

**STRUCTURE NOTES FOR LABDATA.DBF, GIS/Key VERSION 3**  
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**FILE LAYOUT FOR ELECTRONIC DOWN LOAD TO GIS/Key**

Field Name 10 Character	Respon- sibility	Required	Justify	Type	Len	Dec	Notes  (Default parameters)
SITE_ID	user	X *	L	C	15		Well or sampling location as labeled on the GIS\Key Map. An entry in SITE_ID is required for all Primary results, duplicates, and splits. Spike results may be associated with samples from another location, and therefore SITE_ID is not required although recommended if appropriate.
SP_ID	user		L	C	7		In version 3.x and newer, this field is no longer used.
SAMP_TYPE	lab	X		C	1		Sample types are <W>ater, <S>oil, Sediment, Solid. Others sample types can be added, but these are not supported by GIS\Key. The import routine requires < W, S> entry.
RES_CODE	lab	X	L	C	4		Preliminary code used to determine the type of chemical result. <b>See notes for valid entries.</b> RES_CODE is used by the LabBuild routine to derive the GIS\Key RES_TYPE and RES_CLASS fields. Initially assigned by the lab and modified as required by the user to reflect sample status not known by the lab.
RES_CLASS	GIS	internal		C	1		Assigned by LabBuild from the RES_CODE field, this code refers to the type of result received from the lab. Allowable RES_CLASS entries are <P>primary/duplicate/split <C>ontrol sample <B>lank sample  and <S>pike sample.
RES_TYPE	GIS	internal	L	C	3		Assigned by LabBuild from the RES_CODE field, this code works in conjunction with RES_CLASS to describe the type of result. It consists of a one character code, a test sequence number, and a result occurrence.
RES_COLUMN	lab			C	1		The column number of a multiple column test. RES_COLUMN should = 0 for the result set of record of a record. This corresponds to a RES_CODE result set occurrence = 0 for the result set of record. For other result sets, the column number of the test should be given. Used primarily for IRPIMS reporting.
RES_ORIG	lab	X*	L	C	3		Points to the originating result of a result set of record in a multiple column or dilution test. A result set of the record may be a combination of one or more column/dilution tests. The RES_ORIG points to the result in the test run from which the result of the record came and should equal the last 3 characters of the RES_CODE for that result. Used primarily for IRPIMS reporting.
SURROG_FLG	lab	X*		L	1		The field is set to "T" for a surrogate result and "F" for all other result types. <b>Same as Is_surrog.</b>
SAMP_ID	user		L	C	25		SAMP_ID is the unique identifier provided to the laboratory on the sample bottle.
SAMP_ID2	user		L	C	25		SAMP_ID2 is used ONLY for Field Spike Duplicates or for Blind Control Sample Duplicates.
SAMP_DATE	user	X *		D	8		Date sample was collected (MM/DD/YY format). Required for all results except blanks, spikes and control samples.
SAMP_TIME	lab/user	X *		C	5		Time sample was collected (HH:MM 24hr format). Required for all primary, duplicate, split, blank, and surrogate results but not required for spike and control sample results. If not required and not specified, the import routine enters a default of 00:00.
SAMP_DEPTH	user	X *		N	8	3	Depth below ground surface in meters (metric) or feet (American) at which sample was collected. Required for SAMP_TYPE = <S>, Recommended for SAMP_TYPE = <W>. Depths above ground surface are assigned a negative number. Note that primary key in American version is based on depth measurements to a hundredth of a foot only.
S_DEPTH	user			N	8	3	Depth below ground surface in feet to the top of the sample interval range.
E_DEPTH	user			N	8	3	Depth below ground surface in feet to the bottom of the sample interval range.
CASE_ID	user	X *	L	C	5		Case and blank Ids or case and QA/QC IDs are used to associate primary results with quality control results. CASE_ID is a required entry for quality control data and should be entered for primary results if quality control data is being entered. For small projects, many GIS\Key users use sampling event as CASE_ID. IRPIMS projects should enter the IRPIMS site in the CASE_ID.
SDG_ID	lab/user	X*	L	C	25		SDG or sample delivery group ID. This field (in combination with CASE_ID) is used to associate rinsate blank results with primary results. Required for rinsate blanks.Required for rinsate blanks.Required for rinsate blanks.

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QAQC_ID	lab	X*	L	C	25		QA/QC Batch ID's are normally assigned only by labs. This field is used to associate laboratory quality control results (i.e. method blanks, lab blanks, matrix spikes, control samples) with primary results. QAQC_ID entries must uniquely identify each batch of samples analyzed by the laboratory and may not be repeated. Required for method blanks. <b>Same as Lbatch_id.</b>
BLANK_ID	lab/ user	X*	L	C	25		Field Blank identifier. BLANK_ID is used with CASE_ID to associate field blank results with primary results. Required for field blanks.
TCL_ID	user		L	C	10		In version 3.x and newer this field is not used.
TCL_TYPE	user	X		C	1		In version 3.x and newer this field is mapped to <b>LM_CODE</b> (lab method code). Used to differentiate lists of constituents for the same lab and method. This should typically be 'A' for Automatic.
METHOD_ID	lab/user	X	L	C	10		Test Method identification.
EXTRACTION	lab		L	C	6		Extraction method code. The import routine requires definition of entries in the GIS/Key database.
LAB_ID	user		L	C	5		Lab ID code.
SEQ_NUM	GIS	internal	R	C	3		Used to order the compounds in a LabMethod (SEQ_NUM=1 for the first compound on a LabMethod). When editing results after data import, the sequence number controls the order in which the results are viewed. LabBuild assigns a SEQ_NUM based on the SEQ_NUM of the chemicals defined in the LabMethod. If a LabMethod definition is not found in the project, the SEQ_NUM assignment is based on the order within the LabMethod in LABDATA.dbf.
SPLIT_ID	user	X *	L	C	10		SPLIT_ID records the LabMethod of the first split sample of the primary sample. This field is left blank unless the record is for a primary result and a split sample was analyzed. Required for primary results to associate with split results (otherwise splits will be orphaned).
SPLIT_ID2	user	X *	L	C	10		SPLIT_ID2 records the LabMethod of the second split sample of the primary sample. This field is left blank unless the record is for a primary result and a second split sample was analyzed. The second split result, entered as a separate record, will be orphaned unless this field is filled in for the primary result record.
LSAMP_ID	lab		L	C	15		Lab sample ID.
LSAMP_ID2	lab		L	C	15		Lab sample ID of duplicates, entered by the lab for known-control sample duplicates and lab spike duplicates.
LAB_CAS_ID	lab	X *	R	C	11		CAS Registry number assigned by the Lab for the constituent. Either a LAB_CAS_ID or a LAB_CHEM must be included with each record. The import routine requires any LAB_CAS_ID to match a CAS_NUM in GIS\Key COMPOUND.DBF.
CAS_NUM	GIS	internal	R	C	11		CAS number from the GIS\Key compound.dbf. This is internally assigned based on a match with LAB_CHEM or LAB_CAS_ID, with preference given to LAB_CAS_ID.
LAB_CHEM	lab	X *	L	C	40		Constituent name from lab. Either a LAB_CAS_ID or a LAB_CHEM must be included with each result. If LAB_CHEM is used, then it must match a GIS\Key COMPOUND.DBF alias.
NAME	GIS	internal	L	C	40		Constituent name assigned by comparing LAB_CHEM to COMPOUND.DBF. If LAB_CAS_ID is used without a matching LAB_CHEM, NAME is assigned based on alias 0 in GIS\Key Database.
ALIAS_NUM	GIS	internal	R	C	2		Alias numbers are internally assigned by comparing LAB_CAS_ID and LAB_CHEM to COMPOUND.DBF.
CONC	lab	X *	L	C	11		Utilized to store constituent concentrations for primary results, duplicates, splits & blanks and concentrations added to spikes and control samples. The field is left blank for surrogates. Warning code generated when CONC and LIMIT1 are both left blank for primary results, duplicates, splits and blanks. Stored as a character string to preserve significant figures. May be expressed in scientific notation (e.g. 1.3E03). All entries must be numeric with the exception of "E" (i.e. scientific notation), "+", or a "+/-". A "+" after concentration amount means greater than while a concentration followed by "+/-" and a number expresses an uncertainty factor.

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LIMIT1	lab	X *	L	C	10		Detection Limit 1 for a sample result. Stored as a character string to preserve the significant figures. May be expressed in scientific notation (e.g. 1.3E03). Required for primary results, duplicates, splits & blanks if CONC is blank. Left blank for control samples, matrix spikes and surrogates. All entries must be numeric with the exception of "E" (i.e. scientific notation) or "?". A "?" means that the detection limit is unknown. The entered detection limit should reflect dilution. Generally, LIMIT1 refers to the method detection limit. However, GIS\Key places no restrictions on the use of this field.
DL_FLAG	lab	X *	L	C	2		Place a {<} in this field if the result is non-detect, otherwise leave it blank. Required for primary results, duplicates, splits and blanks. The field is left blank for control samples, matrix spikes and surrogates. For IRPIMS files, DL_FLAG corresponds to the PARVQ field. DL_FLAG corresponds to RF_FLAG on the data entry screen.
UNITS	lab	X *	L	C	5		Reported units of concentration. GIS\Key can automatically convert concentrations in mg/l, mg/kg, ug/l, ug/kg, ppm, ppb, and %. Other units are allowed but will generate warning codes.
LIMIT2	lab		L	C	10		Practical quantitation limit for a blank or primary sample result. Format limitations for LIMIT2 are the same as described for LIMIT1. The entered quantitation limit should reflect dilution. GIS\Key places no restrictions on the use of this field.
INSTRUMENT	lab		L	C	20		Identifying number or name of laboratory equipment used to perform the analysis. Used primarily for Air Force reporting.
CALIBRATE	lab		L	C	20		Calibration reference number for the test. Used primarily for Air Force reporting.
SPIKE_DUP	GIS	internal		L	1		Flag indicating a spike control sample duplicate record. Information is combined in the same record as the spike or control sample.
TEST_ORIG	Lab/ user		L	C	3		Used for spikes to identify the res_type of the sample that was spiked.
S_CONC	Lab		L	C	9		Spike concentration for surrogates if reported. <b>For version 3.x the CONC field is copied into S_CONC for matrix spikes and control samples if the field is empty.</b>
RECOVER	lab	X *		N	3		Constituent Recovery in %. Required for spike, surrogate, and control sample results. The field is left blank for primary samples, duplicates, splits and blanks. Supplied by the Lab for surrogates, lab matrix spikes and known control samples.
D_RECOVER	lab	X *		N	3		Duplicate constituent recovery in %. Required for spike and control sample duplicates results. The field is left blank for primary sample, duplicates, splits, blanks, and surrogates. Supplied by the Lab for lab matrix spikes and known control samples.
T_CONC	Lab/user		L	C	11		Target concentration for spikes (i.e. calculated total of concentration in sample plus concentration spiked).
R_CONC	lab		L	C	11		Measured concentration in control samples and spiked samples. Supplied by the Lab for lab matrix spikes, field matrix spikes, blind control samples and known control samples.
D_CONC	lab		L	C	11		Measured concentration in duplicate control samples and spiked samples. Supplied by the Lab for lab matrix spikes, field matrix spikes, blind control samples, and known control samples.
RPD	lab			N	3		Relative Percent Difference (RPD). Supplied by the Lab for matrix spike and control samples that are run in duplicate. When RES_CODES DL#/DF#/DB#/DK# are used, the RPD is entered with these records.
B_RECOVER	lab			N	3		Lower percent recovery goal for surrogates, spikes, and control samples and spikes reported by the Laboratory.
E_RECOVER	lab			N	3		Upper percent recovery goal for surrogates, spikes, and control samples reported by the Laboratory.
MAX_RPD	lab			N	3		Maximum relative percent difference goal for control samples and spikes reported by the Laboratory.
PF_CODE	lab/user	X		C	1		Preparation Fraction Code. Required and must match a code in GIS\Key database. Standard codes include "T" (total), "D" (dissolved), "A" (Acid Rain Extraction), "C" (TCLP Extraction), "E" (EPTOX Extraction), "S" (California Wet Extraction), "W" (Deionized Water Extraction).

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CR_C	lab			C	1		CLP data concentration "C" column. The import routine requires entry to match a code defined in GIS\Key Database.
CR_M	lab		L	C	2		CLP data method "M" column. The import routine requires entry to match a code defined in GIS\Key Database.
CR_Q	lab		L	C	3		CLP data qualifier "Q" column. The import routine requires entry(s) to match 1 character code(s) defined in the GIS\Key Database.
ER_Q	user		L	C	3		Expert review data qualifier. The import routine requires entry(s) to match 1 character code(s) defined in the GIS\Key Database.
ER_R1	user		L	C	2		Expert review reason 1 "R1" code. The import routine requires entry to match a defined code in GIS\Key Database.
ER_R2	user		L	C	2		Expert review reason 2 "R2" code. The import routine requires entry to match a defined code in GIS\Key Database.
ER_R3	user		L	C	2		Expert review reason 3 "R3" code. The suggested use of this field is to track updates. The import routine requires entry to match a defined code in GIS\Key Database.
FILTERED	user	X		C	1		Was sample field filtered, <Y>es, <N>o, or <U>nknown.
PRESERVED	user			C	1		Sample preservation code, "H" = HCl, "N" = HNO3, "S" = H2SO4, "U" = unknown, "" = none, and "O" = other sample preservation code.
ICED	user	X		C	1		Field preservation Code, "Y" = stored/shipped on ice, "N" = stored/shipped at ambient temperature, "U" = Unknown.
CUSTODY	lab	X*	L	C	25		Chain of custody ID. Used to associate travel blanks with primary samples. Required for travel blanks.
DILUTION	lab	X*		N	7	2	Dilution factor for sample run ranging from 0.01 to 9999. A required field for all primary results, duplicates, splits and blank results. The field is left blank for all other results.
PROG_TYPE	GIS/user	X		C	1		Program codes are required for all results. The import routine requires codes to be defined in GIS\Key Database. Program codes must be identical for all chemical results for a particular sample. <b>Same as PT_Code.</b>
RECEIVED	lab			D	8		Date sample was received by the Lab (MM/DD/YY format).
REC_TIME	lab			C	5		Time sample was received by the Lab (HH:MM 24hr format).
PREPARED	lab			D	8		Date sample was prepared or extracted by the Lab (MM/DD/YY format).
PREP_TIME	lab			C	5		Time sample was prepared or extracted by the Lab (HH:MM 24hr format).
TESTED	lab			D	8		Date sample was analyzed by the Lab (MM/DD/YY format for American Version).
TEST_TIME	lab			C	5		Time sample was analyzed by the Lab (HH:MM 24hr format).
REPORTED	lab			D	8		Date sample was reported by the Lab (MM/DD/YY format for American Version).
APPROVED	lab			D	8		Date sample was result approved by the Lab (MM/DD/YY format for American Version).
LOT_NUMBER	lab/ user		L	C	4		IRPIMS lot control number (LOTCTLNUM) used to associate primary samples with QC.
SA_CODE	lab/ user		L	C	3		IRPIMS sample type code (SA_CODE) used to identify the type of sample collected.
MATRIX	lab/ user		L	C	2		IRPIMS sampling matrix code.
BASIS	lab/ user			C	1		Used to indicate whether results are reported on a (W)et or (D)ry basis. Required for soil results.
MOISTURE	lab/ user			N	4	1	Percent moisture of a soil sample.
EXC_CODE	GIS	internal	L	C	30		Exception codes are generated by the checking routine to alert the user to errors with the record. <b>Same as X_Error.</b>

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Field Name 10 Character	Respon- sibility	Required	Justify	Type	Len	Dec	Notes  (Default parameters)
WARN_CODE	GIS	internal	L	C	20		Warning codes are generated by the import routine to alert the user to possible problems with the record. Warning codes do not prevent user from appending LABDATA.DBF file to the project database. <b>Same as X_Warn.</b>
BUILD_FLAG	GIS	internal		C	1		Internal flag used during the LabBuild process.
NOTE	lab/ user		L	C	20		Lab/user notes for samples (i.e. placed in CSAMPLE.DBF). May be expanded to 50 characters.
TEST_NOTE	lab/user		L	C	20		Lab/user notes for tests (i.e. placed in CTEST.DBF). May be expanded to 50 characters.
UNCERT_1	Lab		L	C	10		Radiological uncertainty.
UNCERT_2	Lab		L	C	10		Radiological uncertainty.
RAD_LIMIT3	Lab		L	C	10		Third reporting limit associated with radiological results.
LR_Q	Lab		L	C	3		Laboratory qualifier field for radiological results.
RAD_FLAG	Lab/user	X*		L	1		Logical field set "T" (true) for radiological results. Assumed false if blank. Required for radiological data.
DUP_RPD	Lab			N	3		Relative percent difference goal for primary duplicates.
SPLIT_RPD	Lab			N	3		Relative percent difference goal for primary splits.
PRIME_LAB	User			C	5		Primary Lab_id of primary sample for a Split.

**ALLOWABLE VALUES FOR RES\_CODE FIELD**

RES CODES	DESCRIPTION	RES CODES	DESCRIPTION
PP0<1-9>	Primary Results	CB[1-9]<1-9>	Blind Control Sample
PD[1-9]<1-9>	Duplicate	CK[1-9]<1-9>	Known Control Sample
PS[1-2]<1-9>	Split	SL[1-9]<1-9>	Lab Spike
BF[1-9]<1-9>	Field Blanks	SF[1-9]<1-9>	Field Spike
BL[1-9]<1-9>	Lab Blanks	DL[1-9]<1-9>	Duplicate Lab Spike
BM[1-9]<1-9>	Method Blanks	DF[1-9]<1-9>	Duplicate Field Spike
BR[1-9]<1-9>	Rinsate Blanks	DB[1-9]<1-9>	Duplicate Blind Control Sample
BT[1-9]<1-9>	Travel Blanks	DK[1-9]<1-9>	Duplicate Known Control Sample
Numbers in [] denote test sequence numbers			
Numbers in <> denote result set occurrence			

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## PRIMARY KEYS AND NOTES

### DUPLICATE RECORD KEY FOR PRIMARIES, DUPLICATES AND SPLITS (RES\_CODE = PP0#, PD##, PS##):

SAMP\_TYPE + SITE\_ID + SAMP\_DATE + SAMP\_TIME + SAMP\_DEPTH + RES\_CODE + LAB\_ID + METHOD\_ID + PF\_CODE + CAS\_NUM

### DUPLICATE RECORD KEY FOR BLANKS (RES\_CODE = BR##, BM##, BT##, BF##):

SAMP\_TYPE + CASE\_ID + BLANK\_ID + RES\_CODE + LAB\_ID + METHOD\_ID + PF\_CODE + CAS\_NUM

### DUPLICATE RECORD KEY FOR SPIKES AND CONTROL SAMPLES (RES\_CODE = SF##, SL##, CB##, CK##):

SAMP\_TYPE + CASE\_ID + QAQC\_ID + RES\_CODE + LAB\_ID + METHOD\_ID + PF\_CODE + CAS\_NUM

### ASSIGNING RES\_CODE SEQUENCE NUMBERS [1-9]:

The test sequence number refers to a sample sequence used to differentiate test results that otherwise have the same primary key. For example, a test sequence number of 2 for a duplicate sample would mean that the result set is for the second of 2 duplicate samples originating from the same primary sample. A test sequence number of 2 for a method blank would mean that 2 method blanks were run for the same batch (QAQC\_ID). Note that matrix spikes and control samples and their duplicates should always have matching test sequence numbers.

### ASSIGNING RES\_CODE RESULT SET OCCURRENCES <1-9>:

The result set occurrence is used to differentiate multiple column or dilution runs of the same sample and test method that otherwise have the same primary key. Occurrence = 1 is the set of record and the set used for reporting and graphics.

### ASSIGNING RES\_ORIG CODES

RES\_ORIG codes are equal to the last three characters of RES\_CODES for all results except when multiple column/dilution runs are being reported and the result being reported is for the combined "best estimate" result. In this case, the RES\_ORIG code equals the last three characters of the RES\_CODE of the originating column/dilution run.

### ADDITIONAL GUIDANCE FOR FIELD/LAB MATRIX SPIKE DUPLICATES AND BLIND/KNOWN CONTROL SAMPLE DUPLICATES:

Field/lab matrix spike duplicate and blind/known control sample duplicate concentrations are always entered in the D\_CONC field, with recoveries in the D\_RECOVER field. Spike and control sample duplicates may be entered as individual records using RES\_CODES DL##, DF##, DB##, DK##, or can be combined with the record storing the original spike or control sample when using RES\_CODES SL##, SF##, CB##, CK##.