seq Input)</i>
library_strategy	string	R	The library strategy, from the point of view of EGA/SRA <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata</i>

Continued on next page

Table 2.2.7 – continued from previous page

Name	Type	Need	Description / Values
experimental_group_id	string	R	Identifier of the experimental group who did the experiment (See CV A.5)
features	compound[] <i>feature=value*units</i> (array seps ;)	R	The known features/experimental conditions about the Chip-Seq Input experiment feature → (See CV A.13)
raw_data_repository	integer	R	Public repository where raw data is submitted (#) (See CV A.9)
raw_data_accession	compound <i>accession;url</i>	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase (See CV A.6)
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms
extraction_protocol	text	R	The protocol used to isolate the extracted material <i>It corresponds with IHEC Level 0 EXTRACTION_PROTOCOL (Chromatin Accessibility, WGBS, MeDIP-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq)</i>

2.2.8 Chip-Seq

This concept extends [AbstractExperimentExtraction](#)

Table 2.2.8: Chip-Seq

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> Relates to Analyzed Sample Data File (sample_id)
experiment_type	string	R	Type of experiment: 'Histone H3K4me1','Histone H3K4me3','Histone H3K9me3','Histone H3K9ac','Histone H3K27me3', 'Histone H3K36me3', etc... <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (Chip-Seq)</i>
library_strategy	string	R	The library strategy, from the point of view of EGA/SRA <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata</i>
experimental_group_id	string	R	Identifier of the experimental group who did the experiment (See CV A.5)
features	compound[] <i>feature=value*units</i> (array seps ;)	R	The known features/experimental conditions about the Chip-Seq experiment feature → (See CV A.14)
raw_data_repository	integer	R	Public repository where raw data is submitted (#) (See CV A.9)

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Table 2.2.8 – continued from previous page

Name	Type	Need	Description / Values
raw_data_accession	compound accession;url	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase (<i>See CV A.6</i>)
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms
extraction_protocol	text	R	The protocol used to isolate the extracted material <i>It corresponds with IHEC Level 0 EXTRACTION_PROTOCOL (Chromatin Accessibility, WGBS, MeDIP-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq)</i>

2.2.9 mRNA-seq

This concept extends [AbstractExperimentExtraction](#)

Table 2.2.9: mRNA-seq

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> Relates to Analyzed Sample Data File (sample_id)
experiment_type	string	R	Type of experiment: mRNA-seq <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (mRNA-seq)</i>
library_strategy	string	R	The library strategy, from the point of view of EGA/SRA <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata</i>
experimental_group_id	string	R	Identifier of the experimental group who did the experiment (<i>See CV A.5</i>)
features	compound[] feature=value*units (array sep ;)	R	The known features/experimental conditions about the mRNA-seq experiment feature → (<i>See CV A.15</i>)
raw_data_repository	integer	R	Public repository where raw data is submitted (#) (<i>See CV A.9</i>)
raw_data_accession	compound accession;url	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase (<i>See CV A.6</i>)
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms
extraction_protocol	text	R	The protocol used to isolate the extracted material <i>It corresponds with IHEC Level 0 EXTRACTION_PROTOCOL (Chromatin Accessibility, WGBS, MeDIP-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq)</i>

2.2.10 smRNA-seq

This concept extends [AbstractExperimentExtraction](#)

Table 2.2.10: smRNA-seq

Name	Type	Need	Description / Values
experiment_id	string	I	Unique identifier for the experiment performed on a sample
analyzed_sample_id	string	R	<i>Unique identifier for the sample assigned by data provider</i> Relates to Analyzed Sample Data File (sample_id)
experiment_type	string	R	Type of experiment: smRNA-seq <i>It corresponds with IHEC Level 0 EXPERIMENT_TYPE (smRNA-Seq)</i>
library_strategy	string	R	The library strategy, from the point of view of EGA/SRA <i>It corresponds with /EXPERIMENT_SET/EXPERIMENT/DESIGN/LIBRARY_DESCRIPTOR/LIBRARY_STRATEGY , from EGA/SRA 1.2 metadata</i>
experimental_group_id	string	R	Identifier of the experimental group who did the experiment (See CV A.5)
features	compound[] <i>feature=value*units</i> (array seps ;)	R	The known features/experimental conditions about the smRNA-seq experiment feature → (See CV A.16)
raw_data_repository	integer	R	Public repository where raw data is submitted (#) (See CV A.9)
raw_data_accession	compound <i>accession;url</i>	O	Accession and URL for referencing the raw data at the public repository
platform	integer	R	Platform or technology used in the detection phase (See CV A.6)
seq_coverage	decimal	O	Sequence coverage if analyzed by sequencing platforms
extraction_protocol	text	R	The protocol used to isolate the extracted material <i>It corresponds with IHEC Level 0 EXTRACTION_PROTOCOL (Chromatin Accessibility, WGBS, MeDIP-Seq, Chip-Seq Input, Chip-Seq, mRNA-seq, smRNA-Seq)</i>

2.3 Gene Expression

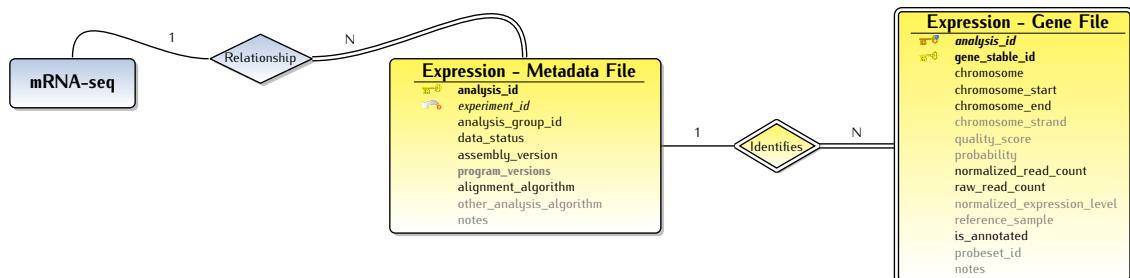


Figure 2.3: Gene Expression Sub-Schema

2.3.1 Expression – Metadata File

Expression [exp] – Metadata File [m]

Table 2.3.1: Expression – Metadata File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples
experiment_id	string	R	Unique identifier for the experiment performed on a sample Relates to mRNA-seq (experiment_id)
analysis_group_id	string	R	Identifier of the analysis group (i.e. the one who prepared/run the pipeline) (See CV A.5)
data_status	integer	R	The status of the analysis over the associated raw data -1 ↪ Withdrawn 0 ↪ Only raw data available 1 ↪ Raw data available (analysis in process) 2 ↪ Raw and analysis data available (analysis finished)
assembly_version	integer	R	Version of reference genome assembly (See CV A.8)
program_versions	compound[] program:version (array seps ;)	D	The versions of (some of) the programs used for the analysis
alignment_algorithm	compound name;url	R	Name of alignment algorithm and URL to written protocol
other_analysis_algorithm	compound[] name;url (array seps ,)	O	Names of other analysis algorithms. Separate multiple algorithms by commas.
notes	text	O	Optional field to leave notes

2.3.2 Expression – Gene File

Expression [exp] – Gene File [g]

Table 2.3.2: Expression – Gene File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples Relates to Expression – Metadata File (analysis_id)
gene_stable_id	string	I	For annotated gene, use Ensembl gene ID. Otherwise, use assemblyBuild_chr_start_end where assemblyBuild is hg19.
chromosome	string	R	Name of the chromosome containing the experimentally detected feature (mutation, variation, expression, ...) (See CV A.7)
chromosome_start	integer	R	Start position of the mutation/variation on the chromosome
chromosome_end	integer	R	End position of the mutation/variation on the chromosome

Continued on next page

Table 2.3.2 – continued from previous page

Name	Type	Need	Description / Values
chromosome_strand	integer	0	Strand where it was detected the mutation/variation on the chromosome -1 ↳ Reverse strand 1 ↳ Forward strand
quality_score	decimal	0	Average quality score for the mutation/variation call
probability	decimal	0	Probability of the mutation/variation call
normalized_read_count	decimal	R	Normalized count of sequencing reads if analyzed by sequencing platforms
raw_read_count	integer	R	Raw count of sequencing reads if analyzed by sequencing platforms
normalized_expression_level	decimal	0	Normalized value of expression level if analyzed by microarray platforms
reference_sample	string	0	ID of the reference analyzed sample if differential expression is measured
is_annotated	boolean	R	If it is true, it indicate if the expressed fragment is annotated in GENCODE/Ensembl (i.e. gene_stable_id contains a Ensembl Gene Identifier)
probeset_id	string	0	ID of the probeset used in microarray if analyzed by microarray platform
notes	text	0	Optional field to leave notes

2.4 Exon Junction

The following diagram, based on the one from ICGC DCC manual, illustrates how junction_id should be generated, how junction_read_count, exon1_number_bases and exon2_number_bases are calculated:

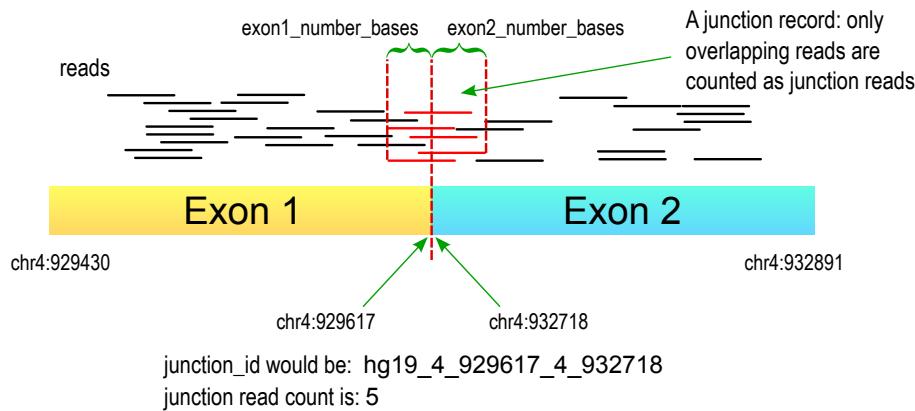


Figure 2.4: Junction Read Count explanation

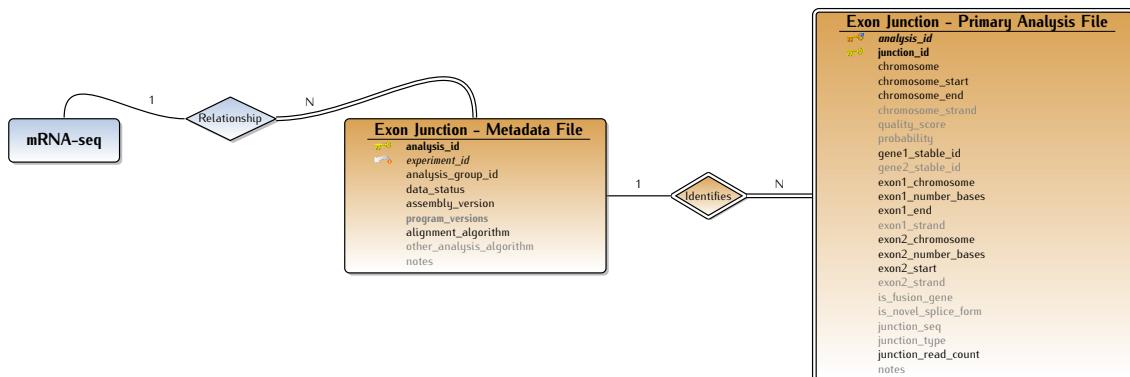


Figure 2.5: Exon Junction Sub-Schema

2.4.1 Exon Junction – Metadata File

Exon Junction [jcn] – Metadata File [m]

Table 2.4.1: Exon Junction – Metadata File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples
experiment_id	string	R	Unique identifier for the experiment performed on a sample Relates to mRNA-seq (experiment_id)
analysis_group_id	string	R	Identifier of the analysis group (i.e. the one who prepared/run the pipeline) (See CV A.5)
data_status	integer	R	The status of the analysis over the associated raw data -1 ↳ Withdrawn 0 ↳ Only raw data available 1 ↳ Raw data available (analysis in process) 2 ↳ Raw and analysis data available (analysis finished)
assembly_version	integer	R	Version of reference genome assembly (See CV A.8)
program_versions	compound[] program:version (array seps ;)	D	The versions of (some of) the programs used for the analysis
alignment_algorithm	compound name;url	R	Name of alignment algorithm and URL to written protocol
other_analysis_algorithm	compound[] name;url (array seps ,)	O	Names of other analysis algorithms. Separate multiple algorithms by commas.
notes	text	O	Optional field to leave notes

2.4.2 Exon Junction – Primary Analysis File

Exon Junction [jcn] – Primary Analysis File [p]

Table 2.4.2: Exon Junction – Primary Analysis File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples Relates to Exon Junction – Metadata File (analysis_id)
junction_id	string	I	For known exons, use exonID1_exonID2 where exonID1 and exonID2 are Ensembl IDs of the 5' and 3' exons, respectively. For novel or putative exons, use assemblyBuild_exon1chr_exon1end_exon2chr_exon2start where assemblyBuild is hg18 or hg19; exon1chr and exon2chr are the chromosomes of the 5' and 3' exons, respectively; exon1end is the end position of the 5' exon; exon2start is the start position of the 3' exon.

Continued on next page

Table 2.4.2 – continued from previous page

Name	Type	Need	Description / Values
chromosome	string	R	Name of the chromosome containing the experimentally detected feature (mutation, variation, expression, ...) <i>(See CV A.7)</i>
chromosome_start	integer	R	Start position of the mutation/variation on the chromosome
chromosome_end	integer	R	End position of the mutation/variation on the chromosome
chromosome_strand	integer	O	Strand where it was detected the mutation/variation on the chromosome -1 ↳ Reverse strand 1 ↳ Forward strand
quality_score	decimal	O	Average quality score for the mutation/variation call
probability	decimal	O	Probability of the mutation/variation call
gene1_stable_id	string	R	Stable ID of the gene containing the 5' exon at the junction. For GENCODE/Ensembl annotated gene, use Ensembl gene ID. For putative and novel gene, use assemblyBuild_chr_start_end where assemblyBuild can be hg18 or hg19.
gene2_stable_id	string	O	In the case of a fusion gene, provide the Stable ID of the gene containing the 3' exon at the junction. For GENCODE/Ensembl annotated genes, use Ensembl gene ID. For putative and novel genes, use assemblyBuild_chr_start_end where assemblyBuild can be hg18 or hg19.
exon1_chromosome	string	R	Name of the chromosome containing the 5' exon (#) <i>(See CV A.7)</i>
exon1_number_bases	integer	R	Number of bases from 5' exon
exon1_end	integer	R	End position of the 5' exon on the chromosome
exon1_strand	integer	O	Chromosome strand of the 5' exon -1 ↳ Reverse strand 1 ↳ Forward strand
exon2_chromosome	string	R	Name of the chromosome containing the 3' exon (#) <i>(See CV A.7)</i>
exon2_number_bases	integer	R	Number of bases from 3' exon
exon2_start	integer	R	Start position of the 3' exon on the chromosome
exon2_strand	integer	O	Chromosome strand of the 3' exon -1 ↳ Reverse strand 1 ↳ Forward strand
is_fusion_gene	boolean	O	Indicate if the function is the result of a fusion gene
is_novel_splice_form	boolean	O	Indicate if the splice form is novel
junction_seq	string	O	Provide junction sequence if either is_fusion_gene or is_novel_splice_form is true
junction_type	integer	O	Type of junction 1 ↳ Canonical 2 ↳ Non-canonical 3 ↳ U12
junction_read_count	integer	R	Count of sequencing reads that span across exons
notes	text	O	Optional field to leave notes

2.5 Protein-DNA interactions

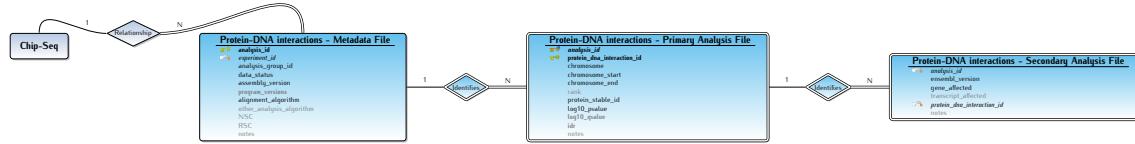


Figure 2.6: Protein-DNA interactions Sub-Schema

2.5.1 Protein-DNA interactions – Metadata File

Protein-DNA [pdna] – Metadata File [m]

Table 2.5.1: Protein-DNA interactions – Metadata File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples
experiment_id	string	R	Unique identifier for the experiment performed on a sample Relates to Chip-Seq (experiment_id)
analysis_group_id	string	R	Identifier of the analysis group (i.e. the one who prepared/run the pipeline) (See CV A.5)
data_status	integer	R	The status of the analysis over the associated raw data -1 ↪ Withdrawn 0 ↪ Only raw data available 1 ↪ Raw data available (analysis in process) 2 ↪ Raw and analysis data available (analysis finished)
assembly_version	integer	R	Version of reference genome assembly (See CV A.8)
program_versions	compound[] program:version (array seps ;)	D	The versions of (some of) the programs used for the analysis
alignment_algorithm	compound name;url	R	Name of alignment algorithm and URL to written protocol
other_analysis_algorithm	compound[] name;url (array seps ,)	O	Names of other analysis algorithms. Separate multiple algorithms by commas.
NSC	decimal	O	Normalized strand cross-correlation of the analysis (see ENCODE quality metrics)
RSC	decimal	O	Relative strand cross-correlation of the analysis (see ENCODE quality metrics)
notes	text	O	Optional field to leave notes

2.5.2 Protein-DNA interactions – Primary Analysis File

Protein-DNA [pdna] – Primary Analysis File [p]

Table 2.5.2: Protein-DNA interactions – Primary Analysis File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples Relates to Protein-DNA interactions – Metadata File (analysis_id)
protein_dna_interaction_id	string	I	Unique identifier for the protein-DNA interaction
chromosome	string	R	Name of the chromosome containing the experimentally detected feature (mutation, variation, expression, ...) (See CV A.7)
chromosome_start	integer	R	Start position of the mutation/variation on the chromosome
chromosome_end	integer	R	End position of the mutation/variation on the chromosome
rank	compound[] rank:value (array seps ;)	O	Kind of used ranking and its value, in the form "rank:value". As it can hold more than one value, they are separated by semicolons
protein_stable_id	string	R	Stable id of the interacting protein, antibody or protein complex
log10_pvalue	decimal	R	-log10(p-value)
log10_qvalue	decimal	D	-log10(q-value) , which available for peaks, but not for broad peaks
idr	decimal	D	Irreproducible discovery rate
notes	text	O	Optional field to leave notes

2.5.3 Protein-DNA interactions – Secondary Analysis File

Protein-DNA [pdna] – Secondary Analysis File [s]

Table 2.5.3: Protein-DNA interactions – Secondary Analysis File

Name	Type	Need	Description / Values
analysis_id	string	R	Unique identifier for the analysis performed for a particular set of samples Relates to Protein-DNA interactions – Primary Analysis File (analysis_id)
ensembl_version	integer	R	Version of Ensembl gene build used for annotation (or the version of Ensembl gene build integrated into used GENCODE build)
gene_affected	string[] (array seps)	R	Gene affected. Use Ensembl gene id, separated by when there is more than one. If no gene is affected, don't put an entry (See external CV description A.1)
transcript_affected	string[] (array seps)	O	Transcript on the protein-DNA interaction area. Use Ensembl transcript id. Separate multiple transcripts with vertical bars in the form of transcriptA transcriptB transcriptC (See external CV description A.2)
protein_dna_interaction_id	string	R	Unique identifier for the protein-DNA interaction Relates to Protein-DNA interactions – Primary Analysis File (protein_dna_interaction_id)
notes	text	O	Optional field to leave notes

2.6 Regulatory Regions

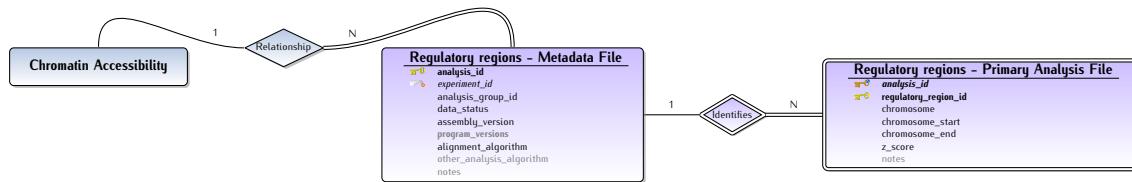


Figure 2.7: Regulatory Regions Sub-Schema

2.6.1 Regulatory regions – Metadata File

Regulatory regions [rreg] – Metadata File [m]

Table 2.6.1: Regulatory regions – Metadata File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples
experiment_id	string	R	Unique identifier for the experiment performed on a sample Relates to <i>Chromatin Accessibility (experiment_id)</i>
analysis_group_id	string	R	Identifier of the analysis group (i.e. the one who prepared/run the pipeline) (See CV A.5)
data_status	integer	R	The status of the analysis over the associated raw data -1 ↪ Withdrawn 0 ↪ Only raw data available 1 ↪ Raw data available (analysis in process) 2 ↪ Raw and analysis data available (analysis finished)
assembly_version	integer	R	Version of reference genome assembly (See CV A.8)
program_versions	compound[] program:version (array seps ;)	D	The versions of (some of) the programs used for the analysis
alignment_algorithm	compound name;url	R	Name of alignment algorithm and URL to written protocol
other_analysis_algorithm	compound[] name;url (array seps ,)	O	Names of other analysis algorithms. Separate multiple algorithms by commas.
notes	text	O	Optional field to leave notes

2.6.2 Regulatory regions – Primary Analysis File

Regulatory regions [rreg] – Primary Analysis File [p]

Table 2.6.2: Regulatory regions – Primary Analysis File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples Relates to Regulatory regions – Metadata File (analysis_id)
regulatory_region_id	string	I	Unique identifier for the identified regulatory region
chromosome	string	R	Name of the chromosome containing the experimentally detected feature (mutation, variation, expression, ...) (See CV A.7)
chromosome_start	integer	R	Start position of the mutation/variation on the chromosome
chromosome_end	integer	R	End position of the mutation/variation on the chromosome
z_score	decimal	R	Combined z-score of the 250bp window for each tag
notes	text	O	Optional field to leave notes

2.7 DNA *-lation (Methylation, Hydroxy-Methylation, Formylation, etc...)

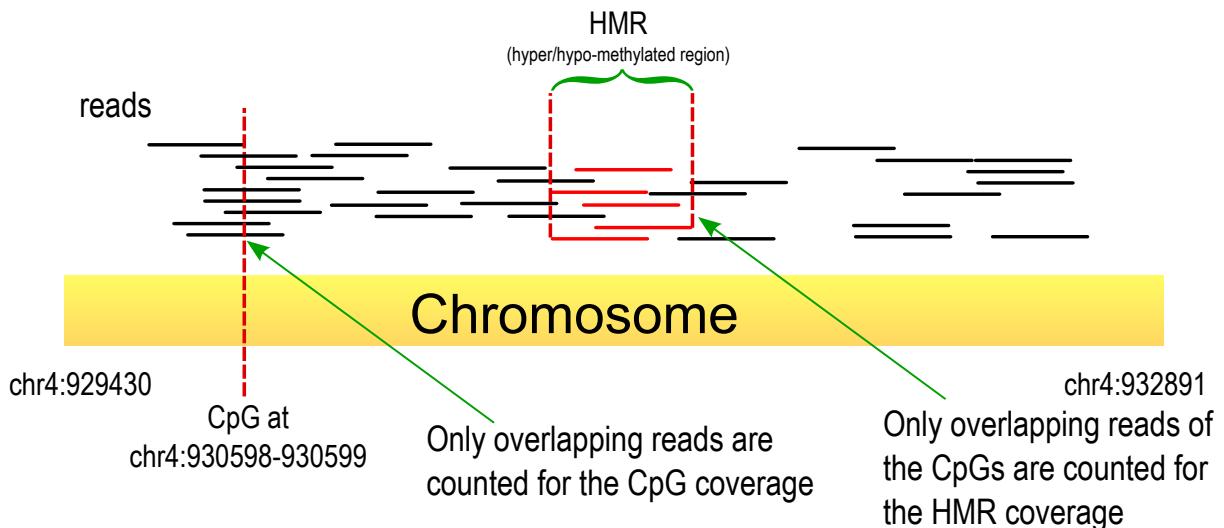


Figure 2.8: Cytosine, CpG and HMR explanation

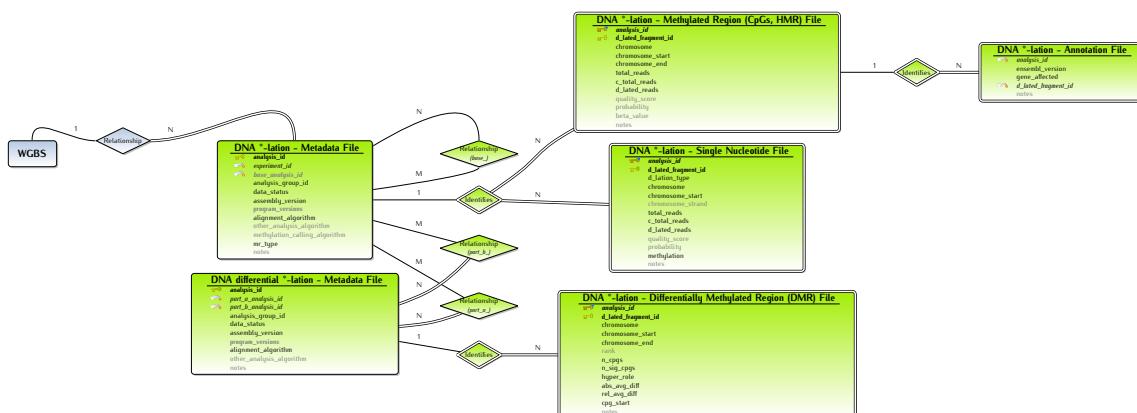


Figure 2.9: DNA *-lation (Methylation, Hydroxy-Methylation, Formylation, etc...) Sub-Schema

2.7.1 DNA *-lation – Metadata File

DNA *-lation [dlat] – Metadata File [m]

Table 2.7.1: DNA *-lation – Metadata File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples
experiment_id	string	R	Unique identifier for the experiment performed on a sample Relates to WGBS (experiment_id)
base_analysis_id	string[] (array sdeps ,)	D	Unique identifier for the analysis performed for a particular set of samples Relates to DNA *-lation – Metadata File (analysis_id)
analysis_group_id	string	R	Identifier of the analysis group (i.e. the one who prepared/run the pipeline) (See CV A.5)
data_status	integer	R	The status of the analysis over the associated raw data -1 ↪ Withdrawn 0 ↪ Only raw data available 1 ↪ Raw data available (analysis in process) 2 ↪ Raw and analysis data available (analysis finished)
assembly_version	integer	R	Version of reference genome assembly (See CV A.8)
program_versions	compound[] <i>program:version</i> (array sdeps ;)	D	The versions of (some of) the programs used for the analysis
alignment_algorithm	compound <i>name;url</i>	R	Name of alignment algorithm and URL to written protocol
other_analysis_algorithm	compound[] <i>name;url</i> (array sdeps ,)	O	Names of other analysis algorithms. Separate multiple algorithms by commas.
methylation_calling_algorithm	compound <i>name;url</i>	O	Name of variation calling algorithm and URL to written protocol
mr_type	string	R	The type of methylated region site c ↪ Single nucleotide *-lation cpg ↪ CpG dinucleotide hyper ↪ Hyper-methylated region hypo ↪ Hypo-methylated region
notes	text	O	Optional field to leave notes

2.7.2 DNA *-lation – Single Nucleotide File

DNA *-lation [dlat] – Single Nucleotide File [n]

Continued on next page

Table 2.7.2 – continued from previous page

Name	Type	Need	Description / Values
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Table 2.7.2: DNA *-lation – Single Nucleotide File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples Relates to DNA *-lation – Metadata File (analysis_id)
d_lated_fragment_id	string	I	Unique identifier for the methylated fragment, in the form d'*lationType chromosome_chromosomeStart_-chromosomeEnd
d_lation_type	string	R	Type of DNA *-lation (Methylation, Hydroxy-Methylation, Formylation, etc...) $m \mapsto$ Methylation (cytosine) $hm \mapsto$ Hydroxy-Methylation (cytosine) $hmU \mapsto$ Hydroxy-Methylation (uracil) $f \mapsto$ Formylation (cytosine) $ca \mapsto$ Carboxylation (cytosine)
chromosome	string	R	Name of the chromosome containing the experimentally detected feature (mutation, variation, expression, ...) (See CV A.7)
chromosome_start	integer	R	Start position of the mutation/variation on the chromosome
chromosome_strand	integer	O	Strand where it was detected the mutation/variation on the chromosome $-1 \mapsto$ Reverse strand $1 \mapsto$ Forward strand
total_reads	decimal	R	Total number of reads over this position/segment, either identifying or not a cytosine, for sequencing platforms. Mean reads depth for other technologies
c_total_reads	decimal	R	Reads which has identified this position as a cytosine
d_lated_reads	decimal	R	Reads which has identified this position as a DNA *lated cytosine
quality_score	decimal	O	Quality score for the DNA *-lation call
probability	decimal	O	Probability of the DNA *-lation call
methylation	decimal	R	DNA *-lation beta value (or average methylation) for interrogated site
notes	text	O	Optional field to leave notes

2.7.3 DNA *-lation – Methylated Region (CpGs, HMR) File

DNA *-lation [dlat] – Methylated Region File [mr] for CpGs and hypo/hyper-methylated regions

Table 2.7.3: DNA *-lation – Methylated Region (CpGs, HMR) File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples Relates to DNA *-lation – Metadata File (analysis_id)
d_lated_fragment_id	string	I	Unique identifier for the methylated fragment, in the form d'*lationType chromosome_chromosomeStart_-chromosomeEnd

Continued on next page

Table 2.7.3 – continued from previous page

Name	Type	Need	Description / Values
chromosome	string	R	Name of the chromosome containing the experimentally detected feature (mutation, variation, expression, ...) (See CV A.7)
chromosome_start	integer	R	Start position of the mutation/variation on the chromosome
chromosome_end	integer	R	End position of the mutation/variation on the chromosome
total_reads	decimal	R	Total number of reads over this position/segment, either identifying or not a cytosine, for sequencing platforms. Mean reads depth for other technologies
c_total_reads	decimal	R	Reads which has identified this position as a cytosine
d_lated_reads	decimal	R	Reads which has identified this position as a DNA *lated cytosine
quality_score	decimal	0	Quality score for the DNA *-lation call
probability	decimal	0	Probability of the DNA *-lation call
beta_value	decimal	0	DNA *-lation beta value (or average methylation or) for interrogated site
notes	text	0	Optional field to leave notes

2.7.4 DNA *-lation - Annotation File

DNA *-lation [dlat] - Annotation File [s]

Table 2.7.4: DNA *-lation - Annotation File

Name	Type	Need	Description / Values
analysis_id	string	R	Unique identifier for the analysis performed for a particular set of samples Relates to DNA *-lation - Methylated Region (CpGs, HMR) File (analysis_id)
ensembl_version	integer	R	Version of Ensembl gene build used for annotation (or the version of Ensembl gene build integrated into used GENCODE build)
gene_affected	string[] (array seps)	R	Gene affected. Use Ensembl gene id, separated by when there is more than one. If no gene is affected, don't put an entry (See external CV description A.1)
d_lated_fragment_id	string	R	Unique identifier for the methylated fragment, in the form d'*lationType chromosome_chromosomeStart_-chromosomeEnd Relates to DNA *-lation - Methylated Region (CpGs, HMR) File (d_lated_fragment_id)
notes	text	0	Optional field to leave notes

2.7.5 DNA differential *-lation - Metadata File

DNA differential *-lation [dlat] - Metadata File [dm]

Table 2.7.5: DNA differential *-lation – Metadata File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples
part_a_analysis_id	string[] (array sdeps ,)	R	Unique identifier for the analysis performed for a particular set of samples Relates to DNA *-lation – Metadata File (analysis_id)
part_b_analysis_id	string[] (array sdeps ,)	R	Unique identifier for the analysis performed for a particular set of samples Relates to DNA *-lation – Metadata File (analysis_id)
analysis_group_id	string	R	Identifier of the analysis group (i.e. the one who prepared/run the pipeline) (See CV A.5)
data_status	integer	R	The status of the analysis over the associated raw data -1 ↪ Withdrawn 0 ↪ Only raw data available 1 ↪ Raw data available (analysis in process) 2 ↪ Raw and analysis data available (analysis finished)
assembly_version	integer	R	Version of reference genome assembly (See CV A.8)
program_versions	compound[] <i>program:version</i> (array sdeps ;)	D	The versions of (some of) the programs used for the analysis
alignment_algorithm	compound <i>name;url</i>	R	Name of alignment algorithm and URL to written protocol
other_analysis_algorithm	compound[] <i>name;url</i> (array sdeps ,)	O	Names of other analysis algorithms. Separate multiple algorithms by commas.
notes	text	O	Optional field to leave notes

2.7.6 DNA *-lation – Differentially Methylated Region (DMR) File

DNA *-lation [dlat] – Differentially Methylated Region File [dmr]

Table 2.7.6: DNA *-lation – Differentially Methylated Region (DMR) File

Name	Type	Need	Description / Values
analysis_id	string	I	Unique identifier for the analysis performed for a particular set of samples Relates to DNA differential *-lation – Metadata File (analysis_id)
d_lated_fragment_id	string	I	Unique identifier for the methylated fragment, in the form d'*lationType chromosome_chromosomeStart_-chromosomeEnd
chromosome	string	R	Name of the chromosome containing the experimentally detected feature (mutation, variation, expression, ...) (See CV A.7)
chromosome_start	integer	R	Start position of the mutation/variation on the chromosome

Continued on next page

Table 2.7.6 – continued from previous page

Name	Type	Need	Description / Values
chromosome_end	integer	R	End position of the mutation/variation on the chromosome
rank	compound[] <i>rank:value</i> (array seps ;)	O	Kind of used ranking and its value, in the form "rank:value". As it can hold more than one value, they are separated by semicolons
n_cpgs	integer	R	Number of CpGs in the DMR
n_sig_cpgs	integer	R	Number of significant CpGs in the DMR (z_score > 3 or < -3)
hyper_role	string	R	Which participant had the hypermethylation role in the comparison? A ↪ The hyper methylation role was given to participant A B ↪ The hyper methylation role was given to participant B
abs_avg_diff	decimal	R	Average of absolute methylation difference for the DMR
rel_avg_diff	decimal	R	Average of relative methylation difference for the DMR
cpg_start	integer[] (array seps ,)	R	The coordinates of the CpGs used for the calculation of this differentially methylated region
notes	text	O	Optional field to leave notes

Appendix A

Controlled Vocabularies

A.1 Ensembl Genes

This controlled vocabulary has 62069 terms

Valid Ensembl Genes identifiers

(See it at http://jan2013.archive.ensembl.org/Homo_sapiens/Info/Index)

A.2 Ensembl Transcripts

This controlled vocabulary has 213272 terms

Valid Ensembl Transcript identifiers

(See it at http://jan2013.archive.ensembl.org/Homo_sapiens/Info/Index)

A.3 Cell Ontology

This controlled vocabulary has 4299 terms

The Cell Ontology is designed as a structured controlled vocabulary for cell types \$Revision: 1.113 \$ See PMID:15693950, PMID:12799354, PMID:20123131, PMID:21208450; Contact Alexander Diehl, adiehl@buffalo.edu, University at Buffalo.

Table A.3.1: Cell Ontology

Key	Description
CHEBI:23367	molecular entity
CHEBI:24431	chemical entity
CHEBI:24651	hydroxides
CHEBI:25179	melanin
CHEBI:25806	oxygen molecular entity
CHEBI:26195	polyphenol
CHEBI:33243	natural product
CHEBI:33304	chalcogen molecular entity
CHEBI:33579	main group molecular entity
CHEBI:33582	carbon group molecular entity
CHEBI:33608	hydrogen molecular entity
CHEBI:33674	s-block molecular entity
CHEBI:33675	p-block molecular entity
CHEBI:33822	organic hydroxy compound

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
CHEBI:36357	Polyatomic entity
CHEBI:37577	Heteroatomic molecular entity
CHEBI:50860	Organic molecular entity
CL:0000000	Cell
CL:0000001	Primary cultured cell
CL:0000002	Immortal cell line cell
CL:0000003	Native cell
CL:0000005	Fibroblast neural crest derived
CL:0000006	Neuronal receptor cell
CL:0000007	Early embryonic cell
CL:0000008	Migratory cranial neural crest cell
CL:0000010	Cultured cell
CL:0000011	Migratory trunk neural crest cell
CL:0000014	Germ line stem cell
CL:0000015	Male germ cell
CL:0000016	Male germ line stem cell
CL:0000017	Spermatocyte
CL:0000018	Spermatid
CL:0000019	Sperm
CL:0000020	Spermatogonium
CL:0000021	Female germ cell
CL:0000022	Female germ line stem cell
CL:0000023	Oocyte
CL:0000024	Oogonial cell
CL:0000025	Egg
CL:0000026	Invertebrate nurse cell
CL:0000027	Smooth muscle cell neural crest derived
CL:0000028	CNS neuron (sensu Nematoda and Protostomia)
CL:0000029	Neuron neural crest derived
CL:0000030	Glioblast
CL:0000031	Neuroblast
CL:0000032	Neuroplacodal cell
CL:0000033	Apocrine cell
CL:0000034	Stem cell
CL:0000035	Single fate stem cell
CL:0000036	Epithelial fate stem cell
CL:0000037	Hematopoietic stem cell
CL:0000038	Erythroid progenitor cell
CL:0000039	Germ line cell
CL:0000040	Monoblast
CL:0000041	Mature eosinophil
CL:0000042	Neutrophilic myeloblast
CL:0000043	Mature basophil
CL:0000047	Neuronal stem cell
CL:0000048	Multi fate stem cell
CL:0000049	Common myeloid progenitor
CL:0000050	Megakaryocyte-erythroid progenitor cell
CL:0000051	Common lymphoid progenitor
CL:0000052	Totipotent stem cell
CL:0000054	Bone matrix secreting cell
CL:0000055	Non-terminally differentiated cell

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
CL:0000056	myoblast
CL:0000057	fibroblast
CL:0000058	chondroblast
CL:0000059	ameloblast
CL:0000060	odontoblast
CL:0000061	cementoblast
CL:0000062	osteoblast
CL:0000064	ciliated cell
CL:0000065	ependymal cell
CL:0000066	epithelial cell
CL:0000067	ciliated epithelial cell
CL:0000068	duct epithelial cell
CL:0000069	branched duct epithelial cell
CL:0000071	blood vessel endothelial cell
CL:0000072	non-branched duct epithelial cell
CL:0000073	barrier epithelial cell
CL:0000075	columnar/cuboidal epithelial cell
CL:0000076	squamous epithelial cell
CL:0000077	mesothelial cell
CL:0000078	peridermal cell
CL:0000079	stratified epithelial cell
CL:0000080	circulating cell
CL:0000081	blood cell
CL:0000082	epithelial cell of lung
CL:0000083	epithelial cell of pancreas
CL:0000084	T cell
CL:0000085	germ line stem cell (<i>sensu Vertebrata</i>)
CL:0000086	germ line stem cell (<i>sensu Nematoda and Protostomia</i>)
CL:0000087	male germ line stem cell (<i>sensu Nematoda and Protostomia</i>)
CL:0000088	female germ line stem cell (<i>sensu Nematoda and Protostomia</i>)
CL:0000089	male germ line stem cell (<i>sensu Vertebrata</i>)
CL:0000090	female germ line stem cell (<i>sensu Vertebrata</i>)
CL:0000091	Kupffer cell
CL:0000092	osteoclast
CL:0000094	granulocyte
CL:0000095	neuron associated cell
CL:0000096	mature neutrophil
CL:0000097	mast cell
CL:0000098	sensory epithelial cell
CL:0000099	interneuron
CL:0000100	motor neuron
CL:0000101	sensory neuron
CL:0000102	polymodal neuron
CL:0000103	bipolar neuron
CL:0000104	multipolar neuron
CL:0000105	pseudounipolar neuron
CL:0000106	unipolar neuron
CL:0000107	autonomic neuron
CL:0000108	cholinergic neuron

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
CL:0000109	adrenergic neuron
CL:0000110	peptidergic neuron
CL:0000111	peripheral neuron
CL:0000112	columnar neuron
CL:0000113	mononuclear phagocyte
CL:0000114	surface ectodermal cell
CL:0000115	endothelial cell
CL:0000116	pioneer neuron
CL:0000117	CNS neuron (sensu Vertebrata)
CL:0000118	basket cell
CL:0000119	Golgi cell
CL:0000120	granule cell
CL:0000121	Purkinje cell
CL:0000122	stellate cell
CL:0000123	neuron associated cell (sensu Vertebrata)
CL:0000124	glial cell (sensu Nematoda and Protostomia)
CL:0000125	glial cell
CL:0000126	macrogliial cell
CL:0000127	astrocyte
CL:0000128	oligodendrocyte
CL:0000129	microglial cell
CL:0000130	neuron associated cell (sensu Nematoda and Proto-stomia)
CL:0000131	gut endothelial cell
CL:0000132	corneal endothelial cell
CL:0000133	neurectodermal cell
CL:0000134	mesenchymal cell
CL:0000135	fibrocyte
CL:0000136	fat cell
CL:0000137	osteocyte
CL:0000138	chondrocyte
CL:0000140	odontocyte
CL:0000141	cementocyte
CL:0000142	hyalocyte
CL:0000143	guidepost cell
CL:0000145	professional antigen presenting cell
CL:0000146	simple columnar epithelial cell
CL:0000147	pigment cell
CL:0000148	melanocyte
CL:0000149	visual pigment cell
CL:0000150	glandular epithelial cell
CL:0000151	secretory cell
CL:0000152	exocrine cell
CL:0000153	GAG secreting cell
CL:0000154	protein secreting cell
CL:0000155	peptic cell
CL:0000157	surfactant secreting cell
CL:0000158	Clara cell
CL:0000159	seromucus secreting cell
CL:0000160	goblet cell
CL:0000161	acid secreting cell

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
CL:0000162	parietal cell
CL:0000163	endocrine cell
CL:0000164	enteroendocrine cell
CL:0000165	neuroendocrine cell
CL:0000166	chromaffin cell
CL:0000167	peptide hormone secreting cell
CL:0000168	insulin secreting cell
CL:0000169	type B pancreatic cell
CL:0000170	glucagon secreting cell
CL:0000171	pancreatic A cell
CL:0000172	somatostatin secreting cell
CL:0000173	pancreatic D cell
CL:0000174	steroid hormone secreting cell
CL:0000175	luteal cell
CL:0000176	ecdysteroid secreting cell
CL:0000177	testosterone secreting cell
CL:0000178	Leydig cell
CL:0000179	progesterone secreting cell
CL:0000180	estradiol secreting cell
CL:0000181	metabolising cell
CL:0000182	hepatocyte
CL:0000183	contractile cell
CL:0000185	myoepithelial cell
CL:0000186	myofibroblast cell
CL:0000187	muscle cell
CL:0000188	skeletal muscle cell
CL:0000189	slow muscle cell
CL:0000190	fast muscle cell
CL:0000192	smooth muscle cell
CL:0000193	cardiac muscle cell (<i>sensu Arthropoda</i>)
CL:0000196	flight muscle cell
CL:0000197	receptor cell
CL:0000198	pain receptor cell
CL:0000199	mechanoreceptor cell
CL:0000200	touch receptor cell
CL:0000202	auditory hair cell
CL:0000203	gravity sensitive cell
CL:0000204	acceleration receptive cell
CL:0000205	thermoreceptor cell
CL:0000206	chemoreceptor cell
CL:0000207	olfactory receptor cell
CL:0000208	pH receptor cell
CL:0000209	taste receptor cell
CL:0000210	photoreceptor cell
CL:0000211	electrically active cell
CL:0000212	absorptive cell
CL:0000213	lining cell
CL:0000214	synovial cell
CL:0000215	barrier cell
CL:0000216	Sertoli cell
CL:0000217	insulating cell

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
CL:0000218	myelinating Schwann cell
CL:0000219	motile cell
CL:0000221	ectodermal cell
CL:0000222	mesodermal cell
CL:0000223	endodermal cell
CL:0000225	anucleate cell
CL:0000226	single nucleate cell
CL:0000227	binucleate cell
CL:0000228	multinucleate cell
CL:0000232	erythrocyte
CL:0000233	platelet
CL:0000234	phagocyte
CL:0000235	macrophage
CL:0000236	B cell
CL:0000237	keratinizing barrier epithelial cell
CL:0000238	non keratinizing barrier epithelial cell
CL:0000239	brush border epithelial cell
CL:0000240	stratified squamous epithelial cell
CL:0000241	stratified cuboidal epithelial cell
CL:0000242	Merkel cell
CL:0000243	glial cell (<i>sensu Vertebrata</i>)
CL:0000244	transitional epithelial cell
CL:0000246	Mauthner neuron
CL:0000247	Rohon-Beard neuron
CL:0000249	hatching gland cell
CL:0000251	extramedullary cell
CL:0000253	eurydendroid cell
CL:0000255	eukaryotic cell
CL:0000256	uric acid accumulating cell
CL:0000257	Mycetozoan cell
CL:0000259	aggregate cell
CL:0000261	anterior cell
CL:0000263	vegetative cell (<i>sensu Mycetozoa</i>)
CL:0000265	anterior like cell
CL:0000267	prespore cell
CL:0000269	prestalk cell
CL:0000271	prestalk A cell
CL:0000273	prestalk AB cell
CL:0000275	prestalk B cell
CL:0000279	prestalk O cell
CL:0000281	pstAB/ALC
CL:0000283	pstO/ALC
CL:0000285	stalk cell
CL:0000286	hyphal cell
CL:0000287	eye photoreceptor cell
CL:0000289	chemotactic amoeboid cell (<i>sensu Mycetozoa</i>)
CL:0000291	spore (<i>sensu Mycetozoa</i>)
CL:0000293	structural cell
CL:0000295	somatotropin secreting cell
CL:0000300	gamete
CL:0000301	pole cell

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
CL:0000306	crystallin accumulating cell
CL:0000307	tracheal epithelial cell
CL:0000308	metal ion accumulating cell
CL:0000309	copper accumulating cell
CL:0000310	iron accumulating cell
CL:0000311	keratin accumulating cell
CL:0000312	keratinocyte
CL:0000313	serous secreting cell
CL:0000314	milk secreting cell
CL:0000315	tears secreting cell
CL:0000317	sebum secreting cell
CL:0000318	sweat secreting cell
CL:0000319	mucus secreting cell
CL:0000321	seminal fluid secreting cell
CL:0000322	pneumocyte
CL:0000323	lysozyme secreting cell
CL:0000324	metanephric mesenchyme stem cell
CL:0000325	stuff accumulating cell
CL:0000326	glycogen accumulating cell
CL:0000327	extracellular matrix secreting cell
CL:0000328	myelin accumulating cell
CL:0000329	oxygen accumulating cell
CL:0000333	migratory neural crest cell
CL:0000334	vegetative cell (sensu Fungi)
CL:0000335	mesenchyme condensation cell
CL:0000336	adrenal medulla chromaffin cell
CL:0000337	neuroblast (sensu Vertebrata)
CL:0000338	neuroblast (sensu Nematoda and Protostomia)
CL:0000339	glioblast (sensu Vertebrata)
CL:0000340	glioblast (sensu Nematoda and Protostomia)
CL:0000341	pigment cell (sensu Nematoda and Protostomia)
CL:0000342	pigment cell (sensu Vertebrata)
CL:0000343	visual pigment cell (sensu Vertebrata)
CL:0000345	dental papilla cell
CL:0000346	hair follicle dermal papilla cell
CL:0000347	scleral cell
CL:0000348	choroidal cell of the eye
CL:0000349	extraembryonic cell
CL:0000350	amnioserosal cell
CL:0000351	trophoblast cell
CL:0000352	epiblast cell
CL:0000353	blastoderm cell
CL:0000354	blastemal cell
CL:0000355	muscle stem cell
CL:0000356	hair matrix stem cell
CL:0000357	stratified epithelial stem cell
CL:0000358	sphincter associated smooth muscle cell
CL:0000359	vascular associated smooth muscle cell
CL:0000360	morula cell
CL:0000361	gastrula cell
CL:0000362	epidermal cell

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
CL:0000365	zygote
CL:0000367	sheath cell (sensu Nematoda)
CL:0000371	protoplast
CL:0000372	tormogen cell
CL:0000373	histoblast
CL:0000374	trichogen cell
CL:0000376	humidity receptor cell
CL:0000377	tracheoblast
CL:0000378	support cell (sensu Nematoda and Protostomia)
CL:0000379	sensory processing neuron
CL:0000380	thecogen cell
CL:0000381	neurosecretory neuron
CL:0000382	scolopidium
CL:0000383	nephrogenic mesenchyme stem cell
CL:0000384	ligament cell
CL:0000385	prohemocyte (sensu Nematoda and Protostomia)
CL:0000386	attachment cell
CL:0000387	hemocyte (sensu Nematoda and Protostomia)
CL:0000388	tendon cell
CL:0000389	socket cell (sensu Nematoda)
CL:0000390	blood cell (sensu Nematoda and Protostomia)
CL:0000391	podocyte (sensu Diptera)
CL:0000392	crystal cell
CL:0000393	electrically responsive cell
CL:0000394	plasmacyte
CL:0000395	procrysal cell
CL:0000396	lamellocyte
CL:0000397	ganglion interneuron
CL:0000398	polygonal cell
CL:0000401	macrophage (sensu Diptera)
CL:0000402	CNS interneuron
CL:0000404	electrically signaling cell
CL:0000405	neuroepidermoblast
CL:0000406	CNS short range interneuron
CL:0000407	scolopidial ligament cell
CL:0000408	male gamete
CL:0000409	scolopidial sheath cell
CL:0000410	CNS long range interneuron
CL:0000411	flatworm hypodermal cell
CL:0000412	polyploid cell
CL:0000413	haploid cell
CL:0000415	diploid cell
CL:0000416	polytene cell
CL:0000417	endopolyploid cell
CL:0000418	arcade cell
CL:0000419	seam cell
CL:0000420	syncytial epithelial cell
CL:0000421	coelomocyte
CL:0000422	mitogenic signaling cell
CL:0000423	tip cell
CL:0000424	excretory cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0000425	pore cell
CL:0000426	scaffold cell
CL:0000427	GLR cell
CL:0000428	yolk cell
CL:0000429	imaginal disc cell
CL:0000430	xanthophore
CL:0000431	iridophore
CL:0000432	reticular cell
CL:0000434	eccrine cell
CL:0000435	alkali secreting cell
CL:0000436	vaginal lubricant secreting cell
CL:0000437	gonadtroph
CL:0000438	luteinizing hormone secreting cell
CL:0000439	prolactin secreting cell
CL:0000440	melanocyte stimulating hormone secreting cell
CL:0000441	follicle stem cell
CL:0000442	follicular dendritic cell
CL:0000443	calcitonin secreting cell
CL:0000444	obliquely striated muscle cell
CL:0000445	apoptosis fated cell
CL:0000446	chief cell of parathyroid gland
CL:0000447	carbohydrate secreting cell
CL:0000448	white fat cell
CL:0000449	brown fat cell
CL:0000451	dendritic cell
CL:0000452	thyroid hormone secreting cell
CL:0000453	Langerhans cell
CL:0000454	epinephrine secreting cell
CL:0000456	mineralocorticoid secreting cell
CL:0000457	biogenic amine secreting cell
CL:0000458	serotonin secreting cell
CL:0000459	norepinephrin secreting cell
CL:0000460	glucocorticoid secreting cell
CL:0000462	adepithelial cell
CL:0000463	epidermal cell (sensu arthropoda)
CL:0000464	epidermoblast
CL:0000465	cardioblast (sensu Arthropoda)
CL:0000467	adrenocorticotropic hormone secreting cell
CL:0000468	neuroglioblast
CL:0000469	ganglion mother cell
CL:0000470	digestive enzyme secreting cell
CL:0000473	defensive cell
CL:0000474	pericardial nephrocyte
CL:0000476	thyrotroph
CL:0000477	follicle cell
CL:0000478	oxytocin stimulating hormone secreting cell
CL:0000479	vasopressin stimulating hormone secreting cell
CL:0000480	secretin stimulating hormone secreting cell
CL:0000481	cholecystokin stimulating hormone secreting cell
CL:0000482	juvenile hormone secreting cell
CL:0000483	bombesin stimulating hormone secreting cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0000484	connective tissue type mast cell
CL:0000485	mucosal type mast cell
CL:0000486	garland cell
CL:0000487	oenocyte
CL:0000488	visible light photoreceptor cell
CL:0000489	scotopic photoreceptor cell
CL:0000490	photopic photoreceptor cell
CL:0000492	CD4-positive helper T cell
CL:0000494	UV sensitive photoreceptor cell
CL:0000495	blue sensitive photoreceptor cell
CL:0000496	green sensitive photoreceptor cell
CL:0000497	red sensitive photoreceptor cell
CL:0000498	inhibitory interneuron
CL:0000499	stromal cell
CL:0000500	follicular epithelial cell
CL:0000501	granulosa cell
CL:0000502	type D enteroendocrine cell
CL:0000503	theca cell
CL:0000504	enterochromaffin-like cell
CL:0000505	substance P secreting cell
CL:0000506	enkephalin secreting cell
CL:0000507	endorphin secreting cell
CL:0000508	type G enteroendocrine cell
CL:0000509	gastrin secreting cell
CL:0000510	paneth cell
CL:0000511	androgen binding protein secreting cell
CL:0000512	paracrine cell
CL:0000513	cardiac muscle myoblast
CL:0000514	smooth muscle myoblast
CL:0000515	skeletal muscle myoblast
CL:0000516	perineuronal satellite cell
CL:0000517	macrophage derived foam cell
CL:0000518	phagocyte (<i>sensu Vertebrata</i>)
CL:0000519	phagocyte (<i>sensu Nematoda and Protostomia</i>)
CL:0000520	prokaryotic cell
CL:0000521	fungus cell
CL:0000523	mononuclear cytotrophoblast cell
CL:0000524	spheroplast
CL:0000525	syncytiotrophoblast cell
CL:0000526	afferent neuron
CL:0000527	efferent neuron
CL:0000528	nitrogenic neuron
CL:0000529	pigmented epithelial cell
CL:0000530	primary neuron
CL:0000531	primary sensory neuron
CL:0000532	CAP motoneuron
CL:0000533	primary motor neuron
CL:0000534	primary interneuron
CL:0000535	secondary neuron
CL:0000536	secondary motor neuron
CL:0000540	neuron

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Table A.3.1 – continued from previous page

Key	Description
CL:0000541	melanoblast
CL:0000542	lymphocyte
CL:0000544	slowly adapting mechanoreceptor cell
CL:0000545	T-helper 1 cell
CL:0000546	T-helper 2 cell
CL:0000547	proerythroblast
CL:0000548	animal cell
CL:0000549	basophilic erythroblast
CL:0000550	polychromatophilic erythroblast
CL:0000551	unimodal nocireceptor
CL:0000552	orthochromatic erythroblast
CL:0000553	megakaryocyte progenitor cell
CL:0000554	gastrin stimulating hormone secreting cell
CL:0000555	neuronal brush cell
CL:0000556	megakaryocyte
CL:0000557	granulocyte monocyte progenitor cell
CL:0000558	reticulocyte
CL:0000559	promonocyte
CL:0000560	band form neutrophil
CL:0000561	amacrine cell
CL:0000562	nucleate erythrocyte
CL:0000563	endospore
CL:0000564	neutrophilic promyelocyte
CL:0000565	fat body cell
CL:0000566	angioblastic mesenchymal cell
CL:0000567	polymodal nocireceptor
CL:0000568	APUD cell
CL:0000569	cardiac mesenchymal cell
CL:0000570	parafollicular cell
CL:0000571	leucophore
CL:0000573	retinal cone cell
CL:0000574	erythrophore
CL:0000575	corneal epithelial cell
CL:0000576	monocyte
CL:0000577	type EC enteroendocrine cell
CL:0000578	experimentally modified cell in vitro
CL:0000579	border follicle cell
CL:0000580	neutrophilic myelocyte
CL:0000581	peritoneal macrophage
CL:0000582	neutrophilic metamyelocyte
CL:0000583	alveolar macrophage
CL:0000584	enterocyte
CL:0000586	germ cell
CL:0000587	cold sensing thermoreceptor cell
CL:0000588	odontoclast
CL:0000589	cochlear inner hair cell
CL:0000590	small luteal cell
CL:0000591	warmth sensing thermoreceptor cell
CL:0000592	large luteal cell
CL:0000593	androgen secreting cell
CL:0000594	skeletal muscle satellite cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0000595	enucleate erythrocyte
CL:0000596	sexual spore
CL:0000597	microconidium
CL:0000598	pyramidal cell
CL:0000599	conidium
CL:0000600	heterokaryon
CL:0000601	outer hair cell
CL:0000602	pressoreceptor cell
CL:0000603	dikaryon
CL:0000604	retinal rod cell
CL:0000605	fungus asexual spore
CL:0000606	macroconidium
CL:0000607	ascospore
CL:0000608	zygospore
CL:0000609	vestibular hair cell
CL:0000611	eosinophil progenitor cell
CL:0000612	eosinophilic myelocyte
CL:0000613	basophil progenitor cell
CL:0000614	basophilic myelocyte
CL:0000615	basidiospore
CL:0000617	GABAergic neuron
CL:0000618	sheath cell
CL:0000619	support cell (sensu Nematoda)
CL:0000621	fusion competent myoblast
CL:0000622	acinar cell
CL:0000623	natural killer cell
CL:0000624	CD4-positive, alpha-beta T cell
CL:0000625	CD8-positive, alpha-beta T cell
CL:0000626	olfactory granule cell
CL:0000627	transporting cell
CL:0000628	photosynthetic cell
CL:0000629	storage cell
CL:0000630	supportive cell
CL:0000631	labyrinth supporting cell
CL:0000632	hepatic stellate cell
CL:0000633	Hensen cell
CL:0000634	Claudius cell
CL:0000635	Deiter's cell
CL:0000636	Mueller cell
CL:0000637	chromophil cell of anterior pituitary gland
CL:0000638	acidophil cell of pars distalis of adenohypophysis
CL:0000639	basophil cell of pars distalis of adenohypophysis
CL:0000641	chromophobe cell
CL:0000642	folliculostellate cell
CL:0000644	Bergmann glial cell
CL:0000645	pituicyte
CL:0000646	basal cell
CL:0000647	multinucleated giant cell
CL:0000648	kidney granular cell
CL:0000649	prickle cell
CL:0000650	mesangial cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0000651	neck cell
CL:0000652	pinealocyte
CL:0000653	glomerular visceral epithelial cell
CL:0000654	primary oocyte
CL:0000655	secondary oocyte
CL:0000656	primary spermatocyte
CL:0000657	secondary spermatocyte
CL:0000658	cuticle secreting cell
CL:0000659	eggshell secreting cell
CL:0000660	glycocalyx secreting cell
CL:0000661	distal tip cell (<i>sensu Nematoda</i>)
CL:0000662	neuroglioblast (<i>sensu Nematoda</i>)
CL:0000663	valve cell
CL:0000664	closable valve cell
CL:0000665	permanently open valve cell
CL:0000666	fenestrated cell
CL:0000667	collagen secreting cell
CL:0000669	pericyte cell
CL:0000670	primordial germ cell
CL:0000671	centripetally migrating follicle cell
CL:0000673	Kenyon cell
CL:0000674	interfollicle cell
CL:0000675	female gamete
CL:0000676	cap cell
CL:0000677	gut absorptive cell
CL:0000678	commisural neuron
CL:0000679	glutamatergic neuron
CL:0000680	muscle precursor cell
CL:0000681	radial glial cell
CL:0000682	M cell
CL:0000683	ependymoglia cell
CL:0000684	littoral cell of liver
CL:0000686	cerebrospinal fluid secreting cell
CL:0000687	R1 photoreceptor cell
CL:0000688	perijunctional fibroblast
CL:0000689	myoendocrine cell
CL:0000690	R2 photoreceptor cell
CL:0000691	stellate interneuron
CL:0000692	terminal Schwann cell
CL:0000693	neurogliaform cell
CL:0000694	R3 photoreceptor cell
CL:0000695	Cajal-Retzius cell
CL:0000696	PP cell
CL:0000697	R4 photoreceptor cell
CL:0000699	paraganglial type 1 cell
CL:0000700	dopaminergic neuron
CL:0000701	paraganglia type 2 cell
CL:0000702	R5 photoreceptor cell
CL:0000703	sustentacular cell
CL:0000704	endothelial tip cell
CL:0000705	R6 photoreceptor cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0000706	choroid plexus epithelial cell
CL:0000707	R7 photoreceptor cell
CL:0000708	leptomeningeal cell
CL:0000709	R8 photoreceptor cell
CL:0000710	neurecto-epithelial cell
CL:0000711	cumulus cell
CL:0000712	stratum granulosum cell
CL:0000713	corona radiata cell
CL:0000715	embryonic crystal cell
CL:0000716	lymph gland crystal cell
CL:0000717	fusimotor neuron
CL:0000718	cone cell (<i>sensu Endopterygota</i>)
CL:0000719	posterior cone cell (<i>sensu Endopterygota</i>)
CL:0000720	anterior cone cell (<i>sensu Endopterygota</i>)
CL:0000721	equatorial cone cell (<i>sensu Endopterygota</i>)
CL:0000722	cystoblast
CL:0000723	somatic stem cell
CL:0000724	heterocyst
CL:0000725	nitrogen fixing cell
CL:0000726	chlamydospore
CL:0000727	primary pigment cell
CL:0000728	secondary pigment cell
CL:0000729	tertiary pigment cell
CL:0000730	leading edge cell
CL:0000731	urothelial cell
CL:0000732	amoeboid cell
CL:0000733	lymph gland plasmacyte
CL:0000734	embryonic gland plasmacyte
CL:0000735	lymph gland hemocyte
CL:0000736	embryonic gland hemocyte
CL:0000737	striated muscle cell
CL:0000738	leukocyte
CL:0000740	retinal ganglion cell
CL:0000741	spinal accessory motor neuron
CL:0000742	periarticular chondrocyte
CL:0000743	hypertrophic chondrocyte
CL:0000744	columnar chondrocyte
CL:0000745	horizontal cell
CL:0000746	cardiac muscle cell
CL:0000747	cyanophore
CL:0000748	retinal bipolar neuron
CL:0000749	ON-bipolar cell
CL:0000750	OFF-bipolar cell
CL:0000751	rod bipolar cell
CL:0000752	cone retinal bipolar cell
CL:0000753	type 1 cone bipolar cell (<i>sensu Mus</i>)
CL:0000754	type 2 cone bipolar cell (<i>sensu Mus</i>)
CL:0000755	type 3 cone bipolar cell (<i>sensu Mus</i>)
CL:0000756	type 4 cone bipolar cell (<i>sensu Mus</i>)
CL:0000757	type 5 cone bipolar cell (<i>sensu Mus</i>)
CL:0000758	type 6 cone bipolar cell (<i>sensu Mus</i>)

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Table A.3.1 – continued from previous page

Key	Description
CL:0000759	type 7 cone bipolar cell (sensu Mus)
CL:0000760	type 8 cone bipolar cell (sensu Mus)
CL:0000761	type 9 cone bipolar cell (sensu Mus)
CL:0000762	nucleated thrombocyte
CL:0000763	myeloid cell
CL:0000764	erythroid lineage cell
CL:0000765	erythroblast
CL:0000766	myeloid leukocyte
CL:0000767	basophil
CL:0000768	immature basophil
CL:0000769	basophilic metamyelocyte
CL:0000770	band form basophil
CL:0000771	eosinophil
CL:0000772	immature eosinophil
CL:0000773	eosinophilic metamyelocyte
CL:0000774	band form eosinophil
CL:0000775	neutrophil
CL:0000776	immature neutrophil
CL:0000777	mesangial phagocyte
CL:0000778	mononuclear osteoclast
CL:0000779	multinuclear osteoclast
CL:0000780	multinuclear odontoclast
CL:0000781	mononuclear odontoclast
CL:0000782	myeloid dendritic cell
CL:0000783	multinucleated phagocyte
CL:0000784	plasmacytoid dendritic cell
CL:0000785	mature B cell
CL:0000786	plasma cell
CL:0000787	memory B cell
CL:0000788	naive B cell
CL:0000789	alpha-beta T cell
CL:0000790	immature alpha-beta T cell
CL:0000791	mature alpha-beta T cell
CL:0000792	CD4-positive, CD25-positive, alpha-beta regulatory T cell
CL:0000793	CD4-positive, alpha-beta intraepithelial T cell
CL:0000794	CD8-positive, alpha-beta cytotoxic T cell
CL:0000795	CD8-positive, alpha-beta regulatory T cell
CL:0000796	CD8-alpha-beta-positive, alpha-beta intraepithelial T cell
CL:0000797	alpha-beta intraepithelial T cell
CL:0000798	gamma-delta T cell
CL:0000799	immature gamma-delta T cell
CL:0000800	mature gamma-delta T cell
CL:0000801	gamma-delta intraepithelial T cell
CL:0000802	CD8-alpha alpha positive, gamma-delta intraepithelial T cell
CL:0000803	CD4-negative CD8-negative gamma-delta intraepithelial T cell
CL:0000805	immature single positive thymocyte
CL:0000806	DN2 thymocyte

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Table A.3.1 – continued from previous page

Key	Description
CL:0000807	DN3 thymocyte
CL:0000808	DN4 thymocyte
CL:0000809	double-positive, alpha-beta thymocyte
CL:0000810	CD4-positive, alpha-beta thymocyte
CL:0000811	CD8-positive, alpha-beta thymocyte
CL:0000813	memory T cell
CL:0000814	mature NK T cell
CL:0000815	regulatory T cell
CL:0000816	immature B cell
CL:0000817	precursor B cell
CL:0000818	transitional stage B cell
CL:0000819	B-1 B cell
CL:0000820	B-1a B cell
CL:0000821	B-1b B cell
CL:0000822	B-2 B cell
CL:0000823	immature natural killer cell
CL:0000824	mature natural killer cell
CL:0000825	pro-NK cell
CL:0000826	pro-B cell
CL:0000827	pro-T cell
CL:0000828	thromboblast
CL:0000829	basophilic myeloblast
CL:0000830	basophilic promyelocyte
CL:0000831	mast cell progenitor
CL:0000832	eosinophilic myeloblast
CL:0000833	eosinophilic promyelocyte
CL:0000834	neutrophil progenitor cell
CL:0000835	myeloblast
CL:0000836	promyelocyte
CL:0000837	hematopoietic multipotent progenitor cell
CL:0000838	lymphoid lineage restricted progenitor cell
CL:0000839	myeloid lineage restricted progenitor cell
CL:0000840	immature conventional dendritic cell
CL:0000841	mature conventional dendritic cell
CL:0000842	mononuclear cell
CL:0000843	follicular B cell
CL:0000844	germinal center B cell
CL:0000845	marginal zone B cell
CL:0000846	vestibular dark cell
CL:0000847	ciliated olfactory receptor neuron
CL:0000848	microvillous olfactory receptor neuron
CL:0000849	crypt olfactory receptor neuron
CL:0000850	serotonergic neuron
CL:0000851	neuromast mantle cell
CL:0000852	neuromast support cell
CL:0000853	olfactory epithelial support cell
CL:0000854	interneuromast cell
CL:0000855	sensory hair cell
CL:0000856	neuromast hair cell
CL:0000857	slow muscle myoblast
CL:0000858	fast muscle myoblast

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Table A.3.1 – continued from previous page

Key	Description
CL:0000860	classical monocyte
CL:0000861	elicited macrophage
CL:0000862	suppressor macrophage
CL:0000863	inflammatory macrophage
CL:0000864	tissue-resident macrophage
CL:0000865	gastrointestinal tract (lamina propria) macrophage
CL:0000866	thymic macrophage
CL:0000867	secondary lymphoid organ macrophage
CL:0000868	lymph node macrophage
CL:0000869	tonsillar macrophage
CL:0000870	Peyer's patch macrophage
CL:0000871	splenic macrophage
CL:0000872	splenic marginal zone macrophage
CL:0000873	splenic metallophilic macrophage
CL:0000874	splenic red pulp macrophage
CL:0000875	non-classical monocyte
CL:0000876	splenic white pulp macrophage
CL:0000877	splenic tingible body macrophage
CL:0000878	central nervous system macrophage
CL:0000879	meningeal macrophage
CL:0000880	choroid-plexus macrophage
CL:0000881	perivascular macrophage
CL:0000882	thymic medullary macrophage
CL:0000883	thymic cortical macrophage
CL:0000884	mucosa-associated lymphoid tissue macrophage
CL:0000885	gut-associated lymphoid tissue macrophage
CL:0000886	nasal and bronchial associated lymphoid tissue macrophage
CL:0000887	lymph node subcapsular sinus macrophage
CL:0000888	lymph node tingible body macrophage
CL:0000889	myeloid suppressor cell
CL:0000890	alternatively activated macrophage
CL:0000891	foam cell
CL:0000892	smooth muscle cell derived foam cell
CL:0000893	thymocyte
CL:0000894	DN1 thymic pro-T cell
CL:0000895	naive thymus-derived CD4-positive, alpha-beta T cell
CL:0000896	activated CD4-positive, alpha-beta T cell
CL:0000897	CD4-positive, alpha-beta memory T cell
CL:0000898	naive T cell
CL:0000899	T-helper 17 cell
CL:0000900	naive thymus-derived CD8-positive, alpha-beta T cell
CL:0000901	Tr1 cell
CL:0000902	induced T-regulatory cell
CL:0000903	natural T-regulatory cell
CL:0000904	central memory CD4-positive, alpha-beta T cell
CL:0000905	effector memory CD4-positive, alpha-beta T cell
CL:0000906	activated CD8-positive, alpha-beta T cell
CL:0000907	central memory CD8 positive, alpha-beta T cell
CL:0000908	CD8-positive, alpha-beta cytokine secreting effector T cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0000909	CD8-positive, alpha-beta memory T cell
CL:0000910	cytotoxic T cell
CL:0000911	effector T cell
CL:0000912	helper T cell
CL:0000913	effector memory CD8-positive, alpha-beta T cell
CL:0000914	immature NK T cell
CL:0000915	CD8-alpha-alpha-positive, alpha-beta intraepithelial T cell
CL:0000916	dendritic epidermal T cell
CL:0000917	Tc1 cell
CL:0000918	Tc2 cell
CL:0000919	CD8-positive, CD25-positive, alpha-beta regulatory T cell
CL:0000920	CD8-positive, CD28-negative, alpha-beta regulatory T cell
CL:0000921	type I NK T cell
CL:0000922	type II NK T cell
CL:0000923	CD4-positive type I NK T cell
CL:0000924	CD4-negative, CD8-negative type I NK T cell
CL:0000925	activated CD4-positive type I NK T cell
CL:0000926	CD4-positive type I NK T cell secreting interferon-gamma
CL:0000927	CD4-positive type I NK T cell secreting interleukin-4
CL:0000928	activated CD4-negative, CD8-negative type I NK T cell
CL:0000929	CD4-negative, CD8-negative type I NK T cell secreting interferon-gamma
CL:0000930	CD4-negative, CD8-negative type I NK T cell secreting interleukin-4
CL:0000931	activated type II NK T cell
CL:0000932	type II NK T cell secreting interferon-gamma
CL:0000933	type II NK T cell secreting interleukin-4
CL:0000934	CD4-positive, alpha-beta cytotoxic T cell
CL:0000935	CD4-negative, CD8-negative, alpha-beta intraepithelial T cell
CL:0000936	early lymphoid progenitor
CL:0000937	pre-natural killer cell
CL:0000938	CD56-bright cytokine secreting natural killer cell
CL:0000939	cytotoxic CD56-dim natural killer cell
CL:0000940	mucosal invariant T cell
CL:0000941	thymic conventional dendritic cell
CL:0000942	thymic plasmacytoid dendritic cell
CL:0000943	Be1 Cell
CL:0000944	Be2 cell
CL:0000945	lymphocyte of B lineage
CL:0000946	antibody secreting cell
CL:0000947	IgE plasma cell
CL:0000948	IgE memory B cell
CL:0000949	IgD plasmablast
CL:0000950	IgE plasmablast
CL:0000951	IgE short lived plasma cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0000952	preBCR-positive large pre-B-II cell
CL:0000953	preBCR-negative large pre-B-II cell
CL:0000954	small pre-B-II cell
CL:0000955	pre-B-II cell
CL:0000956	pre-B-I cell
CL:0000957	large pre-B-II cell
CL:0000958	T1 B cell
CL:0000959	T2 B cell
CL:0000960	T3 B cell
CL:0000961	Bm1 B cell
CL:0000962	Bm2 B cell
CL:0000963	Bm3-delta B cell
CL:0000964	Bm2' B cell
CL:0000965	Bm3 B cell
CL:0000966	Bm4 B cell
CL:0000967	Bm5 B cell
CL:0000968	Be cell
CL:0000969	regulatory B cell
CL:0000970	unswitched memory B cell
CL:0000971	IgM memory B cell
CL:0000972	class switched memory B cell
CL:0000973	IgA memory B cell
CL:0000974	long lived plasma cell
CL:0000975	short lived plasma cell
CL:0000976	IgA short lived plasma cell
CL:0000977	IgG short lived plasma cell
CL:0000978	IgM short lived plasma cell
CL:0000979	IgG memory B cell
CL:0000980	plasmablast
CL:0000981	double negative memory B cell
CL:0000982	IgG plasmablast
CL:0000983	IgM plasmablast
CL:0000984	IgA plasmablast
CL:0000985	IgG plasma cell
CL:0000986	IgM plasma cell
CL:0000987	IgA plasma cell
CL:0000988	hematopoietic cell
CL:0000989	CD11c-low plasmacytoid dendritic cell
CL:0000990	conventional dendritic cell
CL:0000991	CD11c-negative plasmacytoid dendritic cell
CL:0000992	immature CD11c-low plasmacytoid dendritic cell
CL:0000993	mature CD11c-low plasmacytoid dendritic cell
CL:0000994	immature CD11c-negative plasmacytoid dendritic cell
CL:0000995	CD34-positive, CD38-positive common myeloid progenitor OR CD34-positive, CD38-positive common lymphoid progenitor
CL:0000996	mature CD11c-negative plasmacytoid dendritic cell
CL:0000997	immature CD8_alpha-negative CD11b-positive dendritic cell
CL:0000998	CD8_alpha-negative CD11b-negative dendritic cell
CL:0000999	CD4-positive CD11b-positive dendritic cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0001000	CD8_alpha-positive CD11b-negative dendritic cell
CL:0001001	immature CD8_alpha-negative CD11b-negative dendritic cell
CL:0001002	mature CD8_alpha-negative CD11b-negative dendritic cell
CL:0001003	mature CD8_alpha-negative CD11b-positive dendritic cell
CL:0001004	immature CD8_alpha-positive CD11b-negative dendritic cell
CL:0001005	mature CD8_alpha-positive CD11b-negative dendritic cell
CL:0001006	dermal dendritic cell
CL:0001007	interstitial dendritic cell
CL:0001008	Kit and Sca1-positive hematopoietic stem cell
CL:0001009	immature dermal dendritic cell
CL:0001010	mature dermal dendritic cell
CL:0001011	immature interstitial dendritic cell
CL:0001012	CD7-negative lymphoid progenitor OR granulocyte monocyte progenitor
CL:0001013	mature interstitial dendritic cell
CL:0001014	CD1a-positive Langerhans cell
CL:0001015	CD8_alpha-low Langerhans cell
CL:0001016	immature CD1a-positive Langerhans cell
CL:0001017	mature CD1a-positive Langerhans cell
CL:0001018	immature CD8_alpha-low Langerhans cell
CL:0001019	CD115-positive monocyte OR common dendritic progenitor
CL:0001020	mature CD8_alpha-low Langerhans cell
CL:0001021	CD34-positive, CD38-positive common lymphoid progenitor
CL:0001022	CD115-positive monocyte
CL:0001023	Kit-positive, CD34-positive common myeloid progenitor
CL:0001024	CD34-positive, CD38-negative hematopoietic stem cell
CL:0001025	Kit-positive, Sca1-positive common lymphoid progenitor
CL:0001026	CD34-positive, CD38-positive common myeloid progenitor
CL:0001027	CD7-negative lymphoid progenitor cell
CL:0001028	CD7-positive lymphoid progenitor cell
CL:0001029	common dendritic progenitor
CL:0001030	CD117-positive common myeloid progenitor OR CD217-positive common lymphoid progenitor
CL:0001031	cerebellar granule cell
CL:0001032	cortical granule cell
CL:0001033	hippocampal granule cell
CL:0001034	cell in vitro
CL:0001035	bone cell
CL:0001039	terminally differentiated osteoblast
CL:0001040	non-terminally differentiated osteoblast

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Table A.3.1 – continued from previous page

Key	Description
CL:0001041	CD8-positive, CXCR3-positive, alpha-beta regulatory T cell
CL:0001042	T-helper 22 cell
CL:0001658	visual pigment cell (<i>sensu</i> Nematoda and Protostomia)
CL:0002000	Kit-positive erythroid progenitor cell
CL:0002001	CD34-positive, CD38-positive granulocyte monocyte progenitor
CL:0002002	Kit-positive granulocyte monocyte progenitor
CL:0002003	CD34-positive, GlyA-negative erythroid progenitor cell
CL:0002004	CD34-negative, GlyA-negative proerythroblast
CL:0002005	CD34-positive, CD38-positive megakaryocyte erythroid progenitor cell
CL:0002006	Kit-positive, CD34-negative megakaryocyte erythroid progenitor cell
CL:0002007	Kit-low, CD34-positive eosinophil progenitor cell
CL:0002008	CD34-positive, CD38-positive eosinophil progenitor cell
CL:0002009	macrophage dendritic cell progenitor
CL:0002010	pre-conventional dendritic cell
CL:0002011	Kit-positive macrophage dendritic cell progenitor
CL:0002012	Kit-low proerythroblast
CL:0002013	GlyA-positive basophilic erythroblast
CL:0002014	Kit-negative, Ly-76 high basophilic erythroblast
CL:0002015	Kit-negative, Ly-76 high polychromatophilic erythroblast
CL:0002016	CD71-low, GlyA-positive polychromatic erythroblast
CL:0002017	Kit-negative, Ly-76 high orthochromatophilic erythroblasts
CL:0002018	CD71-negative, GlyA-positive orthochromatic erythroblast
CL:0002019	Ly-76 high reticulocyte
CL:0002020	GlyA-positive reticulocytes
CL:0002021	GlyA-positive erythrocyte
CL:0002022	Ly-76 high positive erythrocyte
CL:0002023	CD34-positive, CD41-positive, CD42-positive megakaryocyte progenitor cell
CL:0002024	Kit-positive megakaryocyte progenitor cell
CL:0002025	CD34-positive, CD41-positive, CD42-negative megakaryocyte progenitor cell
CL:0002026	CD34-negative, CD41-positive, CD42-positive megakaryocyte cell
CL:0002027	CD9-positive, CD41-positive megakaryocyte cell
CL:0002028	basophil mast progenitor cell
CL:0002029	Fc-epsilon R1alpha-low mast cell progenitor
CL:0002030	Fc-epsilon R1alpha-high basophil progenitor cell
CL:0002031	hematopoietic lineage restricted progenitor cell
CL:0002032	hematopoietic oligopotent progenitor cell
CL:0002033	short term hematopoietic stem cell
CL:0002034	long term hematopoietic stem cell
CL:0002035	Slamf1-negative multipotent progenitor cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0002036	Slamf1-positive multipotent progenitor cell
CL:0002037	CD2-positive, CD5-positive, CD44-positive alpha-beta intraepithelial T cell
CL:0002038	T follicular helper cell
CL:0002039	immature NK T cell stage I
CL:0002040	immature NK T cell stage II
CL:0002041	immature NK T cell stage III
CL:0002042	immature NK T cell stage IV
CL:0002043	CD34-positive, CD38-negative multipotent progenitor cell
CL:0002044	Kit-positive, integrin beta7-high basophil mast progenitor cell
CL:0002045	Fraction A pre-pro B cell
CL:0002046	early pro-B cell
CL:0002047	Fraction B precursor B cell
CL:0002048	late pro-B cell
CL:0002049	Fraction C precursor B cell
CL:0002050	Fraction C' precursor B cell
CL:0002051	CD38-high pre-BCR positive cell
CL:0002052	Fraction D precursor B cell
CL:0002053	CD22-positive, CD38-low small pre-B cell
CL:0002054	Fraction E immature B cell
CL:0002055	CD38-negative immature B cell
CL:0002056	Fraction F mature B cell
CL:0002057	CD14-positive, CD16-negative classical monocyte
CL:0002058	Gr1-low non-classical monocyte
CL:0002059	CD8alpha-positive thymic conventional dendritic cell
CL:0002060	melanophase
CL:0002061	T-helper 9 cell
CL:0002062	type I pneumocyte
CL:0002063	type II pneumocyte
CL:0002064	pancreatic acinar cell
CL:0002066	Feyrter cell
CL:0002067	type A enterocrine cell
CL:0002068	Purkinje myocyte
CL:0002069	type II vestibular sensory cell
CL:0002070	type I vestibular sensory cell
CL:0002071	enterocyte of epithelium of large intestine
CL:0002072	nodal myocyte
CL:0002073	transitional myocyte
CL:0002074	myocardial endocrine cell
CL:0002075	brush cell of tracheobronchial tree
CL:0002076	endo-epithelial cell
CL:0002077	ecto-epithelial cell
CL:0002078	meso-epithelial cell
CL:0002079	pancreatic ductal cell
CL:0002080	pancreatic centro-acinar cell
CL:0002081	type II cell of carotid body
CL:0002082	type II cell of adrenal medulla
CL:0002083	type I cell of adrenal medulla
CL:0002084	Boettcher cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0002085	tanycyte
CL:0002086	specialized cardiac myocyte
CL:0002087	nongranular leukocyte
CL:0002088	interstitial cell of Cajal
CL:0002089	nuocyte
CL:0002090	polar body
CL:0002091	primary polar body
CL:0002092	bone marrow cell
CL:0002093	secondary polar body
CL:0002094	interstitial cell of ovary
CL:0002095	hilus cell of ovary
CL:0002096	internodal tract myocyte
CL:0002097	cortical cell of adrenal gland
CL:0002098	regular cardiac myocyte
CL:0002099	type I cell of adrenal cortex
CL:0002100	regular interventricular cardiac myocyte
CL:0002101	CD38-positive naive B cell
CL:0002102	CD38-negative naive B cell
CL:0002103	IgG-positive double negative memory B cell
CL:0002104	IgG-negative double negative memory B cell
CL:0002105	CD38-positive IgG memory B cell
CL:0002106	IgD-positive CD38-positive IgG memory B cell
CL:0002107	IgD-negative CD38-positive IgG memory B cell
CL:0002108	CD38-negative IgG memory B cell
CL:0002109	B220-positive CD38-positive naive B cell
CL:0002110	B220-low CD38-positive naive B cell
CL:0002111	CD38-negative unswitched memory B cell
CL:0002112	B220-positive CD38-negative unswitched memory B cell
CL:0002113	B220-low CD38-negative unswitched memory B cell
CL:0002114	CD38-positive unswitched memory B cell
CL:0002115	B220-positive CD38-positive unswitched memory B cell
CL:0002116	B220-low CD38-positive unswitched memory B cell
CL:0002117	IgG-negative class switched memory B cell
CL:0002118	CD38-negative IgG-negative class switched memory B cell
CL:0002119	CD38-positive IgG-negative class switched memory B cell
CL:0002120	CD24-positive CD38-negative IgG-negative class switched memory B cell
CL:0002121	CD24-negative CD38-negative IgG-negative class switched memory B cell
CL:0002122	B220-positive CD38-positive IgG-negative class switched memory B cell
CL:0002123	B220-low CD38-positive IgG-negative class switched memory B cell
CL:0002124	CD27-positive gamma-delta T cell
CL:0002125	CD27-negative gamma-delta T cell
CL:0002126	CD25-positive, CD27-positive immature gamma-delta T cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0002127	innate effector T cell
CL:0002128	Tc17 cell
CL:0002129	regular atrial cardiac myocyte
CL:0002130	regular interatrial cardiac myocyte
CL:0002131	regular ventricular cardiac myocyte
CL:0002132	stromal cell of ovary
CL:0002133	stromal cell of ovarain cortex
CL:0002134	stromal cell of ovarian medulla
CL:0002135	nonkeratinized cell of epidermis
CL:0002136	type II cell of adrenal cortex
CL:0002137	type III cell of adrenal cortex
CL:0002138	endothelial cell of lymphatic vessel
CL:0002139	endothelial cell of vascular tree
CL:0002140	acinar cell of sebaceous gland
CL:0002141	active chief cell of parathyroid gland
CL:0002142	dark cell of eccrine sweat gland
CL:0002143	dark chief cell of parathyroid cell
CL:0002144	capillary endothelial cell
CL:0002145	ciliated columnar cell of tracheobronchial tree
CL:0002146	clear cell of eccrine sweat gland
CL:0002147	clear chief cell of parathyroid cell
CL:0002148	dental pulp cell
CL:0002149	epithelial cell of uterus
CL:0002150	epithelioid macrophage
CL:0002151	late promyelocyte
CL:0002152	columnar cell of endocervix
CL:0002153	corneocyte
CL:0002154	early promyelocyte
CL:0002155	echinocyte
CL:0002157	endosteal cell
CL:0002158	external epithelial cell of tympanic membrane
CL:0002159	general ecto-epithelial cell
CL:0002160	basal external epithelial cell of tympanic membrane
CL:0002161	superficial external epithelial cell of tympanic membrane
CL:0002162	internal epithelial cell of tympanic membrane
CL:0002163	internal pillar cell of cochlea
CL:0002164	external pillar cell of cochlea
CL:0002165	phalangeal cell
CL:0002166	epithelial cell of Malassez
CL:0002167	olfactory epithelial cell
CL:0002168	border cell of cochlea
CL:0002169	basal cell of olfactory epithelium
CL:0002170	keratinized cell of the oral mucosa
CL:0002171	globose cell of olfactory epithelium
CL:0002172	interdental cell of cochlea
CL:0002173	extraglomerular mesangial cell
CL:0002174	follicular cell of ovary
CL:0002175	primary follicular cell of ovary
CL:0002176	secondary follicular cell of ovary

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Table A.3.1 – continued from previous page

Key	Description
CL:0002177	folliculostellate cell of pars distalis of adenohypophysis
CL:0002178	epithelial cell of stomach
CL:0002179	foveolar cell of stomach
CL:0002180	mucous cell of stomach
CL:0002181	mucus neck cell of gastric gland
CL:0002182	surface mucosal cell of stomach
CL:0002183	stem cell of gastric gland
CL:0002184	basal proper cell of olfactory epithelium
CL:0002187	basal cell of epidermis
CL:0002188	glomerular endothelial cell
CL:0002189	granular cell of epidermis
CL:0002190	squamous cell of epidermis
CL:0002191	granulocytopoietic cell
CL:0002192	metamyelocyte
CL:0002193	myelocyte
CL:0002194	monopoietic cell
CL:0002195	hepatic stem cell
CL:0002196	hepatic oval stem cell
CL:0002197	inactive chief cell of parathyroid gland
CL:0002198	oncocyte
CL:0002199	oxyphil cell of parathyroid gland
CL:0002200	oxyphil cell of thyroid
CL:0002201	renal beta-intercalated cell
CL:0002202	epithelial cell of tracheobronchial tree
CL:0002203	Brush cell of epithelium proper of large intestine
CL:0002204	brush cell
CL:0002205	brush cell of lobular bronchiole
CL:0002206	brush cell of terminal bronchiole
CL:0002207	brush cell of trachea
CL:0002208	brush cell of bronchus
CL:0002209	intermediate epitheliocyte
CL:0002210	red muscle cell
CL:0002211	type I muscle cell
CL:0002212	type II muscle cell
CL:0002213	white muscle cell
CL:0002214	type IIa muscle cell
CL:0002215	type IIb muscle cell
CL:0002216	intermediate muscle cell
CL:0002217	intermediate trophoblast
CL:0002218	immature dendritic epithelial T cell precursor
CL:0002219	anchoring trophoblasts
CL:0002220	interstitial cell of pineal gland
CL:0002221	keratinized squamous cell of esophagus
CL:0002222	vertebrate lens cell
CL:0002223	anterior lens cell
CL:0002224	lens epithelial cell
CL:0002225	secondary lens fiber
CL:0002226	non-nucleated secondary lens fiber
CL:0002227	nucleated secondary lens fiber
CL:0002228	primary lens fiber

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Table A.3.1 – continued from previous page

Key	Description
CL:0002229	light chief cell of parathyroid gland
CL:0002231	epithelial cell of prostate
CL:0002232	epithelial cell of prostatic duct
CL:0002233	epithelial cell of prostatic acinus
CL:0002234	basal cell of prostatic acinus
CL:0002235	luminal cell of prostatic acinus
CL:0002236	basal epithelial cell of prostatic duct
CL:0002237	luminal epithelial cell of prostatic duct
CL:0002238	male gonocyte
CL:0002239	ooblast
CL:0002240	marrow fibroblast
CL:0002241	pulmonary interstitial fibroblast
CL:0002242	nucleate cell
CL:0002243	smooth muscle cell of sphincter of pupil
CL:0002244	squamous cell of ectocervix
CL:0002246	peripheral blood stem cell
CL:0002247	pleural macrophage
CL:0002248	pluripotent stem cell
CL:0002249	primitive cardiac myocyte
CL:0002250	intestinal crypt stem cell
CL:0002251	epithelial cell of alimentary canal
CL:0002252	epithelial cell of esophagus
CL:0002253	epithelial cell of large intestine
CL:0002254	epithelial cell of small intestine
CL:0002255	stromal cell of endometrium
CL:0002256	supporting cell of carotid body
CL:0002257	epithelial cell of thyroid gland
CL:0002258	thyroid follicular cell
CL:0002259	neuroepithelial stem cell
CL:0002260	epithelial cell of parathyroid gland
CL:0002261	endothelial cell of viscerocranial mucosa
CL:0002262	endothelial cell of sinusoid
CL:0002263	transitional cell of parathyroid gland
CL:0002264	type A cell of stomach
CL:0002265	type D cell of colon
CL:0002266	type D cell of small intestine
CL:0002267	type D cell of stomach
CL:0002268	P/D1 enteroendocrine cell
CL:0002269	vasoactive intestinal peptide secreting cell
CL:0002270	type EC2 enteroendocrine cell
CL:0002271	type EC1 enteroendocrine cell
CL:0002272	motilin secreting cell
CL:0002273	type ECL enteroendocrine cell
CL:0002274	histamine secreting cell
CL:0002275	pancreatic PP cell
CL:0002277	type I enteroendocrine cell
CL:0002278	GIP cell
CL:0002279	type L enteroendocrine cell
CL:0002280	type N enteroendocrine cell
CL:0002281	type S enteroendocrine cell
CL:0002282	type TG enteroendocrine cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0002283	ecto-epithelial cell of viscerocranial mucosa
CL:0002284	type X enteroendocrine cell
CL:0002285	type III taste bud cell
CL:0002286	type II taste cell
CL:0002287	type IV taste receptor cell
CL:0002288	type V taste receptor cell
CL:0002289	type I taste bud cell
CL:0002290	Y chromosome-bearing sperm cell
CL:0002291	X chromosome-bearing sperm cell
CL:0002292	type I cell of carotid body
CL:0002293	epithelial cell of thymus
CL:0002294	type-1 epithelial cell of thymus
CL:0002295	type-6 epithelial cell of thymus
CL:0002296	type-4 epithelial cell of thymus
CL:0002297	type-3 epithelial cell of thymus
CL:0002298	type-5 epithelial cell of thymus
CL:0002299	type-2 epithelial cell of thymus
CL:0002300	type-7 epithelial cell of thymus
CL:0002301	type B synovial cell
CL:0002302	type A synovial cell
CL:0002303	pigmented ciliary epithelial cell
CL:0002304	non-pigmented ciliary epithelial cell
CL:0002305	epithelial cell of distal tubule
CL:0002306	epithelial cell of proximal tubule
CL:0002307	brush border cell of the proximal tubule
CL:0002308	epithelial cell of skin gland
CL:0002309	corticotroph
CL:0002310	mammosomatotroph
CL:0002311	mammotroph
CL:0002312	somatotroph
CL:0002313	endocrine-paracrine cell of prostate gland
CL:0002314	external supporting cell of vestibular epithelium
CL:0002315	supporting cell of cochlea
CL:0002316	supporting cell of vestibular epithelium
CL:0002317	external limiting cell of vestibular epithelium
CL:0002318	peripheral blood mesothelial cell
CL:0002319	neural cell
CL:0002320	connective tissue cell
CL:0002321	embryonic cell
CL:0002322	embryonic stem cell
CL:0002323	amniocyte
CL:0002324	myoepithelial cell of mammary gland
CL:0002325	mammary alveolar cell
CL:0002326	luminal epithelial cell of mammary gland
CL:0002327	mammary epithelial cell
CL:0002328	bronchial epithelial cell
CL:0002329	basal epithelial cell of tracheobronchial tree
CL:0002330	undifferentiated cell of bronchus epithelium
CL:0002332	ciliated cell of the bronchus
CL:0002333	neural crest derived fat cell
CL:0002334	preadipocyte

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Table A.3.1 – continued from previous page

Key	Description
CL:0002335	brown preadipocyte
CL:0002336	buccal mucosa cell
CL:0002337	keratinocyte stem cell
CL:0002338	CD56-positive, CD161-positive immature natural killer cell
CL:0002339	prostate stem cell
CL:0002340	luminal cell of prostate epithelium
CL:0002341	basal cell of prostate epithelium
CL:0002342	circulating endothelial cell
CL:0002343	decidual natural killer cell
CL:0002344	CD56-negative, CD161-positive immature natural killer cell
CL:0002345	CD27-low, CD11b-low immature natural killer cell
CL:0002346	Dx5-negative, NK1.1-positive immature natural killer cell
CL:0002347	CD27-high, CD11b-high natural killer cell
CL:0002348	CD27-low, CD11b-high natural killer cell
CL:0002349	CD27-high, CD11b-low natural killer cell
CL:0002350	endocardial cell
CL:0002351	progenitor cell of endocrine pancreas
CL:0002352	gestational hematopoietic stem cell
CL:0002353	fetal liver hematopoietic progenitor cell
CL:0002354	yolk sac hematopoietic stem cell
CL:0002355	primitive red blood cell
CL:0002356	primitive reticulocyte
CL:0002357	fetal derived definitive erythrocyte
CL:0002358	pyrenocyte
CL:0002359	placental hematopoietic stem cell
CL:0002360	AGM hematopoietic stem cell
CL:0002361	primitive erythroid progenitor
CL:0002362	granule cell precursor
CL:0002363	keratocyte
CL:0002364	cortical thymic epithelial cell
CL:0002365	medullary thymic epithelial cell
CL:0002366	myometrial cell
CL:0002367	trabecular meshwork cell
CL:0002368	respiratory epithelial cell
CL:0002369	fungal spore
CL:0002370	respiratory goblet cell
CL:0002371	somatic cell
CL:0002372	myotube
CL:0002373	growth hormone releasing hormone secreting cell
CL:0002374	ear hair cell
CL:0002375	Schwann cell precursor
CL:0002376	non-myelinating Schwann cell
CL:0002377	immature Schwann cell
CL:0002378	immature Vgamma2-positive fetal thymocyte
CL:0002379	meningothelial cell
CL:0002380	oospore
CL:0002381	uninucleate conidium
CL:0002382	multinucleate conidium

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Table A.3.1 – continued from previous page

Key	Description
CL:0002383	conidium of conidiophore head
CL:0002384	uninucleate macroconidium
CL:0002385	blastoconidium
CL:0002386	multinucleate macroconidium
CL:0002387	arthroconidium
CL:0002388	multinucleate arthroconidium
CL:0002389	uninucleate arthroconidium
CL:0002390	uninucleate blastconidium
CL:0002391	multinucleate blastoconidium
CL:0002393	intermediate monocyte
CL:0002394	CD141-positive myeloid dendritic cell
CL:0002395	Gr1-high classical monocyte
CL:0002396	CD14-low, CD16-positive monocyte
CL:0002397	CD14-positive, CD16-positive monocyte
CL:0002398	Gr1-positive, CD43-positive monocyte
CL:0002399	CD1c-positive myeloid dendritic cell
CL:0002400	Fraction B/C precursor B cell
CL:0002401	mature dendritic epithelial T cell precursor
CL:0002402	Peyer's patch B cell
CL:0002403	mature Vgamma2-positive fetal thymocyte
CL:0002404	fetal thymocyte
CL:0002405	gamma-delta thymocyte
CL:0002406	immature Vgamma2-positive thymocyte
CL:0002407	mature Vgamma2-positive thymocyte
CL:0002408	immature Vgamma2-negative thymocyte
CL:0002409	mature Vgamma2-negative thymocyte
CL:0002410	pancreatic stellate cell
CL:0002411	Vgamma1.1-positive, Vdelta6.3-negative thymocyte
CL:0002412	Vgamma1.1-positive, Vdelta6.3-positive thymocyte
CL:0002413	mature Vgamma1.1-positive, Vdelta6.3-negative thymocyte
CL:0002414	immature Vgamma1.1-positive, Vdelta6.3-negative thymocyte
CL:0002415	immature Vgamma1.1-positive, Vdelta6.3-positive thymocyte
CL:0002416	mature Vgamma1.1-positive, Vdelta6.3-positive thymocyte
CL:0002417	primitive erythroid lineage cell
CL:0002418	hemangioblast
CL:0002419	mature T cell
CL:0002420	immature T cell
CL:0002421	nucleated reticulocyte
CL:0002422	enucleated reticulocyte
CL:0002423	DN2a thymocyte
CL:0002424	DN2b thymocyte
CL:0002425	early T lineage precursor
CL:0002426	CD11b-positive, CD27-positive natural killer cell
CL:0002427	resting double-positive thymocyte
CL:0002428	double-positive blast
CL:0002429	CD69-positive double-positive thymocyte

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Key	Description
CL:0002430	CD4-intermediate, CD8-positive double-positive thymocyte
CL:0002431	CD4-positive, CD8-intermediate double-positive thymocyte
CL:0002432	CD24-positive, CD4 single-positive thymocyte
CL:0002433	CD69-positive, CD4-positive single-positive thymocyte
CL:0002434	CD24-positive, CD8 single-positive thymocyte
CL:0002435	CD69-positive, CD8-positive single-positive thymocyte
CL:0002436	mature CD4 single-positive thymocyte
CL:0002437	mature CD8 single-positive thymocyte
CL:0002438	NK1.1-positive natural killer cell
CL:0002439	NKG2A-positive natural killer cell
CL:0002440	Ly49D-positive natural killer cell
CL:0002441	CD94-positive natural killer cell
CL:0002442	CD94-negative, Ly49Cl-negative natural killer cell
CL:0002443	Ly49Cl-positive natural killer cell
CL:0002444	Ly49H-positive natural killer cell
CL:0002445	Ly49D-negative natural killer cell
CL:0002446	Ly49Cl-negative natural killer cell
CL:0002447	CD94-negative natural killer cell
CL:0002448	Ly49H-negative natural killer cell
CL:0002449	CD94-positive Ly49Cl-positive natural killer cell
CL:0002450	tether cell
CL:0002451	mammary stem cell
CL:0002453	oligodendrocyte precursor cell
CL:0002454	Cd4-negative, CD8_alpha-negative, CD11b-positive dendritic cell
CL:0002455	CD8_alpha-negative plasmacytoid dendritic cell
CL:0002456	CD8_alpha-positive plasmacytoid dendritic cell
CL:0002457	epidermal Langerhans cell
CL:0002458	langerin-positive dermal dendritic cell
CL:0002459	langerin-negative dermal dendritic cell
CL:0002460	CD8alpha-negative thymic conventional dendritic cell
CL:0002461	CD103-positive dendritic cell
CL:0002462	adipose dendritic cell
CL:0002463	SIRPa-positive adipose dendritic cell
CL:0002464	SIRPa-negative adipose dendritic cell
CL:0002465	CD11b-positive dendritic cell
CL:0002466	small intestine serosal dendritic cell
CL:0002467	Gr1-high myeloid suppressor cell
CL:0002468	Gr1-low myeloid suppressor cell
CL:0002469	MHC-II-negative classical monocyte
CL:0002470	MHC-II-positive classical monocyte
CL:0002471	MHC-II-negative non-classical monocyte
CL:0002472	MHC-II-low non-classical monocyte
CL:0002473	MHC-II-high non-classical monocyte
CL:0002474	lymphoid MHC-II-negative classical monocyte
CL:0002475	lymphoid MHC-II-negative non-classical monocyte
CL:0002476	bone marrow macrophage

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Key	Description
CL:0002477	adipose macrophage
CL:0002478	F4/80-negative adipose macrophage
CL:0002479	F4/80-positive adipose macrophage
CL:0002480	nasal mucosa goblet cell
CL:0002481	peritubular myoid cell
CL:0002482	dermal melanocyte
CL:0002483	hair follicle melanocyte
CL:0002484	epithelial melanocyte
CL:0002485	retinal melanocyte
CL:0002486	strial intermediate cell
CL:0002487	cutaneous/subcutaneous mechanoreceptor cell
CL:0002488	trophoblast giant cell
CL:0002489	double negative thymocyte
CL:0002490	organ of Corti supporting cell
CL:0002491	auditory epithelial cell
CL:0002492	strial marginal cell
CL:0002493	strial basal cell
CL:0002494	cardiocyte
CL:0002495	fetal cardiomyocyte
CL:0002496	intraepithelial lymphocyte
CL:0002497	primary trophoblast giant cell
CL:0002498	secondary trophoblast giant cell
CL:0002499	spongiotrophoblast cell
CL:0002500	P enteroendocrine cell
CL:0002501	type D1 enteroendocrine cell
CL:0002502	type M enteroendocrine cell
CL:0002503	adventitial cell
CL:0002504	enteric smooth muscle cell
CL:0002505	liver CD103-negative dendritic cell
CL:0002506	liver CD103-positive dendritic cell
CL:0002507	langerin-positive lymph node dendritic cell
CL:0002508	langerin-negative, CD103-negative lymph node dendritic cell
CL:0002509	CD103-positive, langerin-positive lymph node dendritic cell
CL:0002510	CD103-negative, langerin-positive lymph node dendritic cell
CL:0002511	CD11b-low, CD103-negative, langerin-negative lymph node dendritic cell
CL:0002512	CD11b-high, CD103-negative, langerin-negative lymph node dendritic cell
CL:0002513	Vgamma5-positive CD8alpha alpha positive gamma-delta intraepithelial T cell
CL:0002514	Vgamma5-negative CD8alpha alpha positive gamma-delta intraepithelial T cell
CL:0002515	interrenal norepinephrine type cell
CL:0002516	interrenal chromaffin cell
CL:0002517	interrenal epinephrin secreting cell
CL:0002518	kidney epithelial cell
CL:0002519	interrenal epithelial cell
CL:0002520	nephrocyte

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Key	Description
CL:0002521	subcutaneous fat cell
CL:0002522	renal filtration cell
CL:0002523	mesonephric glomerular visceral epithelial cell
CL:0002524	disseminated nephrocyte
CL:0002525	metanephric glomerular visceral epithelial cell
CL:0002526	CD14-positive dermal dendritic cell
CL:0002527	immature CD14-positive dermal dendritic cell
CL:0002528	mature CD14-positive dermal dendritic cell
CL:0002529	CD1a-positive dermal dendritic cell
CL:0002530	immature CD1a-positive dermal dendritic cell
CL:0002531	mature CD1a-positive dermal dendritic cell
CL:0002532	CD16-positive myeloid dendritic cell
CL:0002533	immature CD16-positive myeloid dendritic cell
CL:0002534	mature CD16-positive myeloid dendritic cell
CL:0002535	epithelial cell of cervix
CL:0002536	amniotic epithelial cell
CL:0002537	amnion mesenchymal stem cell
CL:0002538	intrahepatic bile duct epithelial cell
CL:0002539	aortic smooth muscle cell
CL:0002540	mesenchymal stem cell of the bone marrow
CL:0002541	chorionic membrane mesenchymal stem cell
CL:0002543	vein endothelial cell
CL:0002544	aortic endothelial cell
CL:0002545	thoracic aorta endothelial cell
CL:0002546	embryonic blood vessel endothelial progenitor cell
CL:0002547	fibroblast of the aortic adventitia
CL:0002548	cardiac fibroblast
CL:0002549	fibroblast of choroid plexus
CL:0002550	fibroblast of the conjunctiva
CL:0002551	fibroblast of dermis
CL:0002552	fibroblast of gingiva
CL:0002553	fibroblast of lung
CL:0002554	fibroblast of lymphatic vessel
CL:0002555	fibroblast of mammary gland
CL:0002556	fibroblast of periodontium
CL:0002557	fibroblast of pulmonary artery
CL:0002558	fibroblast of villous mesenchymal
CL:0002559	hair follicle cell
CL:0002560	inner root sheath cell
CL:0002561	outer root sheath cell
CL:0002562	hair germinal matrix cell
CL:0002563	intestinal epithelial cell
CL:0002564	nucleus pulposus cell of intervertebral disc
CL:0002565	iris pigment epithelial cell
CL:0002566	dark melanocyte
CL:0002567	light melanocyte
CL:0002568	mesenchymal stem cell of Wharton's jelly
CL:0002569	mesenchymal stem cell of umbilical cord
CL:0002570	mesenchymal stem cell of adipose
CL:0002571	hepatic mesenchymal stem cell
CL:0002572	vertebral mesenchymal stem cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0002573	Schwann cell
CL:0002574	stromal cell of pancreas
CL:0002575	central nervous system pericyte
CL:0002576	perineural cell
CL:0002577	placental epithelial cell
CL:0002578	mesenteric preadipocyte
CL:0002579	omentum preadipocyte
CL:0002580	preadipocyte of the breast
CL:0002581	perirenal preadipocyte
CL:0002582	visceral preadipocyte
CL:0002583	subcutaneous preadipocyte
CL:0002584	renal cortical epithelial cell
CL:0002585	retinal blood vessel endothelial cell
CL:0002586	retinal pigment epithelial cell
CL:0002588	smooth muscle cell of the umbilical vein
CL:0002589	smooth muscle cell of the brachiocephalic vasculature
CL:0002590	smooth muscle cell of the brain vasculature
CL:0002591	smooth muscle cell of the pulmonary artery
CL:0002592	smooth muscle cell of the coronary artery
CL:0002593	smooth muscle cell of the internal thoracic artery
CL:0002594	smooth muscle cell of the umbilical artery
CL:0002595	smooth muscle cell of the subclavian artery
CL:0002596	smooth muscle cell of the carotid artery
CL:0002597	smooth muscle cell of bladder
CL:0002598	bronchial smooth muscle cell
CL:0002599	smooth muscle cell of the esophagus
CL:0002600	smooth muscle cell of trachea
CL:0002601	uterine smooth muscle cell
CL:0002602	annulus pulposus cell
CL:0002603	astrocyte of the cerebellum
CL:0002604	astrocyte of the hippocampus
CL:0002605	astrocyte of the cerebral cortex
CL:0002606	astrocyte of the spinal cord
CL:0002607	migratory enteric neural crest cell
CL:0002608	hippocampal neuron
CL:0002609	neuron of cerebral cortex
CL:0002610	raphe nuclei neuron
CL:0002611	neuron of the dorsal spinal cord
CL:0002612	neuron of the ventral spinal cord
CL:0002613	striatum neuron
CL:0002614	neuron of the substantia nigra
CL:0002615	adipocyte of omentum tissue
CL:0002616	perirenal adipocyte cell
CL:0002617	adipocyte of breast
CL:0002618	endothelial cell of umbilical vein
CL:0002619	adult endothelial progenitor cell
CL:0002620	skin fibroblast
CL:0002621	gingival epithelial cell
CL:0002622	prostate stromal cell
CL:0002623	acinar cell of salivary gland
CL:0002624	paneth cell of the appendix

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Table A.3.1 – continued from previous page

Key	Description
CL:0002625	seminiferous tubule epithelial cell
CL:0002626	immature astrocyte
CL:0002627	mature astrocyte
CL:0002628	immature microglial cell
CL:0002629	mature microglial cell
CL:0002630	actinomycete-type spore
CL:0002631	epithelial cell of upper respiratory tract
CL:0002632	epithelial cell of lower respiratory tract
CL:0002633	respiratory basal cell
CL:0002634	epithelial cell of anal column
CL:0002635	nonkeratinized epithelial cell of anal column
CL:0002636	nonkeratinized epithelial cell of inferior part of anal canal
CL:0002637	keratinized epithelial cell of the anal canal
CL:0002638	bronchioalveolar stem cell
CL:0002639	amniotic stem cell
CL:0002640	amniotic epithelial stem cell
CL:0002641	epithelial cell of esophageal gland proper
CL:0002642	epithelial cell of esophageal cardiac gland
CL:0002643	nonkeratinized cell of stratum corneum of esophageal epithelium
CL:0002644	endo-epithelial cell of tympanic part of viscerocranial mucosa
CL:0002645	endo-epithelial cell of pharyngotympanic part of viscerocranial mucosa
CL:0002646	epithelial cell of buccal part of viscerocranial mucosa
CL:0002647	epithelial cell of anterior palatal part of viscerocranial mucosa
CL:0002648	epithelial cell of nasal part of viscerocranial mucosa
CL:0002649	epithelial cell of gingival part of viscerocranial mucosa
CL:0002650	epithelial cell of paranasal sinus part of viscerocranial mucosa
CL:0002651	endothelial cell of venous sinus of spleen
CL:0002652	endothelial cell of high endothelial venule
CL:0002653	squamous endothelial cell
CL:0002654	epithelial cell of stratum corneum of esophageal epithelium
CL:0002655	epithelial cell of stratum spinosum of esophageal epithelium
CL:0002656	glandular cell of endometrium
CL:0002657	glandular cell of esophagus
CL:0002658	glandular cell of the large intestine
CL:0002659	glandular cell of stomach
CL:0002660	luminal cell of acinus of lactiferous gland
CL:0002661	luminal cell of lactiferous terminal ductal lobular unit
CL:0002662	luminal cell of lactiferous duct
CL:0002663	myocardial endocrine cell of atrium
CL:0002664	cardioblast
CL:0002665	otic fibrocyte
CL:0002666	type 2 otic fibrocyte
CL:0002667	type 5 otic fibrocyte

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Table A.3.1 – continued from previous page

Key	Description
CL:0002668	type 4 otic fibrocyte
CL:0002669	type 3 otic fibrocyte
CL:0002670	type 1 otic fibrocyte
CL:0002671	endothelial stalk cell
CL:0002672	retinal progenitor cell
CL:0002673	tongue muscle cell
CL:0002674	H minus
CL:0002675	H plus
CL:0002676	neural crest derived neuroblast
CL:0002677	naive regulatory T cell
CL:0002678	memory regulatory T cell
CL:0002679	natural helper lymphocyte
CL:0002680	PP cell of intestine
CL:0002681	kidney cortical cell
CL:0005000	spinal cord interneuron
CL:0005001	iridoblast
CL:0005002	xanthoblast
CL:0005003	leucoblast
CL:0005004	pigment erythroblast
CL:0005005	cyanoblast
CL:0005006	ionocyte
CL:0005007	Kolmer-Agduhr neuron
CL:0005008	macular hair cell
CL:0005009	renal principal cell
CL:0005010	renal intercalated cell
CL:0005011	renal alpha-intercalated cell
CL:0005012	multi-ciliated epithelial cell
CL:0005013	single ciliated epithelial cell
CL:0005014	auditory epithelial support cell
CL:0005015	inner phalangeal cell
CL:0005018	ghrelin secreting cell
CL:0005019	pancreatic epsilon cell
CL:0005020	lymphangioblast
CL:0005021	mesenchymal lymphangioblast
CL:0005022	vascular lymphangioblast
CL:0007000	preameloblast
CL:0007001	skeletogenic cell
CL:0007002	precementoblast
CL:0007003	preodontoblast
CL:0007004	premigratory neural crest cell
CL:0007005	notochordal cell
CL:0007006	chordamesodermal cell
CL:0007007	notochordal sheath cell
CL:0007008	notochordal vacuole cell
CL:0007009	prechondroblast
CL:0007010	preosteoblast
CL:0007011	enteric neuron
CL:0007012	non-terminally differentiated odontoblast
CL:0007013	terminally differentiated odontoblast
CL:0007014	cell line cell
CL:0007015	mortal cell line cell

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Table A.3.1 – continued from previous page

Key	Description
CL:0007016	adaxial cell
CL:0009000	sensory neuron of spinal nerve
CL:0011000	dorsal horn interneuron
CL:0011001	spinal cord motor neuron
CL:0011002	lateral motor column neuron
CL:0011003	magnocellular neurosecretory cell
CL:0011004	lens fiber cell
CL:0011005	GABAergic interneuron
CL:0011006	lugaro cell
CL:1000082	stretch receptor cell
CL:1000083	stratified keratinized epithelial stem cell
CL:1000085	stratified non keratinized epithelial stem cell
CL:1000191	pillar cell
CL:1000274	trophectodermal cell
CL:1000275	smooth muscle cell of small intestine
CL:1000276	smooth muscle fiber of duodenum
CL:1000277	smooth muscle fiber of jejunum
CL:1000278	smooth muscle fiber of ileum
CL:1000279	smooth muscle cell of large intestine
CL:1000280	smooth muscle cell of colon
CL:1000281	smooth muscle cell of cecum
CL:1000282	smooth muscle fiber of ascending colon
CL:1000283	smooth muscle fiber of transverse colon
CL:1000284	smooth muscle fiber of descending colon
CL:1000285	smooth muscle cell of sigmoid colon
CL:1000286	smooth muscle cell of rectum
CL:1000287	myocyte of anterior internodal tract
CL:1000288	myocyte of atrial branch of anterior internodal tract
CL:1000289	myocyte of atrial septal branch of anterior internodal tract
CL:1000290	myocyte of middle internodal tract
CL:1000291	myocyte of posterior internodal tract
CL:1000296	epithelial cell of urethra
CL:1000298	mesothelial cell of dura mater
CL:1000299	fibroblast of connective tissue of prostate
CL:1000300	fibroblast of outer membrane of prostatic capsule
CL:1000301	fibroblast of subepithelial connective tissue of prostatic gland
CL:1000302	fibroblast of papillary layer of dermis
CL:1000303	fibroblast of areolar connective tissue
CL:1000304	fibroblast of connective tissue of nonglandular part of prostate
CL:1000305	fibroblast of connective tissue of glandular part of prostate
CL:1000306	fibroblast of tunica adventitia of artery
CL:1000307	fibroblast of dense regular elastic tissue
CL:1000308	fibrocyte of adventitia of ureter
CL:1000309	epicardial adipocyte
CL:1000310	adipocyte of epicardial fat of right ventricle
CL:1000311	adipocyte of epicardial fat of left ventricle
CL:1000312	bronchial goblet cell

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Table A.3.1 – continued from previous page

Key	Description
CL:1000313	gastric goblet cell
CL:1000314	goblet cell of epithelium of gastric cardiac gland
CL:1000315	goblet cell of epithelium of principal gastric gland
CL:1000316	goblet cell of epithelium of small intestine
CL:1000317	goblet cell of epithelium of intestinal villus
CL:1000318	goblet cell of epithelium of crypt of lieberkuhn of small intestine
CL:1000319	goblet cell of epithelium proper of small intestine
CL:1000320	goblet cell of epithelium of large intestine
CL:1000321	goblet cell of epithelium of crypt of lieberkuhn of large intestine
CL:1000322	pancreatic goblet cell
CL:1000323	goblet cell of epithelium of pyloric gland
CL:1000324	goblet cell of epithelium proper of duodenum
CL:1000325	goblet cell of epithelium proper of jejunum
CL:1000326	goblet cell of epithelium proper of ileum
CL:1000327	goblet cell of epithelium proper of appendix
CL:1000328	goblet cell of epithelium proper of large intestine
CL:1000329	tracheal goblet cell
CL:1000330	serous cell of epithelium of trachea
CL:1000331	serous cell of epithelium of bronchus
CL:1000332	serous cell of epithelium of terminal bronchiole
CL:1000333	serous cell of epithelium of lobular bronchiole
CL:1000334	enterocyte of epithelium of small intestine
CL:1000335	enterocyte of epithelium of intestinal villus
CL:1000337	enterocyte of epithelium of duodenal gland
CL:1000338	enterocyte of epithelium of crypt of lieberkuhn of small intestine
CL:1000339	enterocyte of epithelium proper of small intestine
CL:1000340	enterocyte of epithelium proper of duodenum
CL:1000341	enterocyte of epithelium proper of jejunum
CL:1000342	enterocyte of epithelium proper of ileum
CL:1000343	paneth cell of epithelium of small intestine
CL:1000344	paneth cell of epithelium proper of small intestine
CL:1000345	paneth cell of epithelium of crypt of lieberkuhn of small intestine
CL:1000346	vacuolar absorptive cell of epithelium proper of large intestine
CL:1000347	vacuolar absorptive cell of epithelium of colon
CL:1000348	basal cell of epithelium of trachea
CL:1000349	basal cell of epithelium of bronchus
CL:1000350	basal cell of epithelium of terminal bronchiole
CL:1000351	basal cell of epithelium of respiratory bronchiole
CL:1000352	basal cell of epithelium of lobular bronchiole
CL:1000353	microfold cell of epithelium of small intestine
CL:1000354	microfold cell of epithelium of intestinal villus
CL:1000355	microfold cell of epithelium proper of small intestine
CL:1000356	microfold cell of epithelium proper of duodenum
CL:1000357	microfold cell of epithelium proper of jejunum
CL:1000358	microfold cell of epithelium proper of ileum
CL:1000359	microfold cell of epithelium proper of appendix

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Table A.3.1 – continued from previous page

Key	Description
CL:1000360	microfold cell of epithelium proper of large intestine
CL:1000361	transitional myocyte of interatrial septum
CL:1000362	transitional myocyte of interventricular septum
CL:1000363	transitional myocyte of atrial branch of anterior internodal tract
CL:1000364	transitional myocyte of anterior internodal tract
CL:1000365	transitional myocyte of atrial septal branch of anterior internodal tract
CL:1000366	transitional myocyte of middle internodal tract
CL:1000367	transitional myocyte of posterior internodal tract
CL:1000368	transitional myocyte of anterior division of left branch of atrioventricular bundle
CL:1000369	transitional myocyte of septal division of left branch of atrioventricular bundle
CL:1000370	transitional myocyte of left branch of atrioventricular bundle
CL:1000371	transitional myocyte of right branch of atrioventricular bundle
CL:1000372	transitional myocyte of atrial part of atrioventricular bundle
CL:1000373	transitional myocyte of ventricular part of atrioventricular bundle
CL:1000374	transitional myocyte of posterior division of left branch of atrioventricular bundle
CL:1000375	myocardial endocrine cell of septal division of left branch of atrioventricular bundle
CL:1000376	purkinje myocyte of interventricular septum
CL:1000377	dense-core granulated cell of epithelium of trachea
CL:1000378	type 1 vestibular sensory cell of stato-acoustic epithelium
CL:1000379	type 1 vestibular sensory cell of epithelium of macula of utricle of membranous labyrinth
CL:1000380	type 1 vestibular sensory cell of epithelium of macula of saccule of membranous labyrinth
CL:1000381	type 1 vestibular sensory cell of epithelium of crista of ampulla of semicircular duct of membranous labyrinth
CL:1000382	type 2 vestibular sensory cell of stato-acoustic epithelium
CL:1000383	type 2 vestibular sensory cell of epithelium of macula of utricle of membranous labyrinth
CL:1000384	type 2 vestibular sensory cell of epithelium of macula of saccule of membranous labyrinth
CL:1000385	type 2 vestibular sensory cell of epithelium of crista of ampulla of semicircular duct of membranous labyrinth
CL:1000391	melanocyte of eyelid
CL:1000394	myoepithelial cell of intralobular lactiferous duct
CL:1000397	endothelial cell of venous sinus of red pulp of spleen
CL:1000398	endothelial cell of hepatic sinusoid
CL:1000405	epithelial cell of appendix
CL:1000409	myocyte of sinoatrial node
CL:1000410	myocyte of atrioventricular node
CL:1000411	endothelial cell of peyer's patch

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Table A.3.1 – continued from previous page

Key	Description
CL:1000412	endothelial cell of arteriole
CL:1000413	endothelial cell of artery
CL:1000414	endothelial cell of venule
CL:1000415	epithelial cell of gall bladder
CL:1000416	myoepithelial cell of lactiferous gland
CL:1000417	myoepithelial cell of sweat gland
CL:1000418	myoepithelial cell of lactiferous alveolus
CL:1000419	myoepithelial cell of lactiferous duct
CL:1000420	myoepithelial cell of terminal lactiferous duct
CL:1000424	chromaffin cell of paraaortic body
CL:1000425	chromaffin cell of paraganglion
CL:1000426	chromaffin cell of adrenal gland
CL:1000427	adrenal cortex chromaffin cell
CL:1000428	stem cell of epidermis
CL:1000432	conjunctival epithelial cell
CL:1000433	epithelial cell of lacrimal canaliculus
CL:1000434	epithelial cell of external acoustic meatus
CL:1000435	epithelial cell of lacrimal duct
CL:1000436	epithelial cell of lacrimal sac
CL:1000437	epithelial cell of nasolacrimal duct
CL:1000438	epithelial cell of wall of inferior part of anal canal
CL:1000441	epithelial cell of viscerocranial mucosa
CL:1000442	urothelial cell of trigone of urinary bladder
CL:1000443	ciliary muscle cell
CL:1000444	mesothelial cell of anterior chamber of eye
CL:1000445	myoepithelial cell of dilator pupillae
CL:1000447	epithelial cell of stratum germinativum of esophagus
CL:1000448	epithelial cell of sweat gland
CL:1000449	epithelial cell of nephron
CL:1000450	epithelial cell of glomerular capsule
CL:1000451	epithelial cell of visceral layer of glomerular capsule
CL:1000452	parietal epithelial cell
CL:1000453	epithelial cell of intermediate tubule
CL:1000454	kidney collecting duct epithelial cell
CL:1000456	mesothelial cell of parietal peritoneum
CL:1000457	mesothelial cell of visceral peritoneum
CL:1000458	melanocyte of skin
CL:1000465	chromaffin cell of ovary
CL:1000466	chromaffin cell of right ovary
CL:1000467	chromaffin cell of left ovary
CL:1000468	myoepithelial cell of acinus of lactiferous gland
CL:1000469	myoepithelial cell of main lactiferous duct
CL:1000470	myoepithelial cell of primary lactiferous duct
CL:1000471	myoepithelial cell of secondary lactiferous duct
CL:1000472	myoepithelial cell of tertiary lactiferous duct
CL:1000473	myoepithelial cell of quarternary lactiferous duct
CL:1000477	cardiac pacemaker cell of sinoatrial node
CL:1000478	transitional myocyte of sinoatrial node
CL:1000479	purkinje myocyte of atrioventricular node
CL:1000480	transitional myocyte of internodal tract
CL:1000481	transitional myocyte of atrioventricular bundle

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Table A.3.1 – continued from previous page

Key	Description
CL:1000482	myocardial endocrine cell of interventricular septum
CL:1000483	purkinje myocyte of internodal tract
CL:1000484	purkinje myocyte of atrioventricular bundle
CL:1000486	basal cell of urothelium
CL:1000487	smooth muscle cell of prostate
CL:1000488	cholangiocyte
CL:1000489	reticular cell of splenic cord
CL:1000490	mesothelial cell of peritoneum
CL:1000491	mesothelial cell of pleura
CL:1000492	mesothelial cell of parietal pleura
CL:1000493	mesothelial cell of visceral pleura
CL:1000494	epithelial cell of renal tubule
CL:1000495	goblet cell of small intestine
CL:1000497	kidney cell
CL:1000500	kidney interstitial cell
CL:1000504	kidney medulla cell
CL:1000505	kidney pelvis cell
CL:1000507	kidney tubule cell
CL:1000510	kidney glomerular epithelial cell
CL:1000546	kidney medulla collecting duct epithelial cell
CL:1000547	kidney inner medulla collecting duct epithelial cell
CL:1000548	kidney outer medulla collecting duct epithelial cell
CL:1000549	kidney cortex collecting duct epithelial cell
CL:1000550	kidney papillary duct principal epithelial cell
CL:1000596	inner renal cortex cell
CL:1000597	papillary tips cell
CL:1000600	lower urinary tract cell
CL:1000601	ureteral cell
CL:1000606	kidney nerve cell
CL:1000612	kidney corpuscle cell
CL:1000615	kidney cortex tubule cell
CL:1000616	kidney outer medulla cell
CL:1000617	kidney inner medulla cell
CL:1000618	juxtaglomerular complex cell
CL:1000681	kidney cortex interstitial cell
CL:1000682	kidney medulla interstitial cell
CL:1000691	kidney interstitial myofibroblast
CL:1000692	kidney interstitial fibroblast
CL:1000693	kidney interstitial fibrocyte
CL:1000695	kidney interstitial alternatively activated macrophage
CL:1000696	kidney interstitial inflammatory macrophage
CL:1000697	kidney interstitial suppressor macrophage
CL:1000698	kidney resident macrophage
CL:1000699	kidney resident dendritic cell
CL:1000702	kidney pelvis smooth muscle cell
CL:1000703	kidney pelvis urothelial cell
CL:1000706	ureter urothelial cell
CL:1000708	ureter adventitial cell
CL:1000714	kidney cortex collecting duct principal cell
CL:1000715	kidney cortex collecting duct intercalated cell
CL:1000716	kidney outer medulla collecting duct principal cell

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Table A.3.1 – continued from previous page

Key	Description
CL:1000717	kidney outer medulla collecting duct intercalated cell
CL:1000718	kidney inner medulla collecting duct principal cell
CL:1000719	kidney inner medulla collecting duct intercalated cell
CL:1000720	kidney papillary duct intercalated cell
CL:1000721	kidney papillary duct principal cell
CL:1000742	glomerular mesangial cell
CL:1000746	glomerular cell
CL:1000768	kidney connecting tubule epithelial cell
CL:1000803	kidney inner medulla interstitial cell
CL:1000804	kidney outer medulla interstitial cell
CL:1000838	kidney proximal convoluted tubule epithelial cell
CL:1000839	kidney proximal straight tubule epithelial cell
CL:1000849	kidney distal convoluted tubule epithelial cell
CL:1000850	macula densa epithelial cell
CL:1000854	kidney blood vessel cell
CL:1000891	kidney arterial blood vessel cell
CL:1000892	kidney capillary endothelial cell
CL:1000893	kidney venous blood vessel cell
CL:1000909	kidney loop of henle epithelial cell
CL:1000979	ureter smooth muscle cell
CL:1001005	glomerular capillary endothelial cell
CL:1001006	kidney afferent arteriole cell
CL:1001009	kidney efferent arteriole cell
CL:1001016	kidney loop of henle ascending limb epithelial cell
CL:1001021	kidney loop of henle descending limb epithelial cell
CL:1001033	peritubular capillary endothelial cell
CL:1001036	vasa recta cell
CL:1001045	kidney cortex artery cell
CL:1001052	kidney cortex vein cell
CL:1001064	kidney artery smooth muscle cell
CL:1001066	kidney arteriole smooth muscle cell
CL:1001068	kidney venous system smooth muscle cell
CL:1001096	kidney afferent arteriole endothelial cell
CL:1001097	kidney afferent arteriole smooth muscle cell
CL:1001099	kidney efferent arteriole endothelial cell
CL:1001100	kidney efferent arteriole smooth muscle cell
CL:1001106	kidney loop of henle thick ascending limb epithelial cell
CL:1001107	kidney loop of henle thin ascending limb epithelial cell
CL:1001108	kidney loop of henle medullary thick ascending limb epithelial cell
CL:1001109	kidney loop of henle cortical thick ascending limb epithelial cell
CL:1001111	kidney loop of henle thin descending limb epithelial cell
CL:1001123	kidney outer medulla peritubular capillary cell
CL:1001124	kidney cortex peritubular capillary cell
CL:1001126	inner renal medulla vasa recta cell
CL:1001127	outer renal medulla vasa recta cell
CL:1001131	vasa recta ascending limb cell

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Table A.3.1 – continued from previous page

Key	Description
CL:1001135	arcuate artery cell
CL:1001138	interlobular artery cell
CL:1001142	arcuate vein cell
CL:1001145	interlobular vein cell
CL:1001209	inner medulla vasa recta ascending limb cell
CL:1001210	outer medulla vasa recta ascending limb cell
CL:1001213	arcuate artery endothelial cell
CL:1001214	arcuate artery smooth muscle cell
CL:1001216	interlobular artery endothelial cell
CL:1001217	interlobular artery smooth muscle cell
CL:1001220	arcuate vein endothelial cell
CL:1001221	arcuate vein smooth muscle cell
CL:1001223	interlobular vein endothelial cell
CL:1001224	interlobular vein smooth muscle cell
CL:1001225	kidney collecting duct cell
CL:1001285	vasa recta descending limb cell
CL:1001286	inner medulla vasa recta descending limb cell
CL:1001287	outer medulla vasa recta descending limb cell
CL:1001318	renal interstitial pericyte
CL:1001319	bladder cell
CL:1001320	urethra cell
CL:1001428	bladder urothelial cell
CL:1001430	urethra urothelial cell
CL:1001431	kidney collecting duct principal cell
CL:1001432	kidney collecting duct intercalated cell
CL:1001433	epithelial cell of exocrine pancreas
CL:1001434	olfactory bulb interneuron
CL:1001435	periglomerular cell
CL:1001436	hair-tylotrich neuron
CL:1001437	hair-down neuron
CL:1001451	sensory neuron of dorsal root ganglion
CL:1001474	medium spiny neuron
CL:1001502	mitral cell
CL:1001503	olfactory bulb tufted cell
CL:1001505	parvocellular neurosecretory cell
CL:1001509	glycinergic neuron
CL:1001516	intestinal enteroendocrine cell
CL:1001517	stomach enteroendocrine cell
CL:1001561	vomeronasal sensory neuron
CL:1001566	bronchioalveolar stem cells
CL:1001567	lung endothelial cell
CL:1001568	pulmonary artery endothelial cell
CL:1001569	hippocampal interneuron
CL:1001571	hippocampal pyramidal neuron
CP:0000000	neutrophilic cytoplasm
CP:0000025	lobed nucleus
CP:0000027	acidophilic cytoplasm
CP:0000028	basophilic cytoplasm
CP:0000035	polychromatophilic cytoplasm
CP:0000037	increased nucleus size
CP:0000039	banded nucleus

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Key	Description
CP:0000040	reniform nucleus
CP:0000043	cartwheel heterochromatin
GO:0000003	reproduction
GO:0000018	regulation of DNA recombination
GO:0000087	M phase of mitotic cell cycle
GO:0000226	microtubule cytoskeleton organization
GO:0000278	mitotic cell cycle
GO:0000279	M phase
GO:0000280	nuclear division
GO:0000323	lytic vacuole
GO:0000785	chromatin
GO:0000791	euchromatin
GO:0000792	heterochromatin
GO:0001501	skeletal system development
GO:0001503	ossification
GO:0001525	angiogenesis
GO:0001553	luteinization
GO:0001568	blood vessel development
GO:0001578	microtubule bundle formation
GO:0001649	osteoblast differentiation
GO:0001667	ameboidal cell migration
GO:0001675	acrosome assembly
GO:0001773	myeloid dendritic cell activation
GO:0001775	cell activation
GO:0001776	leukocyte homeostasis
GO:0001782	B cell homeostasis
GO:0001783	B cell apoptotic process
GO:0001816	cytokine production
GO:0001817	regulation of cytokine production
GO:0001818	negative regulation of cytokine production
GO:0001820	serotonin secretion
GO:0001894	tissue homeostasis
GO:0001906	cell killing
GO:0001909	leukocyte mediated cytotoxicity
GO:0001913	T cell mediated cytotoxicity
GO:0001942	hair follicle development
GO:0001944	vasculature development
GO:0001974	blood vessel remodeling
GO:0002200	somatic diversification of immune receptors
GO:0002204	somatic recombination of immunoglobulin genes involved in immune response
GO:0002208	somatic diversification of immunoglobulins involved in immune response
GO:0002215	defense response to nematode
GO:0002227	innate immune response in mucosa
GO:0002228	natural killer cell mediated immunity
GO:0002244	hematopoietic progenitor cell differentiation
GO:0002249	lymphocyte anergy
GO:0002250	adaptive immune response
GO:0002251	organ or tissue specific immune response
GO:0002252	immune effector process

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Table A.3.1 – continued from previous page

Key	Description
GO:0002260	lymphocyte homeostasis
GO:0002263	cell activation involved in immune response
GO:0002274	myeloid leukocyte activation
GO:0002285	lymphocyte activation involved in immune response
GO:0002286	T cell activation involved in immune response
GO:0002287	alpha-beta T cell activation involved in immune response
GO:0002288	NK T cell activation involved in immune response
GO:0002292	T cell differentiation involved in immune response
GO:0002293	alpha-beta T cell differentiation involved in immune response
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response
GO:0002312	B cell activation involved in immune response
GO:0002313	mature B cell differentiation involved in immune response
GO:0002314	germinal center B cell differentiation
GO:0002335	mature B cell differentiation
GO:0002339	B cell selection
GO:0002343	peripheral B cell selection
GO:0002344	B cell affinity maturation
GO:0002349	histamine production involved in inflammatory response
GO:0002351	serotonin production involved in inflammatory response
GO:0002366	leukocyte activation involved in immune response
GO:0002367	cytokine production involved in immune response
GO:0002369	T cell cytokine production
GO:0002376	immune system process
GO:0002377	immunoglobulin production
GO:0002381	immunoglobulin production involved in immunoglobulin mediated immune response
GO:0002385	mucosal immune response
GO:0002386	immune response in mucosal-associated lymphoid tissue
GO:0002387	immune response in gut-associated lymphoid tissue
GO:0002395	immune response in nasopharyngeal-associated lymphoid tissue
GO:0002432	granuloma formation
GO:0002440	production of molecular mediator of immune response
GO:0002443	leukocyte mediated immunity
GO:0002449	lymphocyte mediated immunity
GO:0002456	T cell mediated immunity
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002461	tolerance induction dependent upon immune response
GO:0002465	peripheral tolerance induction
GO:0002467	germinal center formation
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I

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Table A.3.1 – continued from previous page

Key	Description
GO:0002478	antigen processing and presentation of exogenous peptide antigen
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
GO:0002507	tolerance induction
GO:0002514	B cell tolerance induction
GO:0002515	B cell anergy
GO:0002520	immune system development
GO:0002521	leukocyte differentiation
GO:0002532	production of molecular mediator involved in inflammatory response
GO:0002536	respiratory burst involved in inflammatory response
GO:0002537	nitric oxide production involved in inflammatory response
GO:0002538	arachidonic acid metabolite production involved in inflammatory response
GO:0002539	prostaglandin production involved in inflammatory response
GO:0002540	leukotriene production involved in inflammatory response
GO:0002544	chronic inflammatory response
GO:0002548	monocyte chemotaxis
GO:0002562	somatic diversification of immune receptors via germline recombination within a single locus
GO:0002566	somatic diversification of immune receptors via somatic mutation
GO:0002573	myeloid leukocyte differentiation
GO:0002574	thrombocyte differentiation
GO:0002634	regulation of germinal center formation
GO:0002637	regulation of immunoglobulin production
GO:0002643	regulation of tolerance induction
GO:0002645	positive regulation of tolerance induction
GO:0002652	regulation of tolerance induction dependent upon immune response
GO:0002654	positive regulation of tolerance induction dependent upon immune response
GO:0002658	regulation of peripheral tolerance induction
GO:0002660	positive regulation of peripheral tolerance induction
GO:0002679	respiratory burst involved in defense response
GO:0002682	regulation of immune system process
GO:0002683	negative regulation of immune system process
GO:0002684	positive regulation of immune system process
GO:0002685	regulation of leukocyte migration
GO:0002687	positive regulation of leukocyte migration
GO:0002688	regulation of leukocyte chemotaxis
GO:0002690	positive regulation of leukocyte chemotaxis
GO:0002694	regulation of leukocyte activation
GO:0002695	negative regulation of leukocyte activation
GO:0002696	positive regulation of leukocyte activation

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Table A.3.1 – continued from previous page

Key	Description
GO:0002697	regulation of immune effector process
GO:0002699	positive regulation of immune effector process
GO:0002700	regulation of production of molecular mediator of immune response
GO:0002703	regulation of leukocyte mediated immunity
GO:0002706	regulation of lymphocyte mediated immunity
GO:0002712	regulation of B cell mediated immunity
GO:0002775	antimicrobial peptide production
GO:0002776	antimicrobial peptide secretion
GO:0002790	peptide secretion
GO:0002819	regulation of adaptive immune response
GO:0002821	positive regulation of adaptive immune response
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0002825	regulation of T-helper 1 type immune response
GO:0002827	positive regulation of T-helper 1 type immune response
GO:0002828	regulation of type 2 immune response
GO:0002830	positive regulation of type 2 immune response
GO:0002889	regulation of immunoglobulin mediated immune response
GO:0002901	mature B cell apoptotic process
GO:0002902	regulation of B cell apoptotic process
GO:0002905	regulation of mature B cell apoptotic process
GO:0003001	generation of a signal involved in cell-cell signaling
GO:0003006	developmental process involved in reproduction
GO:0003008	system process
GO:0003012	muscle system process
GO:0003013	circulatory system process
GO:0003674	molecular_function
GO:0004871	signal transducer activity
GO:0004872	receptor activity
GO:0004888	transmembrane signaling receptor activity
GO:0005044	scavenger receptor activity
GO:0005215	transporter activity
GO:0005488	binding
GO:0005575	cellular_component
GO:0005576	extracellular region
GO:0005615	extracellular space
GO:0005622	intracellular
GO:0005623	cell
GO:0005634	nucleus
GO:0005694	chromosome
GO:0005730	nucleolus
GO:0005737	cytoplasm
GO:0005764	lysosome
GO:0005766	primary lysosome

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Table A.3.1 – continued from previous page

Key	Description
GO:0005773	vacuole
GO:0005794	Golgi apparatus
GO:0005840	ribosome
GO:0005886	plasma membrane
GO:0005887	integral to plasma membrane
GO:0005902	microvillus
GO:0005929	cilium
GO:0006022	aminoglycan metabolic process
GO:0006023	aminoglycan biosynthetic process
GO:0006024	glycosaminoglycan biosynthetic process
GO:0006082	organic acid metabolic process
GO:0006139	nucleobase-containing compound metabolic process
GO:0006259	DNA metabolic process
GO:0006310	DNA recombination
GO:0006323	DNA packaging
GO:0006520	cellular amino acid metabolic process
GO:0006544	glycine metabolic process
GO:0006545	glycine biosynthetic process
GO:0006725	cellular aromatic compound metabolic process
GO:0006790	sulfur compound metabolic process
GO:0006801	superoxide metabolic process
GO:0006807	nitrogen compound metabolic process
GO:0006810	transport
GO:0006811	ion transport
GO:0006812	cation transport
GO:0006837	serotonin transport
GO:0006869	lipid transport
GO:0006897	endocytosis
GO:0006909	phagocytosis
GO:0006915	apoptotic process
GO:0006921	cellular component disassembly involved in execution phase of apoptosis
GO:0006928	cellular component movement
GO:0006935	chemotaxis
GO:0006936	muscle contraction
GO:0006937	regulation of muscle contraction
GO:0006939	smooth muscle contraction
GO:0006940	regulation of smooth muscle contraction
GO:0006950	response to stress
GO:0006952	defense response
GO:0006954	inflammatory response
GO:0006955	immune response
GO:0006959	humoral immune response
GO:0006996	organelle organization
GO:0006997	nucleus organization
GO:0007010	cytoskeleton organization
GO:0007017	microtubule-based process
GO:0007049	cell cycle
GO:0007067	mitosis
GO:0007113	endomitotic cell cycle
GO:0007126	meiosis

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Table A.3.1 – continued from previous page

Key	Description
GO:0007135	meiosis II
GO:0007140	male meiosis
GO:0007142	male meiosis II
GO:0007143	female meiosis
GO:0007147	female meiosis II
GO:0007154	cell communication
GO:0007267	cell-cell signaling
GO:0007275	multicellular organismal development
GO:0007276	gamete generation
GO:0007281	germ cell development
GO:0007283	spermatogenesis
GO:0007286	spermatid development
GO:0007288	sperm axoneme assembly
GO:0007289	spermatid nucleus differentiation
GO:0007292	female gamete generation
GO:0007399	nervous system development
GO:0007507	heart development
GO:0007548	sex differentiation
GO:0007585	respiratory gaseous exchange
GO:0007586	digestion
GO:0007589	body fluid secretion
GO:0007596	blood coagulation
GO:0007599	hemostasis
GO:0007600	sensory perception
GO:0007601	visual perception
GO:0007605	sensory perception of sound
GO:0007606	sensory perception of chemical stimulus
GO:0007608	sensory perception of smell
GO:0007610	behavior
GO:0008015	blood circulation
GO:0008104	protein localization
GO:0008150	biological_process
GO:0008152	metabolic process
GO:0008219	cell death
GO:0008283	cell proliferation
GO:0008284	positive regulation of cell proliferation
GO:0008285	negative regulation of cell proliferation
GO:0008289	lipid binding
GO:0008406	gonad development
GO:0008509	anion transmembrane transporter activity
GO:0008544	epidermis development
GO:0008585	female gonad development
GO:0008652	cellular amino acid biosynthetic process
GO:0009058	biosynthetic process
GO:0009059	macromolecule biosynthetic process
GO:0009069	serine family amino acid metabolic process
GO:0009070	serine family amino acid biosynthetic process
GO:0009266	response to temperature stimulus
GO:0009296	flagellum assembly
GO:0009306	protein secretion
GO:0009314	response to radiation

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Table A.3.1 – continued from previous page

Key	Description
GO:0009416	response to light stimulus
GO:0009566	fertilization
GO:0009581	detection of external stimulus
GO:0009582	detection of abiotic stimulus
GO:0009583	detection of light stimulus
GO:0009584	detection of visible light
GO:0009590	detection of gravity
GO:0009593	detection of chemical stimulus
GO:0009605	response to external stimulus
GO:0009607	response to biotic stimulus
GO:0009611	response to wounding
GO:0009612	response to mechanical stimulus
GO:0009617	response to bacterium
GO:0009624	response to nematode
GO:0009628	response to abiotic stimulus
GO:0009629	response to gravity
GO:0009653	anatomical structure morphogenesis
GO:0009887	organ morphogenesis
GO:0009888	tissue development
GO:0009893	positive regulation of metabolic process
GO:0009914	hormone transport
GO:0009987	cellular process
GO:0010604	positive regulation of macromolecule metabolic process
GO:0010817	regulation of hormone levels
GO:0010876	lipid localization
GO:0010927	cellular component assembly involved in morphogenesis
GO:0010941	regulation of cell death
GO:0012501	programmed cell death
GO:0012505	endomembrane system
GO:0012506	vesicle membrane
GO:0014046	dopamine secretion
GO:0014706	striated muscle tissue development
GO:0015031	protein transport
GO:0015075	ion transmembrane transporter activity
GO:0015103	inorganic anion transmembrane transporter activity
GO:0015106	bicarbonate transmembrane transporter activity
GO:0015669	gas transport
GO:0015671	oxygen transport
GO:0015695	organic cation transport
GO:0015833	peptide transport
GO:0015837	amine transport
GO:0015844	monoamine transport
GO:0015850	organic hydroxy compound transport
GO:0015872	dopamine transport
GO:0015874	norepinephrine transport
GO:0016020	membrane
GO:0016021	integral to membrane
GO:0016023	cytoplasmic membrane–bounded vesicle
GO:0016043	cellular component organization

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Table A.3.1 – continued from previous page

Key	Description
GO:0016048	detection of temperature stimulus
GO:0016050	vesicle organization
GO:0016053	organic acid biosynthetic process
GO:0016064	immunoglobulin mediated immune response
GO:0016192	vesicle-mediated transport
GO:0016265	death
GO:0016444	somatic cell DNA recombination
GO:0016445	somatic diversification of immunoglobulins
GO:0016446	somatic hypermutation of immunoglobulin genes
GO:0016447	somatic recombination of immunoglobulin gene segments
GO:0016477	cell migration
GO:0017145	stem cell division
GO:0019219	regulation of nucleobase-containing compound metabolic process
GO:0019222	regulation of metabolic process
GO:0019724	B cell mediated immunity
GO:0019730	antimicrobial humoral response
GO:0019752	carboxylic acid metabolic process
GO:0019814	immunoglobulin complex
GO:0019815	B cell receptor complex
GO:0019882	antigen processing and presentation
GO:0019884	antigen processing and presentation of exogenous antigen
GO:0019953	sexual reproduction
GO:0021700	developmental maturation
GO:0022008	neurogenesis
GO:0022402	cell cycle process
GO:0022403	cell cycle phase
GO:0022404	molting cycle process
GO:0022405	hair cycle process
GO:0022411	cellular component disassembly
GO:0022412	cellular process involved in reproduction in multicellular organism
GO:0022414	reproductive process
GO:0022600	digestive system process
GO:0022602	ovulation cycle process
GO:0022603	regulation of anatomical structure morphogenesis
GO:0022607	cellular component assembly
GO:0022857	transmembrane transporter activity
GO:0022891	substrate-specific transmembrane transporter activity
GO:0022892	substrate-specific transporter activity
GO:0023052	signaling
GO:0023061	signal release
GO:0030030	cell projection organization
GO:0030031	cell projection assembly
GO:0030072	peptide hormone secretion
GO:0030073	insulin secretion
GO:0030097	hemopoiesis
GO:0030098	lymphocyte differentiation
GO:0030099	myeloid cell differentiation

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Table A.3.1 – continued from previous page

Key	Description
GO:0030101	natural killer cell activation
GO:0030103	vasopressin secretion
GO:0030141	secretory granule
GO:0030154	cell differentiation
GO:0030182	neuron differentiation
GO:0030183	B cell differentiation
GO:0030198	extracellular matrix organization
GO:0030202	heparin metabolic process
GO:0030203	glycosaminoglycan metabolic process
GO:0030210	heparin biosynthetic process
GO:0030217	T cell differentiation
GO:0030218	erythrocyte differentiation
GO:0030219	megakaryocyte differentiation
GO:0030221	basophil differentiation
GO:0030222	eosinophil differentiation
GO:0030223	neutrophil differentiation
GO:0030224	monocyte differentiation
GO:0030225	macrophage differentiation
GO:0030252	growth hormone secretion
GO:0030261	chromosome condensation
GO:0030262	apoptotic nuclear changes
GO:0030263	apoptotic chromosome condensation
GO:0030316	osteoclast differentiation
GO:0030317	sperm motility
GO:0030334	regulation of cell migration
GO:0030335	positive regulation of cell migration
GO:0030529	ribonucleoprotein complex
GO:0030593	neutrophil chemotaxis
GO:0030595	leukocyte chemotaxis
GO:0030659	cytoplasmic vesicle membrane
GO:0030667	secretory granule membrane
GO:0030851	granulocyte differentiation
GO:0030855	epithelial cell differentiation
GO:0031090	organelle membrane
GO:0031224	intrinsic to membrane
GO:0031226	intrinsic to plasma membrane
GO:0031268	pseudopodium organization
GO:0031294	lymphocyte costimulation
GO:0031323	regulation of cellular metabolic process
GO:0031325	positive regulation of cellular metabolic process
GO:0031347	regulation of defense response
GO:0031348	negative regulation of defense response
GO:0031349	positive regulation of defense response
GO:0031410	cytoplasmic vesicle
GO:0031974	membrane-enclosed lumen
GO:0031981	nuclear lumen
GO:0031982	vesicle
GO:0031988	membrane-bounded vesicle
GO:0032101	regulation of response to external stimulus
GO:0032102	negative regulation of response to external stimulus
GO:0032103	positive regulation of response to external stimulus

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Table A.3.1 – continued from previous page

Key	Description
GO:0032274	gonadotropin secretion
GO:0032275	luteinizing hormone secretion
GO:0032394	MHC class Ib receptor activity
GO:0032501	multicellular organismal process
GO:0032502	developmental process
GO:0032504	multicellular organism reproduction
GO:0032606	type I interferon production
GO:0032609	interferon-gamma production
GO:0032611	interleukin-1 beta production
GO:0032612	interleukin-1 production
GO:0032613	interleukin-10 production
GO:0032616	interleukin-13 production
GO:0032620	interleukin-17 production
GO:0032623	interleukin-2 production
GO:0032626	interleukin-22 production
GO:0032633	interleukin-4 production
GO:0032635	interleukin-6 production
GO:0032637	interleukin-8 production
GO:0032638	interleukin-9 production
GO:0032640	tumor necrosis factor production
GO:0032649	regulation of interferon-gamma production
GO:0032689	negative regulation of interferon-gamma production
GO:0032814	regulation of natural killer cell activation
GO:0032816	positive regulation of natural killer cell activation
GO:0032844	regulation of homeostatic process
GO:0032879	regulation of localization
GO:0032880	regulation of protein localization
GO:0032940	secretion by cell
GO:0032943	mononuclear cell proliferation
GO:0032944	regulation of mononuclear cell proliferation
GO:0032945	negative regulation of mononuclear cell proliferation
GO:0032989	cellular component morphogenesis
GO:0032991	macromolecular complex
GO:0032997	Fc receptor complex
GO:0033001	Fc-gamma receptor III complex
GO:0033036	macromolecule localization
GO:0033151	V(D)J recombination
GO:0033152	immunoglobulin V(D)J recombination
GO:0033363	secretory granule organization
GO:0033365	protein localization to organelle
GO:0033366	protein localization to secretory granule
GO:0033371	T cell secretory granule organization
GO:0033374	protein localization to T cell secretory granule
GO:0033375	protease localization to T cell secretory granule
GO:0033380	granzyme B localization to T cell secretory granule
GO:0034101	erythrocyte homeostasis
GO:0034102	erythrocyte clearance
GO:0034613	cellular protein localization
GO:0034641	cellular nitrogen compound metabolic process
GO:0035010	encapsulation of foreign target
GO:0035051	cardiac cell differentiation

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Table A.3.1 – continued from previous page

Key	Description
GO:0035082	axoneme assembly
GO:0035084	flagellar axoneme assembly
GO:0035369	pre-B cell receptor complex
GO:0035710	CD4-positive, alpha-beta T cell activation
GO:0035929	steroid hormone secretion
GO:0035930	corticosteroid hormone secretion
GO:0035931	mineralocorticoid secretion
GO:0035933	glucocorticoid secretion
GO:0035935	androgen secretion
GO:0035936	testosterone secretion
GO:0035937	estrogen secretion
GO:0035938	estradiol secretion
GO:0036160	melanocyte-stimulating hormone secretion
GO:0036161	calcitonin secretion
GO:0038023	signaling receptor activity
GO:0038024	cargo receptor activity
GO:0040011	locomotion
GO:0040012	regulation of locomotion
GO:0040017	positive regulation of locomotion
GO:0042060	wound healing
GO:0042088	T-helper 1 type immune response
GO:0042092	type 2 immune response
GO:0042093	T-helper cell differentiation
GO:0042098	T cell proliferation
GO:0042101	T cell receptor complex
GO:0042105	alpha-beta T cell receptor complex
GO:0042106	gamma-delta T cell receptor complex
GO:0042110	T cell activation
GO:0042113	B cell activation
GO:0042127	regulation of cell proliferation
GO:0042129	regulation of T cell proliferation
GO:0042130	negative regulation of T cell proliferation
GO:0042221	response to chemical stimulus
GO:0042267	natural killer cell mediated cytotoxicity
GO:0042303	molting cycle
GO:0042330	taxis
GO:0042470	melanosome
GO:0042475	odontogenesis of dentin-containing tooth
GO:0042476	odontogenesis
GO:0042481	regulation of odontogenesis
GO:0042483	negative regulation of odontogenesis
GO:0042492	gamma-delta T cell differentiation
GO:0042554	superoxide anion generation
GO:0042571	immunoglobulin complex, circulating
GO:0042582	azurophil granule
GO:0042588	zymogen granule
GO:0042589	zymogen granule membrane
GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I
GO:0042592	homeostatic process
GO:0042611	MHC protein complex

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Table A.3.1 – continued from previous page

Key	Description
GO:0042613	MHC class II protein complex
GO:0042633	hair cycle
GO:0042638	exogen
GO:0042692	muscle cell differentiation
GO:0042698	ovulation cycle
GO:0042701	progesterone secretion
GO:0042742	defense response to bacterium
GO:0042886	amide transport
GO:0042981	regulation of apoptotic process
GO:0042995	cell projection
GO:0043011	myeloid dendritic cell differentiation
GO:0043062	extracellular structure organization
GO:0043064	flagellum organization
GO:0043067	regulation of programmed cell death
GO:0043129	surfactant homeostasis
GO:0043133	hindgut contraction
GO:0043134	regulation of hindgut contraction
GO:0043170	macromolecule metabolic process
GO:0043208	glycosphingolipid binding
GO:0043226	organelle
GO:0043227	membrane–bounded organelle
GO:0043228	non-membrane–bounded organelle
GO:0043229	intracellular organelle
GO:0043231	intracellular membrane–bounded organelle
GO:0043232	intracellular non-membrane–bounded organelle
GO:0043233	organelle lumen
GO:0043234	protein complex
GO:0043235	receptor complex
GO:0043277	apoptotic cell clearance
GO:0043367	CD4-positive, alpha-beta T cell differentiation
GO:0043368	positive T cell selection
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation
GO:0043384	pre-T cell receptor complex
GO:0043436	oxoacid metabolic process
GO:0044057	regulation of system process
GO:0044058	regulation of digestive system process
GO:0044085	cellular component biogenesis
GO:0044237	cellular metabolic process
GO:0044238	primary metabolic process
GO:0044249	cellular biosynthetic process
GO:0044260	cellular macromolecule metabolic process
GO:0044272	sulfur compound biosynthetic process
GO:0044281	small molecule metabolic process
GO:0044283	small molecule biosynthetic process
GO:0044421	extracellular region part
GO:0044422	organelle part
GO:0044424	intracellular part
GO:0044425	membrane part

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Table A.3.1 – continued from previous page

Key	Description
GO:0044427	chromosomal part
GO:0044428	nuclear part
GO:0044433	cytoplasmic vesicle part
GO:0044444	cytoplasmic part
GO:0044446	intracellular organelle part
GO:0044459	plasma membrane part
GO:0044464	cell part
GO:0044699	single-organism process
GO:0044700	single organism signaling
GO:0044702	single organism reproductive process
GO:0044707	single-multicellular organism process
GO:0044710	single-organism metabolic process
GO:0044711	single-organism biosynthetic process
GO:0044763	single-organism cellular process
GO:0045058	T cell selection
GO:0045063	T-helper 1 cell differentiation
GO:0045064	T-helper 2 cell differentiation
GO:0045087	innate immune response
GO:0045137	development of primary sexual characteristics
GO:0045184	establishment of protein localization
GO:0045190	isotype switching
GO:0045191	regulation of isotype switching
GO:0045321	leukocyte activation
GO:0045443	juvenile hormone secretion
GO:0045444	fat cell differentiation
GO:0045453	bone resorption
GO:0045457	ecdysteroid secretion
GO:0045580	regulation of T cell differentiation
GO:0045582	positive regulation of T cell differentiation
GO:0045595	regulation of cell differentiation
GO:0045597	positive regulation of cell differentiation
GO:0045619	regulation of lymphocyte differentiation
GO:0045621	positive regulation of lymphocyte differentiation
GO:0045622	regulation of T-helper cell differentiation
GO:0045624	positive regulation of T-helper cell differentiation
GO:0045625	regulation of T-helper 1 cell differentiation
GO:0045627	positive regulation of T-helper 1 cell differentiation
GO:0045628	regulation of T-helper 2 cell differentiation
GO:0045630	positive regulation of T-helper 2 cell differentiation
GO:0045730	respiratory burst
GO:0045765	regulation of angiogenesis
GO:0045766	positive regulation of angiogenesis
GO:0045830	positive regulation of isotype switching
GO:0045911	positive regulation of DNA recombination
GO:0045935	positive regulation of nucleobase-containing compound metabolic process
GO:0046394	carboxylic acid biosynthetic process
GO:0046483	heterocycle metabolic process
GO:0046545	development of primary female sexual characteristics
GO:0046625	sphingolipid binding
GO:0046629	gamma-delta T cell activation

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Table A.3.1 – continued from previous page

Key	Description
GO:0046631	alpha-beta T cell activation
GO:0046632	alpha-beta T cell differentiation
GO:0046634	regulation of alpha-beta T cell activation
GO:0046635	positive regulation of alpha-beta T cell activation
GO:0046637	regulation of alpha-beta T cell differentiation
GO:0046638	positive regulation of alpha-beta T cell differentiation
GO:0046649	lymphocyte activation
GO:0046651	lymphocyte proliferation
GO:0046660	female sex differentiation
GO:0046849	bone remodeling
GO:0046864	isoprenoid transport
GO:0046865	terpenoid transport
GO:0046879	hormone secretion
GO:0046903	secretion
GO:0048002	antigen processing and presentation of peptide antigen
GO:0048103	somatic stem cell division
GO:0048134	germ-line cyst formation
GO:0048136	male germ-line cyst formation
GO:0048137	spermatocyte division
GO:0048232	male gamete generation
GO:0048240	sperm capacitation
GO:0048241	epinephrine transport
GO:0048242	epinephrine secretion
GO:0048243	norepinephrine secretion
GO:0048285	organelle fission
GO:0048289	isotype switching to IgE isotypes
GO:0048293	regulation of isotype switching to IgE isotypes
GO:0048295	positive regulation of isotype switching to IgE isotypes
GO:0048305	immunoglobulin secretion
GO:0048468	cell development
GO:0048469	cell maturation
GO:0048477	oogenesis
GO:0048511	rhythmic process
GO:0048513	organ development
GO:0048514	blood vessel morphogenesis
GO:0048515	spermatid differentiation
GO:0048518	positive regulation of biological process
GO:0048519	negative regulation of biological process
GO:0048520	positive regulation of behavior
GO:0048522	positive regulation of cellular process
GO:0048523	negative regulation of cellular process
GO:0048534	hematopoietic or lymphoid organ development
GO:0048583	regulation of response to stimulus
GO:0048584	positive regulation of response to stimulus
GO:0048585	negative regulation of response to stimulus
GO:0048608	reproductive structure development
GO:0048609	multicellular organismal reproductive process
GO:0048610	cellular process involved in reproduction
GO:0048646	anatomical structure formation involved in morphogenesis

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Table A.3.1 – continued from previous page

Key	Description
GO:0048699	generation of neurons
GO:0048731	system development
GO:0048738	cardiac muscle tissue development
GO:0048770	pigment granule
GO:0048771	tissue remodeling
GO:0048820	hair follicle maturation
GO:0048856	anatomical structure development
GO:0048869	cellular developmental process
GO:0048870	cell motility
GO:0048871	multicellular organismal homeostasis
GO:0048872	homeostasis of number of cells
GO:0048875	chemical homeostasis within a tissue
GO:0048878	chemical homeostasis
GO:0050432	catecholamine secretion
GO:0050670	regulation of lymphocyte proliferation
GO:0050672	negative regulation of lymphocyte proliferation
GO:0050673	epithelial cell proliferation
GO:0050678	regulation of epithelial cell proliferation
GO:0050679	positive regulation of epithelial cell proliferation
GO:0050708	regulation of protein secretion
GO:0050714	positive regulation of protein secretion
GO:0050727	regulation of inflammatory response
GO:0050728	negative regulation of inflammatory response
GO:0050729	positive regulation of inflammatory response
GO:0050776	regulation of immune response
GO:0050777	negative regulation of immune response
GO:0050778	positive regulation of immune response
GO:0050789	regulation of biological process
GO:0050793	regulation of developmental process
GO:0050794	regulation of cellular process
GO:0050795	regulation of behavior
GO:0050817	coagulation
GO:0050863	regulation of T cell activation
GO:0050864	regulation of B cell activation
GO:0050865	regulation of cell activation
GO:0050866	negative regulation of cell activation
GO:0050867	positive regulation of cell activation
GO:0050868	negative regulation of T cell activation
GO:0050870	positive regulation of T cell activation
GO:0050871	positive regulation of B cell activation
GO:0050877	neurological system process
GO:0050878	regulation of body fluid levels
GO:0050886	endocrine process
GO:0050896	response to stimulus
GO:0050900	leukocyte migration
GO:0050906	detection of stimulus involved in sensory perception
GO:0050907	detection of chemical stimulus involved in sensory perception
GO:0050908	detection of light stimulus involved in visual perception
GO:0050909	sensory perception of taste

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Table A.3.1 – continued from previous page

Key	Description
GO:0050910	detection of mechanical stimulus involved in sensory perception of sound
GO:0050911	detection of chemical stimulus involved in sensory perception of smell
GO:0050912	detection of chemical stimulus involved in sensory perception of taste
GO:0050920	regulation of chemotaxis
GO:0050921	positive regulation of chemotaxis
GO:0050951	sensory perception of temperature stimulus
GO:0050953	sensory perception of light stimulus
GO:0050954	sensory perception of mechanical stimulus
GO:0050955	thermoception
GO:0050960	detection of temperature stimulus involved in thermoception
GO:0050961	detection of temperature stimulus involved in sensory perception
GO:0050962	detection of light stimulus involved in sensory perception
GO:0050974	detection of mechanical stimulus involved in sensory perception
GO:0050975	sensory perception of touch
GO:0050976	detection of mechanical stimulus involved in sensory perception of touch
GO:0050982	detection of mechanical stimulus
GO:0051023	regulation of immunoglobulin secretion
GO:0051024	positive regulation of immunoglobulin secretion
GO:0051046	regulation of secretion
GO:0051047	positive regulation of secretion
GO:0051049	regulation of transport
GO:0051050	positive regulation of transport
GO:0051052	regulation of DNA metabolic process
GO:0051054	positive regulation of DNA metabolic process
GO:0051093	negative regulation of developmental process
GO:0051094	positive regulation of developmental process
GO:0051132	NK T cell activation
GO:0051146	striated muscle cell differentiation
GO:0051171	regulation of nitrogen compound metabolic process
GO:0051173	positive regulation of nitrogen compound metabolic process
GO:0051179	localization
GO:0051216	cartilage development
GO:0051222	positive regulation of protein transport
GO:0051223	regulation of protein transport
GO:0051234	establishment of localization
GO:0051239	regulation of multicellular organismal process
GO:0051241	negative regulation of multicellular organismal process
GO:0051249	regulation of lymphocyte activation
GO:0051250	negative regulation of lymphocyte activation
GO:0051251	positive regulation of lymphocyte activation
GO:0051270	regulation of cellular component movement

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Table A.3.1 – continued from previous page

Key	Description
GO:0051272	positive regulation of cellular component movement
GO:0051276	chromosome organization
GO:0051301	cell division
GO:0051321	meiotic cell cycle
GO:0051327	M phase of meiotic cell cycle
GO:0051458	corticotropin secretion
GO:0051606	detection of stimulus
GO:0051641	cellular localization
GO:0051649	establishment of localization in cell
GO:0051674	localization of cell
GO:0051704	multi-organism process
GO:0051707	response to other organism
GO:0051716	cellular response to stimulus
GO:0051768	nitric-oxide synthase 2 biosynthetic process
GO:0051861	glycolipid binding
GO:0051937	catecholamine transport
GO:0055007	cardiac muscle cell differentiation
GO:0060054	positive regulation of epithelial cell proliferation involved in wound healing
GO:0060089	molecular transducer activity
GO:0060249	anatomical structure homeostasis
GO:0060255	regulation of macromolecule metabolic process
GO:0060326	cell chemotaxis
GO:0060341	regulation of cellular localization
GO:0060374	mast cell differentiation
GO:0060429	epithelium development
GO:0060537	muscle tissue development
GO:0060591	chondroblast differentiation
GO:0060986	endocrine hormone secretion
GO:0061061	muscle structure development
GO:0061448	connective tissue development
GO:0061458	reproductive system development
GO:0065007	biological regulation
GO:0065008	regulation of biological quality
GO:0070013	intracellular organelle lumen
GO:0070091	glucagon secretion
GO:0070201	regulation of establishment of protein localization
GO:0070227	lymphocyte apoptotic process
GO:0070228	regulation of lymphocyte apoptotic process
GO:0070253	somatostatin secretion
GO:0070254	mucus secretion
GO:0070278	extracellular matrix constituent secretion
GO:0070459	prolactin secretion
GO:0070460	thyroid-stimulating hormone secretion
GO:0070661	leukocyte proliferation
GO:0070663	regulation of leukocyte proliferation
GO:0070664	negative regulation of leukocyte proliferation
GO:0070727	cellular macromolecule localization
GO:0070820	tertiary granule
GO:0070887	cellular response to chemical stimulus
GO:0070925	organelle assembly

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Table A.3.1 – continued from previous page

Key	Description
GO:0070998	sensory perception of gravity
GO:0070999	detection of mechanical stimulus involved in sensory perception of gravity
GO:0071103	DNA conformation change
GO:0071695	Anatomical structure maturation
GO:0071702	organic substance transport
GO:0071704	organic substance metabolic process
GO:0071705	nitrogen compound transport
GO:0071706	tumor necrosis factor superfamily cytokine production
GO:0071707	immunoglobulin heavy chain V-D-J recombination
GO:0071708	immunoglobulin light chain V-J recombination
GO:0071735	IgG immunoglobulin complex
GO:0071736	IgG immunoglobulin complex, circulating
GO:0071738	IgD immunoglobulin complex
GO:0071739	IgD immunoglobulin complex, circulating
GO:0071742	IgE immunoglobulin complex
GO:0071743	IgE immunoglobulin complex, circulating
GO:0071745	IgA immunoglobulin complex
GO:0071746	IgA immunoglobulin complex, circulating
GO:0071753	IgM immunoglobulin complex
GO:0071754	IgM immunoglobulin complex, circulating
GO:0071840	cellular component organization or biogenesis
GO:0071887	leukocyte apoptotic process
GO:0071944	cell periphery
GO:0071971	extracellular vesicular exosome assembly
GO:0072358	cardiovascular system development
GO:0072359	circulatory system development
GO:0072593	reactive oxygen species metabolic process
GO:0080090	regulation of primary metabolic process
GO:0080134	regulation of response to stress
GO:0090022	regulation of neutrophil chemotaxis
GO:0090023	positive regulation of neutrophil chemotaxis
GO:0090257	regulation of muscle system process
GO:0090304	nucleic acid metabolic process
GO:0097186	amelogenesis
GO:0097194	execution phase of apoptosis
GO:0097285	cell-type specific apoptotic process
GO:1901135	carbohydrate derivative metabolic process
GO:1901137	carbohydrate derivative biosynthetic process
GO:1901342	regulation of vasculature development
GO:1901360	organic cyclic compound metabolic process
GO:1901564	organonitrogen compound metabolic process
GO:1901566	organonitrogen compound biosynthetic process
GO:1901576	organic substance biosynthetic process
GO:1901605	alpha-amino acid metabolic process
GO:1901607	alpha-amino acid biosynthetic process
GO:2000026	regulation of multicellular organismal development
GO:2000027	regulation of organ morphogenesis
GO:2000106	regulation of leukocyte apoptotic process
GO:2000145	regulation of cell motility
GO:2000147	positive regulation of cell motility

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Table A.3.1 – continued from previous page

Key	Description
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation
PATO:0000001	quality
PATO:0000050	life span
PATO:0000051	morphology
PATO:0000052	shape
PATO:0000068	qualitative
PATO:0000069	deviation(from_normal)
PATO:0000117	size
PATO:0000165	time
PATO:0000261	maturity
PATO:0000406	curved
PATO:0000411	circular
PATO:0000461	normal
PATO:0000586	increased size
PATO:0000587	decreased size
PATO:0000947	elliptic
PATO:0001018	physical quality
PATO:0001241	physical object quality
PATO:0001374	ploidy
PATO:0001375	haploid
PATO:0001393	euploid
PATO:0001394	diploid
PATO:0001396	cellular quality
PATO:0001397	cellular potency
PATO:0001400	unipotent
PATO:0001401	oligopotent
PATO:0001402	multipotent
PATO:0001404	nucleate quality
PATO:0001405	anucleate
PATO:0001406	binucleate
PATO:0001407	mononucleate
PATO:0001501	immature
PATO:0001591	curvature
PATO:0001604	decreased life span
PATO:0001789	domed
PATO:0001857	concave
PATO:0001871	reniform
PATO:0001873	cylindrical
PATO:0001874	discoid
PATO:0001908	multinucleate
PATO:0001979	lobed
PATO:0001995	organismal quality
PATO:0002005	concavity
PATO:0002006	2-D shape
PATO:0002007	convex 3-D shape
PATO:0002008	concave 3-D shape
PATO:0002039	biconcave
PATO:0002070	affinity

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Table A.3.1 – continued from previous page

Key	Description
PATO:0002094	basophilic
PATO:0002182	molecular quality
PATO:0002266	3-D shape
PATO:0002300	increased quality
PATO:0002301	decreased quality
PATO:0002303	decreased object quality
PATO:0002305	increased object quality
PATO:0002318	superelliptic
PR:000000001	protein
PR:000001002	CD19 molecule
PR:000001003	CD34 molecule
PR:000001004	CD4 molecule
PR:000001005	integrin alpha with A domain
PR:000001006	receptor-type tyrosine-protein phosphatase C
PR:000001008	integrin alpha-2
PR:000001010	integrin alpha-E
PR:000001012	integrin alpha-M
PR:000001013	integrin alpha-X
PR:000001014	receptor-type tyrosine-protein phosphatase C isoform CD45R
PR:000001015	receptor-type tyrosine-protein phosphatase C isoform CD45RA
PR:000001017	receptor-type tyrosine-protein phosphatase C isoform CD45RO
PR:000001018	CD3 subunit with immunoglobulin domain
PR:000001020	CD3 epsilon
PR:000001022	neural cell adhesion molecule
PR:000001023	neural cell adhesion molecule NCAM
PR:000001024	neural cell adhesion molecule 1
PR:000001025	C-type lectin with multiple lectin domains
PR:000001026	lymphocyte antigen 75
PR:000001083	CD2 molecule
PR:000001084	T-cell surface glycoprotein CD8 alpha chain
PR:000001094	rhodopsin-like G-protein coupled receptor
PR:000001128	chemokine receptor
PR:000001197	chemokine receptor CCR1/3/1L
PR:000001199	C-C chemokine receptor type 2
PR:000001201	C-C chemokine receptor type 5
PR:000001202	C-C chemokine receptor type 6
PR:000001203	C-C chemokine receptor type 7
PR:000001206	CX3C chemokine receptor 1
PR:000001207	C-X-C chemokine receptor type 3
PR:000001208	C-X-C chemokine receptor type 4
PR:000001209	C-X-C chemokine receptor type 5
PR:000001226	high affinity interleukin-8 receptor
PR:000001254	chemokine receptor CCR1
PR:000001255	chemokine receptor CCR3
PR:000001256	high affinity interleukin-8 receptor A
PR:000001257	high affinity interleukin-8 receptor B
PR:000001281	ADP-ribosyl cyclase
PR:000001288	B-cell receptor CD22

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Table A.3.1 – continued from previous page

Key	Description
PR:000001289	membrane-spanning 4-domains subfamily A member 1
PR:000001290	B7-related protein
PR:000001292	C-type lectin domain family 4 member C
PR:000001293	C-type lectin domain family 4 member K
PR:000001300	CD209 molecule
PR:000001307	CD44 molecule
PR:000001308	CD48 molecule
PR:000001310	CD83 molecule
PR:000001318	L-selectin
PR:000001319	SLAM family member 5
PR:000001320	alpha-(1,3)-fucosyltransferase
PR:000001326	bone marrow stromal antigen 2
PR:000001327	cadherin
PR:000001332	carcinoembryonic antigen-related cell adhesion molecule 8
PR:000001337	complement receptor type 1
PR:000001338	complement receptor type 2
PR:000001343	CD69 molecule
PR:000001344	ectonucleotide pyrophosphatase/phosphodiesterase family member 3
PR:000001345	endoglin
PR:000001350	forkhead box protein P3
PR:000001352	glycophorin
PR:000001355	immunoglobulin gamma Fc receptor II/III/IV
PR:000001356	immunoglobulin gamma Fc receptor I
PR:000001380	interleukin-2 receptor subunit alpha
PR:000001381	interleukin-2 receptor subunit beta
PR:000001398	leukocyte immunoglobulin-like receptor subfamily A member 4
PR:000001402	killer cell lectin-like receptor subfamily D member 1
PR:000001403	tetraspanin
PR:000001408	ADP-ribosyl cyclase 1
PR:000001412	CD86 molecule
PR:000001431	N-formyl peptide receptor
PR:000001438	CD80 molecule
PR:000001444	cadherin-5
PR:000001447	epithelial cadherin
PR:000001456	alpha-(1,3)-fucosyltransferase FUT4
PR:000001460	glycophorin-A
PR:000001465	high affinity immunoglobulin gamma Fc receptor I
PR:000001479	low affinity immunoglobulin gamma Fc region receptor II
PR:000001481	low affinity immunoglobulin gamma Fc region receptor II-b
PR:000001483	low affinity immunoglobulin gamma Fc region receptor III
PR:000001580	fMet-Leu-Phe receptor
PR:000001753	transcription factor NF-kappa-B
PR:000001785	prominin
PR:000001786	prominin-1
PR:000001800	5'-nucleotidase

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Table A.3.1 – continued from previous page

Key	Description
PR:000001806	C-type lectin domain family 6 member A
PR:000001807	C-type lectin domain family 7 member A
PR:000001809	CD59-like glycoprotein
PR:000001810	CSF-1/PDGF receptor-type tyrosine-protein kinase
PR:000001813	EGF-like module-containing mucin-like hormone receptor-like 1
PR:000001832	SIRP/SHPS-1 family protein
PR:000001833	SLAM family member 1
PR:000001835	T-box transcription factor TBX21
PR:000001836	CD7 molecule
PR:000001838	T-cell surface glycoprotein CD1
PR:000001839	T-cell surface glycoprotein CD5
PR:000001841	T-cell-specific surface glycoprotein CD28
PR:000001843	Thy-1 membrane glycoprotein
PR:000001844	arginase-1
PR:000001850	cathepsin K
PR:000001852	cytotoxic T-lymphocyte protein 4
PR:000001858	immunoglobulin iota chain
PR:000001859	immunoglobulin lambda-like polypeptide 1
PR:000001860	inducible T-cell costimulator
PR:000001861	integrin beta
PR:000001865	interleukin-3 receptor class 2 alpha chain
PR:000001867	interleukin-5 receptor subunit alpha
PR:000001869	interleukin-7 receptor subunit alpha
PR:000001874	KLRB1-like protein
PR:000001879	leukosialin
PR:000001880	low affinity immunoglobulin epsilon Fc receptor
PR:000001883	lysosome-associated membrane protein
PR:000001884	macrophage receptor MARCO
PR:000001885	macrophage scavenger receptor types I and II
PR:000001888	membrane alanyl aminopeptidase-like metallopeptidase
PR:000001889	CD14 molecule
PR:000001892	CD33 molecule
PR:000001893	natural cytotoxicity triggering receptor 1
PR:000001896	natural killer cell receptor 2B4
PR:000001897	natural killer cell receptor NKG2
PR:000001898	nephrilysin
PR:000001902	nuclear receptor ROR-gamma
PR:000001903	paired box protein PAX-5
PR:000001905	platelet glycoprotein 4
PR:000001907	platelet glycoprotein Ib alpha chain
PR:000001919	programmed cell death protein 1
PR:000001925	scavenger receptor cysteine-rich type 1 protein M130
PR:000001927	sialic acid-binding Ig-like lectin 5
PR:000001931	sialoadhesin
PR:000001932	signal transducer CD24
PR:000001935	syndecan-1
PR:000001937	tartrate-resistant acid phosphatase type 5
PR:000001938	thrombomodulin-like receptor

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Table A.3.1 – continued from previous page

Key	Description
PR:000001941	trans-acting T-cell-specific transcription factor GATA-3
PR:000001944	transcription factor PU.1
PR:000001945	transferrin receptor protein 1
PR:000001950	tumor necrosis factor ligand superfamily member 5
PR:000001954	tumor necrosis factor receptor superfamily member 11A
PR:000001963	CD27 molecule
PR:000001968	tyrosine-protein phosphatase non-receptor type substrate 1
PR:000001969	urokinase plasminogen activator surface receptor
PR:000001971	vascular endothelial growth factor receptor
PR:000002001	FL cytokine receptor
PR:000002023	NKG2-A/NKG2-B type II integral membrane protein
PR:000002025	T-cell surface glycoprotein CD1a
PR:000002027	T-cell surface glycoprotein CD1c
PR:000002028	T-cell surface glycoprotein CD1d
PR:000002031	aminopeptidase N
PR:000002037	complement component C1q receptor
PR:000002039	glutamyl aminopeptidase
PR:000002062	macrophage colony-stimulating factor 1 receptor
PR:000002064	macrosialin
PR:000002065	mast/stem cell growth factor receptor
PR:000002105	thrombomodulin
PR:000002112	vascular endothelial growth factor receptor 2
PR:000002972	macrophage mannose receptor 1
PR:000002976	ly-6-like protein
PR:000002977	killer cell lectin-like receptor subfamily B member 1C
PR:000002978	lymphocyte antigen 6G
PR:000002979	lymphocyte antigen 6A-2/6E-1
PR:000002980	lymphocyte antigen 6C
PR:000002981	lymphocyte antigen 76
PR:000003450	B-cell lymphoma 6 protein
PR:000003455	nuclear receptor ROR-gamma isoform 2
PR:000003457	V(D)J recombination-activating protein 1
PR:000003460	V(D)J recombination-activating protein 2
PR:000003463	eomesodermin
PR:000003466	perforin-1
PR:000003469	early growth response protein 2
PR:000003499	granzyme B
PR:000003505	leukocyte granule-associated proteinase
PR:000003506	T-brain transcription factor
PR:000003516	lactosylceramide 4-alpha-galactosyltransferase
PR:000005178	CD9 molecule
PR:000005307	CCAAT/enhancer-binding protein alpha
PR:000005310	CCAAT/enhancer-binding protein epsilon
PR:000006169	cell surface glycoprotein CD200 receptor 3
PR:000006172	CD209 molecule-like protein B
PR:000006611	DNA nucleotidylexotransferase
PR:000007152	eosinophil peroxidase

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Table A.3.1 – continued from previous page

Key	Description
PR:000007431	high affinity immunoglobulin epsilon receptor subunit alpha
PR:000007597	proto-oncogene c-Fos
PR:000007857	erythroid transcription factor
PR:000007858	endothelial transcription factor GATA-2
PR:000007939	glial fibrillary acidic protein
PR:000008467	hemoglobin subunit zeta
PR:000008857	hemoglobin subunit beta-1
PR:000008982	interleukin-17 receptor B
PR:000008994	interleukin-1 receptor-like 1
PR:000009127	integrin alpha-IIb
PR:000009129	integrin alpha-4
PR:000009143	integrin beta-7
PR:000009616	T-cell surface glycoprotein YE1/48
PR:000009618	killer cell lectin-like receptor 3
PR:000009619	killer cell lectin-like receptor 4
PR:000009623	killer cell lectin-like receptor 8
PR:000009725	neutrophil gelatinase-associated lipocalin
PR:000009766	galectin-1
PR:000009978	lactotransferrin
PR:000010329	tyrosine-protein kinase Mer
PR:000010543	myeloperoxidase
PR:000010799	myb proto-oncogene protein
PR:000011178	nuclear factor NF-kappa-B p100 subunit
PR:000014046	non-secretory ribonuclease
PR:000014047	eosinophil cationic protein
PR:000014362	runt-related transcription factor 1
PR:000016043	T-cell acute lymphocytic leukemia protein 1
PR:000016401	transmembrane emp24 domain-containing protein 1
PR:000018263	amino acid chain
PR:000018264	proteolytic cleavage product
PR:000021082	bone marrow proteoglycan proteolytic cleavage product
PR:000022006	eosinophil granule major basic protein
PR:000025402	T cell receptor co-receptor CD8
PR:000025403	T-cell surface glycoprotein CD8 alpha chain isoform 1
PR:000025796	integrin alpha
PR:000025797	integrin alpha lacking A domain
UBERON:0000002	uterine cervix
UBERON:0000004	olfactory apparatus
UBERON:0000006	islet of Langerhans
UBERON:0000007	pituitary gland
UBERON:0000009	submucosa
UBERON:0000010	peripheral nervous system
UBERON:0000015	anatomical boundary
UBERON:0000016	endocrine pancreas
UBERON:0000017	exocrine pancreas
UBERON:0000019	camera-type eye
UBERON:0000020	sense organ
UBERON:0000025	tube

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Key	Description
UBERON:0000029	lymph node
UBERON:0000030	lamina propria
UBERON:0000033	head
UBERON:0000042	serous membrane
UBERON:0000043	tendon
UBERON:0000044	dorsal root ganglion
UBERON:0000045	ganglion
UBERON:0000047	simple eye
UBERON:0000054	macula
UBERON:0000055	vessel
UBERON:0000056	ureter
UBERON:0000057	urethra
UBERON:0000058	duct
UBERON:0000059	large intestine
UBERON:0000060	anatomical wall
UBERON:0000061	anatomical structure
UBERON:0000062	organ
UBERON:0000063	organ segment
UBERON:0000064	organ part
UBERON:0000065	respiratory tract
UBERON:0000072	segment of respiratory tract
UBERON:0000073	regional part of nervous system
UBERON:0000074	renal glomerulus
UBERON:0000075	subdivision of skeletal system
UBERON:0000076	external ectoderm
UBERON:0000077	mixed endoderm/mesoderm-derived structure
UBERON:0000078	mixed ectoderm/mesoderm/endoderm-derived structure
UBERON:0000079	male reproductive system
UBERON:0000080	mesonephros
UBERON:0000083	mesonephric tubule
UBERON:0000084	ureteric bud
UBERON:0000085	morula
UBERON:0000087	inner cell mass
UBERON:0000091	bilaminar disc
UBERON:0000094	membrane organ
UBERON:0000102	lung vasculature
UBERON:0000115	lung epithelium
UBERON:0000117	respiratory tube
UBERON:0000118	lung bud
UBERON:0000119	cell layer
UBERON:0000121	perineurium
UBERON:0000122	neuron projection bundle
UBERON:0000125	neural nucleus
UBERON:0000153	anterior region of body
UBERON:0000158	membranous layer
UBERON:0000160	intestine
UBERON:0000162	cloaca
UBERON:0000163	embryonic cloaca
UBERON:0000164	primitive urogenital sinus
UBERON:0000165	mouth

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0000168	segment of colon
UBERON:0000170	pair of lungs
UBERON:0000171	respiration organ
UBERON:0000173	amniotic fluid
UBERON:0000178	blood
UBERON:0000179	haemolymphatic fluid
UBERON:0000203	pallium
UBERON:0000204	ventral part of telencephalon
UBERON:0000211	ligament
UBERON:0000305	amnion
UBERON:0000307	blastula
UBERON:0000310	breast
UBERON:0000325	gastric gland
UBERON:0000333	intestinal gland
UBERON:0000344	mucosa
UBERON:0000349	limbic system
UBERON:0000353	parenchyma
UBERON:0000358	blastocyst
UBERON:0000362	renal medulla
UBERON:0000365	urothelium
UBERON:0000369	corpus striatum
UBERON:0000379	tracheal mucosa
UBERON:0000383	musculature of body
UBERON:0000397	colonic epithelium
UBERON:0000410	bronchial mucosa
UBERON:0000412	dermal papilla
UBERON:0000414	mucous gland
UBERON:0000415	artery wall
UBERON:0000428	prostate epithelium
UBERON:0000444	lymphoid follicle
UBERON:0000454	cerebral subcortex
UBERON:0000458	endocervix
UBERON:0000459	uterine wall
UBERON:0000463	portion of organism substance
UBERON:0000464	anatomical space
UBERON:0000465	material anatomical entity
UBERON:0000466	immaterial anatomical entity
UBERON:0000467	anatomical system
UBERON:0000468	multi-cellular organism
UBERON:0000470	cell part
UBERON:0000471	compound organ component
UBERON:0000473	testis
UBERON:0000474	female reproductive system
UBERON:0000475	organism subdivision
UBERON:0000477	anatomical cluster
UBERON:0000478	extraembryonic structure
UBERON:0000479	tissue
UBERON:0000480	anatomical group
UBERON:0000481	multi-tissue structure
UBERON:0000483	epithelium
UBERON:0000484	simple cuboidal epithelium

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0000485	simple columnar epithelium
UBERON:0000486	multilaminar epithelium
UBERON:0000487	simple squamous epithelium
UBERON:0000488	atypical epithelium
UBERON:0000489	cavitated compound organ
UBERON:0000490	unilaminar epithelium
UBERON:0000915	thoracic segment of trunk
UBERON:0000916	abdomen
UBERON:0000922	embryo
UBERON:0000923	germ layer
UBERON:0000924	ectoderm
UBERON:0000925	endoderm
UBERON:0000926	mesoderm
UBERON:0000930	stomodeum
UBERON:0000931	proctodeum
UBERON:0000945	stomach
UBERON:0000947	aorta
UBERON:0000948	heart
UBERON:0000949	endocrine system
UBERON:0000955	brain
UBERON:0000956	cerebral cortex
UBERON:0000958	medulla
UBERON:0000964	cornea
UBERON:0000965	lens of camera-type eye
UBERON:0000966	retina
UBERON:0000970	eye
UBERON:0000974	neck
UBERON:0000977	pleura
UBERON:0000982	skeletal joint
UBERON:0000990	reproductive system
UBERON:0000991	gonad
UBERON:0000992	female gonad
UBERON:0000995	uterus
UBERON:0000996	vagina
UBERON:0001003	epidermis
UBERON:0001004	respiratory system
UBERON:0001005	respiratory airway
UBERON:0001007	digestive system
UBERON:0001008	excretory system
UBERON:0001009	circulatory system
UBERON:0001013	adipose tissue
UBERON:0001015	musculature
UBERON:0001016	nervous system
UBERON:0001017	central nervous system
UBERON:0001021	nerve
UBERON:0001023	dendrite
UBERON:0001024	neurite
UBERON:0001032	sensory system
UBERON:0001040	yolk sac
UBERON:0001041	foregut
UBERON:0001042	chordate pharynx

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0001043	esophagus
UBERON:0001044	salivary gland
UBERON:0001045	midgut
UBERON:0001046	hindgut
UBERON:0001048	primordium
UBERON:0001049	neural tube
UBERON:0001052	rectum
UBERON:0001062	anatomical entity
UBERON:0001064	ventral pancreatic duct
UBERON:0001066	intervertebral disk
UBERON:0001091	calcareous tooth
UBERON:0001096	wall of esophagus
UBERON:0001130	vertebral column
UBERON:0001132	parathyroid gland
UBERON:0001133	cardiac muscle tissue
UBERON:0001134	skeletal muscle tissue
UBERON:0001135	smooth muscle tissue
UBERON:0001136	mesothelium
UBERON:0001137	dorsum
UBERON:0001140	renal vein
UBERON:0001153	caecum
UBERON:0001154	vermiform appendix
UBERON:0001155	colon
UBERON:0001156	ascending colon
UBERON:0001157	transverse colon
UBERON:0001158	descending colon
UBERON:0001159	sigmoid colon
UBERON:0001160	fundus of stomach
UBERON:0001162	cardia of stomach
UBERON:0001166	pylorus
UBERON:0001167	wall of stomach
UBERON:0001168	wall of small intestine
UBERON:0001169	wall of large intestine
UBERON:0001173	biliary tree
UBERON:0001178	visceral peritoneum
UBERON:0001179	peritoneal cavity
UBERON:0001199	mucosa of stomach
UBERON:0001204	mucosa of small intestine
UBERON:0001205	submucosa of small intestine
UBERON:0001207	mucosa of large intestine
UBERON:0001211	Peyer's patch
UBERON:0001212	duodenal gland
UBERON:0001213	intestinal villus
UBERON:0001224	renal pelvis
UBERON:0001225	cortex of kidney
UBERON:0001228	renal papilla
UBERON:0001229	renal corpuscle
UBERON:0001230	glomerular capsule
UBERON:0001231	nephron tubule
UBERON:0001232	collecting duct of renal tubule
UBERON:0001235	adrenal cortex

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0001236	adrenal medulla
UBERON:0001237	paraaortic body
UBERON:0001238	lamina propria of small intestine
UBERON:0001242	intestinal mucosa
UBERON:0001249	spleen lymphoid follicle
UBERON:0001250	red pulp of spleen
UBERON:0001251	marginal zone of spleen
UBERON:0001252	adventitia of ureter
UBERON:0001254	urothelium of ureter
UBERON:0001255	urinary bladder
UBERON:0001256	wall of urinary bladder
UBERON:0001257	trigone of urinary bladder
UBERON:0001259	mucosa of urinary bladder
UBERON:0001262	wall of intestine
UBERON:0001263	pancreatic acinus
UBERON:0001264	pancreas
UBERON:0001266	splenic cord
UBERON:0001276	epithelium of stomach
UBERON:0001277	intestinal epithelium
UBERON:0001278	epithelium of large intestine
UBERON:0001280	liver parenchyma
UBERON:0001281	hepatic sinusoid
UBERON:0001285	nephron
UBERON:0001287	proximal convoluted tubule
UBERON:0001288	loop of Henle
UBERON:0001289	descending limb of loop of Henle
UBERON:0001290	proximal straight tubule
UBERON:0001291	thick ascending limb of loop of Henle
UBERON:0001292	distal convoluted tubule
UBERON:0001293	outer medulla of kidney
UBERON:0001294	inner medulla of kidney
UBERON:0001296	myometrium
UBERON:0001305	ovarian follicle
UBERON:0001310	umbilical artery
UBERON:0001343	seminiferous tubule of testis
UBERON:0001347	white adipose tissue
UBERON:0001348	brown adipose tissue
UBERON:0001351	lacrimal sac
UBERON:0001352	external acoustic meatus
UBERON:0001353	anal region
UBERON:0001366	parietal peritoneum
UBERON:0001434	skeletal system
UBERON:0001443	chest
UBERON:0001444	subdivision of head
UBERON:0001456	face
UBERON:0001468	intervertebral joint
UBERON:0001473	lymphatic vessel
UBERON:0001474	bone
UBERON:0001515	thoracic aorta
UBERON:0001529	brachiocephalic artery
UBERON:0001533	subclavian artery

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0001552	arcuate artery
UBERON:0001555	digestive tract
UBERON:0001556	lower urinary tract
UBERON:0001557	upper respiratory tract
UBERON:0001558	lower respiratory tract
UBERON:0001560	neck of organ
UBERON:0001606	muscle of iris
UBERON:0001607	sphincter pupillae
UBERON:0001608	dilatator pupillae
UBERON:0001621	coronary artery
UBERON:0001630	muscle organ
UBERON:0001637	artery
UBERON:0001638	vein
UBERON:0001678	temporal bone
UBERON:0001690	ear
UBERON:0001691	external ear
UBERON:0001694	petrous part of temporal bone
UBERON:0001703	neurocranium
UBERON:0001708	jaw skeleton
UBERON:0001711	eyelid
UBERON:0001735	tonsillar ring
UBERON:0001744	lymphoid tissue
UBERON:0001745	secondary nodular lymphoid tissue
UBERON:0001747	parenchyma of thyroid gland
UBERON:0001750	lacrimal apparatus
UBERON:0001751	dentine
UBERON:0001752	enamel
UBERON:0001753	cementum
UBERON:0001754	dental pulp
UBERON:0001756	middle ear
UBERON:0001758	periodontium
UBERON:0001763	odontogenic papilla
UBERON:0001765	mammary duct
UBERON:0001766	anterior chamber of eyeball
UBERON:0001768	uvea
UBERON:0001769	iris
UBERON:0001770	lacrimal canaliculus
UBERON:0001773	sclera
UBERON:0001775	ciliary body
UBERON:0001776	optic choroid
UBERON:0001777	substantia propria of cornea
UBERON:0001778	ciliary epithelium
UBERON:0001780	spinal nerve
UBERON:0001781	layer of retina
UBERON:0001782	pigmented layer of retina
UBERON:0001800	sensory ganglion
UBERON:0001801	anterior segment of eyeball
UBERON:0001802	posterior segment of eyeball
UBERON:0001803	epithelium of lens
UBERON:0001811	conjunctiva
UBERON:0001820	sweat gland

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0001821	sebaceous gland
UBERON:0001826	nasal cavity mucosa
UBERON:0001828	gingiva
UBERON:0001839	bony labyrinth
UBERON:0001840	semicircular canal
UBERON:0001844	cochlea
UBERON:0001846	internal ear
UBERON:0001849	membranous labyrinth
UBERON:0001850	lacrimal duct
UBERON:0001851	cortex
UBERON:0001853	utricle of membranous labyrinth
UBERON:0001854	saccule of membranous labyrinth
UBERON:0001855	cochlear duct of membranous labyrinth
UBERON:0001856	semicircular duct
UBERON:0001862	vestibular labyrinth
UBERON:0001869	cerebral hemisphere
UBERON:0001886	choroid plexus
UBERON:0001890	forebrain
UBERON:0001891	midbrain
UBERON:0001893	telencephalon
UBERON:0001894	diencephalon
UBERON:0001895	metencephalon
UBERON:0001898	hypothalamus
UBERON:0001901	epithelium of trachea
UBERON:0001902	epithelium of small intestine
UBERON:0001911	mammary gland
UBERON:0001912	lobule of lactiferous gland
UBERON:0001915	endothelium of capillary
UBERON:0001917	endothelium of artery
UBERON:0001930	paraventricular nucleus of hypothalamus
UBERON:0001948	regional part of spinal cord
UBERON:0001949	gingival epithelium
UBERON:0001954	Ammon's horn
UBERON:0001955	epithelium of respiratory bronchiole
UBERON:0001958	epithelium of terminal bronchiole
UBERON:0001959	white pulp of spleen
UBERON:0001961	mucosa-associated lymphoid tissue
UBERON:0001962	gut-associated lymphoid tissue
UBERON:0001963	bronchial-associated lymphoid tissue
UBERON:0001973	substance of tooth
UBERON:0001976	epithelium of esophagus
UBERON:0001979	venule
UBERON:0001980	arteriole
UBERON:0001981	blood vessel
UBERON:0001982	capillary
UBERON:0001983	crypt of Lieberkuhn
UBERON:0001986	endothelium
UBERON:0001987	placenta
UBERON:0001992	papillary layer of dermis
UBERON:0001994	hyaline cartilage
UBERON:0001995	fibrocartilage

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0001997	olfactory epithelium
UBERON:0002005	enteric nervous system
UBERON:0002006	cortex of lymph node
UBERON:0002012	pulmonary artery
UBERON:0002018	synovial membrane of synovial joint
UBERON:0002020	gray matter of neuraxis
UBERON:0002027	stratum corneum of epidermis
UBERON:0002028	hindbrain
UBERON:0002031	epithelium of bronchus
UBERON:0002036	striated muscle tissue
UBERON:0002037	cerebellum
UBERON:0002038	substantia nigra
UBERON:0002046	thyroid gland
UBERON:0002048	lung
UBERON:0002049	vasculature
UBERON:0002050	embryonic structure
UBERON:0002051	epithelium of bronchiole
UBERON:0002053	zona glomerulosa of adrenal gland
UBERON:0002061	truncus arteriosus
UBERON:0002066	umbilical vein
UBERON:0002067	dermis
UBERON:0002072	hypodermis
UBERON:0002073	hair follicle
UBERON:0002075	viscus
UBERON:0002080	heart right ventricle
UBERON:0002081	cardiac atrium
UBERON:0002082	cardiac ventricle
UBERON:0002084	heart left ventricle
UBERON:0002085	interatrial septum
UBERON:0002091	entire appendicular skeleton
UBERON:0002094	interventricular septum
UBERON:0002095	mesentery
UBERON:0002097	skin of body
UBERON:0002099	cardiac septum
UBERON:0002100	trunk
UBERON:0002104	visual system
UBERON:0002105	vestibulo-auditory system
UBERON:0002106	spleen
UBERON:0002107	liver
UBERON:0002108	small intestine
UBERON:0002110	gallbladder
UBERON:0002111	artery smooth muscle tissue
UBERON:0002113	kidney
UBERON:0002114	duodenum
UBERON:0002115	jejunum
UBERON:0002116	ileum
UBERON:0002118	right ovary
UBERON:0002119	left ovary
UBERON:0002120	pronephros
UBERON:0002123	cortex of thymus
UBERON:0002124	medulla of thymus

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0002165	endocardium
UBERON:0002169	alveolar sac
UBERON:0002185	bronchus
UBERON:0002186	bronchiole
UBERON:0002187	terminal bronchiole
UBERON:0002188	respiratory bronchiole
UBERON:0002190	subcutaneous adipose tissue
UBERON:0002193	hemolymphoid system
UBERON:0002194	capsule of lymph node
UBERON:0002196	adenohypophysis
UBERON:0002199	integument
UBERON:0002200	vasculature of head
UBERON:0002201	vasculature of trunk
UBERON:0002203	vasculature of eye
UBERON:0002204	musculoskeletal system
UBERON:0002209	fibrous joint
UBERON:0002211	nerve root
UBERON:0002213	cartilaginous joint
UBERON:0002214	macula of utricle of membranous labyrinth
UBERON:0002216	symphysis
UBERON:0002217	synovial joint
UBERON:0002227	spiral organ of cochlea
UBERON:0002240	spinal cord
UBERON:0002241	chondrocranium
UBERON:0002242	nucleus pulposus
UBERON:0002255	vomeronasal organ
UBERON:0002256	dorsal horn of spinal cord
UBERON:0002257	ventral horn of spinal cord
UBERON:0002261	dorsal root of spinal cord
UBERON:0002264	olfactory bulb
UBERON:0002268	olfactory organ
UBERON:0002271	periventricular zone of hypothalamus
UBERON:0002275	reticular formation
UBERON:0002276	lamina of spiral limbus
UBERON:0002282	stria vascularis of cochlear duct
UBERON:0002294	biliary system
UBERON:0002296	dorsal mesentery
UBERON:0002299	alveolus of lung
UBERON:0002303	juxtaglomerular apparatus
UBERON:0002305	layer of hippocampus
UBERON:0002308	nucleus of brain
UBERON:0002313	hippocampus pyramidal layer
UBERON:0002315	gray matter of spinal cord
UBERON:0002319	mesangium
UBERON:0002320	glomerular mesangium
UBERON:0002321	extraglomerular mesangium
UBERON:0002323	coelomic cavity lumen
UBERON:0002325	epithelium of urethra
UBERON:0002328	notochord
UBERON:0002329	somite
UBERON:0002330	exocrine system

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0002331	umbilical cord
UBERON:0002335	macula densa
UBERON:0002342	neural crest
UBERON:0002346	neurectoderm
UBERON:0002348	epicardium
UBERON:0002349	myocardium
UBERON:0002350	conducting system of heart
UBERON:0002351	sinoatrial node
UBERON:0002352	atrioventricular node
UBERON:0002353	atrioventricular bundle
UBERON:0002355	pelvis
UBERON:0002357	serous pericardium
UBERON:0002358	peritoneum
UBERON:0002360	meninx
UBERON:0002363	dura mater
UBERON:0002364	tympanic membrane
UBERON:0002365	exocrine gland
UBERON:0002367	prostate gland
UBERON:0002368	endocrine gland
UBERON:0002369	adrenal gland
UBERON:0002370	thymus
UBERON:0002371	bone marrow
UBERON:0002372	tonsil
UBERON:0002376	muscle of head
UBERON:0002384	connective tissue
UBERON:0002385	muscle tissue
UBERON:0002390	hematopoietic system
UBERON:0002392	nasolacrimal duct
UBERON:0002394	bile duct
UBERON:0002400	parietal pleura
UBERON:0002401	visceral pleura
UBERON:0002405	immune system
UBERON:0002406	pericardial sac
UBERON:0002407	pericardium
UBERON:0002410	autonomic nervous system
UBERON:0002412	vertebra
UBERON:0002416	integumental system
UBERON:0002417	abdominal segment of trunk
UBERON:0002418	cartilage tissue
UBERON:0002419	skin gland
UBERON:0002420	basal ganglion
UBERON:0002421	hippocampal formation
UBERON:0002423	hepatobiliary system
UBERON:0002424	oral epithelium
UBERON:0002425	visceral serous pericardium
UBERON:0002435	striatum
UBERON:0002456	internal thoracic artery
UBERON:0002465	lymphoid system
UBERON:0002469	esophagus mucosa
UBERON:0002481	bone tissue
UBERON:0002485	prostate duct

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0002495	long bone
UBERON:0002499	cochlear labyrinth
UBERON:0002506	iris epithelium
UBERON:0002512	corpus luteum
UBERON:0002513	endochondral bone
UBERON:0002517	basicranium
UBERON:0002518	otolith organ
UBERON:0002521	elastic tissue
UBERON:0002523	tunica intima
UBERON:0002530	gland
UBERON:0002532	epiblast (generic)
UBERON:0002539	pharyngeal arch
UBERON:0002546	cranial placode
UBERON:0002553	anatomical cavity
UBERON:0002600	limbic lobe
UBERON:0002616	regional part of brain
UBERON:0002619	regional part of cerebral cortex
UBERON:0002680	regional part of metencephalon
UBERON:0002780	regional part of forebrain
UBERON:0002784	regional part of diencephalon
UBERON:0002791	regional part of telencephalon
UBERON:0002950	regional part of midbrain
UBERON:0003022	lobe parts of cerebral cortex
UBERON:0003037	septum
UBERON:0003048	regional part of hypothalamus
UBERON:0003050	olfactory placode
UBERON:0003051	ear vesicle
UBERON:0003055	periderm
UBERON:0003056	pre-chordal neural plate
UBERON:0003057	chordal neural plate
UBERON:0003059	presomitic mesoderm
UBERON:0003060	pronephric duct
UBERON:0003061	blood island
UBERON:0003063	prechordal plate
UBERON:0003064	intermediate mesoderm
UBERON:0003067	dorsolateral placode
UBERON:0003068	axial mesoderm
UBERON:0003069	otic placode
UBERON:0003071	eye primordium
UBERON:0003072	optic cup
UBERON:0003073	lens placode
UBERON:0003074	mesonephric duct
UBERON:0003075	neural plate
UBERON:0003076	posterior neural tube
UBERON:0003077	paraxial mesoderm
UBERON:0003080	anterior neural tube
UBERON:0003081	lateral plate mesoderm
UBERON:0003082	myotome
UBERON:0003083	trunk neural crest
UBERON:0003084	heart primordium
UBERON:0003089	sclerotome

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0003091	thyroid primordium
UBERON:0003099	cranial neural crest
UBERON:0003100	female organism
UBERON:0003101	male organism
UBERON:0003102	surface structure
UBERON:0003103	compound organ
UBERON:0003104	mesenchyme
UBERON:0003124	chorion
UBERON:0003126	trachea
UBERON:0003128	cranium
UBERON:0003129	skull
UBERON:0003133	reproductive organ
UBERON:0003134	female reproductive organ
UBERON:0003135	male reproductive organ
UBERON:0003210	blood-cerebrospinal fluid barrier
UBERON:0003214	mammary gland alveolus
UBERON:0003215	alveolus
UBERON:0003220	metanephric mesenchyme
UBERON:0003241	epithelium of utricle
UBERON:0003242	epithelium of saccule
UBERON:0003244	epithelium of mammary gland
UBERON:0003258	endoderm of foregut
UBERON:0003281	mesentery of stomach
UBERON:0003294	gland of foregut
UBERON:0003295	pharyngeal gland
UBERON:0003296	gland of diencephalon
UBERON:0003297	gland of integumental system
UBERON:0003332	submucosa of duodenum
UBERON:0003338	ganglion of peripheral nervous system
UBERON:0003350	epithelium of mucosa
UBERON:0003351	pharyngeal epithelium
UBERON:0003353	epithelium of hindgut
UBERON:0003386	smooth muscle of eye
UBERON:0003408	gland of gut
UBERON:0003422	mesenchyme of umbilical cord
UBERON:0003454	small intestine Peyer's patch
UBERON:0003455	inner renal medulla loop of henle
UBERON:0003457	head bone
UBERON:0003462	facial bone
UBERON:0003469	respiratory system artery
UBERON:0003487	skin sebaceous gland
UBERON:0003496	head blood vessel
UBERON:0003497	abdomen blood vessel
UBERON:0003498	heart blood vessel
UBERON:0003504	respiratory system blood vessel
UBERON:0003509	arterial blood vessel
UBERON:0003513	trunk blood vessel
UBERON:0003517	kidney blood vessel
UBERON:0003527	kidney capillary
UBERON:0003528	brain grey matter
UBERON:0003566	head connective tissue

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0003567	abdomen connective tissue
UBERON:0003586	trunk connective tissue
UBERON:0003643	respiratory system arterial blood vessel
UBERON:0003644	kidney arterial blood vessel
UBERON:0003672	dentition
UBERON:0003688	omentum
UBERON:0003697	abdominal wall
UBERON:0003704	intrahepatic bile duct
UBERON:0003714	neural tissue
UBERON:0003729	mouth mucosa
UBERON:0003820	prostate bud
UBERON:0003835	abdominal segment blood vessel
UBERON:0003838	abdominal segment connective tissue
UBERON:0003856	odontogenic mesenchyme
UBERON:0003869	presumptive ganglion
UBERON:0003886	body cavity precursor
UBERON:0003887	intraembryonic coelom
UBERON:0003891	stroma
UBERON:0003893	capsule
UBERON:0003894	liver primordium
UBERON:0003909	sinusoid
UBERON:0003913	tooth-like structure
UBERON:0003914	epithelial tube
UBERON:0003915	endothelial tube
UBERON:0003918	kidney mesenchyme
UBERON:0003920	venous blood vessel
UBERON:0003921	pancreas primordium
UBERON:0003922	pancreatic bud
UBERON:0003923	dorsal pancreatic bud
UBERON:0003924	ventral pancreatic bud
UBERON:0003928	digestive system duct
UBERON:0003929	gut epithelium
UBERON:0003937	sex gland
UBERON:0003947	brain ventricle/choroid plexus
UBERON:0003956	aqueous drainage system
UBERON:0003975	internal female genitalia
UBERON:0004001	olfactory bulb layer
UBERON:0004043	semicircular canal ampulla
UBERON:0004086	brain ventricle
UBERON:0004088	ocular region
UBERON:0004089	midface
UBERON:0004111	anatomical conduit
UBERON:0004117	pharyngeal pouch
UBERON:0004119	endoderm-derived structure
UBERON:0004120	mesoderm-derived structure
UBERON:0004121	ectoderm-derived structure
UBERON:0004122	genitourinary system
UBERON:0004128	optic vesicle
UBERON:0004134	proximal tubule
UBERON:0004135	distal tubule
UBERON:0004136	intermediate tubule

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0004139	cardiogenic plate
UBERON:0004140	heart field
UBERON:0004141	heart tube
UBERON:0004145	outflow tract
UBERON:0004146	His-Purkinje system
UBERON:0004151	cardiac chamber
UBERON:0004160	proepicardium
UBERON:0004161	septum transversum
UBERON:0004175	internal reproductive organ
UBERON:0004176	external reproductive organ
UBERON:0004177	hemopoietic organ
UBERON:0004178	aorta smooth muscle tissue
UBERON:0004179	prostate glandular acinus
UBERON:0004185	endodermal gut
UBERON:0004186	olfactory bulb mitral cell layer
UBERON:0004188	glomerular epithelium
UBERON:0004189	glomerular endothelium
UBERON:0004190	glomerulus vasculature
UBERON:0004193	loop of Henle ascending limb thin segment
UBERON:0004198	comma-shaped body
UBERON:0004199	S-shaped body
UBERON:0004201	kidney outer medulla inner stripe
UBERON:0004202	kidney outer medulla outer stripe
UBERON:0004208	nephrogenic mesenchyme
UBERON:0004209	renal vesicle
UBERON:0004211	nephron epithelium
UBERON:0004212	glomerular capillary
UBERON:0004227	kidney pelvis smooth muscle
UBERON:0004234	iris smooth muscle
UBERON:0004237	blood vessel smooth muscle
UBERON:0004277	eye muscle
UBERON:0004288	skeleton
UBERON:0004290	dermomyotome
UBERON:0004291	heart rudiment
UBERON:0004294	glomerular capillary endothelium
UBERON:0004340	allantois
UBERON:0004348	optic eminence
UBERON:0004362	pharyngeal arch 1
UBERON:0004363	aortic arch
UBERON:0004456	entire sense organ system
UBERON:0004457	cavity lining
UBERON:0004458	body cavity or lining
UBERON:0004461	musculature of head
UBERON:0004490	cardiac muscle tissue of atrium
UBERON:0004493	cardiac muscle tissue of myocardium
UBERON:0004535	cardiovascular system
UBERON:0004536	lymph vasculature
UBERON:0004537	blood vasculature
UBERON:0004571	systemic arterial system
UBERON:0004572	arterial system
UBERON:0004573	systemic artery

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
UBERON:0004582	venous system
UBERON:0004590	sphincter muscle
UBERON:0004638	blood vessel endothelium
UBERON:0004639	afferent arteriole
UBERON:0004640	efferent arteriole
UBERON:0004645	urinary bladder urothelium
UBERON:0004647	liver lobule
UBERON:0004663	aorta wall
UBERON:0004664	aorta tunica adventitia
UBERON:0004681	vestibular system
UBERON:0004684	raphe nuclei
UBERON:0004695	arterial system smooth muscle
UBERON:0004700	arterial system endothelium
UBERON:0004715	annulus fibrosus disci intervertebralis
UBERON:0004716	conceptus
UBERON:0004719	arcuate vein
UBERON:0004721	crista ampullaris
UBERON:0004723	interlobular artery
UBERON:0004726	vasa recta
UBERON:0004732	segmental subdivision of nervous system
UBERON:0004733	segmental subdivision of hindbrain
UBERON:0004734	gastrula
UBERON:0004755	skeletal tissue
UBERON:0004761	cartilaginous neurocranium
UBERON:0004765	skeletal element
UBERON:0004770	articular system
UBERON:0004775	outer renal medulla vasa recta
UBERON:0004776	inner renal medulla vasa recta
UBERON:0004780	gastrointestinal system lamina propria
UBERON:0004782	gastrointestinal system serosa
UBERON:0004785	respiratory system mucosa
UBERON:0004786	gastrointestinal system mucosa
UBERON:0004787	urethra urothelium
UBERON:0004788	kidney pelvis urothelium
UBERON:0004797	blood vessel layer
UBERON:0004801	cervix epithelium
UBERON:0004802	respiratory tract epithelium
UBERON:0004807	respiratory system epithelium
UBERON:0004808	gastrointestinal system epithelium
UBERON:0004810	nephron tubule epithelium
UBERON:0004813	seminiferous tubule epithelium
UBERON:0004815	lower respiratory tract epithelium
UBERON:0004819	kidney epithelium
UBERON:0004820	bile duct epithelium
UBERON:0004821	pulmonary alveolus epithelium
UBERON:0004823	intrahepatic bile duct epithelium
UBERON:0004852	cardiovascular system endothelium
UBERON:0004854	gastrointestinal system mesentery
UBERON:0004872	splanchnic layer of lateral plate mesoderm
UBERON:0004874	somatopleure
UBERON:0004875	nephrogenic cord

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
UBERON:0004876	urogenital ridge
UBERON:0004880	chordamesoderm
UBERON:0004894	alveolar wall
UBERON:0004902	urogenital sinus epithelium
UBERON:0004905	articulation
UBERON:0004906	ectodermal gut
UBERON:0004907	lower digestive tract
UBERON:0004909	epithelium of gonad
UBERON:0004910	epithelium of male gonad
UBERON:0004911	epithelium of female gonad
UBERON:0004912	biliary bud
UBERON:0004921	subdivision of digestive tract
UBERON:0004923	organ component layer
UBERON:0004996	mucosa of cardia of stomach
UBERON:0004998	mucosa of pylorus
UBERON:0005039	mucosa of bronchiole
UBERON:0005057	immune organ
UBERON:0005058	hemolymphoid system gland
UBERON:0005062	neural fold
UBERON:0005068	neural rod
UBERON:0005081	ureter ureteric bud
UBERON:0005085	ectodermal placode
UBERON:0005086	hair follicle placode
UBERON:0005087	tooth placode
UBERON:0005088	sebaceous gland placode
UBERON:0005089	sweat gland placode
UBERON:0005090	muscle structure
UBERON:0005095	kidney rudiment
UBERON:0005096	descending thin limb
UBERON:0005097	renal connecting tubule
UBERON:0005103	mesonephric epithelium
UBERON:0005153	epithelial bud
UBERON:0005154	epithelial cord
UBERON:0005156	reproductive structure
UBERON:0005157	epithelial fold
UBERON:0005162	multi cell component structure
UBERON:0005164	ascending limb of loop of Henle
UBERON:0005167	papillary duct
UBERON:0005168	interlobular vein
UBERON:0005169	interstitial tissue
UBERON:0005171	hepatic duct
UBERON:0005172	abdomen organ
UBERON:0005173	abdominal segment organ
UBERON:0005174	back organ
UBERON:0005176	tooth enamel organ
UBERON:0005177	trunk organ
UBERON:0005178	thoracic cavity organ
UBERON:0005179	pelvis organ
UBERON:0005185	renal medulla collecting duct
UBERON:0005186	outer renal medulla collecting duct
UBERON:0005187	inner renal medulla collecting duct

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
UBERON:0005211	renal medulla interstitium
UBERON:0005212	testis interstitial tissue
UBERON:0005213	outer renal medulla interstitium
UBERON:0005214	inner renal medulla interstitium
UBERON:0005215	kidney interstitium
UBERON:0005253	head mesenchyme
UBERON:0005256	trunk mesenchyme
UBERON:0005267	renal cortex collecting duct
UBERON:0005268	renal cortex artery
UBERON:0005269	renal cortex vein
UBERON:0005270	renal cortex interstitium
UBERON:0005271	juxtamedullary cortex
UBERON:0005272	peritubular capillary
UBERON:0005281	ventricular system of central nervous system
UBERON:0005282	ventricular system of brain
UBERON:0005283	tela choroidea
UBERON:0005284	brain vasculature
UBERON:0005291	embryonic tissue
UBERON:0005292	extraembryonic tissue
UBERON:0005294	genital ridge
UBERON:0005295	sex cord
UBERON:0005296	ovary sex cord
UBERON:0005297	testis sex cord
UBERON:0005311	mammary placode
UBERON:0005317	pulmonary artery endothelium
UBERON:0005321	mesonephric smooth muscle tissue
UBERON:0005333	mammary bud
UBERON:0005358	ventricle of nervous system
UBERON:0005366	olfactory lobe
UBERON:0005376	olfactory bulb external plexiform layer
UBERON:0005377	olfactory bulb glomerular layer
UBERON:0005384	nasal cavity epithelium
UBERON:0005388	photoreceptor array
UBERON:0005389	transparent eye structure
UBERON:0005396	carotid artery segment
UBERON:0005398	female reproductive gland
UBERON:0005399	male reproductive gland
UBERON:0005406	perirenal fat
UBERON:0005409	gastrointestinal system
UBERON:0005423	developing anatomical structure
UBERON:0005424	presumptive retinal pigmented epithelium
UBERON:0005426	lens vesicle
UBERON:0005427	corneal primordium
UBERON:0005428	vagal neural crest
UBERON:0005432	aortic sac
UBERON:0005497	non-neural ectoderm
UBERON:0005498	primitive heart tube
UBERON:0005562	thymus primordium
UBERON:0005564	gonad primordium
UBERON:0005597	lung primordium
UBERON:0005602	dorsal mesogastrium

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0005629	vascular plexus
UBERON:0005631	extraembryonic membrane
UBERON:0005721	pronephric mesoderm
UBERON:0005725	olfactory system
UBERON:0005728	extraembryonic mesoderm
UBERON:0005734	tunica adventitia of blood vessel
UBERON:0005742	adventitia
UBERON:0005744	cranial conduit
UBERON:0005749	glomerular tuft
UBERON:0005750	glomerular parietal epithelium
UBERON:0005751	visceral layer of glomerular capsule
UBERON:0005754	rostral part of nephrogenic cord
UBERON:0005760	urorectal septum
UBERON:0005795	embryonic uterus
UBERON:0005800	segment of aorta
UBERON:0005856	developing mesenchymal condensation
UBERON:0005863	cartilaginous condensation
UBERON:0005866	pre-cartilage condensation
UBERON:0005872	1st arch pharyngeal cleft
UBERON:0005879	pharyngeal cleft
UBERON:0005891	coelomic epithelium
UBERON:0005904	duct of male reproductive system
UBERON:0005906	serous sac
UBERON:0005908	conjunctival sac
UBERON:0005910	transitional epithelium
UBERON:0005911	endo-epithelium
UBERON:0005913	zone of bone organ
UBERON:0005932	bulb of hair follicle
UBERON:0005933	hair root sheath
UBERON:0005941	hair inner root sheath
UBERON:0005942	hair outer root sheath
UBERON:0005969	reticulum trabeculare
UBERON:0005971	amniotic fold
UBERON:0005983	heart layer
UBERON:0005985	coronary vessel
UBERON:0005986	left branch of atrioventricular bundle
UBERON:0005987	right branch of atrioventricular bundle
UBERON:0006003	skin adnexa
UBERON:0006004	hair follicle matrix region
UBERON:0006082	fundus of urinary bladder
UBERON:0006215	rhombic lip
UBERON:0006235	foregut-midgut junction
UBERON:0006238	future brain
UBERON:0006242	gall bladder primordium
UBERON:0006266	nasolacrimal groove
UBERON:0006267	notochordal plate
UBERON:0006268	notochordal process
UBERON:0006293	spleen primordium
UBERON:0006311	chamber of eyeball
UBERON:0006341	outer renal medulla peritubular capillary
UBERON:0006376	premacula segment of distal straight tubule

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0006444	annulus fibrosus
UBERON:0006524	alveolar system
UBERON:0006534	renal convoluted tubule
UBERON:0006541	outer medulla inner stripe loop of henle
UBERON:0006542	outer medulla outer stripe loop of henle
UBERON:0006544	kidney vasculature
UBERON:0006553	renal duct
UBERON:0006554	urinary system structure
UBERON:0006555	excretory tube
UBERON:0006558	lymphatic part of lymphoid system
UBERON:0006561	non-lymphatic part of lymphoid system
UBERON:0006562	pharynx
UBERON:0006568	hypothalamic nucleus
UBERON:0006569	diencephalic nucleus
UBERON:0006595	presumptive endoderm
UBERON:0006598	presumptive structure
UBERON:0006601	presumptive ectoderm
UBERON:0006603	presumptive mesoderm
UBERON:0006660	muscle layer
UBERON:0006725	spiral ligament
UBERON:0006799	glandular epithelium
UBERON:0006800	anatomical line
UBERON:0006815	areolar connective tissue
UBERON:0006846	groove
UBERON:0006851	renal cortex peritubular capillary
UBERON:0006853	renal cortex tubule
UBERON:0006854	distal straight tubule postmacula segment
UBERON:0006855	ureter muscle layer
UBERON:0006858	adrenal/interrenal gland
UBERON:0006866	terminal part of digestive tract
UBERON:0006876	vasculature of organ
UBERON:0006877	vasculature of liver
UBERON:0006904	head mesenchyme from mesoderm
UBERON:0006914	squamous epithelium
UBERON:0006915	stratified squamous epithelium
UBERON:0006924	stomach glandular epithelium
UBERON:0006925	digestive gland
UBERON:0006929	glandular columnar epithelium
UBERON:0006931	stomach glandular region mucosa
UBERON:0006932	vestibular epithelium
UBERON:0006934	sensory epithelium
UBERON:0006935	crista ampullaris neuroepithelium
UBERON:0006937	inner ear epithelium
UBERON:0006955	uterine epithelium
UBERON:0006965	vascular cord
UBERON:0007005	cardiac mesoderm
UBERON:0007010	cleaving embryo
UBERON:0007026	primitive gut
UBERON:0007100	circulatory organ
UBERON:0007123	pharyngeal pouch 2
UBERON:0007135	neural keel

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
UBERON:0007196	tracheobronchial tree
UBERON:0007204	brachiocephalic vasculature
UBERON:0007213	mesenchyme derived from head neural crest
UBERON:0007238	1st arch maxillary component
UBERON:0007240	tunica adventitia of artery
UBERON:0007245	nuclear complex of neuraxis
UBERON:0007277	presumptive hindbrain
UBERON:0007280	presumptive endocardium
UBERON:0007282	presumptive segmental plate
UBERON:0007284	presumptive neural plate
UBERON:0007285	presumptive paraxial mesoderm
UBERON:0007297	presumptive pronephric mesoderm
UBERON:0007303	pharyngeal vasculature
UBERON:0007324	pancreatic lobe
UBERON:0007329	pancreatic duct
UBERON:0007376	outer epithelial layer
UBERON:0007383	enveloping layer of ectoderm
UBERON:0007497	developing epithelial placode
UBERON:0007499	epithelial sac
UBERON:0007500	epithelial tube open at both ends
UBERON:0007503	epithelial vesicle
UBERON:0007521	smooth muscle sphincter
UBERON:0007524	dense mesenchyme tissue
UBERON:0007530	migrating mesenchyme population
UBERON:0007592	ciliated columnar epithelium
UBERON:0007601	ciliated epithelium
UBERON:0007616	layer of synovial tissue
UBERON:0007625	pigment epithelium of eye
UBERON:0007645	future meninx
UBERON:0007647	ectomeninx
UBERON:0007684	uriniferous tubule
UBERON:0007685	region of nephron tubule
UBERON:0007687	kidney field
UBERON:0007689	thyroid diverticulum
UBERON:0007690	early pharyngeal endoderm
UBERON:0007771	epidermis gland
UBERON:0007798	vascular system
UBERON:0007806	connecting stalk
UBERON:0007811	craniocervical region
UBERON:0007844	cartilaginous element
UBERON:0007845	regular connective tissue
UBERON:0007846	dense regular connective tissue
UBERON:0007914	head or neck bone
UBERON:0008001	irregular bone
UBERON:0008193	pneumatized bone
UBERON:0008229	craniocervical region musculature
UBERON:0008404	proximale tubular epithelium
UBERON:0008408	distal tubular epithelium
UBERON:0008425	mammary ridge
UBERON:0008780	inner cell mass derived epiblast
UBERON:0008814	pharyngeal system

Continued on next page

Table A.3.1 – continued from previous page

Key	Description
UBERON:0008816	embryonic head
UBERON:0008835	hepatic diverticulum
UBERON:0008836	liver bud
UBERON:0008859	cardiac gastric gland
UBERON:0008861	pyloric gastric gland
UBERON:0008874	pulmonary acinus
UBERON:0008883	osteoid
UBERON:0008886	pulmonary vascular system
UBERON:0008947	respiratory primordium
UBERON:0008987	renal parenchyma
UBERON:0009034	stomach region
UBERON:0009089	inner medulla vasa recta descending limb
UBERON:0009090	outer medulla vasa recta descending limb
UBERON:0009091	vasa recta ascending limb
UBERON:0009092	inner medulla vasa recta ascending limb
UBERON:0009093	outer medulla vasa recta ascending limb
UBERON:0009095	tip of renal papilla
UBERON:0009113	thymic region
UBERON:0009117	indifferent gonad
UBERON:0009122	adenohypophyseal placode
UBERON:0009123	otic cup
UBERON:0009142	entire mesenchyme
UBERON:0009143	developing esophageal region
UBERON:0009145	pharyngeal region
UBERON:0009196	indifferent external genitalia
UBERON:0009201	nephric duct
UBERON:0009202	vasa recta descending limb
UBERON:0009210	pharyngeal membrane
UBERON:0009213	pharyngeal membrane of 1st arch
UBERON:0009497	epithelium of foregut-midgut junction
UBERON:0009550	endoderm of foregut-midgut junction
UBERON:0009566	intestinal submucosa
UBERON:0009569	subdivision of trunk
UBERON:0009616	presumptive midbrain
UBERON:0009617	head paraxial mesoderm
UBERON:0009618	trunk paraxial mesoderm
UBERON:0009623	spinal nerve root
UBERON:0009661	midbrain nucleus
UBERON:0009663	telencephalic nucleus
UBERON:0009664	gut mesentery
UBERON:0009722	entire pharyngeal arch endoderm
UBERON:0009753	adrenal gland cortex zone
UBERON:0009773	renal tubule
UBERON:0009778	pleural sac
UBERON:0009842	acinus
UBERON:0009843	prostate epithelial cord
UBERON:0009845	urogenital sinus mesenchyme
UBERON:0009846	embryonic cloacal epithelium
UBERON:0009847	prostate field
UBERON:0009854	digestive tract diverticulum
UBERON:0009856	sac

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0009859	endosteum
UBERON:0009870	zone of stomach
UBERON:0009881	anterior lateral plate mesoderm
UBERON:0009889	secondary heart field
UBERON:0009911	lobule
UBERON:0009916	wall of ureter
UBERON:0009919	ureter smooth muscle
UBERON:0009950	olfactory bulb plexiform layer
UBERON:0009954	vomeronasal system
UBERON:0009955	neurogenic placode
UBERON:0010009	aggregate regional part of brain
UBERON:0010011	collection of basal ganglia
UBERON:0010039	food storage organ
UBERON:0010047	oral gland
UBERON:0010077	cuboidal epithelium
UBERON:0010092	future metencephalon
UBERON:0010131	conducting tissue of heart
UBERON:0010133	neuroendocrine gland
UBERON:0010141	primitive sex cord of indifferent gonad
UBERON:0010147	male accessory sex gland
UBERON:0010188	protuberance
UBERON:0010191	aortic system
UBERON:0010226	future cardiac ventricle
UBERON:0010227	future cardiac atrium
UBERON:0010230	eyeball of camera-type eye
UBERON:0010260	umbilical blood vessel
UBERON:0010286	midbrain neural tube
UBERON:0010302	amnioserosa
UBERON:0010303	extraembryonic epithelium
UBERON:0010312	immature eye
UBERON:0010313	neural crest-derived structure
UBERON:0010314	structure with developmental contribution from neural crest
UBERON:0010316	germ layer / neural crest
UBERON:0010323	cranial skeletal system
UBERON:0010363	endochondral element
UBERON:0010364	dermal skeleton
UBERON:0010365	odontoid tissue
UBERON:0010368	pulmonary lobule
UBERON:0010371	ecto-epithelium
UBERON:0010375	pancreas dorsal primordium
UBERON:0010376	pancreas ventral primordium
UBERON:0010409	eye surface
UBERON:0010422	primary nodular lymphoid tissue
UBERON:0010498	pseudostratified columnar epithelium
UBERON:0010499	pseudostratified ciliated columnar epithelium
UBERON:0010523	microcirculatory vessel
UBERON:0010532	primitive nephron
UBERON:0010743	meningeal cluster
UBERON:0010912	subdivision of skeleton
UBERON:0010913	vertebral element

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Table A.3.1 – continued from previous page

Key	Description
UBERON:0010959	craniocervical muscle
UBERON:0010996	articular cartilage of joint
UBERON:0011094	vertebra cartilaginous condensation
UBERON:0011095	vertebra pre-cartilage condensation
UBERON:0011134	nonsynovial joint
UBERON:0011135	intervertebral cartilage
UBERON:0011137	axial skeletal system
UBERON:0011138	post-cranial axial skeletal system
UBERON:0011143	upper urinary tract
UBERON:0011148	submucosal gland
UBERON:0011156	facial skeleton
UBERON:0011158	primary subdivision of skull
UBERON:0011159	primary subdivision of cranial skeletal system
UBERON:0011216	organ system subdivision
UBERON:0011222	intra-ocular muscle
UBERON:0011249	appendicular skeletal system
UBERON:0011272	embryonic skin basal layer
UBERON:0011300	gray matter of telencephalon
UBERON:0011362	cranial blood vasculature
UBERON:0011585	cell condensation
UBERON:0011587	pre-dentine
UBERON:0011588	pre-enamel
UBERON:0011595	jaw region
UBERON:0011676	axial subdivision of organism
UBERON:0011814	non-neurogenic ectodermal placode
UBERON:0011817	follicle placode
UBERON:0011821	irregular connective tissue
UBERON:0011823	dense connective tissue
UBERON:0011825	loose connective tissue
UBERON:0011892	anterior uvea
UBERON:0011932	pilosebaceous unit
UBERON:0011953	stomach glandular region
UBERON:0011997	coelom
UBERON:0012069	epithelium-associated lymphoid tissue
UBERON:0012274	columnar epithelium
UBERON:0012275	meso-epithelium
UBERON:0012292	embryonic cloacal fold
UBERON:0012313	1st arch maxillary ectoderm
UBERON:0012344	holocrine gland
UBERON:0012361	internal anal region
UBERON:0012429	hemopoietic tissue
UBERON:0012430	tunica fibrosa of eyeball
UBERON:0012469	external anal region
UBERON:0012481	cloacal epithelium
UBERON:0013126	vein of abdomen
UBERON:1000023	spleen pulp
UBERON:1000024	parenchyma of spleen
UBERON:2005260	fenestrated capillary
snap:MaterialEntity	material_entity
snap:Object	object

(See it at <http://cellontology.org/>)

A.4 ISO 3166-1, ISO 3166-2 and UN M.49

This controlled vocabulary has 5096 terms and 33 aliases

<![CDATA[ISO 3166 is the International Standard for country codes and codes for their subdivisions. The purpose of ISO 3166 is to establish internationally recognised codes for the representation of names of countries, territories or areas of geographical interest, and their subdivisions. A complementary classification, related to ISO 3166 is UN M.49 (Standard Country and Area Codes Classifications)]]>

Table A.4.1: ISO 3166-1, ISO 3166-2 and UN M.49

Key	Description
AF	Afghanistan
AX	Åland Islands
AL	Albania
DZ	Algeria
AS	American Samoa
AD	Andorra
AO	Angola
AI	Anguilla
AQ	Antarctica
AG	Antigua and Barbuda
AR	Argentina
AM	Armenia
AW	Aruba
AU	Australia
AT	Austria
AZ	Azerbaijan
BS	Bahamas
BH	Bahrain
BD	Bangladesh
BB	Barbados
BY	Belarus
BE	Belgium
BZ	Belize
BJ	Benin
BM	Bermuda
BT	Bhutan
BO	Bolivia, Plurinational State of
BQ	Bonaire, Sint Eustatius and Saba
BA	Bosnia and Herzegovina
BW	Botswana
BV	Bouvet Island
BR	Brazil
IO	British Indian Ocean Territory
BN	Brunei Darussalam
BG	Bulgaria
BF	Burkina Faso
BI	Burundi
KH	Cambodia
CM	Cameroon
CA	Canada
CV	Cape Verde
KY	Cayman Islands

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
CF	Central African Republic
TD	Chad
CL	Chile
CN	China
CX	Christmas Island
CC	Cocos (Keeling) Islands
CO	Colombia
KM	Comoros
CG	Congo
CD	Congo, The Democratic Republic of the
CK	Cook Islands
CR	Costa Rica
CI	Côte d'Ivoire
HR	Croatia
CU	Cuba
CW	Curaçao
CY	Cyprus
CZ	Czech Republic
DK	Denmark
DJ	Djibouti
DM	Dominica
DO	Dominican Republic
EC	Ecuador
EG	Egypt
SV	El Salvador
GQ	Equatorial Guinea
ER	Eritrea
EE	Estonia
ET	Ethiopia
FK	Falkland Islands (Malvinas)
FO	Faroe Islands
FJ	Fiji
FI	Finland
FR	France
GF	French Guiana
PF	French Polynesia
TF	French Southern Territories
GA	Gabon
GM	Gambia
GE	Georgia
DE	Germany
GH	Ghana
GI	Gibraltar
GR	Greece
GL	Greenland
GD	Grenada
GP	Guadeloupe
GU	Guam
GT	Guatemala
GG	Guernsey
GN	Guinea

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
GW	Guinea-Bissau
GY	Guyana
HT	Haiti
HM	Heard Island and McDonald Islands
VA	Holy See (Vatican City State)
HN	Honduras
HK	Hong Kong
HU	Hungary
IS	Iceland
IN	India
ID	Indonesia
IR	Iran, Islamic Republic of
IQ	Iraq
IE	Ireland
IM	Isle of Man
IL	Israel
IT	Italy
JM	Jamaica
JP	Japan
JE	Jersey
JO	Jordan
KZ	Kazakhstan
KE	Kenya
KI	Kiribati
KP	Korea, Democratic People's Republic of
KR	Korea, Republic of
KW	Kuwait
KG	Kyrgyzstan
LA	Lao People's Democratic Republic
LV	Latvia
LB	Lebanon
LS	Lesotho
LR	Liberia
LY	Libya
LI	Liechtenstein
LT	Lithuania
LU	Luxembourg
MO	Macao
MK	Macedonia, Republic of
MG	Madagascar
MW	Malawi
MY	Malaysia
MV	Maldives
ML	Mali
MT	Malta
MH	Marshall Islands
MQ	Martinique
MR	Mauritania
MU	Mauritius
YT	Mayotte
MX	Mexico

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
FM	Micronesia, Federated States of
MD	Moldova, Republic of
MC	Monaco
MN	Mongolia
ME	Montenegro
MS	Montserrat
MA	Morocco
MZ	Mozambique
MM	Myanmar
NA	Namibia
NR	Nauru
NP	Nepal
NL	Netherlands
NC	New Caledonia
NZ	New Zealand
NI	Nicaragua
NE	Niger
NG	Nigeria
NU	Niue
NF	Norfolk Island
MP	Northern Mariana Islands
NO	Norway
OM	Oman
PK	Pakistan
PW	Palau
PS	Palestine, State of
PA	Panama
PG	Papua New Guinea
PY	Paraguay
PE	Peru
PH	Philippines
PN	Pitcairn
PL	Poland
PT	Portugal
PR	Puerto Rico
QA	Qatar
RE	Réunion
RO	Romania
RU	Russian Federation
RW	Rwanda
BL	Saint Barthélemy
SH	Saint Helena, Ascension and Tristan da Cunha
KN	Saint Kitts and Nevis
LC	Saint Lucia
MF	Saint Martin (French part)
PM	Saint Pierre and Miquelon
VC	Saint Vincent and the Grenadines
WS	Samoa
SM	San Marino
ST	Sao Tome and Principe
SA	Saudi Arabia

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
SN	Senegal
RS	Serbia
SC	Seychelles
SL	Sierra Leone
SG	Singapore
SX	Sint Maarten (Dutch part)
SK	Slovakia
SI	Slovenia
SB	Solomon Islands
SO	Somalia
ZA	South Africa
GS	South Georgia and the South Sandwich Islands
ES	Spain
LK	Sri Lanka
SD	Sudan
SR	Suriname
SS	South Sudan
SJ	Svalbard and Jan Mayen
SZ	Swaziland
SE	Sweden
CH	Switzerland
SY	Syrian Arab Republic
TW	Taiwan, Province of China
TJ	Tajikistan
TZ	Tanzania, United Republic of
TH	Thailand
TL	Timor-Leste
TG	Togo
TK	Tokelau
TO	Tonga
TT	Trinidad and Tobago
TN	Tunisia
TR	Turkey
TM	Turkmenistan
TC	Turks and Caicos Islands
TV	Tuvalu
UG	Uganda
UA	Ukraine
AE	United Arab Emirates
GB	United Kingdom
US	United States
UM	United States Minor Outlying Islands
UY	Uruguay
UZ	Uzbekistan
VU	Vanuatu
VE	Venezuela, Bolivarian Republic of
VN	Viet Nam
VG	Virgin Islands, British
VI	Virgin Islands, U.S.
WF	Wallis and Futuna
EH	Western Sahara

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
YE	Yemen
ZM	Zambia
ZW	Zimbabwe
AD-07	Andorra la Vella
AD-02	Canillo
AD-03	Encamp
AD-08	Escaldes-Engordany
AD-04	La Massana
AD-05	Ordino
AD-06	Sant Julià de Lòria
AE-AZ	Abū aby [Abu Dhabi]
AE-AJ	'Ajmān
AE-FU	Al Fujayrah
AE-SH	Ash Shāriqah
AE-DU	Dubayy
AE-RK	Ra's al Khaymah
AE-UQ	Umm al Qaywayn
AF-BDS	Badakhshān
AF-BDG	Bādgīs
AF-BGL	Baghlān
AF-BAL	Balkh
AF-BAM	Bāmyān
AF-DAY	Dāykundī
AF-FRA	Farāh
AF-FYB	Fāryāb
AF-GHA	Ghaznī
AF-GHO	Ghōr
AF-HEL	Helmand
AF-HER	Herāt
AF-JOW	Jowzjān
AF-KAB	Kābul
AF-KAN	Kandahār
AF-KAP	Kāpīsā
AF-KHO	Khōst
AF-KNR	Kunar
AF-KDZ	Kunduz
AF-LAG	Laghmān
AF-LOG	Lōgar
AF-NAN	Nangarhār
AF-NIM	Nīmrōz
AF-NUR	Nūristān
AF-URU	Uruzgān
AF-PIA	Paktiyyā
AF-PKA	Paktīkā
AF-PAN	Panjshayr
AF-PAR	Parwān
AF-SAM	Samangān
AF-SAR	Sar-e Pul
AF-TAK	Takhār
AF-WAR	Wardak
AF-ZAB	Zābul

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
AG-03	Saint George
AG-04	Saint John
AG-05	Saint Mary
AG-06	Saint Paul
AG-07	Saint Peter
AG-08	Saint Philip
AG-10	Barbuda
AG-11	Redonda
AL-01	Berat
AL-09	Dibër
AL-02	Durrës
AL-03	Elbasan
AL-04	Fier
AL-05	Gjirokastër
AL-06	Korçë
AL-07	Kukës
AL-08	Lezhë
AL-10	Shkodër
AL-11	Tiranë
AL-12	Vlorë
AL-BR	Berat
AL-BU	Bulqizë
AL-DL	Delvinë
AL-DV	Devoll
AL-DI	Dibër
AL-DR	Durrës
AL-EL	Elbasan
AL-FR	Fier
AL-GR	Gramsh
AL-GJ	Gjirokastër
AL-HA	Has
AL-KA	Kavajë
AL-ER	Kolonjë
AL-KO	Korçë
AL-KR	Krujë
AL-KC	Kuçovë
AL-KU	Kukës
AL-KB	Kurbin
AL-LE	Lezhë
AL-LB	Librazhd
AL-LU	Lushnjë
AL-MM	Malësi e Madhe
AL-MK	Mallakastër
AL-MT	Mat
AL-MR	Mirditë
AL-PQ	Peqin
AL-PR	Përmet
AL-PG	Pogradec
AL-PU	Pukë
AL-SR	Sarandë
AL-SK	Skrapar

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
AL-SH	Shkodër
AL-TE	Tepelenë
AL-TR	Tiranë
AL-TP	Tropojë
AL-VL	Vlorë
AM-ER	Erevan
AM-AG	Aragacotn
AM-AR	Ararat
AM-AV	Armavir
AM-GR	Gegarkunik'
AM-KT	Kotayk'
AM-LO	Lory
AM-SH	Sírak
AM-SU	Syunik'
AM-TV	Tavus
AM-VD	Vayoc Jor
AO-BGO	Bengo
AO-BGU	Benguela
AO-BIE	Bié
AO-CAB	Cabinda
AO-CCU	Cuando-Cubango
AO-CNO	Cuanza Norte
AO-CUS	Cuanza Sul
AO-CNN	Cunene
AO-HUA	Huambo
AO-HUI	Huíla
AO-LUA	Luanda
AO-LNO	Lunda Norte
AO-LSU	Lunda Sul
AO-MAL	Malange
AO-MOX	Moxico
AO-NAM	Namibe
AO-UIG	Uíge
AO-ZAI	Zaire
AR-C	Ciudad Autónoma de Buenos Aires
AR-B	Buenos Aires
AR-K	Catamarca
AR-X	Cordoba
AR-W	Corrientes
AR-H	Chaco
AR-U	Chubut
AR-E	Entre Ríos
AR-P	Formosa
AR-Y	Jujuy
AR-L	La Pampa
AR-M	Mendoza
AR-N	Misiones
AR-Q	Neuquen
AR-R	Río Negro
AR-A	Salta
AR-J	San Juan

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
AR-D	San Luis
AR-Z	Santa Cruz
AR-S	Santa Fe
AR-G	Santiago del Estero
AR-V	Tierra del Fuego
AR-T	Tucuman
AT-1	Burgenland
AT-2	Kärnten
AT-3	Niederösterreich
AT-4	Oberösterreich
AT-5	Salzburg
AT-6	Steiermark
AT-7	Tirol
AT-8	Vorarlberg
AT-9	Wien
AU-NSW	New South Wales
AU-QLD	Queensland
AU-SA	South Australia
AU-TAS	Tasmania
AU-VIC	Victoria
AU-WA	Western Australia
AU-ACT	Australian Capital Territory
AU-NT	Northern Territory
AZ-NX	Naxçıvan
AZ-BA	Bakı
AZ-GA	Gənc
AZ-XA	Xankəndi
AZ-LA	Lənkəran
AZ-MI	Mingçevir
AZ-NA	Naftalan
AZ-NV	Naxçıvan
AZ-SM	Sumqayıt
AZ-SA	Şəki
AZ-SR	Şirvan
AZ-YE	Yevlax
AZ-ABS	Abşeron
AZ-AGC	Ağcabədi
AZ-AGM	Ağdam
AZ-AGS	Ağdaş
AZ-AGA	Ağstafa
AZ-AGU	Ağsu
AZ-AST	Astara
AZ-BAB	Babek
AZ-BAL	Balakən
AZ-BEY	Beyləqan
AZ-BAR	Berd
AZ-BIL	Biləsuvar
AZ-CAB	Cəbrayıl
AZ-CAL	Cəlilabad
AZ-CUL	Cülfa
AZ-DAS	Dəşkəsnə

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
AZ-FUZ	Füzuli
AZ-GAD	Gadabay
AZ-GOR	Goranboy
AZ-GOY	Göyçay
AZ-GYG	Göygöl
AZ-HAC	Hacıqabul
AZ-XAC	Xaçmaz
AZ-XIZ	Xızı
AZ-XCI	Xocalı
AZ-XVD	Xocavänd
AZ-IMI	İmişli
AZ-ISM	İsmayıllı
AZ-KAL	Kəlbər
AZ-KAN	Kəngərlı
AZ-KUR	Kürdmir
AZ-QAX	Qax
AZ-QAZ	Qazax
AZ-QOB	Qobustan
AZ-QBA	Quba
AZ-QBI	Qubadlı
AZ-QUS	Qusar
AZ-LAC	Laçın
AZ-LER	Lerik
AZ-LAN	Lənkəran
AZ-MAS	Masallı
AZ-NEF	Neftçala
AZ-OGU	Oğuz
AZ-ORD	Ordubad
AZ-QAB	Qəbəl
AZ-SAT	Saatlı
AZ-SAB	Sabirabad
AZ-SAL	Salyan
AZ-SMX	Samux
AZ-SAD	Sədrək
AZ-SIY	Siyəzən
AZ-SBN	Şabran
AZ-SAH	Şahbuz
AZ-SMI	Şamaxı
AZ-SAK	Şəki
AZ-SKR	Şəmkir
AZ-SAR	Şərur
AZ-SUS	Şuşa
AZ-TAR	Tərtər
AZ-TOV	Tovuz
AZ-UCA	Ucar
AZ-YAR	Yardımlı
AZ-YEV	Yevlax
AZ-ZAQ	Zaqatala
AZ-ZAN	Zəngilan
AZ-ZAR	Zərdab
BA-BIH	Federacija Bosne i Hercegovine

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
BA-SRP	Republika Srpska
BA-05	Bosansko-podrinjski kanton
BA-07	Hercegovačko-neretvanski kanton
BA-10	Kanton br. 10 (Livanjski kanton)
BA-09	Kanton Sarajevo
BA-02	Posavski kanton
BA-06	Srednjobosanski kanton
BA-03	Tuzlanski kanton
BA-01	Unsko-sanski kanton
BA-08	Zapadnohercegovački kanton
BA-04	Zeničko-dobojski kanton
BA-BRC	Brčko distrikt
BB-01	Christ Church
BB-02	Saint Andrew
BB-03	Saint George
BB-04	Saint James
BB-05	Saint John
BB-06	Saint Joseph
BB-07	Saint Lucy
BB-08	Saint Michael
BB-09	Saint Peter
BB-10	Saint Philip
BB-11	Saint Thomas
BD-A	Barisal
BD-B	Chittagong
BD-C	Dhaka
BD-D	Khulna
BD-E	Rajshahi
BD-F	Rangpur
BD-G	Sylhet
BD-05	Bagerhat
BD-01	Bandarban
BD-02	Barguna
BD-06	Barisal
BD-07	Bhola
BD-03	Bogra
BD-04	Brahmanbaria
BD-09	Chandpur
BD-10	Chittagong
BD-12	Chuadanga
BD-08	Comilla
BD-11	Cox's Bazar
BD-13	Dhaka
BD-14	Dinajpur
BD-15	Faridpur
BD-16	Feni
BD-19	Gaibandha
BD-18	Gazipur
BD-17	Gopalganj
BD-20	Habiganj
BD-24	Jaipurhat

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
BD-21	Jamalpur
BD-22	Jessore
BD-25	Jhalakati
BD-23	Jhenaidah
BD-29	Khagrachari
BD-27	Khulna
BD-26	Kishorganj
BD-28	Kurigram
BD-30	Kushtia
BD-31	Lakshmipur
BD-32	Lalmonirhat
BD-36	Madaripur
BD-37	Magura
BD-33	Manikganj
BD-39	Meherpur
BD-38	Moulvibazar
BD-35	Munshiganj
BD-34	Mymensingh
BD-48	Naogaon
BD-43	Narail
BD-40	Narayanganj
BD-42	Narsingdi
BD-44	Natore
BD-45	Nawabganj
BD-41	Netrakona
BD-46	Nilphamari
BD-47	Noakhali
BD-49	Pabna
BD-52	Panchagarh
BD-51	Patuakhali
BD-50	Pirojpur
BD-53	Rajbari
BD-54	Rajshahi
BD-56	Rangamati
BD-55	Rangpur
BD-58	Satkhira
BD-62	Shariatpur
BD-57	Sherpur
BD-59	Sirajganj
BD-61	Sunamganj
BD-60	Sylhet
BD-63	Tangail
BD-64	Thakurgaon
BE-BRU	Bruxelles-Capitale, Région de; Brussels Hoofdstedelijk Gewest
BE-VLG	Vlaams Gewest
BE-WAL	wallonne, Région
BE-VAN	Antwerpen
BE-WBR	Brabant wallon
BE-WHT	Hainaut
BE-WLG	Liège

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
BE-VLI	Limburg
BE-WLX	Luxembourg
BE-WNA	Namur
BE-VOV	Oost-Vlaanderen
BE-VBR	Vlaams-Brabant
BE-VWV	West-Vlaanderen
BF-01	Boucle du Mouhoun
BF-02	Cascades
BF-03	Centre
BF-04	Centre-Est
BF-05	Centre-Nord
BF-06	Centre-Ouest
BF-07	Centre-Sud
BF-08	Est
BF-09	Hauts-Bassins
BF-10	Nord
BF-11	Plateau-Central
BF-12	Sahel
BF-13	Sud-Ouest
BF-BAL	Balé
BF-BAM	Bam
BF-BAN	Banwa
BF-BAZ	Bazèga
BF-BGR	Bougouriba
BF-BLG	Boulgou
BF-BLK	Boulkiemdé
BF-COM	Comoé
BF-GAN	Ganzourgou
BF-GNA	Gnagna
BF-GOU	Gourma
BF-HOU	Houet
BF-IOB	Ioba
BF-KAD	Kadiogo
BF-KEN	Kénédougou
BF-KMD	Komondjari
BF-KMP	Kompienga
BF-KOS	Kossi
BF-KOP	Koulpélogo
BF-KOT	Kouritenga
BF-KOW	Kourwéogo
BF-LER	Léraba
BF-LOR	Loroum
BF-MOU	Mouhoun
BF-NAO	Naouri
BF-NAM	Namentenga
BF-NAY	Nayala
BF-NOU	Noumbiel
BF-OUN	Oubritenga
BF-OUD	Oudalan
BF-PAS	Passoré
BF-PON	Poni

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
BF-SNG	Sanguié
BF-SMT	Sanmatenga
BF-SEN	Séno
BF-SIS	Sissili
BF-SOM	Soum
BF-SOR	Sourou
BF-TAP	Tapoa
BF-TUI	Tui
BF-YAG	Yagha
BF-YAT	Yatenga
BF-ZIR	Ziro
BF-ZON	Zondoma
BF-ZOU	Zoundwéogo
BG-01	Blagoevgrad
BG-02	Burgas
BG-08	Dobrich
BG-07	Gabrovo
BG-26	Haskovo
BG-09	Kardzhali
BG-10	Kyustendil
BG-11	Lovech
BG-12	Montana
BG-13	Pazardzhik
BG-14	Pernik
BG-15	Pleven
BG-16	Plovdiv
BG-17	Razgrad
BG-18	Ruse
BG-27	Shumen
BG-19	Silistra
BG-20	Sliven
BG-21	Smolyan
BG-23	Sofia
BG-22	Sofia-Grad
BG-24	Stara Zagora
BG-25	Targovishte
BG-03	Varna
BG-04	Veliko Tarnovo
BG-05	Vidin
BG-06	Vratsa
BG-28	Yambol
BH-13	Al Manāmah (Al ‘Āṣimah)
BH-14	Al Janūbīyah
BH-15	Al Mu arraq
BH-16	Al Wusṭá
BH-17	Ash Shamālīyah
BI-BB	Bubanza
BI-BM	Bujumbura Mairie
BI-BL	Bujumbura Rural
BI-BR	Bururi
BI-CA	Cankuzo

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
BI-CI	Cibitoke
BI-GI	Gitega
BI-KR	Karuzi
BI-KY	Kayanza
BI-KI	Kirundo
BI-MA	Makamba
BI-MU	Muramvya
BI-MW	Mwaro
BI-NG	Ngozi
BI-RT	Rutana
BI-RY	Ruyigi
BJ-AL	Alibori
BJ-AK	Atakora
BJ-AQ	Atlantique
BJ-BO	Borgou
BJ-CO	Collines
BJ-DO	Donga
BJ-KO	Kouffo
BJ-LI	Littoral
BJ-MO	Mono
BJ-OU	Ouémé
BJ-PL	Plateau
BJ-ZO	Zou
BN-BE	Belait
BN-BM	Brunei-Muara
BN-TE	Temburong
BN-TU	Tutong
BO-H	Chuquisaca
BO-C	Cochabamba
BO-B	El Beni
BO-L	La Paz
BO-O	Oruro
BO-N	Pando
BO-P	Potosí
BO-S	Santa Cruz
BO-T	Tarija
BQ-BO	Bonaire
BQ-SA	Saba
BQ-SE	Sint Eustatius
BR-AC	Acre
BR-AL	Alagoas
BR-AM	Amazonas
BR-AP	Amapá
BR-BA	Bahia
BR-CE	Ceará
BR-ES	Espírito Santo
BR-FN	Fernando de Noronha
BR-GO	Goiás
BR-MA	Maranhão
BR-MG	Minas Gerais
BR-MS	Mato Grosso do Sul

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
BR-MT	Mato Grosso
BR-PA	Pará
BR-PB	Paraíba
BR-PE	Pernambuco
BR-PI	Piauí
BR-PR	Paraná
BR-RJ	Rio de Janeiro
BR-RN	Rio Grande do Norte
BR-RO	Rondônia
BR-RR	Roraima
BR-RS	Rio Grande do Sul
BR-SC	Santa Catarina
BR-SE	Sergipe
BR-SP	São Paulo
BR-TO	Tocantins
BR-DF	Distrito Federal
BS-AC	Acklins
BS-BY	Berry Islands
BS-BI	Bimini
BS-BP	Black Point
BS-CI	Cat Island
BS-CO	Central Abaco
BS-CS	Central Andros
BS-CE	Central Eleuthera
BS-FP	City of Freeport
BS-CK	Crooked Island and Long Cay
BS-EG	East Grand Bahama
BS-EX	Exuma
BS-GC	Grand Cay
BS-HI	Harbour Island
BS-HT	Hope Town
BS-IN	Inagua
BS-LI	Long Island
BS-MC	Mangrove Cay
BS-MG	Mayaguana
BS-MI	Moore's Island
BS-NO	North Abaco
BS-NS	North Andros
BS-NE	North Eleuthera
BS-RI	Ragged Island
BS-RC	Rum Cay
BS-SS	San Salvador
BS-SO	South Abaco
BS-SA	South Andros
BS-SE	South Eleuthera
BS-SW	Spanish Wells
BS-WG	West Grand Bahama
BT-33	Bumthang
BT-12	Chhukha
BT-22	Dagana
BT-GA	Gasa

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Table A.4.1 – continued from previous page

Key	Description
BT-13	Ha
BT-44	Lhuentse
BT-42	Monggar
BT-11	Paro
BT-43	Pemagatshel
BT-23	Punakha
BT-45	Samdrup Jongkha
BT-14	Samtee
BT-31	Sarpang
BT-15	Thimphu
BT-41	Trashigang
BT-TY	Trashi Yangtse
BT-32	Trongsa
BT-21	Tsirang
BT-24	Wangdue Phodrang
BT-34	Zhemgang
BW-CE	Central
BW-GH	Ghanzi
BW-KG	Kgalagadi
BW-KL	Kgatleng
BW-KW	Kweneng
BW-NE	North-East
BW-NW	North-West
BW-SE	South-East
BW-SO	Southern
BY-HM	Horad Minsk
BY-BR	Brèsckaja voblast'
BY-HO	Homel'skaja voblast'
BY-HR	Hrodzenskaja voblast'
BY-MA	Mahilëuskaja voblast'
BY-MI	Minskaja voblast'
BY-VI	Vicebskaja voblast'
BZ-BZ	Belize
BZ-CY	Cayo
BZ-CZL	Corozal
BZ-OW	Orange Walk
BZ-SC	Stann Creek
BZ-TOL	Toledo
CA-AB	Alberta
CA-BC	British Columbia
CA-MB	Manitoba
CA-NB	New Brunswick
CA-NL	Newfoundland and Labrador
CA-NS	Nova Scotia
CA-ON	Ontario
CA-PE	Prince Edward Island
CA-QC	Quebec
CA-SK	Saskatchewan
CA-NT	Northwest Territories
CA-NU	Nunavut
CA-YT	Yukon Territory

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Table A.4.1 – continued from previous page

Key	Description
CD-KN	Kinshasa
CD-BN	Bandundu
CD-BC	Bas-Congo
CD-EQ	Équateur
CD-KW	Kasai-Occidental
CD-KE	Kasai-Oriental
CD-KA	Katanga
CD-MA	Maniema
CD-NK	Nord-Kivu
CD-OR	Orientale
CD-SK	Sud-Kivu
CF-BGF	Bangui
CF-BB	Bamingui-Bangoran
CF-BK	Basse-Kotto
CF-HK	Haute-Kotto
CF-HM	Haut-Mbomou
CF-KG	Kémo-Gribingui
CF-LB	Lobaye
CF-HS	Haute-Sangha / Mambéré-Kadéï
CF-MB	Mbomou
CF-NM	Nana-Mambéré
CF-MP	Ombella-M'poko
CF-UK	Ouaka
CF-AC	Ouham
CF-OP	Ouham-Pendé
CF-VK	Vakaga
CF-KB	Gribingui
CF-SE	Sangha
CG-11	Bouenza
CG-8	Cuvette
CG-15	Cuvette-Ouest
CG-5	Kouilou
CG-2	Lékoumou
CG-7	Likouala
CG-9	Niari
CG-14	Plateaux
CG-12	Pool
CG-13	Sangha
CG-BZV	Brazzaville
CH-AG	Aargau
CH-AI	Appenzell Innerrhoden
CH-AR	Appenzell Ausserrhoden
CH-BE	Bern
CH-BL	Basel-Landschaft
CH-BS	Basel-Stadt
CH-FR	Fribourg
CH-GE	Genève
CH-GL	Glarus
CH-GR	Graubünden
CH-JU	Jura
CH-LU	Luzern

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Table A.4.1 – continued from previous page

Key	Description
CH-NE	Neuchâtel
CH-NW	Nidwalden
CH-OW	Obwalden
CH-SG	Sankt Gallen
CH-SH	Schaffhausen
CH-SO	Solothurn
CH-SZ	Schwyz
CH-TG	Thurgau
CH-TI	Ticino
CH-UR	Uri
CH-VD	Vaud
CH-VS	Valais
CH-ZG	Zug
CH-ZH	Zürich
CI-06	18 Montagnes (Région des)
CI-16	Agnébi (Région de l')
CI-17	Bafing (Région du)
CI-09	Bas-Sassandra (Région du)
CI-10	Denguélé (Région du)
CI-18	Fromager (Région du)
CI-02	Haut-Sassandra (Région du)
CI-07	Lacs (Région des)
CI-01	Lagunes (Région des)
CI-12	Marahoué (Région de la)
CI-19	Moyen-Cavally (Région du)
CI-05	Moyen-Comoé (Région du)
CI-11	Nzï-Comoé (Région)
CI-03	Savanes (Région des)
CI-15	Sud-Bandama (Région du)
CI-13	Sud-Comoé (Région du)
CI-04	Vallée du Bandama (Région de la)
CI-14	Worodouqou (Région du)
CI-08	Zanzan (Région du)
CL-AI	Aisén del General Carlos Ibáñez del Campo
CL-AN	Antofagasta
CL-AR	Araucanía
CL-AP	Arica y Parinacota
CL-AT	Atacama
CL-BI	Bío-Bío
CL-CO	Coquimbo
CL-LI	Libertador General Bernardo O'Higgins
CL-LL	Los Lagos
CL-LR	Los Ríos
CL-MA	Magallanes y Antártica Chilena
CL-ML	Maule
CL-RM	Región Metropolitana de Santiago
CL-TA	Tarapacá
CL-VS	Valparaíso
CM-AD	Adamaoua
CM-CE	Centre
CM-ES	East

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
CM-EN	Far North
CM-LT	Littoral
CM-NO	North
CM-NW	North-West (Cameroon)
CM-SU	South
CM-SW	South-West
CM-OU	West
CN-11	Beijing
CN-50	Chongqing
CN-31	Shanghai
CN-12	Tianjin
CN-34	Anhui
CN-35	Fujian
CN-62	Gansu
CN-44	Guangdong
CN-52	Guizhou
CN-46	Hainan
CN-13	Hebei
CN-23	Heilongjiang
CN-41	Henan
CN-42	Hubei
CN-43	Hunan
CN-32	Jiangsu
CN-36	Jiangxi
CN-22	Jilin
CN-21	Liaoning
CN-63	Qinghai
CN-61	Shaanxi
CN-37	Shandong
CN-14	Shanxi
CN-51	Sichuan
CN-71	Taiwan
CN-53	Yunnan
CN-33	Zhejiang
CN-45	Guangxi
CN-15	Nei Mongol
CN-64	Ningxia
CN-65	Xinjiang
CN-54	Xizang
CN-91	Xianggang (Hong-Kong)
CN-92	Aomen (Macau)
CO-DC	Distrito Capital de Bogotá
CO-AMA	Amazonas
CO-ANT	Antioquia
CO-ARA	Arauca
CO-ATL	Atlántico
CO-BOL	Bolívar
CO-BOY	Boyacá
CO-CAL	Caldas
CO-CAQ	Caquetá
CO-CAS	Casanare

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
CO-CAU	Cauca
CO-CES	Cesar
CO-CHO	Chocó
CO-COR	Córdoba
CO-CUN	Cundinamarca
CO-GUA	Guainía
CO-GUV	Guaviare
CO-HUI	Huila
CO-LAG	La Guajira
CO-MAG	Magdalena
CO-MET	Meta
CO-NAR	Nariño
CO-NSA	Norte de Santander
CO-PUT	Putumayo
CO-QUI	Quindío
CO-RIS	Risaralda
CO-SAP	San Andrés, Providencia y Santa Catalina
CO-SAN	Santander
CO-SUC	Sucre
CO-TOL	Tolima
CO-VAC	Valle del Cauca
CO-VAU	Vaupés
CO-VID	Vichada
CR-A	Alajuela
CR-C	Cartago
CR-G	Guanacaste
CR-H	Heredia
CR-L	Limón
CR-P	Puntarenas
CR-SJ	San José
CU-09	Camagüey
CU-08	Ciego de Ávila
CU-06	Cienfuegos
CU-03	Ciudad de La Habana
CU-12	Granma
CU-14	Guantánamo
CU-11	Holguín
CU-02	La Habana
CU-10	Las Tunas
CU-04	Matanzas
CU-01	Pinar del Río
CU-07	Sancti Spíritus
CU-13	Santiago de Cuba
CU-05	Villa Clara
CU-99	Isla de la Juventud
CV-B	Ilhas de Barlavento
CV-S	Ilhas de Sotavento
CV-BV	Boa Vista
CV-BR	Brava
CV-MA	Maio
CV-MO	Mosteiros

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
CV-PA	Paul
CV-PN	Porto Novo
CV-PR	Praia
CV-RB	Ribeira Brava
CV-RG	Ribeira Grande
CV-RS	Ribeira Grande de Santiago
CV-SL	Sal
CV-CA	Santa Catarina
CV-CF	Santa Catarina de Fogo
CV-CR	Santa Cruz
CV-SD	São Domingos
CV-SF	São Filipe
CV-SO	São Lourenço dos Órgãos
CV-SM	São Miguel
CV-SS	São Salvador do Mundo
CV-SV	São Vicente
CV-TA	Tarrafal
CV-TS	Tarrafal de São Nicolau
CY-04	Ammóchostos
CY-06	Kerýneia
CY-03	Lárnaka
CY-01	Lefkosía
CY-02	Lemesós
CY-05	Páfos
CZ-JC	Jihočeský kraj
CZ-JM	Jihomoravský kraj
CZ-KA	Karlovarský kraj
CZ-KR	Královéhradecký kraj
CZ-LI	Liberecký kraj
CZ-MO	Moravskoslezský kraj
CZ-OL	Olomoucký kraj
CZ-PA	Pardubický kraj
CZ-PL	Plzeňský kraj
CZ-PR	Praha, hlavní město
CZ-ST	Středočeský kraj
CZ-US	Ústecký kraj
CZ-VY	Výsočina
CZ-ZL	Zlínský kraj
CZ-201	Benešov
CZ-202	Beroun
CZ-621	Blansko
CZ-622	Brno-město
CZ-623	Brno-venkov
CZ-801	Bruntál
CZ-624	Břeclav
CZ-511	Česká Lípa
CZ-311	České Budějovice
CZ-312	Český Krumlov
CZ-421	Děčín
CZ-321	Domažlice
CZ-802	Frýdek Místek

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
CZ-611	Havlíčkův Brod
CZ-625	Hodonín
CZ-521	Hradec Králové
CZ-411	Cheb
CZ-422	Chomutov
CZ-531	Chrudim
CZ-512	Jablonec nad Nisou
CZ-711	Jeseník
CZ-522	Jičín
CZ-612	Jihlava
CZ-313	Jindřichův Hradec
CZ-412	Karlovy Vary
CZ-803	Karviná
CZ-203	Kladno
CZ-322	Klatovy
CZ-204	Kolín
CZ-721	Kroměříž
CZ-205	Kutná Hora
CZ-513	Liberec
CZ-423	Litoměřice
CZ-424	Louny
CZ-206	Mělník
CZ-207	Mladá Boleslav
CZ-425	Most
CZ-523	Náchod
CZ-804	Nový Jičín
CZ-208	Nymburk
CZ-712	Olomouc
CZ-805	Opava
CZ-806	Ostrava město
CZ-532	Pardubice
CZ-613	Pelhřimov
CZ-314	Písek
CZ-324	Plzeň jih
CZ-323	Plzeň město
CZ-325	Plzeň sever
CZ-101	Praha 1
CZ-102	Praha 2
CZ-103	Praha 3
CZ-104	Praha 4
CZ-105	Praha 5
CZ-106	Praha 6
CZ-107	Praha 7
CZ-108	Praha 8
CZ-109	Praha 9
CZ-10A	Praha 10
CZ-10B	Praha 11
CZ-10C	Praha 12
CZ-10D	Praha 13
CZ-10E	Praha 14
CZ-10F	Praha 15

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
CZ-209	Praha východ
CZ-20A	Praha západ
CZ-315	Prachatice
CZ-713	Prostějov
CZ-714	Přerov
CZ-20B	Příbram
CZ-20C	Rakovník
CZ-326	Rokycany
CZ-524	Rychnov nad Kněžnou
CZ-514	Semily
CZ-413	Sokolov
CZ-316	Strakonice
CZ-533	Svitavy
CZ-715	Šumperk
CZ-317	Tábor
CZ-327	Tachov
CZ-426	Teplice
CZ-525	Trutnov
CZ-614	Třebíč
CZ-722	Uherské Hradiště
CZ-427	Ústí nad Labem
CZ-534	Ústí nad Orlicí
CZ-723	Vsetín
CZ-626	Vyškov
CZ-724	Zlín
CZ-627	Znojmo
CZ-615	Žďár nad Sázavou
DE-BW	Baden-Württemberg
DE-BY	Bayern
DE-HB	Bremen
DE-HH	Hamburg
DE-HE	Hessen
DE-NI	Niedersachsen
DE-NW	Nordrhein-Westfalen
DE-RP	Rheinland-Pfalz
DE-SL	Saarland
DE-SH	Schleswig-Holstein
DE-BE	Berlin
DE-BB	Brandenburg
DE-MV	Mecklenburg-Vorpommern
DE-SN	Sachsen
DE-ST	Sachsen-Anhalt
DE-TH	Thüringen
DJ-AS	Ali Sabieh
DJ-AR	Arta
DJ-DI	Dikhil
DJ-OB	Obock
DJ-TA	Tadjourah
DJ-DJ	Djibouti
DK-84	Hovedstaden
DK-82	Midtjylland

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
DK-81	Nordjylland
DK-85	Sjælland
DK-83	Syddanmark
DM-02	Saint Andrew
DM-03	Saint David
DM-04	Saint George
DM-05	Saint John
DM-06	Saint Joseph
DM-07	Saint Luke
DM-08	Saint Mark
DM-09	Saint Patrick
DM-10	Saint Paul
DM-01	Saint Peter
DO-01	Distrito Nacional (Santo Domingo)
DO-02	Azua
DO-03	Bahoruco
DO-04	Barahona
DO-05	Dajabón
DO-06	Duarte
DO-08	El Seybo [El Seibo]
DO-09	Espaillat
DO-30	Hato Mayor
DO-10	Independencia
DO-11	La Altagracia
DO-07	La Estrellita [Elías Piña]
DO-12	La Romana
DO-13	La Vega
DO-14	María Trinidad Sánchez
DO-28	Monseñor Nouel
DO-15	Monte Cristi
DO-29	Monte Plata
DO-16	Pedernales
DO-17	Peravia
DO-18	Puerto Plata
DO-19	Salcedo
DO-20	Samaná
DO-21	San Cristóbal
DO-22	San Juan
DO-23	San Pedro de Macorís
DO-24	Sánchez Ramírez
DO-25	Santiago
DO-26	Santiago Rodríguez
DO-27	Valverde
DZ-01	Adrar
DZ-44	Aïn Defla
DZ-46	Aïn Témouchent
DZ-16	Alger
DZ-23	Annaba
DZ-05	Batna
DZ-08	Béchar
DZ-06	Béjaïa

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
DZ-07	Biskra
DZ-09	Blida
DZ-34	Bordj Bou Arréridj
DZ-10	Bouira
DZ-35	Boumerdès
DZ-02	Chlef
DZ-25	Constantine
DZ-17	Djelfa
DZ-32	El Bayadh
DZ-39	El Oued
DZ-36	El Tarf
DZ-47	Ghardaïa
DZ-24	Guelma
DZ-33	Illizi
DZ-18	Jijel
DZ-40	Khenchela
DZ-03	Laghouat
DZ-29	Mascara
DZ-26	Médéa
DZ-43	Mila
DZ-27	Mostaganem
DZ-28	Msila
DZ-45	Naama
DZ-31	Oran
DZ-30	Ouargla
DZ-04	Oum el Bouaghi
DZ-48	Relizane
DZ-20	Saïda
DZ-19	Sétif
DZ-22	Sidi Bel Abbès
DZ-21	Skikda
DZ-41	Souk Ahras
DZ-11	Tamanghasset
DZ-12	Tébessa
DZ-14	Tiaret
DZ-37	Tindouf
DZ-42	Tipaza
DZ-38	Tissemsilt
DZ-15	Tizi Ouzou
DZ-13	Tlemcen
EC-A	Azuay
EC-B	Bolívar
EC-F	Cañar
EC-C	Carchi
EC-X	Cotopaxi
EC-H	Chimborazo
EC-O	El Oro
EC-E	Ecuador
EC-W	Galápagos
EC-G	Guayas
EC-I	Imbabura

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
EC-L	Loja
EC-R	Los Ríos
EC-M	Manabí
EC-S	Morona-Santiago
EC-N	Napo
EC-D	Orellana
EC-Y	Pastaza
EC-P	Pichincha
EC-SE	Santa Elena
EC-SD	Santo Domingo de los Tsáchilas
EC-U	Sucumbíos
EC-T	Tungurahua
EC-Z	Zamora-Chinchipe
EE-37	Harjumaa
EE-39	Hiiumaa
EE-44	Ida-Virumaa
EE-49	Jõgevamaa
EE-51	Järvamaa
EE-57	Lääne-Nigula
EE-59	Lääne-Virumaa
EE-65	Põlvamaa
EE-67	Pärnumaa
EE-70	Raplamaa
EE-74	Saaremaa
EE-78	Tartumaa
EE-82	Valgamaa
EE-84	Viljandimaa
EE-86	Võrumaa
EG-DK	Ad Daqahlīyah
EG-BA	Al Bahr al Ahmar
EG-BH	Al Buhayrah
EG-FYM	Al Fayyūm
EG-GH	Al Gharbiyah
EG-ALX	Al Iskandariyah
EG-IS	Al Ismā'īlīyah
EG-GZ	Al Jīzah
EG-MNF	Al Minūfiyah
EG-MN	Al Minya
EG-C	Al Qāhirah
EG-KB	Al Qalyūbiyah
EG-WAD	Al Wādī al Jadīd
EG-SU	As Sādis min Uktūbar
EG-SHR	Ash Sharqīyah
EG-SUZ	As Suways
EG-ASN	Aswān
EG-AST	Asyūt
EG-BNS	Banī Suwayf
EG-PTS	Būr Sa'īd
EG-DT	Dumyāt
EG-HU	Hulwān
EG-JS	Janūb Sīnā'

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
EG-KFS	Kafr ash Shaykh
EG-MT	Matrūh
EG-KN	Qinā
EG-SIN	Shamal Sīnā'
EG-SHG	Sūhāj
ER-MA	Al Awsaṭ
ER-DU	Al Janūbī
ER-AN	Ansabā
ER-DK	Janūbī al Ba rī al A mar
ER-GB	Qāsh-Barkah
ER-SK	Shimālī al Ba rī al A mar
ES-AN	Andalucía
ES-AR	Aragón
ES-AS	Asturias, Principado de
ES-CN	Canarias
ES-CB	Cantabria
ES-CM	Castilla-La Mancha
ES-CL	Castilla y León
ES-CT	Catalunya
ES-EX	Extremadura
ES-GA	Galicia
ES-IB	Illes Balears
ES-RI	La Rioja
ES-MD	Madrid, Comunidad de
ES-MC	Murcia, Región de
ES-NC	Navarra, Comunidad Foral de / Nafarroako Foru Komunitatea
ES-PV	País Vasco / Euskal Herria
ES-VC	Valenciana, Comunidad / Valenciana, Comunitat
ES-C	A Coruña
ES-VI	Álava
ES-AB	Albacete
ES-A	Alicante
ES-AL	Almería
ES-O	Asturias
ES-AV	Ávila
ES-BA	Badajoz
ES-B	Barcelona
ES-BU	Burgos
ES-CC	Cáceres
ES-CA	Cádiz
ES-S	Cantabria
ES-CS	Castellón
ES-CR	Ciudad Real
ES-CO	Córdoba
ES-CU	Cuenca
ES-GI	Girona
ES-GR	Granada
ES-GU	Guadalajara
ES-SS	Guipúzcoa / Gipuzkoa
ES-H	Huelva

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
ES-HU	Huesca
ES-J	Jaén
ES-LO	La Rioja
ES-GC	Las Palmas
ES-LE	León
ES-L	Lleida
ES-LU	Lugo
ES-M	Madrid
ES-MA	Málaga
ES-MU	Murcia
ES-NA	Navarra / Nafarroa
ES-OR	Ourense
ES-P	Palencia
ES-PM	Balears
ES-PO	Pontevedra
ES-SA	Salamanca
ES-TF	Santa Cruz de Tenerife
ES-SG	Segovia
ES-SE	Sevilla
ES-SO	Soria
ES-T	Tarragona
ES-TE	Teruel
ES-TO	Toledo
ES-V	Valencia / València
ES-VA	Valladolid
ES-BI	Vizcayaa / Bizkaia
ES-ZA	Zamora
ES-Z	Zaragoza
ES-CE	Ceuta
ES-ML	Melilla
ET-AA	Ādīs Ābeba
ET-DD	Dirē Dawa
ET-AF	Āfar
ET-AM	Āmara
ET-BE	Bīnshangul Gumuz
ET-GA	Gambēla Hizboch
ET-HA	Hārerī Hizb
ET-OR	Oromīya
ET-SO	Sumalē
ET-TI	Tigray
ET-SN	YeDeubub Bihēroch Bihēreseboch na Hizboch
FI-01	Ahvenanmaan maakunta
FI-02	Etelä-Karjala
FI-03	Etelä-Pohjanmaa
FI-04	Etelä-Savo
FI-05	Kainuu
FI-06	Kanta-Häme
FI-07	Keski-Pohjanmaa
FI-08	Keski-Suomi
FI-09	Kymenlaakso
FI-10	Lappi

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
FI-11	Pirkanmaa
FI-12	Pohjanmaa
FI-13	Pohjois-Karjala
FI-14	Pohjois-Pohjanmaa
FI-15	Pohjois-Savo
FI-16	Päijät-Häme
FI-17	Satakunta
FI-18	Uusimaa
FI-19	Varsinais-Suomi
FJ-C	Central
FJ-E	Eastern
FJ-N	Northern
FJ-W	Western
FJ-R	Rotuma
FM-TRK	Chuuk
FM-KSA	Kosrae
FM-PNI	Pohnpei
FM-YAP	Yap
FR-A	Alsace
FR-B	Aquitaine
FR-C	Auvergne
FR-P	Basse-Normandie
FR-D	Bourgogne
FR-E	Bretagne
FR-F	Centre
FR-G	Champagne-Ardenne
FR-H	Corse
FR-I	Franche-Comté
FR-Q	Haute-Normandie
FR-J	Île-de-France
FR-K	Languedoc-Roussillon
FR-L	Limousin
FR-M	Lorraine
FR-N	Midi-Pyrénées
FR-O	Nord - Pas-de-Calais
FR-R	Pays de la Loire
FR-S	Picardie
FR-T	Poitou-Charentes
FR-U	Provence-Alpes-Côte d'Azur
FR-V	Rhône-Alpes
FR-01	Ain
FR-02	Aisne
FR-03	Allier
FR-04	Alpes-de-Haute-Provence
FR-06	Alpes-Maritimes
FR-07	Ardèche
FR-08	Ardennes
FR-09	Ariège
FR-10	Aube
FR-11	Aude
FR-12	Aveyron

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Table A.4.1 – continued from previous page

Key	Description
FR-67	Bas-Rhin
FR-13	Bouches-du-Rhône
FR-14	Calvados
FR-15	Cantal
FR-16	Charente
FR-17	Charente-Maritime
FR-18	Cher
FR-19	Corrèze
FR-2A	Corse-du-Sud
FR-21	Côte-d'Or
FR-22	Côtes-d'Armor
FR-23	Creuse
FR-79	Deux-Sèvres
FR-24	Dordogne
FR-25	Doubs
FR-26	Drôme
FR-91	Essonne
FR-27	Eure
FR-28	Eure-et-Loir
FR-29	Finistère
FR-30	Gard
FR-32	Gers
FR-33	Gironde
FR-2B	Haute-Corse
FR-31	Haute-Garonne
FR-43	Haute-Loire
FR-52	Haute-Marne
FR-05	Hautes-Alpes
FR-70	Haute-Saône
FR-74	Haute-Savoie
FR-65	Hautes-Pyrénées
FR-87	Haute-Vienne
FR-68	Haut-Rhin
FR-92	Hauts-de-Seine
FR-34	Hérault
FR-35	Ille-et-Vilaine
FR-36	Indre
FR-37	Indre-et-Loire
FR-38	Isère
FR-39	Jura
FR-40	Landes
FR-41	Loir-et-Cher
FR-42	Loire
FR-44	Loire-Atlantique
FR-45	Loiret
FR-46	Lot
FR-47	Lot-et-Garonne
FR-48	Lozère
FR-49	Maine-et-Loire
FR-50	Manche
FR-51	Marne

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
FR-53	Mayenne
FR-54	Meurthe-et-Moselle
FR-55	Meuse
FR-56	Morbihan
FR-57	Moselle
FR-58	Nièvre
FR-59	Nord
FR-60	Oise
FR-61	Orne
FR-75	Paris
FR-62	Pas-de-Calais
FR-63	Puy-de-Dôme
FR-64	Pyrénées-Atlantiques
FR-66	Pyrénées-Orientales
FR-69	Rhône
FR-71	Saône-et-Loire
FR-72	Sarthe
FR-73	Savoie
FR-77	Seine-et-Marne
FR-76	Seine-Maritime
FR-93	Seine-Saint-Denis
FR-80	Somme
FR-81	Tarn
FR-82	Tarn-et-Garonne
FR-90	Territoire de Belfort
FR-94	Val-de-Marne
FR-95	Val d'Oise
FR-83	Var
FR-84	Vaucluse
FR-85	Vendée
FR-86	Vienne
FR-88	Vosges
FR-89	Yonne
FR-78	Yvelines
FR-GP	Guadeloupe
FR-GF	Guyane
FR-MQ	Martinique
FR-YT	Mayotte
FR-RE	Réunion
FR-CP	Clipperton
FR-NC	Nouvelle-Calédonie
FR-PF	Polynésie française
FR-BL	Saint-Barthélemy
FR-MF	Saint-Martin
FR-PM	Saint-Pierre-et-Miquelon
FR-TF	Terres australes françaises
FR-WF	Wallis-et-Futuna
GA-1	Estuaire
GA-2	Haut-Ogooué
GA-3	Moyen-Ogooué
GA-4	Ngounié

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Table A.4.1 – continued from previous page

Key	Description
GA-5	Nyanga
GA-6	Ogooué-Ivindo
GA-7	Ogooué-Lolo
GA-8	Ogooué-Maritime
GA-9	Woleu-Ntem
GB-ENG	England
GB-SCT	Scotland
GB-WLS	Wales
GB-NIR	Northern Ireland
GB-EAW	England and Wales
GB-GBN	Great Britain
GB-UKM	United Kingdom
GB-BKM	Buckinghamshire
GB-CAM	Cambridgeshire
GB-CMA	Cumbria
GB-DBY	Derbyshire
GB-DEV	Devon
GB-DOR	Dorset
GB-ESX	East Sussex
GB-ESS	Essex
GB-GLS	Gloucestershire
GB-HAM	Hampshire
GB-HRT	Hertfordshire
GB-KEN	Kent
GB-LAN	Lancashire
GB-LEC	Leicestershire
GB-LIN	Lincolnshire
GB-NFK	Norfolk
GB-NYK	North Yorkshire
GB-NTH	Northamptonshire
GB-NTT	Nottinghamshire
GB-OXF	Oxfordshire
GB-SOM	Somerset
GB-STS	Staffordshire
GB-SFK	Suffolk
GB-SRY	Surrey
GB-WAR	Warwickshire
GB-WSX	West Sussex
GB-WOR	Worcestershire
GB-BDG	Barking and Dagenham
GB-BNE	Barnet
GB-BEX	Bexley
GB-BEN	Brent
GB-BRY	Bromley
GB-CMD	Camden
GB-CRY	Croydon
GB-EAL	Ealing
GB-ENF	Enfield
GB-GRE	Greenwich
GB-HCK	Hackney
GB-HMF	Hammersmith and Fulham

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
GB-HRY	Haringey
GB-HRW	Harrow
GB-HAV	Harvering
GB-HIL	Hillingdon
GB-HNS	Hounslow
GB-ISL	Islington
GB-KEC	Kensington and Chelsea
GB-KTT	Kingston upon Thames
GB-LBH	Lambeth
GB-LEW	Lewisham
GB-MRT	Merton
GB-NWM	Newham
GB-RDB	Redbridge
GB-RIC	Richmond upon Thames
GB-SWK	Southwark
GB-STN	Sutton
GB-TWH	Tower Hamlets
GB-WFT	Waltham Forest
GB-WND	Wandsworth
GB-WSM	Westminster
GB-BNS	Barnsley
GB-BIR	Birmingham
GB-BOL	Bolton
GB-BRD	Bradford
GB-BUR	Bury
GB-CLD	Calderdale
GB-COV	Coventry
GB-DNC	Doncaster
GB-DUD	Dudley
GB-GAT	Gateshead
GB-KIR	Kirklees
GB-KWL	Knowsley
GB-LDS	Leeds
GB-LIV	Liverpool
GB-MAN	Manchester
GB-NET	Newcastle upon Tyne
GB-NTY	North Tyneside
GB-OLD	Oldham
GB-RCH	Rochdale
GB-ROT	Rotherham
GB-SHN	St. Helens
GB-SLF	Salford
GB-SAW	Sandwell
GB-SFT	Sefton
GB-SHF	Sheffield
GB-SOL	Solihull
GB-STY	South Tyneside
GB-SKP	Stockport
GB-SND	Sunderland
GB-TAM	Tameside
GB-TRF	Trafford

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
GB-WKF	Wakefield
GB-WLL	Walsall
GB-WGN	Wigan
GB-WRL	Wirral
GB-WLV	Wolverhampton
GB-LND	London, City of
GB-ABE	Aberdeen City
GB-ABD	Aberdeenshire
GB-ANS	Angus
GB-AGB	Argyll and Bute
GB-CLK	Clackmannanshire
GB-DGY	Dumfries and Galloway
GB-DND	Dundee City
GB-EAY	East Ayrshire
GB-EDU	East Dunbartonshire
GB-ELN	East Lothian
GB-ERW	East Renfrewshire
GB-EDH	Edinburgh, City of
GB-ELS	Eilean Siar
GB-FAL	Falkirk
GB-FIF	Fife
GB-GLG	Glasgow City
GB-HLD	Highland
GB-IVC	Inverclyde
GB-MLN	Midlothian
GB-MRY	Moray
GB-NAY	North Ayrshire
GB-NLK	North Lanarkshire
GB-ORK	Orkney Islands
GB-PKN	Perth and Kinross
GB-RFW	Renfrewshire
GB-SCB	Scottish Borders, The
GB-ZET	Shetland Islands
GB-SAY	South Ayrshire
GB-SLK	South Lanarkshire
GB-STG	Stirling
GB-WDU	West Dunbartonshire
GB-WLN	West Lothian
GB-ANT	Antrim
GB-ARD	Ards
GB-ARM	Armagh
GB-BLA	Ballymena
GB-BLY	Ballymoney
GB-BNB	Banbridge
GB-BFS	Belfast
GB-CKF	Carrickfergus
GB-CSR	Castlereagh
GB-CLR	Coleraine
GB-CKT	Cookstown
GB-CGV	Craigavon
GB-DRY	Derry

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
GB-DOW	Down
GB-DGN	Dungannon and South Tyrone
GB-FER	Fermanagh
GB-LRN	Larne
GB-LMV	Limavady
GB-LSB	Lisburn
GB-MFT	Magherafelt
GB-MYL	Moyle
GB-NYM	Newry and Mourne
GB-NTA	Newtownabbey
GB-NDN	North Down
GB-OMH	Omagh
GB-STB	Strabane
GB-BAS	Bath and North East Somerset
GB-BBD	Blackburn with Darwen
GB-BDF	Bedford
GB-BPL	Blackpool
GB-BMH	Bournemouth
GB-BRC	Bracknell Forest
GB-BNH	Brighton and Hove
GB-BST	Bristol, City of
GB-CBF	Central Bedfordshire
GB-CHE	Cheshire East
GB-CHW	Cheshire West and Chester
GB-CON	Cornwall
GB-DAL	Darlington
GB-DER	Derby
GB-DUR	Durham, County
GB-ERY	East Riding of Yorkshire
GB-HAL	Halton
GB-HPL	Hartlepool
GB-HEF	Herefordshire
GB-IOW	Isle of Wight
GB-KHL	Kingston upon Hull
GB-LCE	Leicester
GB-LUT	Luton
GB-MDW	Medway
GB-MDB	Middlesbrough
GB-MIK	Milton Keynes
GB-NEL	North East Lincolnshire
GB-NLN	North Lincolnshire
GB-NSM	North Somerset
GB-NBL	Northumberland
GB-NGM	Nottingham
GB-PTE	Peterborough
GB-PLY	Plymouth
GB-POL	Poole
GB-POR	Portsmouth
GB-RDG	Reading
GB-RCC	Redcar and Cleveland
GB-RUT	Rutland

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
GB-SHR	Shropshire
GB-SLG	Slough
GB-SGC	South Gloucestershire
GB-STH	Southampton
GB-SOS	Southend-on-Sea
GB-STT	Stockton-on-Tees
GB-STE	Stoke-on-Trent
GB-SWD	Swindon
GB-TFW	Telford and Wrekin
GB-THR	Thurrock
GB-TOB	Torbay
GB-WRT	Warrington
GB-WBK	West Berkshire
GB-WNM	Windsor and Maidenhead
GB-WOK	Wokingham
GB-YOR	York
GB-BGW	Blaenau Gwent
GB-BGE	Bridgend;Pen-y-bont ar Ogwr
GB-CAY	Caerphilly;Caerffili
GB-CRF	Cardiff;Caerdydd
GB-CMN	Carmarthenshire;Sir Gaerfyrddin
GB-CGN	Ceredigion;Sir Ceredigion
GB-CWY	Conwy
GB-DEN	Denbighshire;Sir Ddinbych
GB-FLN	Flintshire;Sir y Fflint
GB-GWN	Gwynedd
GB-AGY	Isle of Anglesey;Sir Ynys Môn
GB-MTY	Merthyr Tydfil;Merthyr Tudful
GB-MON	Monmouthshire;Sir Fynwy
GB-NTL	Neath Port Talbot;Castell-nedd Port Talbot
GB-NWP	Newport;Casnewydd
GB-PEM	Pembrokeshire;Sir Benfro
GB-POW	Powys
GB-RCT	Rhondda, Cynon, Taff;Rhondda, Cynon,Taf
GB-SWA	Swansea;Abertawe
GB-TOF	Torfaen;Torfaen
GB-VGL	Vale of Glamorgan, The;Bro Morgannwg
GB-WRX	Wrexham;Wrecsam
GD-01	Saint Andrew
GD-02	Saint David
GD-03	Saint George
GD-04	Saint John
GD-05	Saint Mark
GD-06	Saint Patrick
GD-10	Southern Grenadine Islands
GE-AB	Abkhazia
GE-AJ	Ajaria
GE-TB	Tbilisi
GE-GU	Guria
GE-IM	Imeret'i
GE-KA	Kakhet'i

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
GE-KK	K'vemo K'art'li
GE-MM	Mts'khet'a-Mt'ianet'i
GE-RL	Racha-Lech'khumi-K'vemo Svanet'i
GE-SZ	Samegrelo-Zemo Svanet'i
GE-SJ	Samts'khe-Javakhet'i
GE-SK	Shida K'art'li
GH-AH	Ashanti
GH-BA	Brong-Ahafo
GH-CP	Central
GH-EP	Eastern
GH-AA	Greater Accra
GH-NP	Northern
GH-UE	Upper East
GH-UW	Upper West
GH-TV	Volta
GH-WP	Western
GL-KU	Kommune Kujalleq
GL-SM	Kommuneqarfik Sermersooq
GL-QA	Qaasuitsup Kommunia
GL-QE	Qeqqata Kommunia
GM-L	Lower River
GM-M	Central River
GM-N	North Bank
GM-U	Upper River
GM-W	Western
GM-B	Banjul
GN-B	Boké
GN-F	Faranah
GN-K	Kankan
GN-D	Kindia
GN-L	Labé
GN-M	Mamou
GN-N	Nzérékoré
GN-C	Conakry
GN-BE	Beyla
GN-BF	Boffa
GN-BK	Boké
GN-CO	Coyah
GN-DB	Dabola
GN-DL	Dalaba
GN-DI	Dinguiraye
GN-DU	Dubréka
GN-FA	Faranah
GN-FO	Forécariah
GN-FR	Fria
GN-GA	Gaoual
GN-GU	Guékédou
GN-KA	Kankan
GN-KE	Kérouané
GN-KD	Kindia
GN-KS	Kissidougou

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
GN-KB	Koubia
GN-KN	Koundara
GN-KO	Kouroussa
GN-LA	Labé
GN-LE	Léléouma
GN-LO	Lola
GN-MC	Macenta
GN-ML	Mali
GN-MM	Mamou
GN-MD	Mandiana
GN-NZ	Nzérékoré
GN-PI	Pita
GN-SI	Siguiri
GN-TE	Télimélé
GN-TO	Tougué
GN-YO	Yomou
GQ-C	Región Continental
GQ-I	Región Insular
GQ-AN	Annobón
GQ-BN	Bioko Norte
GQ-BS	Bioko Sur
GQ-CS	Centro Sur
GQ-KN	Kié-Ntem
GQ-LI	Litoral
GQ-WN	Wele-Nzas
GR-A	Anatoliki Makedonia kai Thraki
GR-I	Attiki
GR-G	Dytiki Ellada
GR-C	Dytiki Makedonia
GR-F	Ionia Nisia
GR-D	Ipeiros
GR-B	Kentriki Makedonia
GR-M	Kriti
GR-L	Notio Aigaio
GR-J	Peloponnisos
GR-H	Stereia Ellada
GR-E	Thessalia
GR-K	Voreio Aigaio
GR-69	Agio Oros
GR-13	Achaïa
GR-01	Aitolia kai Akarnania
GR-11	Argolida
GR-12	Arkadia
GR-31	Arta
GR-A1	Attiki
GR-64	Chalkidiki
GR-94	Chania
GR-85	Chios
GR-81	Dodekanisos
GR-52	Drama
GR-71	Evros

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
GR-05	Evrytania
GR-04	Evvoias
GR-63	Florina
GR-07	Fokida
GR-06	Fthiotida
GR-51	Grevena
GR-14	Ileia
GR-53	Imathia
GR-33	Ioannina
GR-91	Irakleio
GR-41	Karditsa
GR-56	Kastoria
GR-55	Kavala
GR-23	Kefallonia
GR-22	Kerkyra
GR-57	Kilkis
GR-15	Korinthia
GR-58	Kozani
GR-82	Kyklades
GR-16	Lakonia
GR-42	Larisa
GR-92	Lasithi
GR-24	Lefkada
GR-83	Lesvos
GR-43	Magnisia
GR-17	Messinia
GR-59	Pella
GR-61	Pieria
GR-34	Preveza
GR-93	Rethymno
GR-73	Rodopi
GR-84	Samos
GR-62	Serres
GR-32	Thesprotia
GR-54	Thessaloniki
GR-44	Trikala
GR-03	Voiotia
GR-72	Xanthi
GR-21	Zakynthos
GT-AV	Alta Verapaz
GT-BV	Baja Verapaz
GT-CM	Chimaltenango
GT-CQ	Chiquimula
GT-PR	El Progreso
GT-ES	Escuintla
GT-GU	Guatemala
GT-HU	Huehuetenango
GT-IZ	Izabal
GT-JA	Jalapa
GT-JU	Jutiapa
GT-PE	Petén

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
GT-QZ	Quetzaltenango
GT-QC	Quiché
GT-RE	Retalhuleu
GT-SA	Sacatepéquez
GT-SM	San Marcos
GT-SR	Santa Rosa
GT-SO	Sololá
GT-SU	Suchitepéquez
GT-TO	Totonicapán
GT-ZA	Zacapa
GW-BS	Bissau
GW-L	Leste
GW-N	Norte
GW-S	Sul
GW-BA	Bafatá
GW-BM	Biombo
GW-BL	Bolama
GW-CA	Cacheu
GW-GA	Gabú
GW-OI	Oio
GW-QU	Quinara
GW-TO	Tombali
GY-BA	Barima-Waini
GY-CU	Cuyuni-Mazaruni
GY-DE	Demerara-Mahaica
GY-EB	East Berbice-Corentyne
GY-ES	Essequibo Islands-West Demerara
GY-MA	Mahaica-Berbice
GY-PM	Pomeroon-Supenaam
GY-PT	Potaro-Siparuni
GY-UD	Upper Demerara-Berbice
GY-UT	Upper Takutu-Upper Essequibo
HN-AT	Atlántida
HN-CL	Colón
HN-CM	Comayagua
HN-CP	Copán
HN-CR	Cortés
HN-CH	Choluteca
HN-EP	El Paraíso
HN-FM	Francisco Morazán
HN-GD	Gracias a Dios
HN-IN	Intibucá
HN-IB	Islas de la Bahía
HN-LP	La Paz
HN-LE	Lempira
HN-OC	Ocotepeque
HN-OL	Olancho
HN-SB	Santa Bárbara
HN-VA	Valle
HN-YO	Yoro
HR-21	Grad Zagreb

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
HR-07	Bjelovarsko-bilogorska županija
HR-12	Brodsko-posavska županija
HR-19	Dubrovačko-neretvanska županija
HR-18	Istarska županija
HR-04	Karlovačka županija
HR-06	Koprivničko-križevačka županija
HR-02	Krapinsko-zagorska županija
HR-09	Ličko-senjska županija
HR-20	Međimurska županija
HR-14	Osječko-baranjska županija
HR-11	Požeško-slavonska županija
HR-08	Primorsko-goranska županija
HR-03	Sisačko-moslavačka županija
HR-17	Splitsko-dalmatinska županija
HR-15	Šibensko-kninska županija
HR-05	Varaždinska županija
HR-10	Virovitičko-podravska županija
HR-16	Vukovarsko-srijemska županija
HR-13	Zadarska županija
HR-01	Zagrebačka županija
HT-AR	Artibonite
HT-CE	Centre
HT-GA	Grande-Anse
HT-ND	Nord
HT-NE	Nord-Est
HT-NO	Nord-Ouest
HT-OU	Ouest
HT-SD	Sud
HT-SE	Sud-Est
HU-BK	Bács-Kiskun
HU-BA	Baranya
HU-BE	Békés
HU-BZ	Borsod-Abaúj-Zemplén
HU-CS	Csongrád
HU-FE	Fejér
HU-GS	Győr-Moson-Sopron
HU-HB	Hajdú-Bihar
HU-HE	Heves
HU-JN	Jász-Nagykun-Szolnok
HU-KE	Komárom-Esztergom
HU-NO	Nógrád
HU-PE	Pest
HU-SO	Somogy
HU-SZ	Szabolcs-Szatmár-Bereg
HU-TO	Tolna
HU-VA	Vas
HU-VE	Veszprém (county)
HU-ZA	Zala
HU-BC	Békéscsaba
HU-DE	Debrecen
HU-DU	Dunaújváros

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
HU-EG	Eger
HU-ER	Érd
HU-GY	Győr
HU-HV	Hódmezővásárhely
HU-KV	Kaposvár
HU-KM	Kecskemét
HU-MI	Miskolc
HU-NK	Nagykanizsa
HU-NY	Nyíregyháza
HU-PS	Pécs
HU-ST	Salgótarján
HU-SN	Sopron
HU-SD	Szeged
HU-SF	Székesfehérvár
HU-SS	Szekszárd
HU-SK	Szolnok
HU-SH	Szombathely
HU-TB	Tatabánya
HU-VM	Veszprém
HU-ZE	Zalaegerszeg
HU-BU	Budapest
ID-JW	Jawa
ID-KA	Kalimantan
ID-ML	Maluku
ID-NU	Nusa Tenggara
ID-IJ	Papua
ID-SL	Sulawesi
ID-SM	Sumatera
ID-AC	Aceh
ID-BA	Bali
ID-BB	Bangka Belitung
ID-BT	Banten
ID-BE	Bengkulu
ID-GO	Gorontalo
ID-JA	Jambi
ID-JB	Jawa Barat
ID-JT	Jawa Tengah
ID-JI	Jawa Timur
ID-KB	Kalimantan Barat
ID-KT	Kalimantan Tengah
ID-KS	Kalimantan Selatan
ID-KI	Kalimantan Timur
ID-KR	Kepulauan Riau
ID-LA	Lampung
ID-MA	Maluku
ID-MU	Maluku Utara
ID-NB	Nusa Tenggara Barat
ID-NT	Nusa Tenggara Timur
ID-PA	Papua
ID-PB	Papua Barat
ID-RI	Riau

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
ID-SR	Sulawesi Barat
ID-SN	Sulawesi Selatan
ID-ST	Sulawesi Tengah
ID-SG	Sulawesi Tenggara
ID-SA	Sulawesi Utara
ID-SB	Sumatra Barat
ID-SS	Sumatra Selatan
ID-SU	Sumatera Utara
ID-JK	Jakarta Raya
ID-YO	Yogyakarta
IE-C	Connacht
IE-L	Leinster
IE-M	Munster
IE-U	Ulster
IE-CW	Carlow
IE-CN	Cavan
IE-CE	Clare
IE-CO	Cork
IE-DL	Donegal
IE-D	Dublin
IE-G	Galway
IE-KY	Kerry
IE-KE	Kildare
IE-KK	Kilkenny
IE-LS	Laois
IE-LM	Leitrim
IE-LK	Limerick
IE-LD	Longford
IE-LH	Louth
IE-MO	Mayo
IE-MH	Meath
IE-MN	Monaghan
IE-OY	Offaly
IE-RN	Roscommon
IE-SO	Sligo
IE-TA	Tipperary
IE-WD	Waterford
IE-WH	Westmeath
IE-WX	Wexford
IE-WW	Wicklow
IL-D	HaDarom
IL-M	HaMerkaz
IL-Z	HaZafon
IL-HA	Hefa
IL-TA	Tel-Aviv
IL-JM	Yerushalayim Al Quds
IN-AP	Andhra Pradesh
IN-AR	Arunachal Pradesh
IN-AS	Assam
IN-BR	Bihar
IN-CT	Chhattisgarh

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Table A.4.1 – continued from previous page

Key	Description
IN-GA	Goa
IN-GJ	Gujarat
IN-HR	Haryana
IN-HP	Himachal Pradesh
IN-JK	Jammu and Kashmir
IN-JH	Jharkhand
IN-KA	Karnataka
IN-KL	Kerala
IN-MP	Madhya Pradesh
IN-MH	Maharashtra
IN-MN	Manipur
IN-ML	Meghalaya
IN-MZ	Mizoram
IN-NL	Nagaland
IN-OR	Orissa
IN-PB	Punjab
IN-RJ	Rajasthan
IN-SK	Sikkim
IN-TN	Tamil Nadu
IN-TR	Trípura
IN-UT	Uttarakhand
IN-UP	Uttar Pradesh
IN-WB	West Bengal
IN-AN	Andaman and Nicobar Islands
IN-CH	Chandigarh
IN-DN	Dadra and Nagar Haveli
IN-DD	Damen and Diu
IN-DL	Delhi
IN-LD	Lakshadweep
IN-PY	Puducherry
IQ-AN	Al Anbar
IQ-BA	Al Basrah
IQ-MU	Al Muthanna
IQ-QA	Al Qadisiyah
IQ-NA	An Najef
IQ-AR	Arbil
IQ-SW	As Sulaymaniyah
IQ-TS	At Ta'mim
IQ-BB	Babil
IQ-BG	Baghdad
IQ-DA	Dahuk
IQ-DQ	Dhi Qar
IQ-DI	Diyala
IQ-KA	Karbala'
IQ-MA	Maysan
IQ-NI	Ninawa
IQ-SD	Salah ad Din
IQ-WA	Wasit
IR-03	Ardabīl
IR-02	Āzarbāyjān-e Gharbī
IR-01	Āzarbāyjān-e Sharqī

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
IR-06	Būshehr
IR-08	Chahār Mahāll va Bakhtīārī
IR-04	Esfahān
IR-14	Fārs
IR-19	Gīlān
IR-27	Golestān
IR-24	Hamadān
IR-23	Hormozgān
IR-05	Ilām
IR-15	Kermān
IR-17	Kermānshāh
IR-29	Khorāsān-e Janūbī
IR-30	Khorāsān-e Razavī
IR-31	Khorāsān-e Shemālī
IR-10	Khūzestān
IR-18	Kohgilūyeh va Būyer Ahmad
IR-16	Kordestān
IR-20	Lorestān
IR-22	Markazī
IR-21	Māzandarān
IR-28	Qazvīn
IR-26	Qom
IR-12	Semnān
IR-13	Sīstān va Balūchestān
IR-07	Tehrān
IR-25	Yazd
IR-11	Zanjān
IS-7	Austurland
IS-1	Höfuðborgarsvæðið
IS-6	Norðurland eystra
IS-5	Norðurland vestra
IS-8	Suðurland
IS-2	Suðurnes
IS-4	Vestfirðir
IS-3	Vesturland
IS-0	Reykjavík
IT-65	Abruzzo
IT-77	Basilicata
IT-78	Calabria
IT-72	Campania
IT-45	Emilia-Romagna
IT-36	Friuli-Venezia Giulia
IT-62	Lazio
IT-42	Liguria
IT-25	Lombardia
IT-57	Marche
IT-67	Molise
IT-21	Piemonte
IT-75	Puglia
IT-88	Sardegna
IT-82	Sicilia

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Table A.4.1 – continued from previous page

Key	Description
IT-52	Toscana
IT-32	Trentino-Alto Adige
IT-55	Umbria
IT-23	Valle d'Aosta
IT-34	Veneto
IT-AG	Agrigento
IT-AL	Alessandria
IT-AN	Ancona
IT-AO	Aosta
IT-AR	Arezzo
IT-AP	Ascoli Piceno
IT-AT	Asti
IT-AV	Avellino
IT-BA	Bari
IT-BT	Barletta-Andria-Trani
IT-BL	Belluno
IT-BN	Benevento
IT-BG	Bergamo
IT-BI	Biella
IT-BO	Bologna
IT-BZ	Bolzano
IT-BS	Brescia
IT-BR	Brindisi
IT-CA	Cagliari
IT-CL	Caltanissetta
IT-CB	Campobasso
IT-CI	Carbonia-Iglesias
IT-CE	Caserta
IT-CT	Catania
IT-CZ	Catanzaro
IT-CH	Chieti
IT-CO	Como
IT-CS	Cosenza
IT-CR	Cremona
IT-KR	Crotone
IT-CN	Cuneo
IT-EN	Enna
IT-FM	Fermo
IT-FE	Ferrara
IT-FI	Firenze
IT-FG	Foggia
IT-FC	Forlì-Cesena
IT-FR	Frosinone
IT-GE	Genova
IT-GO	Gorizia
IT-GR	Grosseto
IT-IM	Imperia
IT-IS	Isernia
IT-SP	La Spezia
IT-AQ	L'Aquila
IT-LT	Latina

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
IT-LE	Lecce
IT-LC	Lecco
IT-LI	Livorno
IT-LO	Lodi
IT-LU	Lucca
IT-MC	Macerata
IT-MN	Mantova
IT-MS	Massa-Carrara
IT-MT	Matera
IT-VS	Medio Campidano
IT-ME	Messina
IT-MI	Milano
IT-MO	Modena
IT-MB	Monza e Brianza
IT-NA	Napoli
IT-NO	Novara
IT-NU	Nuoro
IT-OG	Ogliastra
IT-OT	Olbia-Tempio
IT-OR	Oristano
IT-PD	Padova
IT-PA	Palermo
IT-PR	Parma
IT-PV	Pavia
IT-PG	Perugia
IT-PU	Pesaro e Urbino
IT-PE	Pescara
IT-PC	Piacenza
IT-PI	Pisa
IT-PT	Pistoia
IT-PN	Pordenone
IT-PZ	Potenza
IT-PO	Prato
IT-RG	Ragusa
IT-RA	Ravenna
IT-RC	Reggio Calabria
IT-RE	Reggio Emilia
IT-RI	Rieti
IT-RN	Rimini
IT-RM	Roma
IT-RO	Rovigo
IT-SA	Salerno
IT-SS	Sassari
IT-SV	Savona
IT-SI	Siena
IT-SR	Siracusa
IT-SO	Sondrio
IT-TA	Taranto
IT-TE	Teramo
IT-TR	Terni
IT-TO	Torino

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
IT-TP	Trapani
IT-TN	Trento
IT-TV	Treviso
IT-TS	Trieste
IT-UD	Udine
IT-VA	Varese
IT-VE	Venezia
IT-VB	Verbano-Cusio-Ossola
IT-VC	Vercelli
IT-VR	Verona
IT-VV	Vibo Valentia
IT-VI	Vicenza
IT-VT	Viterbo
JM-13	Clarendon
JM-09	Hanover
JM-01	Kingston
JM-12	Manchester
JM-04	Portland
JM-02	Saint Andrew
JM-06	Saint Ann
JM-14	Saint Catherine
JM-11	Saint Elizabeth
JM-08	Saint James
JM-05	Saint Mary
JM-03	Saint Thomas
JM-07	Trelawny
JM-10	Westmoreland
JO-AJ	'Ajlūn
JO-AQ	Al 'Aqabah
JO-BA	Al Balqā'
JO-KA	Al Karak
JO-MA	Al Mafraq
JO-AM	'Ammān (Al 'Aṣimah)
JO-AT	At Ḥaṭṭīlah
JO-AZ	Az Zarqā'
JO-IR	Irbid
JO-JA	Jarash
JO-MN	Ma'ān
JO-MD	Mādabā
JP-23	Aichi
JP-05	Akita
JP-02	Aomori
JP-12	Chiba
JP-38	Ehime
JP-18	Fukui
JP-40	Fukuoka
JP-07	Fukushima
JP-21	Gifu
JP-10	Gunma
JP-34	Hiroshima
JP-01	Hokkaido

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
JP-28	Hyogo
JP-08	Ibaraki
JP-17	Ishikawa
JP-03	Iwate
JP-37	Kagawa
JP-46	Kagoshima
JP-14	Kanagawa
JP-39	Kochi
JP-43	Kumamoto
JP-26	Kyoto
JP-24	Mie
JP-04	Miyagi
JP-45	Miyazaki
JP-20	Nagano
JP-42	Nagasaki
JP-29	Nara
JP-15	Niigata
JP-44	Oita
JP-33	Okayama
JP-47	Okinawa
JP-27	Osaka
JP-41	Saga
JP-11	Saitama
JP-25	Shiga
JP-32	Shimane
JP-22	Shizuoka
JP-09	Tochigi
JP-36	Tokushima
JP-13	Tokyo
JP-31	Tottori
JP-16	Toyama
JP-30	Wakayama
JP-06	Yamagata
JP-35	Yamaguchi
JP-19	Yamanashi
KE-110	Nairobi Municipality
KE-200	Central
KE-300	Coast
KE-400	Eastern
KE-500	North-Eastern Kaskazini Mashariki
KE-700	Rift Valley
KE-800	Western Magharibi
KG-GB	Bishkek
KG-B	Batken
KG-C	Chü
KG-J	Jalal-Abad
KG-N	Naryn
KG-O	Osh
KG-T	Talas
KG-Y	Ysyk-Köl
KH-23	Krong Kaeb

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
KH-24	Krong Pailin
KH-18	Krong Preah Sihanouk
KH-12	Phnom Penh
KH-2	Battambang
KH-1	Banteay Mean Chey
KH-3	Kampong Cham
KH-4	Kampong Chhnang
KH-5	Kampong Speu
KH-6	Kampong Thom
KH-7	Kampot
KH-8	Kandal
KH-9	Kach Kong
KH-10	Krachoh
KH-11	Mondol Kiri
KH-22	Otdar Mean Chey
KH-15	Pousaat
KH-13	Preah Vihear
KH-14	Prey Veaeng
KH-16	Rotanak Kiri
KH-17	Siem Reab
KH-19	Stueng Traeng
KH-20	Svaay Rieng
KH-21	Taakaev
KI-G	Gilbert Islands
KI-L	Line Islands
KI-P	Phoenix Islands
KN-K	Saint Kitts
KN-N	Nevis
KN-01	Christ Church Nichola Town
KN-02	Saint Anne Sandy Point
KN-03	Saint George Basseterre
KN-04	Saint George Gingerland
KN-05	Saint James Windward
KN-06	Saint John Capisterre
KN-07	Saint John Figtree
KN-08	Saint Mary Cayon
KN-09	Saint Paul Capisterre
KN-10	Saint Paul Charlestown
KN-11	Saint Peter Basseterre
KN-12	Saint Thomas Lowland
KN-13	Saint Thomas Middle Island
KN-15	Trinity Palmetto Point
KM-A	Andjouân (Anjwān)
KM-G	Andjažđja (Anjazījah)
KM-M	Moûhîlî (Mühîlî)
KP-01	P'yöngyang
KP-13	Nasōn (Najin-Sönbong)
KP-02	P'yöngan-namdo
KP-03	P'yöngan-bukto
KP-04	Chagang-do
KP-05	Hwanghae-namdo

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
KP-06	Hwanghae-bukto
KP-07	Kangwŏn-do
KP-08	Hamgyōng-namdo
KP-09	Hamgyōng-bukto
KP-10	Yanggang-do
KR-11	Seoul Teugbyeolsi
KR-26	Busan Gwang'yeogsi
KR-27	Daegu Gwang'yeogsi
KR-30	Daejeon Gwang'yeogsi
KR-29	Gwangju Gwang'yeogsi
KR-28	Incheon Gwang'yeogsi
KR-31	Ulsan Gwang'yeogsi
KR-43	Chungcheongbukdo
KR-44	Chungcheongnamdo
KR-42	Gang'weondo
KR-41	Gyeonggido
KR-47	Gyeongsangbukdo
KR-48	Gyeongsangnamdo
KR-49	Jejudo
KR-45	Jeonrabukdo
KR-46	Jeonranamdo
KW-AH	Al Ahmadi
KW-FA	Al Farwānīyah
KW-JA	Al Jahrrā'
KW-KU	Al Kuwayt (Al 'Āsimah)
KW-HA	Hawallī
KW-MU	Mubārak al Kabīr
KZ-ALA	Almaty
KZ-AST	Astana
KZ-ALM	Almaty oblysy
KZ-AKM	Aqmola oblysy
KZ-AKT	Aqtöbe oblysy
KZ-ATY	Atyraū oblysy
KZ-ZAP	Batys Quzaqstan oblysy
KZ-MAN	Mangghystaū oblysy
KZ-YUZ	Ongtüstik Qazaqstan oblysy
KZ-PAV	Pavlodar oblysy
KZ-KAR	Qaraghandy oblysy
KZ-KUS	Qostanay oblysy
KZ-KZY	Qyzylorda oblysy
KZ-VOS	Shyghys Qazaqstan oblysy
KZ-SEV	Soltüstik Quzaqstan oblysy
KZ-ZHA	Zhambyl oblysy
LA-VT	Vientiane
LA-AT	Attapu
LA-BK	Bokèo
LA-BL	Bolikhhamxai
LA-CH	Champasak
LA-HO	Houaphan
LA-KH	Khammouan
LA-LM	Louang Namtha

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
LA-LP	Louangphabang
LA-OU	Oudômxai
LA-PH	Phêngsali
LA-SL	Salavan
LA-SV	Savannakhét
LA-VI	Vientiane
LA-XA	Xaignabouli
LA-XE	Xékong
LA-XI	Xiangkhoang
LA-XN	Xiasômbooun
LI-01	Balzers
LI-02	Eschen
LI-03	Gamprin
LI-04	Mauren
LI-05	Planken
LI-06	Ruggell
LI-07	Schaan
LI-08	Schellenberg
LI-09	Triesen
LI-10	Triesenberg
LI-11	Vaduz
LB-AK	Aakkâr
LB-BH	Baalbek-Hermel
LB-BI	Béqaa
LB-BA	Beyrouth
LB-AS	Liban-Nord
LB-JA	Liban-Sud
LB-JL	Mont-Liban
LB-NA	Nabaîtyé
LK-1	Basnâhira pa āta
LK-3	Daku u pa āta
LK-2	Madhyama pa āta
LK-5	Næg��nahira pa āta
LK-9	Sabaragamuva pa āta
LK-7	Uturum��eda pa āta
LK-4	Uturu pa āta
LK-8	��va pa āta
LK-6	Vayamba pa āta
LK-52	Amp��ara
LK-71	Anur��dhapura
LK-81	Badulla
LK-51	Ma��dakalapuva
LK-11	K�� amba
LK-31	G��lla
LK-12	Gampaha
LK-33	Hambant��ta
LK-41	Y��panaya
LK-13	Ka utara
LK-21	Mahanuvara
LK-92	K��galla
LK-42	Kilin��chchi

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
LK-61	Kuru ægala
LK-43	Mannārama
LK-22	Mātale
LK-32	Mātarā
LK-82	Mõ arāgala
LK-45	Mulativ
LK-23	Nuvara Ěliya
LK-72	Põ önnaruva
LK-62	Puttalama
LK-91	Ratnapura
LK-53	Triku āmalaya
LK-44	Vavuniyāva
LR-BM	Bomi
LR-BG	Bong
LR-GB	Grand Bassa
LR-CM	Grand Cape Mount
LR-GG	Grand Gedeh
LR-GK	Grand Kru
LR-LO	Lofa
LR-MG	Margibi
LR-MY	Maryland
LR-MO	Montserrado
LR-NI	Nimba
LR-RI	Rivercess
LR-SI	Sinoe
LS-D	Berea
LS-B	Butha-Buthe
LS-C	Leribe
LS-E	Mafeteng
LS-A	Maseru
LS-F	Mohale's Hoek
LS-J	Mokhotlong
LS-H	Qacha's Nek
LS-G	Quthing
LS-K	Thaba-Tseka
LT-AL	Alytaus Apskritis
LT-KU	Kauno Apskritis
LT-KL	Klaipėdos Apskritis
LT-MR	Marijampolės Apskritis
LT-PN	Panėvėžio Apskritis
LT-SA	Šiaulių Apskritis
LT-TA	Tauragės Apskritis
LT-TE	Telšių Apskritis
LT-UT	Utenos Apskritis
LT-VL	Vilniaus Apskritis
LU-D	Diekirch
LU-G	Grevenmacher
LU-L	Luxembourg
LV-001	Aglonas novads
LV-002	Aizkraukles novads
LV-003	Aizputes novads

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
LV-004	Aknīstes novads
LV-005	Alojas novads
LV-006	Alsungas novads
LV-007	Alūksnes novads
LV-008	Amatas novads
LV-009	Apes novads
LV-010	Auces novads
LV-011	Ādažu novads
LV-012	Babītes novads
LV-013	Baldones novads
LV-014	Baltinavas novads
LV-015	Balvu novads
LV-016	Bauskas novads
LV-017	Beverīnas novads
LV-018	Brocēnu novads
LV-019	Burtnieku novads
LV-020	Carnikavas novads
LV-021	Cesvaines novads
LV-022	Cēsu novads
LV-023	Cīblas novads
LV-024	Dagdas novads
LV-025	Daugavpils novads
LV-026	Dobeles novads
LV-027	Dundagas novads
LV-028	Durbes novads
LV-029	Engures novads
LV-030	Ērgļu novads
LV-031	Garkalnes novads
LV-032	Grobiņas novads
LV-033	Gulbenes novads
LV-034	Iecavas novads
LV-035	Ikšķiles novads
LV-036	Ilūkstes novads
LV-037	Inčukalna novads
LV-038	Jaunjelgavas novads
LV-039	Jaunpiebalgas novads
LV-040	Jaunpils novads
LV-041	Jelgavas novads
LV-042	Jēkabpils novads
LV-043	Kandavas novads
LV-044	Kārsavas novads
LV-045	Kocēnu novads
LV-046	Kokneses novads
LV-047	Krāslavas novads
LV-048	Krimuldas novads
LV-049	Krustpils novads
LV-050	Kuldīgas novads
LV-051	Ķeguma novads
LV-052	Ķekavas novads
LV-053	Lielvārdes novads
LV-054	Limbažu novads

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Table A.4.1 – continued from previous page

Key	Description
LV-055	Līgatnes novads
LV-056	Līvānu novads
LV-057	Lubānas novads
LV-058	Ludzas novads
LV-059	Madonas novads
LV-060	Mazsalacas novads
LV-061	Mālpils novads
LV-062	Mārupes novads
LV-063	Mērsraga novads
LV-064	Naukšēnu novads
LV-065	Neretas novads
LV-066	Nīcas novads
LV-067	Ogres novads
LV-068	Olaines novads
LV-069	Ozolnieku novads
LV-070	Pārgaujas novads
LV-071	Pāvilostas novads
LV-072	Pļaviņu novads
LV-073	Preiļu novads
LV-074	Priekules novads
LV-075	Priekuļu novads
LV-076	Raunas novads
LV-077	Rēzeknes novads
LV-078	Riebiņu novads
LV-079	Rojas novads
LV-080	Ropažu novads
LV-081	Rucavas novads
LV-082	Rugāju novads
LV-083	Rundāles novads
LV-084	Rūjienas novads
LV-085	Salas novads
LV-086	Salacgrīvas novads
LV-087	Salaspils novads
LV-088	Saldus novads
LV-089	Saulkrastu novads
LV-090	Sējas novads
LV-091	Siguldas novads
LV-092	Skrīveru novads
LV-093	Skrundas novads
LV-094	Smiltenes novads
LV-095	Stopiņu novads
LV-096	Strenču novads
LV-097	Talsu novads
LV-098	Tērvetes novads
LV-099	Tukuma novads
LV-100	Vaiņodes novads
LV-101	Valkas novads
LV-102	Varakļānu novads
LV-103	Vārkavas novads
LV-104	Vecpiebalgas novads
LV-105	Vecumnieku novads

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
LV-106	Ventspils novads
LV-107	Viesītes novads
LV-108	Viļakas novads
LV-109	Viļānu novads
LV-110	Zilupes novads
LV-DGV	Daugavpils
LV-JEL	Jelgava
LV-JKB	Jēkabpils
LV-JUR	Jūrmala
LV-LPX	Liepāja
LV-REZ	Rēzekne
LV-RIX	Rīga
LV-VMR	Valmiera
LV-VEN	Ventspils
LY-BU	Al Buṭnān
LY-JA	Al Jabal al Akh ar
LY-JG	Al Jabal al Gharbī
LY-JI	Al Jifārah
LY-JU	Al Jufrah
LY-KF	Al Kufrah
LY-MJ	Al Marj
LY-MB	Al Marqab
LY-WA	Al Wāhāt
LY-NQ	An Nuqaṭ al Khams
LY-ZA	Az Zāwiyah
LY-BA	Banghāzī
LY-DR	Darnah
LY-GT	Ghāt
LY-JB	Jaghbūb
LY-MI	Miṣrātah
LY-MQ	Murzuq
LY-NL	Nālūt
LY-SB	Sabhā
LY-SR	Surt
LY-TB	Tarābulus
LY-WD	Wādī al ayāt
LY-WS	Wādī ash Shāṭī
MA-09	Chaouia-Ouardigha
MA-10	Doukhala-Abda
MA-05	Fès-Boulemane
MA-02	Gharb-Chrarda-Beni Hssen
MA-08	Grand Casablanca
MA-14	Guelmim-És Smara
MA-15	Laâyoune-Boujdour-Sakia el Hamra
MA-04	L'Oriental
MA-11	Marrakech-Tensift-Al Haouz
MA-06	Meknès-Tafilalet
MA-16	Oued ed Dahab-Lagouira
MA-07	Rabat-Salé-Zemmour-Zaer
MA-13	Sous-Massa-Draa
MA-12	Tadla-Azilal

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Table A.4.1 – continued from previous page

Key	Description
MA-01	Tanger-Tétouan
MA-03	Taza-Al Hoceima-Taounate
MA-HAO	Al Haouz
MA-HOC	Al Hoceïma
MA-ASZ	Assa-Zag
MA-AZI	Azilal
MA-BEM	Beni Mellal
MA-BES	Ben Slimane
MA-BER	Berkane
MA-BOD	Boujdour (EH)
MA-BOM	Boulemane
MA-CHE	Chefchaouen
MA-CHI	Chichaoua
MA-CHT	Chtouka-Ait Baha
MA-HAJ	El Hajeb
MA-JDI	El Jadida
MA-ERR	Errachidia
MA-ESI	Essaouira
MA-ESM	Es Smara (EH)
MA-FIG	Figuig
MA-GUE	Guelmim
MA-IFR	Ifrane
MA-JRA	Jrada
MA-KES	Kelaat es Sraghna
MA-KEN	Kénitra
MA-KHE	Khemisaet
MA-KHN	Khenifra
MA-KHO	Khouribga
MA-LAA	Laâyoune (EH)
MA-LAR	Larache
MA-MED	Médiouna
MA-MOU	Moulay Yacoub
MA-NAD	Nador
MA-NOU	Nouaceur
MA-OUA	Ouarzazate
MA-OUD	Oued ed Dahab (EH)
MA-SAF	Safi
MA-SEF	Sefrou
MA-SET	Settat
MA-SIK	Sid'l Kacem
MA-TNT	Tan-Tan
MA-TAO	Taounate
MA-TAI	Taourirt
MA-TAR	Taroudant
MA-TAT	Tata
MA-TAZ	Taza
MA-TIZ	Tiznit
MA-ZAG	Zagora
MA-AGD	Agadir-Ida-Outanane
MA-AOU	Aousserd
MA-CAS	Casablanca [Dar el Beïda]

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MA-FAH	Fahs-Beni Makada
MA-FES	Fès-Dar-Dbibegh
MA-INE	Inezgane-Ait Melloul
MA-MMD	Marrakech-Medina
MA-MMN	Marrakech-Menara
MA-MEK	Meknès
MA-MOH	Mohammadia
MA-OUJ	Oujda-Angad
MA-RAB	Rabat
MA-SAL	Salé
MA-SYB	Sidi Youssef Ben Ali
MA-SKH	Skhirate-Témara
MA-TNG	Tanger-Assilah
MA-TET	Tétouan
MC-CO	La Condamine
MC-FO	Fontvieille
MC-JE	Jardin Exotique
MC-CL	La Colle
MC-GA	La Gare
MC-SO	La Source
MC-LA	Larvotto
MC-MA	Malbousquet
MC-MO	Monaco-Ville
MC-MG	Moneghetti
MC-MC	Monte-Carlo
MC-MU	Moulins
MC-PH	Port-Hercule
MC-SR	Saint-Roman
MC-SD	Sainte-Dévote
MC-SP	Spélugues
MC-VR	Vallon de la Rousse
MD-GA	Găgăuzia, Unitatea teritorială autonomă
MD-BA	Bălți
MD-BD	Tighina
MD-CU	Chișinău
MD-AN	Anenii Noi
MD-BS	Basarabeasca
MD-BR	Briceni
MD-CA	Cahul
MD-CT	Cantemir
MD-CL	Călărași
MD-CS	Căușeni
MD-CM	Cimișlia
MD-CR	Criuleni
MD-DO	Dondușeni
MD-DR	Drochia
MD-DU	Dubăsari
MD-ED	Edineț
MD-FA	Făleşti
MD-FL	Florești
MD-GL	Glodeni

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MD-HI	Hînceşti
MD-IA	Ialoveni
MD-LE	Leova
MD-NI	Nisporeni
MD-OC	Ocniţa
MD-OR	Orhei
MD-RE	Rezina
MD-RI	Rîşcani
MD-SI	Sîngerei
MD-SO	Soroca
MD-ST	Străşeni
MD-SD	Şoldăneşti
MD-SV	Ştefan Vodă
MD-TA	Taraclia
MD-TE	Teleneşti
MD-UN	Ungheni
MD-SN	Stînga Nistrului, unitatea teritorială din
ME-01	Andrijevica
ME-02	Bar
ME-03	Berane
ME-04	Bijelo Polje
ME-05	Budva
ME-06	Cetinje
ME-07	Danilovgrad
ME-08	Herceg-Novi
ME-09	Kolašin
ME-10	Kotor
ME-11	Mojkovac
ME-12	Nikšić
ME-13	Plav
ME-14	Pljevlja
ME-15	Plužine
ME-16	Podgorica
ME-17	Rožaje
ME-18	Šavnik
ME-19	Tivat
ME-20	Ulcinj
ME-21	Žabljak
MG-T	Antananarivo
MG-D	Antsiranana
MG-F	Fianarantsoa
MG-M	Mahajanga
MG-A	Toamasina
MG-U	Toliara
MH-L	Ralik chain
MH-T	Ratak chain
MH-ALL	Ailinglaplap
MH-ALK	Ailuk
MH-ARN	Arno
MH-AUR	Aur
MH-EBO	Ebon

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MH-ENI	Enewetak
MH-JAB	Jabat
MH-JAL	Jaluit
MH-KIL	Kili
MH-KWA	Kwajalein
MH-LAE	Lae
MH-LIB	Lib
MH-LIK	Likiep
MH-MAJ	Majuro
MH-MAL	Maloelap
MH-MEJ	Mejit
MH-MIL	Mili
MH-NMK	Namdrik
MH-NMU	Namu
MH-RON	Rongelap
MH-UJA	Ujae
MH-UTI	Utirik
MH-WTN	Wotho
MH-WTJ	Wotje
MK-01	Aerodrom
MK-02	Aračinovo
MK-03	Berovo
MK-04	Bitola
MK-05	Bogdanci
MK-06	Bogovinje
MK-07	Bosilovo
MK-08	Brvenica
MK-09	Butel
MK-77	Centar
MK-78	Centar Župa
MK-79	Čair
MK-80	Čaška
MK-81	Češinovo-Obleševo
MK-82	Čučer Sandevo
MK-21	Debar
MK-22	Debarca
MK-23	Delčevro
MK-25	Demir Hisar
MK-24	Demir Kapija
MK-26	Dojran
MK-27	Dolneni
MK-28	Drugovo
MK-17	Gazi Baba
MK-18	Gevgelija
MK-29	Gjorče Petrov
MK-19	Gostivar
MK-20	Gradsko
MK-34	Ilinden
MK-35	Jegunovce
MK-37	Karbinci
MK-38	Karpoš

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MK-36	Kavadarci
MK-40	Kičevo
MK-39	Kisela Voda
MK-42	Kočani
MK-41	Konče
MK-43	Kratovo
MK-44	Kriva Palanka
MK-45	Krivogaštani
MK-46	Kruševo
MK-47	Kumanovo
MK-48	Lipkovo
MK-49	Lozovo
MK-51	Makedonska Kamenica
MK-52	Makedonski Brod
MK-50	Mavrovo-i-Rostuša
MK-53	Mogila
MK-54	Negotino
MK-55	Novaci
MK-56	Novo Selo
MK-58	Ohrid
MK-57	Oslomej
MK-60	Pehčevo
MK-59	Petrovec
MK-61	Plasnica
MK-62	Prilep
MK-63	Probištip
MK-64	Radoviš
MK-65	Rankovce
MK-66	Resen
MK-67	Rosoman
MK-68	Saraj
MK-70	Sopište
MK-71	Staro Nagoričane
MK-72	Struga
MK-73	Strumica
MK-74	Studeničani
MK-69	Sveti Nikole
MK-83	Štip
MK-84	Šuto Orizari
MK-75	Tearce
MK-76	Tetovo
MK-10	Valandovo
MK-11	Vasilevo
MK-13	Veles
MK-12	Vevčani
MK-14	Vinica
MK-15	Vraneštica
MK-16	Vrapčište
MK-31	Zajas
MK-32	Zelenikovo
MK-33	Zrnovci

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MK-30	Želino
ML-BK0	Bamako
ML-7	Gao
ML-1	Kayes
ML-8	Kidal
ML-2	Koulakoro
ML-5	Mopti
ML-4	Ségou
ML-3	Sikasso
ML-6	Tombouctou
MM-07	Ayeyarwady
MM-02	Bago
MM-03	Magway
MM-04	Mandalay
MM-01	Sagaing
MM-05	Tanintharyi
MM-06	Yangon
MM-14	Chin
MM-11	Kachin
MM-12	Kayah
MM-13	Kayin
MM-15	Mon
MM-16	Rakhine
MM-17	Shan
MN-073	Arhangay
MN-069	Bayanhongor
MN-071	Bayan-Ölgii
MN-067	Bulgan
MN-061	Dornod
MN-063	Dornogovi
MN-059	Dundgovi
MN-057	Dzavhan
MN-065	Govi-Altay
MN-039	Hentiü
MN-043	Hovd
MN-041	Hövsgöl
MN-053	Ömnögovi
MN-055	Övörhangay
MN-049	Selenge
MN-051	Sühbaatar
MN-047	Töv
MN-046	Uvs
MN-1	Ulanbaatar
MN-037	Darhan uul
MN-064	Govi-Sumber
MN-035	Orhon
MR-NKC	Nouakchott
MR-07	Adrar
MR-03	Assaba
MR-05	Brakna
MR-08	Dakhlet Nouadhibou

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MR-04	Gorgol
MR-10	Guidimaka
MR-01	Hodh ech Chargui
MR-02	Hodh el Charbi
MR-12	Inchiri
MR-09	Tagant
MR-11	Tiris Zemmour
MR-06	Trarza
MT-01	Attard
MT-02	Balzan
MT-03	Birgu
MT-04	Birkirkara
MT-05	Birżeppuġa
MT-06	Bormla
MT-07	Dingli
MT-08	Fgura
MT-09	Floriana
MT-10	Fontana
MT-11	Gudja
MT-12	Gżira
MT-13	Ġħajnsielem
MT-14	Ģħarb
MT-15	Ģħargħur
MT-16	Ģħasri
MT-17	Ģħaxaq
MT-18	Hamrun
MT-19	Ikklin
MT-20	Isla
MT-21	Kalkara
MT-22	Kerċem
MT-23	Kirkop
MT-24	Lija
MT-25	Luqa
MT-26	Marsa
MT-27	Marsaskala
MT-28	Marsaxlokk
MT-29	Mdina
MT-30	Mellieħa
MT-31	Mġarr
MT-32	Mosta
MT-33	Mqabba
MT-34	Msida
MT-35	Mtarfa
MT-36	Munxar
MT-37	Nadur
MT-38	Naxxar
MT-39	Paola
MT-40	Pembroke
MT-41	Pietà
MT-42	Qala
MT-43	Qormi

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MT-44	Qrendi
MT-45	Rabat Ĝawdex
MT-46	Rabat Malta
MT-47	Safi
MT-48	San Čiljan
MT-49	San Ċwann
MT-50	San Lawrenz
MT-51	San Pawl il-Baħar
MT-52	Sannat
MT-53	Santa Luċija
MT-54	Santa Venera
MT-55	Stiġgiewi
MT-56	Sliema
MT-57	Swieqi
MT-58	Ta' Xbiex
MT-59	Tarxien
MT-60	Valletta
MT-61	Xagħra
MT-62	Xewkija
MT-63	Xghajra
MT-64	Zabbar
MT-65	Żebbuġ Ĝawdex
MT-66	Żebbuġ Malta
MT-67	Żejtun
MT-68	Żurrieq
MU-BR	Beau Bassin-Rose Hill
MU-CU	Curepipe
MU-PU	Port Louis
MU-QB	Quatre Bornes
MU-VP	Vacoas-Phoenix
MU-AG	Agalega Islands
MU-CC	Cargados Carajos Shoals
MU-RO	Rodrigues Island
MU-BL	Black River
MU-FL	Flacq
MU-GP	Grand Port
MU-MO	Moka
MU-PA	Pamplemousses
MU-PW	Plaines Wilhems
MU-PL	Port Louis
MU-RP	Rivière du Rempart
MU-SA	Savanne
MV-MLE	Male
MV-SU	South
MV-US	Upper South
MV-UN	Upper North
MV-CE	Central
MV-SC	South Central
MV-NC	North Central
MV-NO	North
MV-02	Alifu Alifu

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MV-00	Alifu Dhaalu
MV-20	Baa
MV-17	Dhaalu
MV-14	Faafu
MV-27	Gaafu Alifu
MV-28	Gaafu Dhaalu
MV-29	Gnaviyani
MV-07	Haa Alifu
MV-23	Haa Dhaalu
MV-26	Kaafu
MV-05	Laamu
MV-03	Lhaviyani
MV-12	Meemu
MV-25	Noonu
MV-13	Raa
MV-01	Seenu
MV-24	Shaviyani
MV-08	Thaa
MV-04	Vaavu
MW-C	Central Region
MW-N	Northern Region
MW-S	Southern Region
MW-BA	Balaka
MW-BL	Blantyre
MW-CK	Chikwawa
MW-CR	Chiradzulu
MW-CT	Chitipa
MW-DE	Dedza
MW-DO	Dowa
MW-KR	Karonga
MW-KS	Kasungu
MW-LK	Likoma
MW-LI	Lilongwe
MW-MH	Machinga
MW-MG	Mangochi
MW-MC	Mchinji
MW-MU	Mulanje
MW-MW	Mwanza
MW-MZ	Mzimba
MW-NE	Neno
MW-NB	Nkhata Bay
MW-NK	Nkhotakota
MW-NS	Nsanje
MW-NU	Ntcheu
MW-NI	Ntchisi
MW-PH	Phalombe
MW-RU	Rumphi
MW-SA	Salima
MW-TH	Thyolo
MW-ZO	Zomba
MX-DIF	Distrito Federal

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MX-AGU	Aguascalientes
MX-BCN	Baja California
MX-BCS	Baja California Sur
MX-CAM	Campeche
MX-COA	Coahuila
MX-COL	Colima
MX-CHP	Chiapas
MX-CHH	Chihuahua
MX-DUR	Durango
MX-GUA	Guanajuato
MX-GRO	Guerrero
MX-HID	Hidalgo
MX-JAL	Jalisco
MX-MEX	México
MX-MIC	Michoacán
MX-MOR	Morelos
MX-NAY	Nayarit
MX-NLE	Nuevo León
MX-OAX	Oaxaca
MX-PUE	Puebla
MX-QUE	Querétaro
MX-ROO	Quintana Roo
MX-SLP	San Luis Potosí
MX-SIN	Sinaloa
MX-SON	Sonora
MX-TAB	Tabasco
MX-TAM	Tamaulipas
MX-TLA	Tlaxcala
MX-VER	Veracruz
MX-YUC	Yucatán
MX-ZAC	Zacatecas
MY-14	Wilayah Persekutuan Kuala Lumpur
MY-15	Wilayah Persekutuan Labuan
MY-16	Wilayah Persekutuan Putrajaya
MY-01	Johor
MY-02	Kedah
MY-03	Kelantan
MY-04	Melaka
MY-05	Negeri Sembilan
MY-06	Pahang
MY-08	Perak
MY-09	Perlis
MY-07	Pulau Pinang
MY-12	Sabah
MY-13	Sarawak
MY-10	Selangor
MY-11	Terengganu
MZ-MPM	Maputo (city)
MZ-P	Cabo Delgado
MZ-G	Gaza
MZ-I	Inhambane

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
MZ-B	Manica
MZ-L	Maputo
MZ-N	Nampula
MZ-A	Niassa
MZ-S	Sofala
MZ-T	Tete
MZ-Q	Zambezia
NA-CA	Caprivi
NA-ER	Erlango
NA-HA	Hardap
NA-KA	Karas
NA-KH	Khomas
NA-KU	Kunene
NA-OW	Ohangwena
NA-OK	Okavango
NA-OH	Omaheke
NA-OS	Omusati
NA-ON	Oshana
NA-OT	Oshikoto
NA-OD	Otjozondjupa
NE-8	Niamey
NE-1	Agadez
NE-2	Diffa
NE-3	Dosso
NE-4	Maradi
NE-5	Tahoua
NE-6	Tillabéri
NE-7	Zinder
NG-FC	Abuja Capital Territory
NG-AB	Abia
NG-AD	Adamawa
NG-AK	Akwa Ibom
NG-AN	Anambra
NG-BA	Bauchi
NG-BY	Bayelsa
NG-BE	Benue
NG-BO	Borno
NG-CR	Cross River
NG-DE	Delta
NG-EB	Ebonyi
NG-ED	Edo
NG-EK	Ekiti
NG-EN	Enugu
NG-GO	Gombe
NG-IM	Imo
NG-JI	Jigawa
NG-KD	Kaduna
NG-KN	Kano
NG-KT	Katsina
NG-KE	Kebbi
NG-KO	Kogi

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
NG-KW	Kwara
NG-LA	Lagos
NG-NA	Nassarawa
NG-NI	Niger
NG-OG	Ogun
NG-ON	Ondo
NG-OS	Osun
NG-OY	Oyo
NG-PL	Plateau
NG-RI	Rivers
NG-SO	Sokoto
NG-TA	Taraba
NG-YO	Yobe
NG-ZA	Zamfara
NI-BO	Boaco
NI-CA	Carazo
NI-CI	Chinandega
NI-CO	Chontales
NI-ES	Estelí
NI-GR	Granada
NI-JI	Jinotega
NI-LE	León
NI-MD	Madriz
NI-MN	Managua
NI-MS	Masaya
NI-MT	Matagalpa
NI-NS	Nueva Segovia
NI-SJ	Río San Juan
NI-RI	Rivas
NI-AN	Atlántico Norte
NI-AS	Atlántico Sur
NL-DR	Drenthe
NL-FL	Flevoland
NL-FR	Friesland
NL-GE	Gelderland
NL-GR	Groningen
NL-LI	Limburg
NL-NB	Noord-Brabant
NL-NH	Noord-Holland
NL-OV	Overijssel
NL-UT	Utrecht
NL-ZE	Zeeland
NL-ZH	Zuid-Holland
NL-AW	Aruba
NL-CW	Curaçao
NL-SX	Sint Maarten
NL-BQ1	Bonaire
NL-BQ2	Saba
NL-BQ3	Sint Eustatius
NO-02	Akershus
NO-09	Aust-Agder

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
NO-06	Buskerud
NO-20	Finnmark
NO-04	Hedmark
NO-12	Hordaland
NO-15	Møre og Romsdal
NO-18	Nordland
NO-17	Nord-Trøndelag
NO-05	Oppland
NO-03	Oslo
NO-11	Rogaland
NO-14	Sogn og Fjordane
NO-16	Sør-Trøndelag
NO-08	Telemark
NO-19	Troms
NO-10	Vest-Agder
NO-07	Vestfold
NO-01	Østfold
NO-22	Jan Mayen (Arctic Region)
NO-21	Svalbard (Arctic Region)
NP-1	Madhyamanchal
NP-2	Madhya Pashchimanchal
NP-3	Pashchimanchal
NP-4	Purwanchal
NP-5	Sudur Pashchimanchal
NP-BA	Bagmati
NP-BH	Bheri
NP-DH	Dhawalajiri
NP-GA	Gandaki
NP-JA	Janakpur
NP-KA	Karnali
NP-KO	Kosi
NP-LU	Lumbini
NP-MA	Mahakali
NP-ME	Mechi
NP-NA	Narayani
NP-RA	Rapti
NP-SA	Sagarmatha
NP-SE	Seti
NR-01	Aiwo
NR-02	Anabar
NR-03	Anetan
NR-04	Anibare
NR-05	Baiti
NR-06	Boe
NR-07	Buada
NR-08	Denigomodu
NR-09	Ewa
NR-10	Ijuw
NR-11	Meneng
NR-12	Nibok
NR-13	Uaboe

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Table A.4.1 – continued from previous page

Key	Description
NR-14	Yaren
NZ-N	North Island
NZ-S	South Island
NZ-AUK	Auckland
NZ-BOP	Bay of Plenty
NZ-CAN	Canterbury
NZ-HKB	Hawke's Bay
NZ-MWT	Manawatu-Wanganui
NZ-NTL	Northland
NZ-OTA	Otago
NZ-STL	Southland
NZ-TKI	Taranaki
NZ-WKO	Waikato
NZ-WGN	Wellington
NZ-WTC	West Coast
NZ-GIS	Gisborne District
NZ-MBH	Marlborough District
NZ-NSN	Nelson City
NZ-TAS	Tasman District
NZ-CIT	Chatham Islands Territory
OM-DA	Ad Dākhīlā
OM-BA	Al Bāṭinah
OM-WU	Al Wusṭā
OM-SH	Ash Sharqīyah
OM-ZA	Az Zāhirah
OM-BU	Al Buraymī
OM-MA	Masqaṭ
OM-MU	Musandam
OM-ZU	Zufār
PA-1	Bocas del Toro
PA-4	Chiriquí
PA-2	Coclé
PA-3	Colón
PA-5	Darién
PA-6	Herrera
PA-7	Los Santos
PA-8	Panamá
PA-9	Veraguas
PA-EM	Emberá
PA-KY	Kuna Yala
PA-NB	Ngöbe-Buglé
PE-CAL	El Callao
PE-LMA	Municipalidad Metropolitana de Lima
PE-AMA	Amazonas
PE-ANC	Ancash
PE-APU	Apurímac
PE-ARE	Arequipa
PE-AYA	Ayacucho
PE-CAJ	Cajamarca
PE-CUS	Cusco [Cuzco]
PE-HUV	Huancavelica

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
PE-HUC	Huánuco
PE-ICA	Ica
PE-JUN	Junín
PE-LAL	La Libertad
PE-LAM	Lambayeque
PE-LIM	Lima
PE-LOR	Loreto
PE-MDD	Madre de Dios
PE-MOQ	Moquegua
PE-PAS	Pasco
PE-PIU	Piura
PE-PUN	Puno
PE-SAM	San Martín
PE-TAC	Tacna
PE-TUM	Tumbes
PE-UCA	Ucayali
PG-NCD	National Capital District (Port Moresby)
PG-CPM	Central
PG-CPK	Chimbu
PG-EHG	Eastern Highlands
PG-EBR	East New Britain
PG-ESW	East Sepik
PG-EPW	Enga
PG-GPK	Gulf
PG-MPM	Madang
PG-MRL	Manus
PG-MBA	Milne Bay
PG-MPL	Morobe
PG-NIK	New Ireland
PG-NPP	Northern
PG-SAN	Sandaun
PG-SHM	Southern Highlands
PG-WPD	Western
PG-WHM	Western Highlands
PG-WBK	West New Britain
PG-NSB	Bougainville
PH-14	Autonomous Region in Muslim Mindanao (ARMM)
PH-05	Bicol (Region V)
PH-02	Cagayan Valley (Region II)
PH-40	CALABARZON (Region IV-A)
PH-13	Caraga (Region XIII)
PH-03	Central Luzon (Region III)
PH-07	Central Visayas (Region VII)
PH-15	Cordillera Administrative Region (CAR)
PH-08	Eastern Visayas (Region VIII)
PH-01	Ilocos (Region I)
PH-41	MIMAROPA (Region IV-B)
PH-00	National Capital Region
PH-10	Northern Mindanao (Region X)
PH-11	Davao (Region XI)
PH-12	Soccsksargen (Region XII)

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Table A.4.1 – continued from previous page

Key	Description
PH-06	Western Visayas (Region VI)
PH-09	Zamboanga Peninsula (Region IX)
PH-ABR	Abra
PH-AGN	Agusan del Norte
PH-AGS	Agusan del Sur
PH-AKL	Aklan
PH-ALB	Albay
PH-ANT	Antique
PH-APA	Apayao
PH-AUR	Aurora
PH-BAS	Basilan
PH-BAN	Batasn
PH-BTN	Batanes
PH-BTG	Batangas
PH-BEN	Benguet
PH-BIL	Biliran
PH-BOH	Bohol
PH-BUK	Bukidnon
PH-BUL	Bulacan
PH-CAG	Cagayan
PH-CAN	Camarines Norte
PH-CAS	Camarines Sur
PH-CAM	Camiguin
PH-CAP	Capiz
PH-CAT	Catanduanes
PH-CAV	Cavite
PH-CEB	Cebu
PH-COM	Compostela Valley
PH-DAV	Davao del Norte
PH-DAS	Davao del Sur
PH-DAO	Davao Oriental
PH-DIN	Dinagat Islands
PH-EAS	Eastern Samar
PH-GUI	Guimaras
PH-IFU	Ifugao
PH-ILN	Ilocos Norte
PH-ILS	Ilocos Sur
PH-ILI	Iloilo
PH-ISA	Isabela
PH-KAL	Kalinga-Apayso
PH-LAG	Laguna
PH-LAN	Lanao del Norte
PH-LAS	Lanao del Sur
PH-LUN	La Union
PH-LEY	Leyte
PH-MAG	Maguindanao
PH-MAD	Marinduque
PH-MAS	Masbate
PH-MDC	Mindoro Occidental
PH-MDR	Mindoro Oriental
PH-MSC	Misamis Occidental

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
PH-MSR	Misamis Oriental
PH-MOU	Mountain Province
PH-NEC	Negroe Occidental
PH-NER	Negros Oriental
PH-NCO	North Cotabato
PH-NSA	Northern Samar
PH-NUE	Nueva Ecija
PH-NUV	Nueva Vizcaya
PH-PLW	Palawan
PH-PAM	Pampanga
PH-PAN	Pangasinan
PH-QUE	Quezon
PH-QUI	Quirino
PH-RIZ	Rizal
PH-ROM	Romblon
PH-SAR	Sarangani
PH-SIG	Siquijor
PH-SOR	Sorsogon
PH-SCO	South Cotabato
PH-SLE	Southern Leyte
PH-SUK	Sultan Kudarat
PH-SLU	Sulu
PH-SUN	Surigao del Norte
PH-SUR	Surigao del Sur
PH-TAR	Tarlac
PH-TAW	Tawi-Tawi
PH-WSA	Western Samar
PH-ZMB	Zambales
PH-ZAN	Zamboanga del Norte
PH-ZAS	Zamboanga del Sur
PH-ZSI	Zamboanga Sibugay
PK-IS	Islamabad
PK-BA	Balochistan
PK-KP	Khyber Pakhtunkhwa
PK-PB	Punjab
PK-SD	Sindh
PK-TA	Federally Administered Tribal Areas
PK-JK	Azad Kashmir
PK-GB	Gilgit-Baltistan
PL-DS	Dolnośląskie
PL-KP	Kujawsko-pomorskie
PL-LU	Lubelskie
PL-LB	Lubuskie
PL-LD	Łódzkie
PL-MA	Małopolskie
PL-MZ	Mazowieckie
PL-OP	Opolskie
PL-PK	Podkarpackie
PL-PD	Podlaskie
PL-PM	Pomorskie
PL-SL	Śląskie

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
PL-SK	Świętokrzyskie
PL-WN	Warmińsko-mazurskie
PL-WP	Wielkopolskie
PL-ZP	Zachodniopomorskie
PS-BTH	Bethlehem
PS-DEB	Deir El Balah
PS-GZA	Gaza
PS-HBN	Hebron
PS-JEN	Jenin
PS-JRH	Jericho - Al Aghwar
PS-JEM	Jerusalem
PS-KYS	Khan Yunis
PS-NBS	Nablus
PS-NGZ	North Gaza
PS-QQA	Qalqilya
PS-RFH	Rafah
PS-RBH	Ramallah
PS-SLT	Salfit
PS-TBS	Tubas
PS-TKM	Tulkarm
PT-01	Aveiro
PT-02	Beja
PT-03	Braga
PT-04	Bragança
PT-05	Castelo Branco
PT-06	Coimbra
PT-07	Évora
PT-08	Faro
PT-09	Guarda
PT-10	Leiria
PT-11	Lisboa
PT-12	Portalegre
PT-13	Porto
PT-14	Santarém
PT-15	Setúbal
PT-16	Viana do Castelo
PT-17	Vila Real
PT-18	Viseu
PT-20	Região Autónoma dos Açores
PT-30	Região Autónoma da Madeira
PW-002	Aimeliük
PW-004	Airai
PW-010	Angaur
PW-050	Hatobohei
PW-100	Kayangel
PW-150	Koror
PW-212	Melekeok
PW-214	Ngaraard
PW-218	Ngarchelong
PW-222	Ngardmau
PW-224	Ngatpang

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Table A.4.1 – continued from previous page

Key	Description
PW-226	Ngchesar
PW-227	Ngeremlengui
PW-228	Ngiwal
PW-350	Peleliu
PW-370	Sonsorol
PY-ASU	Asunción
PY-16	Alto Paraguay
PY-10	Alto Paraná
PY-13	Amambay
PY-19	Boquerón
PY-5	Caaguazú
PY-6	Caazapá
PY-14	Canindeyú
PY-11	Central
PY-1	Concepción
PY-3	Cordillera
PY-4	Guairá
PY-7	Itapúa
PY-8	Misiones
PY-12	Ñeembucú
PY-9	Paraguarí
PY-15	Presidente Hayes
PY-2	San Pedro
QA-DA	Ad Dawhah
QA-KH	Al Khawr wa adh Dhakhīrah
QA-WA	Al Wakrah
QA-RA	Ar Rayyan
QA-MS	Ash Shamal
QA-ZA	Az Za'āyin
QA-US	Umm Salal
RO-AB	Alba
RO-AR	Arad
RO-AG	Argeş
RO-BC	Bacău
RO-BH	Bihor
RO-BN	Bistriţa-Năsăud
RO-BT	Botoşani
RO-BV	Braşov
RO-BR	Brăila
RO-BZ	Buzău
RO-CS	Caraş-Severin
RO-CL	Călăraşi
RO-CJ	Cluj
RO-CT	Constanţa
RO-CV	Covasna
RO-DB	Dâmboviţa
RO-DJ	Dolj
RO-GL	Galaţi
RO-GR	Giurgiu
RO-GJ	Gorj
RO-HR	Harghita

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
RO-HD	Hunedoara
RO-IL	Ialomița
RO-IS	Iași
RO-IF	Ilfov
RO-MM	Maramureș
RO-MH	Mehedinți
RO-MS	Mureș
RO-NT	Neamț
RO-OT	Olt
RO-PH	Prahova
RO-SM	Satu Mare
RO-SJ	Sălaj
RO-SB	Sibiu
RO-SV	Suceava
RO-TR	Teleorman
RO-TM	Timiș
RO-TL	Tulcea
RO-VS	Vaslui
RO-VL	Vâlcea
RO-VN	Vrancea
RO-B	București
RS-00	Beograd
RS-KM	Kosovo-Metohija
RS-VO	Vojvodina
RS-14	Borski okrug
RS-11	Braničevski okrug
RS-23	Jablanički okrug
RS-06	Južnobački okrug
RS-04	Južnobanatski okrug
RS-09	Kolubarski okrug
RS-25	Kosovski okrug
RS-28	Kosovsko-Mitrovački okrug
RS-29	Kosovsko-Pomoravski okrug
RS-08	Mačvanski okrug
RS-17	Moravički okrug
RS-20	Nišavski okrug
RS-24	Pčinjski okrug
RS-26	Pećki okrug
RS-22	Pirotski okrug
RS-10	Podunavski okrug
RS-13	Pomoravski okrug
RS-27	Prizrenski okrug
RS-19	Rasinski okrug
RS-18	Raški okrug
RS-01	Severnobački okrug
RS-03	Severnobanatski okrug
RS-02	Srednjebanatski okrug
RS-07	Sremski okrug
RS-12	Šumadijski okrug
RS-21	Toplički okrug
RS-15	Zaječarski okrug

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
RS-05	Zapadnobački okrug
RS-16	Zlatiborski okrug
RU-AD	Adygeya, Respublika
RU-AL	Altay, Respublika
RU-BA	Bashkortostan, Respublika
RU-BU	Buryatiya, Respublika
RU-CE	Chechenskaya Respublika
RU-CU	Chuvashskaya Respublika
RU-DA	Dagestan, Respublika
RU-IN	Respublika Ingusetiya
RU-KB	Kabardino-Balkarskaya Respublika
RU-KL	Kalmykiya, Respublika
RU-KC	Karachayevo-Cherkesskaya Respublika
RU-KR	Kareliya, Respublika
RU-KK	Khakasiya, Respublika
RU-KO	Komi, Respublika
RU-ME	Mariy El, Respublika
RU-MO	Mordoviya, Respublika
RU-SA	Sakha, Respublika [Yakutiya]
RU-SE	Severnaya Osetiya-Alaniya, Respublika
RU-TA	Tatarstan, Respublika
RU-TY	Tyva, Respublika [Tuva]
RU-UD	Udmurtskaya Respublika
RU-ALT	Altayskiy kray
RU-KAM	Kamchatskiy kray
RU-KHA	Khabarovskiy kray
RU-KDA	Krasnodarskiy kray
RU-KYA	Krasnoyarskiy kray
RU-PER	Permskiy kray
RU-PRI	Primorskiy kray
RU-STA	Stavropol'skiy kray
RU-ZAB	Zabajkal'skiy kraj
RU-AMU	Amurskaya oblast'
RU-ARK	Arkhangel'skaya oblast'
RU-AST	Astrakhanskaya oblast'
RU-BEL	Belgorodskaya oblast'
RU-BRY	Bryanskaya oblast'
RU-CHE	Chelyabinskaya oblast'
RU-IRK	Irkutskaya oblast'
RU-IVA	Ivanovskaya oblast'
RU-KGD	Kaliningradskaya oblast'
RU-KLU	Kaluzhskaya oblast'
RU-KEM	Kemerovskaya oblast'
RU-KIR	Kirovskaya oblast'
RU-KOS	Kostromskaya oblast'
RU-KGN	Kurganskaya oblast'
RU-KRS	Kurskaya oblast'
RU-LEN	Leningradskaya oblast'
RU-LIP	Lipetskaya oblast'
RU-MAG	Magadanskaya oblast'
RU-MOS	Moskovskaya oblast'

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
RU-MUR	Murmanskaya oblast'
RU-NIZ	Nizhegorodskaya oblast'
RU-NGR	Novgorodskaya oblast'
RU-NVS	Novosibirskaya oblast'
RU-OMS	Omskaya oblast'
RU-ORE	Orenburgskaya oblast'
RU-ORL	Orlovskaya oblast'
RU-PNZ	Penza kaya oblast'
RU-PSK	Pskovskaya oblast'
RU-ROS	Rostovskaya oblast'
RU-RYA	Ryazanskaya oblast'
RU-SAK	Sakhalinskaya oblast'
RU-SAM	Samaraskaya oblast'
RU-SAR	Saratovskaya oblast'
RU-SMO	Smolenskaya oblast'
RU-SVE	Sverdlovskaya oblast'
RU-TAM	Tambovskaya oblast'
RU-TOM	Tomskaya oblast'
RU-TUL	Tul'skaya oblast'
RU-TVE	Tverskaya oblast'
RU-TYU	Tyumenskaya oblast'
RU-ULY	Ul'yanovskaya oblast'
RU-VLA	Vladimirskaya oblast'
RU-VGG	Volgogradskaya oblast'
RU-VLG	Vologodskaya oblast'
RU-VOR	Voronezhskaya oblast'
RU-YAR	Yaroslavskaya oblast'
RU-MOW	Moskva
RU-SPE	Sankt-Peterburg
RU-YEV	Yevreyskaya avtonomnaya oblast'
RU-CHU	Chukotskiy avtonomnyy okrug
RU-KHM	Khanty-Mansiysky avtonomnyy okrug-Yugra
RU-NEN	Nenetskiy avtonomnyy okrug
RU-YAN	Yamalo-Nenetskiy avtonomnyy okrug
RW-01	Ville de Kigali
RW-02	Est
RW-03	Nord
RW-04	Ouest
RW-05	Sud
SA-11	Al Bāhah
SA-08	Al Ḥudūd ash Shamāliyah
SA-12	Al Jawf
SA-03	Al Madīnah
SA-05	Al Qaṣīm
SA-01	Ar Riyāḍ
SA-04	Ash Sharqīyah
SA-14	'Asīr
SA-06	Hā'il
SA-09	Jīzan
SA-02	Makkah
SA-10	Najrān

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
SA-07	Tabūk
SB-CT	Capital Territory (Honiara)
SB-CE	Central
SB-CH	Choiseul
SB-GU	Guadalcanal
SB-IS	Isabel
SB-MK	Makira
SB-ML	Malaita
SB-RB	Rennell and Bellona
SB-TE	Temotu
SB-WE	Western
SC-01	Anse aux Pins
SC-02	Anse Boileau
SC-03	Anse Etoile
SC-04	Anse Louis
SC-05	Anse Royale
SC-06	Baie Lazare
SC-07	Baie Sainte Anne
SC-08	Beau Vallon
SC-09	Bel Air
SC-10	Bel Ombre
SC-11	Cascade
SC-12	Glacis
SC-13	Grand Anse Mahe
SC-14	Grand Anse Praslin
SC-15	La Digue
SC-16	English River
SC-24	Les Mamelles
SC-17	Mont Buxton
SC-18	Mont Fleuri
SC-19	Plaisance
SC-20	Pointe Larue
SC-21	Port Glaud
SC-25	Roche Caiman
SC-22	Saint Louis
SC-23	Takamaka
SD-RS	Al Ba r al A mar
SD-GZ	Al Jazīrah
SD-KH	Al Kharṭūm
SD-GD	Al Qa ārif
SD-NR	An Nīl
SD-NW	An Nīl al Abya
SD-NB	An Nīl al Azraq
SD-NO	Ash Shamālīyah
SD-DW	Gharb Dārfūr
SD-DS	Janūb Dārfūr
SD-KS	Janūb Kurdufān
SD-KA	Kassalā
SD-DN	Shamāl Dārfūr
SD-KN	Shamāl Kurdufān
SD-DE	Sharq Dārfūr

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
SD-SI	Sinnär
SD-DC	Zalingei
SE-K	Blekinge län
SE-W	Dalarnas län
SE-I	Gotlands län
SE-X	Gävleborgs län
SE-N	Hallands län
SE-Z	Jämtlands län
SE-F	Jönköpings län
SE-H	Kalmar län
SE-G	Kronobergs län
SE-BD	Norrbottens län
SE-M	Skåne län
SE-AB	Stockholms län
SE-D	Södermanlands län
SE-C	Uppsala län
SE-S	Värmlands län
SE-AC	Västerbottens län
SE-Y	Västernorrlands län
SE-U	Västmanlands län
SE-O	Västra Götalands län
SE-T	Örebro län
SE-E	Östergötlands län
SG-01	Central Singapore
SG-02	North East
SG-03	North West
SG-04	South East
SG-05	South West
SG-AC	Ascension
SG-HL	Saint Helena
SG-TA	Tristan da Cunha
SI-001	Ajdovščina
SI-195	Apače
SI-002	Beltinci
SI-148	Benedikt
SI-149	Bistrica ob Sotli
SI-003	Bled
SI-150	Bloke
SI-004	Bohinj
SI-005	Borovnica
SI-006	Bovec
SI-151	Braslovče
SI-007	Brda
SI-008	Brezovica
SI-009	Brežice
SI-152	Cankova
SI-011	Celje
SI-012	Cerkle na Gorenjskem
SI-013	Cerknica
SI-014	Cerkno
SI-153	Cerkvenjak

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
SI-196	Cirkulane
SI-015	Črenšovci
SI-016	Črna na Koroškem
SI-017	Črnomelj
SI-018	Destrnik
SI-019	Divača
SI-154	Dobje
SI-020	Dobrepolje
SI-155	Dobrna
SI-021	Dobrova-Polhov Gradec
SI-156	Dobrovnik/Dobronak
SI-022	Dol pri Ljubljani
SI-157	Dolenjske Toplice
SI-023	Domžale
SI-024	Dornava
SI-025	Dravograd
SI-026	Duplek
SI-027	Gorenja vas-Poljane
SI-028	Gorišnica
SI-207	Gorje
SI-029	Gornja Radgona
SI-030	Gornji Grad
SI-031	Gornji Petrovci
SI-158	Grad
SI-032	Grosuplje
SI-159	Hajdina
SI-160	Hoče-Slivnica
SI-161	Hodoš/Hodos
SI-162	Horjul
SI-034	Hrastnik
SI-035	Hrpelje-Kozina
SI-036	Idrija
SI-037	Ig
SI-038	Ilirska Bistrica
SI-039	Ivančna Gorica
SI-040	Izola/Isola
SI-041	Jesenice
SI-163	Jezersko
SI-042	Juršinci
SI-043	Kamnik
SI-044	Kanal
SI-045	Kidričeve
SI-046	Kobarid
SI-047	Kobilje
SI-048	Kočevje
SI-049	Komen
SI-164	Komenda
SI-050	Koper/Capodistria
SI-197	Kosanjevica na Krki
SI-165	Kostel
SI-051	Kozje

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
SI-052	Kranj
SI-053	Kranjska Gora
SI-166	Križevci
SI-054	Krško
SI-055	Kungota
SI-056	Kuzma
SI-057	Laško
SI-058	Lenart
SI-059	Lendava/Lendva
SI-060	Litija
SI-061	Ljubljana
SI-062	Ljubno
SI-063	Ljutomer
SI-208	Log-Dragomer
SI-064	Logatec
SI-065	Loška dolina
SI-066	Loški Potok
SI-167	Lovrenc na Pohorju
SI-067	Luče
SI-068	Lukovica
SI-069	Majšperk
SI-198	Makole
SI-070	Maribor
SI-168	Markovci
SI-071	Medvode
SI-072	Mengeš
SI-073	Metlika
SI-074	Mežica
SI-169	Miklavž na Dravskem polju
SI-075	Miren-Kostanjevica
SI-170	Mirna Peč
SI-076	Mislinja
SI-199	Mokronog-Trebelno
SI-077	Moravče
SI-078	Moravske Toplice
SI-079	Mozirje
SI-080	Murska Sobota
SI-081	Muta
SI-082	Naklo
SI-083	Nazarje
SI-084	Nova Gorica
SI-085	Novo mesto
SI-086	Odranci
SI-171	Oplotnica
SI-087	Ormož
SI-088	Osilnica
SI-089	Pesnica
SI-090	Piran/Pirano
SI-091	Pivka
SI-092	Podčetrtek
SI-172	Podlehnik

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
SI-093	Podvelka
SI-200	Poljčane
SI-173	Polzela
SI-094	Postojna
SI-174	Prebold
SI-095	Predvor
SI-175	Prevalje
SI-096	Ptuj
SI-097	Puconci
SI-098	Rače-Fram
SI-099	Radeče
SI-100	Radenci
SI-101	Radlje ob Dravi
SI-102	Radovljica
SI-103	Ravne na Koroškem
SI-176	Razkrižje
SI-209	Rečica ob Savinji
SI-201	Renče-Vogrsko
SI-104	Ribnica
SI-177	Ribnica na Pohorju
SI-106	Rogaška Slatina
SI-105	Rogašovci
SI-107	Rogatec
SI-108	Ruše
SI-178	Selnica ob Dravi
SI-109	Semič
SI-110	Sevnica
SI-111	Sežana
SI-112	Slovenj Gradec
SI-113	Slovenska Bistrica
SI-114	Slovenske Konjice
SI-179	Sodražica
SI-180	Solčava
SI-202	Središče ob Dravi
SI-115	Starče
SI-203	Straža
SI-181	Sveta Ana
SI-204	Sveta Trojica v Slovenskih Goricah
SI-182	Sveta Andraž v Slovenskih Goricah
SI-116	Sveti Jurij
SI-210	Sveti Jurij v Slovenskih Goricah
SI-205	Sveti Tomaž
SI-033	Šalovci
SI-183	Šempeter-Vrtojba
SI-117	Šenčur
SI-118	Šentilj
SI-119	Šentjernej
SI-120	Šentjur
SI-211	Šentrupert
SI-121	Škocjan
SI-122	Škofja Loka

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
SI-123	Škofljica
SI-124	Šmarje pri Jelšah
SI-206	Šmarjeske Toplice
SI-125	Šmartno ob Paki
SI-194	Šmartno pri Litiji
SI-126	Šoštanj
SI-127	Štore
SI-184	Tabor
SI-010	Tišina
SI-128	Tolmin
SI-129	Trbovlje
SI-130	Trebnje
SI-185	Trnovska vas
SI-186	Trzin
SI-131	Tržič
SI-132	Turnišče
SI-133	Velenje
SI-187	Velika Polana
SI-134	Velike Lašče
SI-188	Veržej
SI-135	Videm
SI-136	Vipava
SI-137	Vitanje
SI-138	Vodice
SI-139	Vojnik
SI-189	Vransko
SI-140	Vrhnička
SI-141	Vuzenica
SI-142	Zagorje ob Savi
SI-143	Zavrč
SI-144	Zreče
SI-190	Žalec
SI-146	Železniki
SI-191	Žetale
SI-147	Žiri
SI-192	Žirovnica
SI-193	Žužemberk
SK-BC	Banskobystrický kraj
SK-BL	Bratislavský kraj
SK-KI	Košický kraj
SK-NI	Nitriansky kraj
SK-PV	Prešovský kraj
SK-TC	Trenčiansky kraj
SK-TA	Trnavský kraj
SK-ZI	Žilinský kraj
SL-W	Western Area (Freetown)
SL-E	Eastern
SL-N	Northern
SL-S	Southern (Sierra Leone)
SM-01	Acquaviva

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
SM-06	Borgo Maggiore
SM-02	Chiesanuova
SM-03	Domagnano
SM-04	Faetano
SM-05	Fiorentino
SM-08	Montegiardino
SM-07	San Marino
SM-09	Serravalle
SN-DK	Dakar
SN-DB	Diourbel
SN-FK	Fatick
SN-KA	Kaffrine
SN-KL	Kaolack
SN-KE	Kédougou
SN-KD	Kolda
SN-LG	Louga
SN-MT	Matam
SN-SL	Saint-Louis
SN-SE	Sédhiou
SN-TC	Tambacounda
SN-TH	Thiès
SN-ZG	Ziguinchor
SO-AW	Awdal
SO-BK	Bakool
SO-BN	Banaadir
SO-BR	Bari
SO-BY	Bay
SO-GA	Galguduud
SO-GE	Gedo
SO-HI	Hürsan
SO-JD	Jubbada Dhexe
SO-JH	Jubbada Hoose
SO-MU	Mudug
SO-NU	Nugaal
SO-SA	Saneag
SO-SD	Shabeellaha Dhexe
SO-SH	Shabeellaha Hoose
SO-SO	Sool
SO-TO	Togdheer
SO-WO	Woqooyi Galbeed
SR-BR	Brokopondo
SR-CM	Commewijne
SR-CR	Coronie
SR-MA	Marowijne
SR-NI	Nickerie
SR-PR	Para
SR-PM	Paramaribo
SR-SA	Saramacca
SR-SI	Sipaliwini
SR-WA	Wanica
SD-EC	Central Equatoria

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
SD-EE8	Eastern Equatoria
SD-JG	Jonglei
SD-LK	Lakes
SD-BN	Northern Bahr el-Ghazal
SD-UY	Unity
SD-NU	Upper Nile
SD-WR	Warrap
SD-BW	Western Bahr el-Ghazal
SD-EW	Western Equatoria
ST-P	Príncipe
ST-S	São Tomé
SV-AH	Ahuachapán
SV-CA	Cabañas
SV-CU	Cuscatlán
SV-CH	Chalatenango
SV-LI	La Libertad
SV-PA	La Paz
SV-UN	La Unión
SV-MO	Morazán
SV-SM	San Miguel
SV-SS	San Salvador
SV-SA	Santa Ana
SV-SV	San Vicente
SV-SO	Sonsonate
SV-US	Usulután
SY-HA	Al Hasakah
SY-LA	Al Ladhiqiyah
SY-QU	Al Qunaytirah
SY-RA	Ar Raqqah
SY-SU	As Suwayda'
SY-DR	Dar'a
SY-DY	Dayr az Zawr
SY-DI	Dimashq
SY-HL	Halab
SY-HM	Hamah
SY-HI	Homs
SY-ID	Idlib
SY-RD	Rif Dimashq
SY-TA	Tartus
SZ-HH	Hhohho
SZ-LU	Lubombo
SZ-MA	Manzini
SZ-SH	Shiselweni
TD-BA	Al Baṭḥah
TD-LC	Al Buhayrah
TD-BG	Bahr al Ghazāl
TD-BO	Būrkū
TD-HL	Ḩajjar Lamīs
TD-EN	Innīdī
TD-KA	Kānim
TD-LO	Lūqūn al Gharbī

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
TD-LR	Lūqūn ash Sharqī
TD-ND	Madīnat Injamīnā
TD-MA	Māndūl
TD-MO	Māyū Kibbī al Gharbī
TD-ME	Māyū Kibbī ash Sharqī
TD-GR	Qīrā
TD-SA	Salāmāt
TD-MC	Shārī al Awsaṭ
TD-CB	Shārī Bāqirmī
TD-SI	Sīlā
TD-TA	Tānjilī
TD-TI	Tibastī
TD-OD	Waddāy
TD-WF	Wādī Fīrā
TG-C	Région du Centre
TG-K	Région de la Kara
TG-M	Région Maritime
TG-P	Région des Plateaux
TG-S	Région des Savannes
TH-10	Krung Thep Maha Nakhon Bangkok
TH-S	Phatthaya
TH-37	Amnat Charoen
TH-15	Ang Thong
TH-31	Buri Ram
TH-24	Chachoengsao
TH-18	Chai Nat
TH-36	Chaiyaphum
TH-22	Chanthaburi
TH-50	Chiang Mai
TH-57	Chiang Rai
TH-20	Chon Buri
TH-86	Chumphon
TH-46	Kalasin
TH-62	Kamphaeng Phet
TH-71	Kanchanaburi
TH-40	Khon Kaen
TH-81	Krabi
TH-52	Lampang
TH-51	Lamphun
TH-42	Loei
TH-16	Lop Buri
TH-58	Mae Hong Son
TH-44	Maha Sarakham
TH-49	Mukdahan
TH-26	Nakhon Nayok
TH-73	Nakhon Pathom
TH-48	Nakhon Phanom
TH-30	Nakhon Ratchasima
TH-60	Nakhon Sawan
TH-80	Nakhon Si Thammarat
TH-55	Nan

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Table A.4.1 – continued from previous page

Key	Description
TH-96	Narathiwat
TH-39	Nong Bua Lam Phu
TH-43	Nong Khai
TH-12	Nonthaburi
TH-13	Pathum Thani
TH-94	Pattani
TH-82	Phangnga
TH-93	Phatthalung
TH-56	Phayao
TH-67	Phetchabun
TH-76	Phetchaburi
TH-66	Phichit
TH-65	Phitsanulok
TH-54	Phrae
TH-14	Phra Nakhon Si Ayutthaya
TH-83	Phuket
TH-25	Prachin Buri
TH-77	Prachuap Khiri Khan
TH-85	Ranong
TH-70	Ratchaburi
TH-21	Rayong
TH-45	Roi Et
TH-27	Sa Kaeo
TH-47	Sakon Nakhon
TH-11	Samut Prakan
TH-74	Samut Sakhon
TH-75	Samut Songkhram
TH-19	Saraburi
TH-91	Satun
TH-17	Sing Buri
TH-33	Si Sa Ket
TH-90	Songkhla
TH-64	Sukhothai
TH-72	Suphan Buri
TH-84	Surat Thani
TH-32	Surin
TH-63	Tak
TH-92	Trang
TH-23	Trat
TH-34	Ubon Ratchathani
TH-41	Udon Thani
TH-61	Uthai Thani
TH-53	Uttaradit
TH-95	Yala
TH-35	Yasothon
TJ-GB	Gorno-Badakhshan
TJ-KT	Khatlon
TJ-SU	Sughd
TL-AL	Aileu
TL-AN	Ainaro
TL-BA	Baucau

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Table A.4.1 – continued from previous page

Key	Description
TL-BO	Bobonaro
TL-CO	Cova Lima
TL-DI	Díli
TL-ER	Ermera
TL-LA	Lautem
TL-LI	Liquiça
TL-MT	Manatuto
TL-MF	Manufahi
TL-OE	Oecussi
TL-VI	Viqueque
TM-A	Ahal
TM-B	Balkan
TM-D	Daşoguz
TM-L	Lebap
TM-M	Mary
TM-S	Aşgabat
TN-12	Ariana
TN-31	Béja
TN-13	Ben Arous
TN-23	Bizerte
TN-81	Gabès
TN-71	Gafsa
TN-32	Jendouba
TN-41	Kairouan
TN-42	Kasserine
TN-73	Kebili
TN-33	Le Kef
TN-53	Mahdia
TN-14	La Manouba
TN-82	Medenine
TN-52	Monastir
TN-21	Nabeul
TN-61	Sfax
TN-43	Sidi Bouzid
TN-34	Siliana
TN-51	Sousse
TN-83	Tataouine
TN-72	Tozeur
TN-11	Tunis
TN-22	Zaghuan
TO-01	'Eua
TO-02	Ha'apai
TO-03	Niuas
TO-04	Tongatapu
TO-05	Vava'u
TR-01	Adana
TR-02	Aduyaman
TR-03	Afyonkarahisar
TR-04	Ağrı
TR-68	Aksaray
TR-05	Amasya

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
TR-06	Ankara
TR-07	Antalya
TR-75	Ardahan
TR-08	Artvin
TR-09	Aydın
TR-10	Balıkesir
TR-74	Bartın
TR-72	Batman
TR-69	Bayburt
TR-11	Bilecik
TR-12	Bingöl
TR-13	Bitlis
TR-14	Bolu
TR-15	Burdur
TR-16	Bursa
TR-17	Çanakkale
TR-18	Çankırı
TR-19	Çorum
TR-20	Denizli
TR-21	Diyarbakır
TR-81	Düzce
TR-22	Edirne
TR-23	Elazığ
TR-24	Erzincan
TR-25	Erzurum
TR-26	Eskişehir
TR-27	Gaziantep
TR-28	Giresun
TR-29	Gümüşhane
TR-30	Hakkâri
TR-31	Hatay
TR-76	İğdır
TR-32	Isparta
TR-34	İstanbul
TR-35	İzmir
TR-46	Kahramanmaraş
TR-78	Karabük
TR-70	Karaman
TR-36	Kars
TR-37	Kastamonu
TR-38	Kayseri
TR-71	Kırıkkale
TR-39	Kırklareli
TR-40	Kırşehir
TR-79	Kilis
TR-41	Kocaeli
TR-42	Konya
TR-43	Kütahya
TR-44	Malatya
TR-45	Manisa
TR-47	Mardin

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
TR-33	Mersin
TR-48	Muğla
TR-49	Muş
TR-50	Nevşehir
TR-51	Niğde
TR-52	Ordu
TR-80	Osmaniye
TR-53	Rize
TR-54	Sakarya
TR-55	Samsun
TR-56	Şiirt
TR-57	Sinop
TR-58	Sivas
TR-63	Şanlıurfa
TR-73	Şırnak
TR-59	Tekirdağ
TR-60	Tokat
TR-61	Trabzon
TR-62	Tunceli
TR-64	Uşak
TR-65	Van
TR-77	Yalova
TR-66	Yozgat
TR-67	Zonguldak
TT-CTT	Couva-Tabaquite-Talparo
TT-DMN	Diego Martin
TT-ETO	Eastern Tobago
TT-PED	Penal-Debe
TT-PRT	Princes Town
TT-RCM	Rio Claro-Mayaro
TT-SGE	Sangre Grande
TT-SJL	San Juan-Laventille
TT-SIP	Siparia
TT-TUP	Tunapuna-Piarco
TT-WTO	Western Tobago
TT-ARI	Arima
TT-CHA	Chaguanas
TT-PTF	Point Fortin
TT-POS	Port of Spain
TT-SFO	San Fernando
TV-FUN	Funafuti
TV-NMG	Nanumanga
TV-NMA	Nanumea
TV-NIT	Niutao
TV-NUI	Nui
TV-NKF	Nukufetau
TV-NKL	Nukulaelae
TV-VAI	Vaitupu
TW-CHA	Changhua
TW-CYQ	Chiayi
TW-HSQ	Hsinchu

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
TW-HUA	Hualien
TW-ILA	Ilan
TW-KHQ	Kaohsiung
TW-MIA	Miaoli
TW-NAN	Nantou
TW-PEN	Penghu
TW-PIF	Pingtung
TW-TXQ	Taichung
TW-TNQ	Tainan
TW-TPQ	Taipei
TW-TTT	Taitung
TW-TAO	Taoyuan
TW-YUN	Yunlin
TW-CYI	Chiay City
TW-HSZ	Hsinchui City
TW-KEE	Keelung City
TW-TXG	Taichung City
TW-TNN	Tainan City
TW-KHH	Kaohsiung City
TW-TPE	Taipei City
TZ-01	Arusha
TZ-02	Dar-es-Salaam
TZ-03	Dodoma
TZ-04	Iringa
TZ-05	Kagera
TZ-06	Kaskazini Pemba
TZ-07	Kaskazini Unguja
TZ-08	Kigoma
TZ-09	Kilimanjaro
TZ-10	Kusini Pemba
TZ-11	Kusini Unguja
TZ-12	Lindi
TZ-26	Manyara
TZ-13	Mara
TZ-14	Mbeya
TZ-15	Mjini Magharibi
TZ-16	Morogoro
TZ-17	Mtwara
TZ-18	Mwanza
TZ-19	Pwani
TZ-20	Rukwa
TZ-21	Ruvuma
TZ-22	Shinyanga
TZ-23	Singida
TZ-24	Tabora
TZ-25	Tanga
UA-71	Cherkas'ka Oblast'
UA-74	Chernihivs'ka Oblast'
UA-77	Chernivets'ka Oblast'
UA-12	Dnipropetrovs'ka Oblast'
UA-14	Donets'ka Oblast'

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
UA-26	Ivano-Frankivs'ka Oblast'
UA-63	Kharkivs'ka Oblast'
UA-65	Khersons'ka Oblast'
UA-68	Khmel'nyts'ka Oblast'
UA-35	Kirovohrads'ka Oblast'
UA-32	Kyïvs'ka Oblast'
UA-09	Luhans'ka Oblast'
UA-46	L'vivs'ka Oblast'
UA-48	Mykolaïvs'ka Oblast'
UA-51	Odes'ka Oblast'
UA-53	Poltavs'ka Oblast'
UA-56	Rivnens'ka Oblast'
UA-59	Sums 'ka Oblast'
UA-61	Ternopil's'ka Oblast'
UA-05	Vinnyts'ka Oblast'
UA-07	Volyns'ka Oblast'
UA-21	Zakarpats'ka Oblast'
UA-23	Zaporiz'ka Oblast'
UA-18	Zhytomyrs'ka Oblast'
UA-43	Respublika Krym
UA-30	Kyïvs'ka mis'ka rada
UA-40	Sevastopol
UG-C	Central
UG-E	Eastern
UG-N	Northern
UG-W	Western
UG-317	Abim
UG-301	Adjumani
UG-314	Amolatar
UG-216	Amuria
UG-319	Amuru
UG-302	Apac
UG-303	Arua
UG-217	Budaka
UG-223	Bududa
UG-201	Bugiri
UG-224	Bukedea
UG-218	Bukwa
UG-419	Buliisa
UG-401	Bundibugyo
UG-402	Bushenyi
UG-202	Busia
UG-219	Butaleja
UG-318	Dokolo
UG-304	Gulu
UG-403	Hoima
UG-416	Ibanda
UG-203	Iganga
UG-417	Isingiro
UG-204	Jinja
UG-315	Kaabong

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
UG-404	Kabale
UG-405	Kabarole
UG-213	Kaberamaido
UG-101	Kalangala
UG-220	Kaliro
UG-102	Kampala
UG-205	Kamuli
UG-413	Kamwenge
UG-414	Kanungu
UG-206	Kapchorwa
UG-406	Kasese
UG-207	Katakwi
UG-112	Kayunga
UG-407	Kibaale
UG-103	Kiboga
UG-418	Kiruhura
UG-408	Kisoro
UG-305	Kitgum
UG-316	Koboko
UG-306	Kotido
UG-208	Kumi
UG-415	Kyenjojo
UG-307	Lira
UG-104	Luwero
UG-116	Lyantonde
UG-221	Manafwa
UG-320	Maracha
UG-105	Masaka
UG-409	Masindi
UG-214	Mayuge
UG-209	Mbale
UG-410	Mbarara
UG-114	Mityana
UG-308	Moroto
UG-309	Moyo
UG-106	Mpigi
UG-107	Mubende
UG-108	Mukono
UG-311	Nakapiripirit
UG-115	Nakaseke
UG-109	Nakasongola
UG-222	Namutumba
UG-310	Nebbi
UG-411	Ntungamo
UG-321	Oyam
UG-312	Pader
UG-210	Pallisa
UG-110	Rakai
UG-412	Rukungiri
UG-111	Sembabule
UG-215	Sironko

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
UG-211	Soroti
UG-212	Tororo
UG-113	Wakiso
UG-313	Yumbe
UM-81	Baker Island
UM-84	Howland Island
UM-86	Jarvis Island
UM-67	Johnston Atoll
UM-89	Kingman Reef
UM-71	Midway Islands
UM-76	Navassa Island
UM-95	Palmyra Atoll
UM-79	Wake Island
US-AL	Alabama
US-AK	Alaska
US-AZ	Arizona
US-AR	Arkansas
US-CA	California
US-CO	Colorado
US-CT	Connecticut
US-DE	Delaware
US-FL	Florida
US-GA	Georgia
US-HI	Hawaii
US-ID	Idaho
US-IL	Illinois
US-IN	Indiana
US-IA	Iowa
US-KS	Kansas
US-KY	Kentucky
US-LA	Louisiana
US-ME	Maine
US-MD	Maryland
US-MA	Massachusetts
US-MI	Michigan
US-MN	Minnesota
US-MS	Mississippi
US-MO	Missouri
US-MT	Montana
US-NE	Nebraska
US-NV	Nevada
US-NH	New Hampshire
US-NJ	New Jersey
US-NM	New Mexico
US-NY	New York
US-NC	North Carolina
US-ND	North Dakota
US-OH	Ohio
US-OK	Oklahoma
US-OR	Oregon
US-PA	Pennsylvania

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
US-RI	Rhode Island
US-SC	South Carolina
US-SD	South Dakota
US-TN	Tennessee
US-TX	Texas
US-UT	Utah
US-VT	Vermont
US-VA	Virginia
US-WA	Washington
US-WV	West Virginia
US-WI	Wisconsin
US-WY	Wyoming
US-DC	District of Columbia
US-AS	American Samoa
US-GU	Guam
US-MP	Northern Mariana Islands
US-PR	Puerto Rico
US-UM	United States Minor Outlying Islands
US-VI	Virgin Islands
UY-AR	Artigas
UY-CA	Canelones
UY-CL	Cerro Largo
UY-CO	Colonia
UY-DU	Durazno
UY-FS	Flores
UY-FD	Florida
UY-LA	Lavalleja
UY-MA	Maldonado
UY-MO	Montevideo
UY-PA	Paysandú
UY-RN	Río Negro
UY-RV	Rivera
UY-RO	Rocha
UY-SA	Salto
UY-SJ	San José
UY-SO	Soriano
UY-TA	Tacuarembó
UY-TT	Treinta y Tres
UZ-TK	Toshkent
UZ-AN	Andijon
UZ-BU	Buxoro
UZ-FA	Farg'ona
UZ-JI	Jizzax
UZ-NG	Namangan
UZ-NW	Navoiy
UZ-QA	Qashqadaryo
UZ-SA	Samarqand
UZ-SI	Sirdaryo
UZ-SU	Surxondaryo
UZ-TO	Toshkent
UZ-XO	Xorazm

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
UZ-QR	Qoraqalpog'iston Respublikasi
VC-01	Charlotte
VC-06	Grenadines
VC-02	Saint Andrew
VC-03	Saint David
VC-04	Saint George
VC-05	Saint Patrick
VE-W	Dependencias Federales
VE-A	Distrito Federal
VE-Z	Amazonas
VE-B	Anzoátegui
VE-C	Apure
VE-D	Aragua
VE-E	Barinas
VE-F	Bolívar
VE-G	Carabobo
VE-H	Cojedes
VE-Y	Delta Amacuro
VE-I	Falcón
VE-J	Guárico
VE-K	Lara
VE-L	Mérida
VE-M	Miranda
VE-N	Monagas
VE-O	Nueva Esparta
VE-P	Portuguesa
VE-R	Sucre
VE-S	Táchira
VE-T	Trujillo
VE-X	Vargas
VE-U	Yaracuy
VE-V	Zulia
VN-44	An Giang
VN-43	Bà Rịa-Vũng Tàu
VN-54	Bắc Giang
VN-53	Bắc Kạn
VN-55	Bạc Liêu
VN-56	Bắc Ninh
VN-50	Bến Tre
VN-31	Bình Định
VN-57	Bình Dương
VN-58	Bình Phước
VN-40	Bình Thuận
VN-59	Cà Mau
VN-04	Cao Bằng
VN-33	Đắc Lăk
VN-72	Đăk Nông
VN-71	Điện Biên
VN-39	Đồng Nai
VN-45	Đồng Tháp
VN-30	Gia Lai

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
VN-03	Hà Giang
VN-63	Hà Nam
VN-15	Hà Tây
VN-23	Hà Tĩnh
VN-61	Hải Dương
VN-73	Hậu Giang
VN-14	Hoà Bình
VN-66	Hưng Yên
VN-34	Khánh Hòa
VN-47	Kiên Giang
VN-28	Kon Tum
VN-01	Lai Châu
VN-35	Lâm Đồng
VN-09	Lạng Sơn
VN-02	Lào Cai
VN-41	Long An
VN-67	Nam Định
VN-22	Nghệ An
VN-18	Ninh Bình
VN-36	Ninh Thuận
VN-68	Phú Thọ
VN-32	Phú Yên
VN-24	Quảng Bình
VN-27	Quảng Nam
VN-29	Quảng Ngãi
VN-13	Quảng Ninh
VN-25	Quảng Trị
VN-52	Sóc Trăng
VN-05	Sơn La
VN-37	Tây Ninh
VN-20	Thái Bình
VN-69	Thái Nguyên
VN-21	Thanh Hóa
VN-26	Thừa Thiên-Huế
VN-46	Tiền Giang
VN-51	Trà Vinh
VN-07	Tuyên Quang
VN-49	Vĩnh Long
VN-70	Vĩnh Phúc
VN-06	Yên Bái
VN-CT	Cần Thơ
VN-DN	Đà Nẵng
VN-HN	Hà Nội
VN-HP	Hải Phòng
VN-SG	Hồ Chí Minh [Sài Gòn]
VU-MAP	Malampa
VU-PAM	Pénama
VU-SAM	Sanma
VU-SEE	Shéfa
VU-TAE	Taféa
VU-TOB	Torba

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
WS-AA	A'ana
WS-AL	Aiga-i-le-Tai
WS-AT	Atua
WS-FA	Fa'asaleleaga
WS-GE	Gaga'emauga
WS-GI	Gagaifomauga
WS-PA	Palauli
WS-SA	Satupa'itea
WS-TU	Tuamasaga
WS-VF	Va'a-o-Fonoti
WS-VS	Vaisigano
YE-AB	Abyān
YE-AD	'Adan
YE-DA	Ad Dālī'
YE-BA	Al Bay ā'
YE-MU	Al udaydah
YE-JA	Al Jawf
YE-MR	Al Mahrah
YE-MW	Al Ma wīt
YE-AM	'Amrān
YE-DH	Dhamār
YE-HD	a ramawt
YE-HJ	ajjah
YE-IB	Ibb
YE-LA	La ij
YE-MA	Ma'rib
YE-RA	Raymah
YE-SD	Şa'dah
YE-SN	Şan'ā'
YE-SH	Shabwah
YE-TA	Tā'izz
ZA-EC	Eastern Cape
ZA-FS	Free State
ZA-GP	Gauteng
ZA-ZN	Kwazulu-Natal
ZA-LP	Limpopo
ZA-MP	Mpumalanga
ZA-NC	Northern Cape
ZA-NW	North-West (South Africa)
ZA-WC	Western Cape
ZM-02	Central
ZM-08	Copperbelt
ZM-03	Eastern
ZM-04	Luapula
ZM-09	Lusaka
ZM-05	Northern
ZM-06	North-Western
ZM-07	Southern (Zambia)
ZM-01	Western
ZW-BU	Bulawayo
ZW-HA	Harare

Continued on next page

Table A.4.1 – continued from previous page

Key	Description
ZW-MA	Manicaland
ZW-MC	Mashonaland Central
ZW-ME	Mashonaland East
ZW-MW	Mashonaland West
ZW-MV	Masvingo
ZW-MN	Matabeleland North
ZW-MS	Matabeleland South
ZW-MI	Midlands

(See them at http://www.iso.org/iso/country_codes.htm, http://en.wikipedia.org/wiki/ISO_3166-2, <http://unstats.un.org/unsd/methods/m49/m49.htm>, <http://unstats.un.org/unsd/methods/m49/m49regin.htm> and <http://unstats.un.org/unsd/methods/m49/m49alpha.htm>)

Table A.4.2: ISO 3166-1, ISO 3166-2 and UN M.49 aliases

Alias	Key	Description
001	019, 002, 150, 142, 009	World
011	BF, BJ, CI, CV, GH, GM, GN, GW, LR, ML, MR, NE, NG, SH, SL, SN, TG	Western Africa
013	BZ, CR, GT, HN, MX, NI, PA, SV	Central America
014	BI, DJ, ER, ET, KE, KM, MG, MU, MW, MZ, RE, RW, SC, SO, TZ, UG, YT, ZM, ZW	Eastern Africa
142	145, 143, 030, 034, 035	Asia
143	TM, TJ, KG, KZ, UZ	Central Asia
145	AE, AM, AZ, BH, CY, GE, IL, IQ, JO, KW, LB, OM, PS, QA, SA, SY, TR, YE	Western Asia
015	DZ, EG, EH, LY, MA, SD, SS, TN	Northern Africa
150	154, 155, 151, 039, EU	Europe
151	BG, BY, CZ, HU, MD, PL, RO, RU, SK, UA	Eastern Europe
154	GG, IM, JE, AX, DK, EE, FI, FO, GB, IE, IS, LT, LV, NO, SE, SJ	Northern Europe
155	AT, BE, CH, DE, FR, LI, LU, MC, NL	Western Europe
017	AO, CD, CF, CG, CM, GA, GQ, ST, TD	Middle Africa
018	BW, LS, NA, SZ, ZA	Southern Africa
019	021, 013, 029, 005, 003, 419	Americas
002	015, 011, 017, 014, 018	Africa
021	BM, CA, GL, PM, US	Northern America
029	AG, AI, AW, BB, BL, BQ, BS, CU, CW, DM, DO, GD, GP, HT, JM, KN, KY, LC, MF, MQ, MS, PR, SX, TC, TT, VC, VG, VI	Caribbean
003	021, 013, 029	North America
030	CN, HK, JP, KP, KR, MN, MO, TW	Eastern Asia

Continued on next page

Table A.4.2 – continued from previous page

Alias	Key	Description
035	BN, ID, KH, LA, MM, MY, PH, SG, TH, TL, VN	South-Eastern Asia
039	AD, AL, BA, ES, GI, GR, HR, IT, ME, MK, MT, RS, PT, SI, SM, VA	Southern Europe, XK not in UN data
419	013, 029, 005	Latin America and the Caribbean
005	AR, BO, BR, CL, CO, EC, FK, GF, GY, PE, PY, SR, UY, VE	South America
053	AU, NF, NZ	Australia and New Zealand
054	FJ, NC, PG, SB, VU	Melanesia
057	FM, GU, KI, MH, MP, NR, PW	Micronesia
061	AS, CK, NU, PF, PN, TK, TO, TV, WF, WS	Polynesia
034	AF, BD, BT, IN, IR, LK, MV, NP, PK	Southern Asia
009	053, 054, 057, 061, QO	Oceania
QO	AQ, BV, CC, CX, GS, HM, IO, TF, UM	Outlying Oceania
EU	AT, BE, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LT, LU, LV, MT, NL, PL, PT, SE, SI, SK, BG, RO	European Union, see http://europa.eu/abc/european_countries/index_en.htm
ALIAS:EAL	GB-CAM, GB-ESS, GB-HRT, GB-NFK, GB-SFK	East Anglia: United Kingdom region composed of the administrative counties of Norfolk to the north, Suffolk to the south, Cambridgeshire and Essex to the west.

A.5 Institution ID

This controlled vocabulary has 53 terms

Please contact BLUEPRINT DCC if your institution is not listed, or you wish to modify the text

Table A.5.1: Institution ID

ID	Institution
1	Radboud University Nijmegen (H.G. Stunnenberg)
2a	University College London (S. Beck)
2b	University College London (T. Enver)
3a	University of Cambridge (A. Ferguson-Smith)
3b	University of Cambridge (W. H.Ouwéhand)
4	Friedrich Miescher Institute (D. Schübeler)
5	Christian Albrechts University of Kiel (R. Siebert)
6	National Cancer Research Centre Spain (A. Valencia)
7a	Institute of Molecular Oncology Foundation - European Institute of Oncology (P.G. Pelicci)
7b	Institute of Molecular Oncology Foundation - European Institute of Oncology (S. Minucci)
8	European Bioinformatics Institute (P. Flórek)
9a	Wellcome Trust Sanger Institute (M. Stratton)
9b	Wellcome Trust Sanger Institute (D. Adams)
9c	Wellcome Trust Sanger Institute (N. Soranzo)

Continued on next page

Table A.5.1 – continued from previous page

ID	Institution
10	Bellvitge Institute for Biomedical Research (M. Esteller)
11	Centro Nacional de Analysis Genómico (I. Gut)
12a	Max Planck Institute for Bioinformatics (T. Lengauer/C.Bock)
12b	Max Planck Institute for Molecular Genetics (H. Lehrach)
12c	Max Planck Institute for Molecular Genetics (M. Vingron)
12d	Max Planck Institute for Molecular Genetics, Dpt Vertebrate Genomics (M-L Yaspo)
13	University of Saarland (J. Walter)
14	Second University of Naples (L. Altucci)
15a	Centre for Genomic Regulation (X. Estivill)
15b	Centre for Genomic Regulation (R. Guigo)
15c	Centre for Genomic Regulation (T. Graf)
16a	Queen Mary, University of London (D. Leslie/V. Rakyan)
16b	Queen Mary, University of London (J. Fitzgibbon)
17	The Babraham Institute (W. Reik)
18	Cellzome AG (D. Simmons)
19	Diagenode SA (D. Allaer)
20	Olink Genomics (F. Dahl)
21	Genomatix Software GmbH (M. Seifert)
22	Oxford Nanopore Technologies Ltd (S. Willcocks)
23	Siena Biotech SpA (A. Caricasole)
24	Centre of Immunology of Marseille-Luminy (S. Spicuglia)
25	Institut d'Investigacions Biomèdiques August Pi i Sunyer (E. Campo)
26	Weizmann Institute of Science (A. Tanay)
27	Erasmus University Medical Centre Rotterdam (F. Grosveld)
28	Universitaetsklinikum Ulm (B. Böhm)
29	University of Edinburgh (A. Bird)
30	Lund University (A. Lernmark)
31	University of Copenhagen (K. Helin)
32	Sapienza University of Rome (A. Mai)
33	Vivia Biotech S.L. (J. Ballesteros)
34	University of Geneva (M. Dermitzakis, S. Antonorakis)
35	University Medical Centre Groningen (E. Vellenga)
36	Neckar Hospital (Elizabeth Macintyre)
37	Epigenomics AG (R. Wasserkort)
38	University of Duisburg-Essen (R. Küppers)
39	University of Leipzig (M. Löffler)
40	Barcelona Supercomputing Center (D. Torrents)
41	Sigolis (J. Jarvius)
42	Eurice (V. Siegmund)

A.6 Value Codes for Platform or Validation Platform

This controlled vocabulary has 75 terms

Please contact the DCC if your platform/technology is not listed here.

Table A.6.1: Value Codes for Platform or Validation Platform

Key	Platform or Validation Platform
1	PCR
2	qPCR
3	capillary sequencing
4	SOLiD sequencing
5	Illumina GA sequencing
6	454 sequencing
7	Helicos sequencing
8	Affymetrix Genome-Wide Human SNP Array 6.0
9	Affymetrix Genome-Wide Human SNP Array 5.0
10	Affymetrix Mapping 100K Array Set
11	Affymetrix Mapping 500K Array Set
12	Affymetrix Mapping 10K 2.0 Array Set
13	Affymetrix EMET Plus Premier Pack
14	Agilent Whole Human Genome Oligo Microarray Kit
15	Agilent Human Genome 244A
16	Agilent Human Genome 105A
17	Agilent Human CNV Association 2x105K
18	Agilent Human Genome 44K
19	Agilent Human CGH 1x1M
20	Agilent Human CGH 2x400K
21	Agilent Human CGH 4x180K
22	Agilent Human CGH 8x60K
23	Agilent Human CNV 2x400K
24	Agilent Human miRNA Microarray Kit (v2)
25	Agilent Human CpG Island Microarray Kit
26	Agilent Human Promoter ChIP-on-chip Microarray Set
27	Agilent Human SpliceArray
28	Illumina human1m-duo
29	Illumina human660w-quad
30	Illumina humancytosnp-12
31	Illumina human510s-duo
32	Illumina humanmethylation27
33	Illumina goldengate methylation
34	Illumina HumanHT-12 v4.0 beadchip
35	Illumina HumanWG-6 v3.0 beadchip
36	Illumina HumanRef-8 v3.0 beadchip
37	Illumina microRNA Expression Profiling Panel
38	Illumina humanht-16
39	Illumina humanht-17
40	Nimblegen Human CGH 3x720 Whole-Genome v3.0 Array
41	Nimblegen Human CGH 2.1M Whole-Genome v2.0D Array
42	Nimblegen Gene Expression 385K
43	Nimblegen Gene Expression 4x72K
44	Nimblegen Gene Expression 12x135K
45	Nimblegen Human Methylation 2.1M Whole-Genome sets

Continued on next page

Table A.6.1 – continued from previous page

Key	Platform or Validation Platform
46	Nimblegen Human Methylation 385K Whole-Genome sets
47	Nimblegen CGS
48	Illumina Human1M OmniQuad chip
49	PCR and capillary sequencing
50	Custom-designed gene expression array
51	Affymetrix HT Human Genome U133A Array Plate Set
52	Agilent 244K Custom Gene Expression G4502A-07-1
53	Agilent 244K Custom Gene Expression G4502A-07-2
54	Agilent 244K Custom Gene Expression G4502A-07-3
55	Agilent Human Genome CGH Custom Microarray 2x415K
56	Affymetrix Human U133 Plus PM
57	Affymetrix Human U133 Plus 2.0
58	Affymetrix Human Exon 1.0 ST
59	Almac Human CRC
60	Illumina HiSeq
61	Affymetrix Human MIP 330K
62	Affymetrix Human Gene 1.0 ST
63	Illumina Human Omni1-Quad beadchip
64	Sequenom MassARRAY
65	Custom-designed cDNA array
66	Illumina HumanHap550
67	Ion Torrent PGM
68	Illumina GoldenGate Methylation Cancer Panel I
69	Illumina Infinium HumanMethylation450
70	Agilent 8 x 15K Human miRNA-specific microarray
71	M.D. Anderson Reverse Phase Protein Array Core
72	Microsatellite Instability Analysis
73	Agilent 244K Custom Gene Expression G4502A-07
74	Illumina HumanCNV370-Duo v1.0 BeadChip
75	Illumina HumanOmniExpress BeadChip

A.7 Chromosome Names for Reference Genome GRCh37

This controlled vocabulary has 137 terms

Table A.7.1: Chromosome Names for Reference Genome GRCh37

Key	Chromosome Name
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9

Continued on next page

Table A.7.1 – continued from previous page

Key	Chromosome Name
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
X	X
Y	Y
MT	MT
c5_H2	c5_H2
c6_COX	c6_COX
c6_QBL	c6_QBL
NT_113870	NT_113870
NT_113871	NT_113871
NT_113872	NT_113872
NT_113874	NT_113874
NT_113878	NT_113878
NT_113880	NT_113880
NT_113881	NT_113881
NT_113884	NT_113884
NT_113885	NT_113885
NT_113886	NT_113886
NT_113888	NT_113888
NT_113889	NT_113889
NT_113890	NT_113890
NT_113898	NT_113898
NT_113899	NT_113899
NT_113901	NT_113901
NT_113902	NT_113902
NT_113903	NT_113903
NT_113906	NT_113906
NT_113908	NT_113908
NT_113909	NT_113909
NT_113910	NT_113910
NT_113911	NT_113911
NT_113912	NT_113912
NT_113915	NT_113915
NT_113916	NT_113916
NT_113917	NT_113917
NT_113923	NT_113923
NT_113924	NT_113924
NT_113925	NT_113925
NT_113926	NT_113926
NT_113927	NT_113927

Continued on next page

Table A.7.1 – continued from previous page

Key	Chromosome Name
NT_113929	NT_113929
NT_113930	NT_113930
NT_113931	NT_113931
NT_113932	NT_113932
NT_113933	NT_113933
NT_113934	NT_113934
NT_113935	NT_113935
NT_113936	NT_113936
NT_113937	NT_113937
NT_113939	NT_113939
NT_113943	NT_113943
NT_113944	NT_113944
NT_113946	NT_113946
NT_113949	NT_113949
NT_113951	NT_113951
NT_113953	NT_113953
NT_113954	NT_113954
NT_113956	NT_113956
NT_113957	NT_113957
NT_113958	NT_113958
NT_113960	NT_113960
NT_113961	NT_113961
NT_113962	NT_113962
NT_113963	NT_113963
NT_113964	NT_113964
NT_113965	NT_113965
NT_113966	NT_113966
HSCHR17_1	HSCHR17_1
HSCHR17_RANDOM_CTG2	HSCHR17_RANDOM_CTG2
HSCHR17_RANDOM_CTG3	HSCHR17_RANDOM_CTG3
HSCHR19_RANDOM_CTG2	HSCHR19_RANDOM_CTG2
HSCHR1_RANDOM_CTG12	HSCHR1_RANDOM_CTG12
HSCHR1_RANDOM_CTG5	HSCHR1_RANDOM_CTG5
HSCHR4_RANDOM_CTG2	HSCHR4_RANDOM_CTG2
HSCHR4_RANDOM_CTG3	HSCHR4_RANDOM_CTG3
HSCHR6_MHC_APD	HSCHR6_MHC_APD
HSCHR6_MHC_COX	HSCHR6_MHC_COX
HSCHR6_MHC_DBB	HSCHR6_MHC_DBB
HSCHR6_MHC_MANN	HSCHR6_MHC_MANN
HSCHR6_MHC_MCF	HSCHR6_MHC_MCF
HSCHR6_MHC_QBL	HSCHR6_MHC_QBL
HSCHR6_MHC_SSTO	HSCHR6_MHC_SSTO
HSCHR7_RANDOM_CTG1	HSCHR7_RANDOM_CTG1
HSCHR8_RANDOM_CTG1	HSCHR8_RANDOM_CTG1
HSCHR8_RANDOM_CTG4	HSCHR8_RANDOM_CTG4
HSCHR9_RANDOM_CTG2	HSCHR9_RANDOM_CTG2
HSCHR9_RANDOM_CTG4	HSCHR9_RANDOM_CTG4
HSCHR9_RANDOM_CTG5	HSCHR9_RANDOM_CTG5
HSCHRUN_RANDOM_CTG1	HSCHRUN_RANDOM_CTG1
HSCHRUN_RANDOM_CTG10	HSCHRUN_RANDOM_CTG10
HSCHRUN_RANDOM_CTG11	HSCHRUN_RANDOM_CTG11

Continued on next page

Table A.7.1 – continued from previous page

Key	Chromosome Name
HSCHRUN_RANDOM_CTG13	HSCHRUN_RANDOM_CTG13
HSCHRUN_RANDOM_CTG14	HSCHRUN_RANDOM_CTG14
HSCHRUN_RANDOM_CTG15	HSCHRUN_RANDOM_CTG15
HSCHRUN_RANDOM_CTG16	HSCHRUN_RANDOM_CTG16
HSCHRUN_RANDOM_CTG17	HSCHRUN_RANDOM_CTG17
HSCHRUN_RANDOM_CTG2	HSCHRUN_RANDOM_CTG2
HSCHRUN_RANDOM_CTG20	HSCHRUN_RANDOM_CTG20
HSCHRUN_RANDOM_CTG21	HSCHRUN_RANDOM_CTG21
HSCHRUN_RANDOM_CTG22	HSCHRUN_RANDOM_CTG22
HSCHRUN_RANDOM_CTG23	HSCHRUN_RANDOM_CTG23
HSCHRUN_RANDOM_CTG26	HSCHRUN_RANDOM_CTG26
HSCHRUN_RANDOM_CTG29	HSCHRUN_RANDOM_CTG29
HSCHRUN_RANDOM_CTG3	HSCHRUN_RANDOM_CTG3
HSCHRUN_RANDOM_CTG30	HSCHRUN_RANDOM_CTG30
HSCHRUN_RANDOM_CTG31	HSCHRUN_RANDOM_CTG31
HSCHRUN_RANDOM_CTG32	HSCHRUN_RANDOM_CTG32
HSCHRUN_RANDOM_CTG33	HSCHRUN_RANDOM_CTG33
HSCHRUN_RANDOM_CTG34	HSCHRUN_RANDOM_CTG34
HSCHRUN_RANDOM_CTG35	HSCHRUN_RANDOM_CTG35
HSCHRUN_RANDOM_CTG36	HSCHRUN_RANDOM_CTG36
HSCHRUN_RANDOM_CTG4	HSCHRUN_RANDOM_CTG4
HSCHRUN_RANDOM_CTG40	HSCHRUN_RANDOM_CTG40
HSCHRUN_RANDOM_CTG5	HSCHRUN_RANDOM_CTG5
HSCHRUN_RANDOM_CTG6	HSCHRUN_RANDOM_CTG6
HSCHRUN_RANDOM_CTG9	HSCHRUN_RANDOM_CTG9
HSCHR4_1	HSCHR4_1

A.8 Value Codes for Reference Genome Assembly Version

This controlled vocabulary has 7 terms

Table A.8.1: Value Codes for Reference Genome Assembly Version

Key	Reference Genome Assembly Version
1	GRCh37
2	NCBI36
3	GRCh37.p1
4	GRCh37.p2
5	GRCh37.p3
6	GRCh37.p4
7	GRCh37.p5

A.9 Value Codes for Raw Data Repository

This controlled vocabulary has 5 terms

Table A.9.1: Value Codes for Raw Data Repository

Key	Raw Data Repository
1	EGA
2	dbSNP
3	TCGA
4	CGHub
5	GEO

A.10 CV Table wgbsFeatures

This controlled vocabulary has 17 terms

Table A.10.1: CV Table wgbsFeatures

Key	Description
EXTRACTION_PROTOCOL_TYPE_OF SONICATOR	The type of sonicator used for extraction.
EXTRACTION_PROTOCOL_SONICATION_CYCLES	The number of sonication cycles used for extraction.
DNA_PREPARATION_INITIAL_DNA_QNTY	The initial DNA quantity used in preparation.
DNA_PREPARATION_FRAGMENT_SIZE_RANGE	The DNA fragment size range used in preparation.
DNA_PREPARATION_ADAPTER_SEQUENCE	The sequence of the adaptor used in preparation.
DNA_PREPARATION_ADAPTER_LIGATION_PROTOCOL	The protocol used for adaptor ligation.
DNA_PREPARATION_POST-LIGATION_FRAGMENT_SIZE_SELECTION	The fragment size selection after adaptor ligation.
BISULFITE_CONVERSION_PROTOCOL	The bisulfite conversion protocol.
BISULFITE_CONVERSION_PERCENT	The bisulfite conversion percent and how it was determined.
LIBRARY_GENERATION_PCR_TEMPLATE_CONC	The PCR template concentration for library generation.
LIBRARY_GENERATION_PCR_POLYMERASE_TYPE	The PCR polymerase used for library generation
LIBRARY_GENERATION_PCR_THERMOCYCLING_PROGRAM	The thermocycling program used for library generation.
LIBRARY_GENERATION_PCR_NUMBER_CYCLES	The number of PCR cycles used for library generation.
LIBRARY_GENERATION_PCR_F_PRIMER_SEQUENCE	The sequence of the PCR forward primer used for library generation.
LIBRARY_GENERATION_PCR_R_PRIMER_SEQUENCE	The sequence of the PCR reverse primer used for library generation.
LIBRARY_GENERATION_PCR_PRIMER_CONC	The concentration of the PCR primers used for library generation.
LIBRARY_GENERATION_PCR_PRODUCT_ISOLATION_PROTOCOL	The protocol for isolating PCR products used for library generation.

A.11 CV Table medipFeatures

This controlled vocabulary has 11 terms

Table A.11.1: CV Table medipFeatures

Key	Description
EXTRACTION_PROTOCOL_TYPE_OF SONICATOR	The type of sonicator used for extraction.

Continued on next page

Table A.11.1 – continued from previous page

Key	Description
EXTRACTION_PROTOCOL_SONICATION_CYCLES	The number of sonication cycles used for extraction.
MeDIP_PROTOCOL	The MeDIP protocol used.
MeDIP_PROTOCOL_DNA_AMOUNT	The amount of DNA used in the MeDIP protocol.
MeDIP_PROTOCOL_BEAD_TYPE	The type of bead used in the MeDIP protocol.
MeDIP_PROTOCOL_BEAD_AMOUNT	The amount of beads used in the MeDIP protocol.
MeDIP_PROTOCOL_ANTIBODY_AMOUNT	The amount of antibody used in the MeDIP protocol.
MeDIP_ANTIBODY	The specific antibody used in the MeDIP protocol.
MeDIP_ANTIBODY_PROVIDER	The name of the company, laboratory or person that provided the antibody.
MeDIP_ANTIBODY_CATALOG	The catalog from which the antibody was purchased.
MeDIP_ANTIBODY_LOT	The lot identifier of the antibody.

A.12 CV Table mreFeatures

This controlled vocabulary has 4 terms

Table A.12.1: CV Table mreFeatures

Key	Description
MRE_PROTOCOL	The MRE protocol.
MRE_PROTOCOL_CHROMATIN_AMOUNT	The amount of chromatin used in the MRE protocol.
MRE_PROTOCOL_RESTRICTION_ENZYME	The restriction enzyme(s) used in the MRE protocol.
MRE_PROTOCOL_SIZE_FRACTION	The size of the fragments selected in the MRE protocol.

A.13 CV Table csiFeatures

This controlled vocabulary has 4 terms

Table A.13.1: CV Table csiFeatures

Key	Description
EXTRACTION_PROTOCOL_TYPE_OF SONICATOR	The type of sonicator used for extraction.
EXTRACTION_PROTOCOL_SONICATION_CYCLES	The number of sonication cycles used for extraction.
CHIP_PROTOCOL	Input
CHIP_PROTOCOL_CHROMATIN_AMOUNT	The amount of chromatin used in the ChIP protocol.

A.14 CV Table csFeatures

This controlled vocabulary has 13 terms

Table A.14.1: CV Table csFeatures

Key	Description
EXTRACTION_PROTOCOL_TYPE_OF SONICATOR	The type of sonicator used for extraction.
EXTRACTION_PROTOCOL_SONICATION_CYCLES	The number of sonication cycles used for extraction.

Continued on next page

Table A.14.1 – continued from previous page

Key	Description
CHIP_PROTOCOL	The ChIP protocol used.
CHIP_PROTOCOL_CHROMATIN_AMOUNT	The amount of chromatin used in the ChIP protocol.
CHIP_PROTOCOL_BEAD_TYPE	The type of bead used in the ChIP protocol.
CHIP_PROTOCOL_BEAD_AMOUNT	The amount of beads used in the ChIP protocol.
CHIP_PROTOCOL_ANTIBODY_AMOUNT	The amount of antibody used in the ChIP protocol.
CHIP_ANTIBODY	The specific antibody used in the ChIP protocol.
CHIP_ANTIBODY_PROVIDER	The name of the company, laboratory or person that provided the antibody.
CHIP_ANTIBODY_CATALOG	The catalog from which the antibody was purchased.
CHIP_ANTIBODY_LOT	The lot identifier of the antibody.
CHIP_PROTOCOL_CROSSLINK_TIME	The timespan in which the chromatin is crosslinked
LIBRARY_GENERATION_FRAGMENT_SIZE_RANGE	The fragment size range of the preparation.

A.15 CV Table mRNAFeatures

This controlled vocabulary has 30 terms

Table A.15.1: CV Table mRNAFeatures

Key	Description
EXTRACTION_PROTOCOL_MRNA_ENRICHMENT	The mRNA enrichment method used in the extraction protocol.
EXTRACTION_PROTOCOL_FRAGMENTATION	The fragmentation method used in the extraction protocol.
MRNA_PREPARATION_INITIAL_MRNA_QNTY	The initial mRNA quantity used in preparation.
MRNA_PREPARATION_FRAGMENT_SIZE_RANGE	The mRNA fragment size range of the preparation.
RNA_PREPARATION_5'_RNA_ADAPTER_SEQUENCE	The sequence of the 5' RNA adapter used in preparation.
RNA_PREPARATION_3'_RNA_ADAPTER_SEQUENCE	The sequence of the 3' RNA adapter used in preparation.
RNA_PREPARATION_REVERSE_TRANSSCRIPTION_PRIMER_SEQUENCE	The sequence of the primer for reverse transcription used in preparation.
RNA_PREPARATION_5'_DEPHOSPHORYLATION	The protocol for 5' dephosphorylation used in preparation.
RNA_PREPARATION_5'_PHOSPHORYLATION	The protocol for 5' phosphorylation used in preparation.
RNA_PREPARATION_3'_RNA_ADAPTER_LIGATION_PROTOCOL	The protocol for 3' adapter ligation used in preparation.
RNA_PREPARATION_5'_RNA_ADAPTER_LIGATION_PROTOCOL	The protocol for 5' adapter ligation used in preparation.
RNA_PREPARATION_REVERSE_TRANSSCRIPTION_PROTOCOL	The protocol for reverse transcription used in preparation.
LIBRARY_GENERATION_PCR_TEMPLATE_CONC	The PCR template concentration for library generation.
LIBRARY_GENERATION_PCR_POLYMERASE_TYPE	The PCR polymerase used for library generation
LIBRARY_GENERATION_PCR_THERMOCYCLING_PROGRAM	The thermocycling program used for library generation.
LIBRARY_GENERATION_PCR_NUMBER_CYCLES	The number of PCR cycles used for library generation.
LIBRARY_GENERATION_PCR_F_PRIMER_SEQUENCE	The sequence of the PCR forward primer used for library generation.

Continued on next page

Table A.15.1 – continued from previous page

Key	Description
LIBRARY_GENERATION_PCR_R_PRIMER_SEQUENCE	The sequence of the PCR reverse primer used for library generation.
LIBRARY_GENERATION_PCR_PRIMER_CONC	The concentration of the PCR primers used for library generation.
LIBRARY_GENERATION_PCR_PRODUCT_ISOLATION_PROTOCOL	The protocol for isolating PCR products used for library generation.
TEMPLATE_TYPE	mRNA or cDNA - The type of template.
AMPLIFIED	True or False - Is the sample amplified?
PREPARATION_INITIAL_MRNA_QNTY	The initial mRNA quantity used in preparation.
PREPARATION_REVERSE_TRANSSCRIPTION_PROTOCOL	The protocol for reverse transcription used in preparation.
PREPARATION_PCR_NUMBER_CYCLES	The number of PCR cycles used to amplify.
LIBRARY_GENERATION_PROTOCOL	The protocol used to generate the library.
LIBRARY_GENERATION_FRAGMENTATION	The fragmentation method used in the library protocol.
LIBRARY_GENERATION_FRAGMENT_SIZE_RANGE	The fragment size range of the preparation.
LIBRARY_GENERATION_3'_ADAPTER_SEQUENCE	The sequence of the 3' adapter used for library generation.
LIBRARY_GENERATION_5'_ADAPTER_SEQUENCE	The sequence of the 5' adapter used for library generation.

A.16 CV Table smrnaFeatures

This controlled vocabulary has 16 terms

Table A.16.1: CV Table smrnaFeatures

Key	Description
EXTRACTION_PROTOCOL_SMRNA_ENRICHMENT	The smRNA enrichment method used in the extraction protocol.
SMRNA_PREPARATION_INITIAL_SMRNA_QNTY	The initial smRNA quantity used in preparation.
RNA_PREPARATION_5'_RNA_ADAPTER_SEQUENCE	The sequence of the 5' RNA adapter used in preparation.
RNA_PREPARATION_3'_RNA_ADAPTER_SEQUENCE	The sequence of the 3' RNA adapter used in preparation.
RNA_PREPARATION_REVERSE_TRANSSCRIPTION_PRIMER_SEQUENCE	The sequence of the primer for reverse transcription used in preparation.
RNA_PREPARATION_3'_RNA_ADAPTER_LIGATION_PROTOCOL	The protocol for 3' adapter ligation used in preparation.
RNA_PREPARATION_5'_RNA_ADAPTER_LIGATION_PROTOCOL	The protocol for 5' adapter ligation used in preparation.
RNA_PREPARATION_REVERSE_TRANSSCRIPTION_PROTOCOL	The protocol for reverse transcription used in preparation.
LIBRARY_GENERATION_PCR_TEMPLATE_CONC	The PCR template concentration for library generation.
LIBRARY_GENERATION_PCR_POLYMERASE_TYPE	The PCR polymerase used for library generation
LIBRARY_GENERATION_PCR_THERMOCYCLING_PROGRAM	The thermocycling program used for library generation.
LIBRARY_GENERATION_PCR_NUMBER_CYCLES	The number of PCR cycles used for library generation.
LIBRARY_GENERATION_PCR_F_PRIMER_SEQUENCE	The sequence of the PCR forward primer used for library generation.

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Table A.16.1 – continued from previous page

Key	Description
LIBRARY_GENERATION_PCR_R_PRIMER_SEQUENCE	The sequence of the PCR reverse primer used for library generation.
LIBRARY_GENERATION_PCR_PRIMER_CONC	The concentration of the PCR primers used for library generation.
LIBRARY_GENERATION_PCR_PRODUCT_ISOLATION_PROTOCOL	The protocol for isolating PCR products used for library generation.

A.17 CV Table SRALibraryStrategy

This controlled vocabulary has 21 terms

Sequencing technique intended for this library (borrowed from SRA XML 1.2).

Table A.17.1: CV Table SRALibraryStrategy

Key	Description
WGS	Random sequencing of the whole genome.
WXS	Random sequencing of exonic regions selected from the genome.
RNA-Seq	Random sequencing of whole transcriptome.
WCS	Random sequencing of a whole chromosome or other replicon isolated from a genome.
CLONE	Genomic clone based (hierarchical) sequencing.
POOLCLONE	Shotgun of pooled clones (usually BACs and Fosmids).
AMPLICON	Sequencing of overlapping or distinct PCR or RT-PCR products.
BARCODE	DEPRECATED. Sequencing of overlapping or distinct products that have been tagged with a short identifying sequence (barcode). Each sequence read can therefore be assigned to an individual product.
CLONEEND	Clone end (5', 3', or both) sequencing.
FINISHING	Sequencing intended to finish (close) gaps in existing coverage.
ChIP-Seq	Direct sequencing of chromatin immunoprecipitates.
MNase-Seq	Direct sequencing following MNase digestion.
DNase-Hypersensitivity	Sequencing of hypersensitive sites, or segments of open chromatin that are more readily cleaved by DNasel.
Bisulfite-Seq	Sequencing following treatment of DNA with bisulfite to convert cytosine residues to uracil depending on methylation status.
EST	Single pass sequencing of cDNA templates
FL-cDNA	Full-length sequencing of cDNA templates
CTS	Concatenated Tag Sequencing
MRE-Seq	Methylation-Sensitive Restriction Enzyme Sequencing strategy.
MeDIP-Seq	Methylated DNA Immunoprecipitation Sequencing strategy.
MBD-Seq	Direct sequencing of methylated fractions sequencing strategy.
OTHER	Library strategy not listed.