

THE DIFFERENT LEVELS OF AARDB

Descriptions of parameters represented

Colors of cells show linkages between the different levels of AARDB

LOCALITY LEVEL

UDAMS
LocalityID
Map100k
Lat
Long
Coordinate_precision_m
SurfaceElevation_m
Notes and/or Reference
Web link
GenNote
HDatum
VDatum

The locality or collection identifier - blue cell identifies the link to the next level in AARDB. Collection ID; Atlantic coast UDAMS numbers range from 00001 to 11xxx, north to south by region. Other UDAMS numbers are usually field numbers of collectors.
 Informal locality name
 USGS 1:100,000 map quadrangle; informal terms for sites outside the US (e.g., "Peru" or "Baja" or "Europe")
 Latitude measured from maps, GPS, or Google Earth
 Longitude measured from maps, GPS, or Google Earth
 Estimated uncertainty of the lat/lon measurement - in some cases, quite large in spite of apparent precision of the lat/lon value
 Entered where known
 Information related to the collection or other sources of information
 Links to web sites that may have information related to the collection
 Information related to the collection or other sources of information
 Horizontal datum - NAD 27 is default value; if nothing indicated, datum in uncertain. "Google Earth" listed as a datum when used to locate sites

COLLECTION ID LEVEL

CollectionID
UDAMS
SamplingType
SamplingDate
Remark
Current location
Collector

The unique collection from a site -it can be a single shell, a bag of shells, or several bags of shells
 As above - the blue color identifies the link between these two levels of AARDB
 Identifies the collection as coming from core, excavation, spoil pile, beach (surface), etc.
 Date of sampling, if known
 Indicates if the collection or samples have been relocated to another repository. Abbreviations as follows: LACM, Los Angeles County Museum; FLMNH, Florida Museum of Natural History; PRI, Paleontology Research Institute; ANSP, Academy of Nat. Sciences of Philadelphia; DGS, Delaware Geological Survey; NCGS, North Carolina Geological Survey; VMNH, Virginia Museum of Natural History. If blank, collection is currently at Univ. of Delaware.
 The name of the individual(s) who made the collection

SAMPLE LEVEL

SampleID
SampleType
SampleNote
CollectionID
SUBSAMPLE LEVEL
SubSampleID
AltID
ShortReference
SamplePosition
Precursor
ProcedureID
CreationDate
Notes
SampleID

The individual shell that came from the collection listed above and below (purple cell)
 Usually the genus of the sample
 species level often noted here
 As above; the purple color links this level of AARDB with the "Collection ID" above
 A unique identifier of a fragment taken from a specific individual shell; multiple subsamples can, in some cases, be taken from a single shell
 An alternate identification number if needed
 Any publication reference that can be cited for this sample
 The position within the shell where the fragment was cut; numbers from 1 to 10 represent the relative position from hinge to growth edge
 See "subsample procedure" in AARDB
 Date when data began to be entered
 Any comments about the sample or the quality of the analysis or chromatogram(s)
 See "SampleID" in green cell above for link to the preceding level in AARDB

CHROMATOGRAM LEVEL

Date of Run
AnalysisProcedureID
RefNumber
SubSampleID
RunNote
FIDScale

The date of the chromatographic analysis, if known (date of data entry if actual date not known)
 See "analysis procedure" table in AARDB
 The chromatogram number, if known; arbitrary if noted; most chromatograms are in digital form for review
 As above - the unique identifier of a sample fragment
 Notes about the quality of the chromatogram
 A number that ranges from -1 to -50 to indicate the full scale of the GC chromatogram -not recorded in most cases, but an indication of whether the GC peaks were small, medium, or large; medium is ideal.

DLRATIO LEVEL

Date of Run
RefNumber
DLRatio
AminoAcid
RatioType
AnalysisProcedureID
Flag
PeakNote

These two link the subsample above to the data below
 The numerical D/L value read from a specific chromatogram
 One of the many amino acids detected by the different methods used
 Peak area or peak height ratios are usually calculated
 See "analysis procedure" table in AARDB
 If a value is flagged, it is suspect for some reason and is not included in any compilation of the mean D/L values for multiple analyses
 Any note or comment about the quality of the chromatogram peak (large, small, asymmetric, etc.)

Sampled interval: for cores, values are always referenced to core top or to mean sea level; sometimes presented as negative numbers