6 May 2025

MHS GENESIS Laboratory Results
for the
MHS Data Repository (MDR)
(Version 1.01.08)

Future Specification

Revision History

Version	Date	Originator	Para/Tbl/Fig	Description of Change
1.00.00	04/25/2019	S. Keane	Initial Document	Baseline
1.01.00	08/26/2020	S. Keane	Section IV, VI, VII	Update to match output dataset.
1.01.01	11/05/2020	S. Keane	Table 2	Update length of Name fields: FIRST_NAME_P, LAST_NAME_P, PRSNL_COMPL_FNAME, PRSNL_COMPL_LNAME, PRSNL_ORD_FNAME, PRSNL_ORD_LNAME, PRSNL_PERF_FNAME, PRSNL_PERF_LNAME
1.01.02	11/20/2020	S. Keane	Table 2	Remove first/last name fields. Replace with Full Name for Patient, Personnel Performed, Personnel Completing, and Personnel Non-Physician Ordering variables.
1.01.03	04/01/2021	S. Keane	Table 2	Obtain “Reason for Test” from MHS GENESIS Laboratory Orders.
1.01.04	02/17/2022	S. Keane	Section IV	Add Time Slicing, Frequency of processing, and Frequency of updates.
1.01.05	09/20/2023	S. Keane	Entire Document	Add Bulk Data Extract (BDE) Redshift 3.0 feed logic.
1.01.06	03/06/2025	S. Keane	Sections VI and IX	Hide T3 fields Add T5 fields Add Section IX Special Outputs section
1.01.07	04/29/2025	S. Keane	Section VI	Update T5 fields
1.01.08	05/06/2025	S. Keane	Section VII	Remove “Reason for Test”.

MHS GENESIS General Laboratory Results Table

I. BACKGROUND

This specification describes the process required to create the Military Health System (MHS) Data Repository (MDR) GENESIS General Laboratory Results tables based on data received from Cerner PowerInsight Enterprise Data Warehouse (PI-EDW) feeds to the MDR and the MIP Redshift 3.0 feeds.

II. SOURCES

The source data files used to create the MHS GENESIS General Laboratory Results tables are extracted from the MHS GENESIS PI-EDW and MIP Redshift 3.0. The transfer of the raw source extracts is handled by the Solution Delivery Division (SDD) for loading into the MDR for further processing according to routine MDR operations. The format of the raw MHS GENESIS feeds to the MDR is described in the Department of Defense Healthcare Management System Modernization (DHMSM®) Program DRAFT Interface Control Document (ICD) for Bulk Data Extract (BDE).

III. TRANSMISSION (FILES AND FREQUENCY)

MHS GENESIS BDE PI-EDW feeds are provided weekly and MIP Redshift 3.0 feeds are updated daily.

IV. ORGANIZATION AND BATCHING

Source Data: The first step in MDR processing is to batch records received from MHS GENESIS. Raw data batches are stored in /mdr/raw/genesis according to routine MDR operating procedures.

Output Products: The processor outputs separate SAS data sets for Fiscal Year (FY) of data. The processor performs merges and field derivations and must incorporate updates to records across raw data extracts. The output data set fyxx.sas7bdat will be stored in /mdr/pub/genesis/laboratory/results/lab/fyxx.sas7bdat.

Frequency of processing: Data are harvested weekly. Raw data batches are harvested, processed, and appended/updated to the master file. If data are received from a fiscal year not being processed that month, they will be held to batch with all other data received prior to that fiscal year's next update batch.

Frequency of updates:
Current FY: Weekly.
Prior FY: Weekly for one quarter (October, November, and December) then semiannually (April, October).
All years prior to prior FY: Annually (October) or on an as needed basis when data corrections or updates are required.

Archiving (APUB): Use routine archiving rules and procedures of the MDR.

Receiving Filters: There are no receiving filters.

MDR GENESIS General Laboratory Results tables will contain result-records for orders in the MDR GENESIS General Laboratory table. Select result records where Activity Type equals “General Laboratory” and to avoid selecting results for omitted orders, match order records on primary key. All records are provided with the initial batch of data. Thereafter, new and changed records are sent each week.

V. UPDATE PROCESSES

New raw feeds contain either insert or update records. These records shall be used to update the master MDR GENESIS General Laboratory Results datasets. The primary key for the final dataset is EVENT_SK. The processor shall delete duplicates before updating the table. Duplicate records, defined as those with the same primary key. When choosing among duplicate records, the processor shall select the record with the most recent value for the variable: UPDT_DT_TM (update date/time (UPDT_DT_TM) for multiple of records with the same primary key.

VI. FILE MERGES

Table 1a and Table 1b describe the various datasets that are necessary to append many of the fields in the MHS GENESIS General Laboratory Results file.

Table 1a: File Merges from PI-EDW Source Tables

Merge	Key Matching
MHS GENESIS Laboratory Orders	Select records where ACTIVITY_TYPE = 'General Laboratory'. Match on ORDER_SK.
MHS GENESIS Clinical Event	Match on ORDER_SK. Select records where EVENT_CLASS_REF in ('233', '236') and HEALTH_SYSTEM_SOURCE_ID = 18635. Use EVENT_SK for additional matching.
MHS GENESIS Clinical Event Result Associations	Match on EVENT_SK where HEALTH_SYSTEM_SOURCE_ID = 18635.
MHS GENESIS Clinical Event Specimen	Match on EVENT_SK where HEALTH_SYSTEM_SOURCE_ID = 18635.
MHS GENESIS Clinical Event Event Note	Match on EVENT_SK where HEALTH_SYSTEM_SOURCE_ID = 18635.
MHS GENESIS Order Detail	Match on order_sk where HEALTH_SYSTEM_SOURCE_ID = 18635.

Table 1b: File Merges from MIP Redshift 3.0 Source Views

Source Table Name	**View Name**	**Date Matching**	**Key Matching**
MHS GENESIS Orders	genesis_vw.orders		encntr_id, order_id
MHS GENESIS Clinical Event	genesis_vw.clinical_event	valid_until_dt_tm > sysdate	encntr_id, order_id, event_id
MHS GENESIS Clinical Event Specimen	genesis_vw.ce_specimen_coll		event_id
MHS GENESIS Clinical Event Event Note	genesis_vw.ce_event_note		event_id
MHS GENESIS Clinical Event Result Associations	genesis_vw.ref_cd_map_header		ref_cd_map_header_id
MHS GENESIS Clinical Event Result Associations	genesis_vw.ref_cd_map_detail		ref_cd_map_header_id
MHS GENESIS Nomenclature	genesis_vw.nomenclature_id		nomenclature_id
MHS GENESIS Code Value	genesis_vw.code_value		code_value

VII. FILE LAYOUT

Table 2 describes the file layout and derivation rules for the MHS GENESIS General Laboratory Results file. Unless specified, business rules apply to both source tables. Listed by Source table then by SAS Name.

Variable Name	**SAS Name**	**Format**	**PI-EDW 2.4 Field**	**MIP Redshift 3.0 Field**	**Business Rule**
MHS GENESIS Clinical Event					
Clinical Event Key	CLINICAL_EVENT_KEY	N(8)		n/a	2.4 No Transformation. 3.0 NULL.
Critical High	CRITICAL_HIGH	$20.00		critical_high	None.
Critical Low	CRITICAL_LOW	$20.00		critical_low	None.
Result Type	EVENT_CLASS	$27.00	event_class_ref	event_class_cd	put(event_class_ref, $event_class.) as EVENT_CLASS (code set 53).
Result Name	EVENT_CODE	$60.00	event_code_ref	event_cd	put(event_code_ref, $ev_code.) as EVENT_CODE label="Lab Result Name" (code set 72).
Normalcy Indicator	EVENT_NORMACY	$14.00	event_normacy_ref	normalcy_cd	put(EVENT_NORMACY_REF, $ev_norm.) as EVENT_NORMACY (code set 52).
Lab Test ID	EVENT_ORDBL	$40.00		event_cd	None.
Event SK	EVENT_SK	$100.00		event_id	None.
Normal High	NORMAL_HIGH	$20.00		normal_high	None.
Normal Low	NORMAL_LOW	$20.00		normal_low	None.
Performed Date and Time	PERFORMED_DT_TM	E8601DT19.		performed_dt_tm	Format e8601dt.
Performed Date and Time Local	PERFORMED_DT_TM_local	E8601DT.		performed_dt_tm, performed_tz	Convert to Local Time. Format e8601dt.
Personnel Performed ID	PERFORMED_PRSNL	$100.00		performed_prsnl_id	None.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Result Normalcy Flag	RESULT_NORMALCY_FLG	N(8)		normalcy_cd	2.4 No transformation. 3.0 when normalcy_cd in (201, 203, 205, 207, 209, 211) then 2; when 214 then 1; when 217 then 0; else -1.
Result Value	RESULT_VALUE	$255.00		result_val	None.
Result Units	RESULTS_UNITS	$60.00	result_units_ref	result_unit_cd	put(RESULT_UNITS_REF, $unit_ref.) as RESULTS_UNITS (code set 54).
Verified Date and Time	VERIFIED_DT_TM	E8601DT19.	verified_dt_tm	verified_dt_tm	Format e8601dt.
Verified Date and Time Local	VERIFIED_DT_TM_local	E8601DT.	verified_dt_tm	verified_dt_tm, verified_tz	Convert to Local Time. Format e8601dt.
Personnel Verified ID	VERIFIED_PRSNL	$100.00	verified_prsnl	verified_prsnl_id	None.
MHS GENESIS Clinical Event Result Associations					
Lab Observation Name	LAB_OBSERVATION_NAME	$60.00	display	short_string	2.4 Obtain display AS LAB_OBSERVATION_NAME match on REF_CODE_NOMEN = NOMENCLATURE_SK (convert to numeric) from refe_cnref where health_system_source_id = 18635 and active_ind =1 and vocabulary_ref in ('680001', '1220'). 3.0 Obtain short_string as LAB_OBSERVATION_NAME match on ref_cd_map_detail = nomenclature_id where concept_cki ILIKE '%LOINC%' OR source_vocabulary_cd = 680001.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
LOINC Code	LOINC_CODE	$60.00	value	source_identifier	2.4 Obtain value AS LOINC_CODE match on REF_CODE_NOMEN = NOMENCLATURE_SK (convert to numeric) from refe_cnref where health_system_source_id = 18635 and active_ind =1 and vocabulary_ref in ('680001', '1220'). 3.0 Obtain source_identifier as LOINC_CODE match on ref_cd_map_detail = nomenclature_id where concept_cki ILIKE '%LOINC%' OR source_vocabulary_cd = 680001.
LOINC Description	LOINC_DESCRIPTION	$255.00	description	source_string	2.4 Obtain description as LOINC_DESCRIPTION match on REF_CODE_NOMEN = NOMENCLATURE_SK (convert to numeric) from refe_cnref where health_system_source_id = 18635 and active_ind =1 and vocabulary_ref in ('680001', '1220'). 3.0 Obtain source_string as LOINC_DESCRIPTION match on ref_cd_map_detail = nomenclature_id where concept_cki ILIKE '%LOINC%' OR source_vocabulary_cd = 680001.
MHS GENESIS Clinical Event Specimen					
Specimen	SPECIMEN	$38.00	source_type_cd	source_type_cd	put(SOURCE_TYPE_CD, $SPECT.) as SPECIMEN (code set 2052).
MHS GENSIS Clinical Event Note					
Note Entry Method	NOTE_ENTRY_METHOD	$35	entry_method_ref	entry_method_cd	put(ENTRY_METHOD_REF , $entry_method_ref.) as NOTE_ENTRY_METHOD (code set 13).
Note Text 1	NOTE_TEXT_1	$4,000		long_text_id	2.4 No transformation. 3.0 Apply code set 19.
Note Type	NOTE_TYPE	$36	note_type_ref	note_type_cd	put(NOTE_TYPE_REF, $note_type_ref.) as NOTE_TYPE (code set 14).
Personnel					
Personnel Performed EDIPN	PRSNL_PERF_EDIPN	$10.00	prsnl_edipn		2.4 Obtain PRSNL_EDIPN from Personnel; Match on PERFORMED_PRSNL = PRSNL_SK. 3.0 Use performed_prsnl_id as performed_prsnl.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Personnel Performed Test Indicator	PRSNL_PERF_FLAG	$1.00	test_record_ind		2.4 Obtain TEST_RECORD_IND from Personnel; Match on PERFORMED_PRSNL = PRSNL_SK. 3.0 Use performed_prsnl_id as performed_prsnl.
Personnel Performed HIPAA	PRSNL_PERF_HIPAA	$10.00	hipaa1		2.4 Obtain HIPAA1 from Personnel; Match on PERFORMED_PRSNL = PRSNL_SK. 3.0 Use performed_prsnl_id as performed_prsnl.
Personnel Performed Name	PRSNL_PERF_NAME	$61.00	full_name		2.4 Obtain FULL_NAME from Personnel; Match on PERFORMED_PRSNL = PRSNL_SK. 3.0 Use performed_prsnl_id as performed_prsnl.
Personnel Performed MD Flag	PRSNL_PERF_MD_FLAG	N(8)	physician_ind		2.4 Obtain PHYSICIAN_IND from Personnel; Match on PERFORMED_PRSNL = PRSNL_SK. 3.0 Use performed_prsnl_id as performed_prsnl.
Personnel Performed NPI	PRSNL_PERF_NPI	$100.00	npi		2.4 Obtain NPI from Personnel; Match on PERFORMED_PRSNL = PRSNL_SK. 3.0 Use performed_prsnl_id as performed_prsnl.
MHS GENESIS Laboratory Orders					
Accession Number	ACCESSION	$100.00			None.
Alternate Care Value (ACV)	ACV_D	$1.00			None.
ACV Group	ACVGROUP	$15.00			None.
Age Group Common	AGEGRP	$1.00			None.
Beneficiary T17 Region	BEN_T17_REG	$2.00			None.
Beneficiary T3 Region	BEN_T3_REG	$2.00			Hide. Not populated as of Jan 2025.
Beneficiary Category	BENCAT_D	$3.00			None.
Ben Cat Common	COMBEN_D	$1.00			None.
Date Complete	DATE_COMPLETE	$8.00			None.
Person ID	EDIPN	$10.00			None.
Eligibility Group	ELG_GRP	$1.00			None.
Encounter PI-EDW Key	ENCOUNTER_KEY	N(8)		n/a	2.4 No Transformation. 3.0 NULL.
Encounter NK	ENCOUNTER_NK	$100.00		n/a	2.4 No Transformation. 3.0 NULL.
Encounter Key (Secondary)	ENCOUNTER_SK	$100.00		n/a	2.4 No Transformation. 3.0 NULL.
Encounter Type	ENCOUNTER_TYPE	$22.00			None.
Enrollment Group	ENR_GRP	$1.00			None.
Patient Ethnicity	ETHNIC	$1.00			None.

Variable Name	**SAS Name**	**Format**	**PI-EDW 2.4 Field**	**MIP Redshift 3.0 Field**	**Business Rule**
Lab Test Name	EVENT_CATALOG	$60.00			None.
Financial Information Number (FIN)	FIN_E	$40.00			None.
Fiscal Month	FM	$2.00			None.
Fiscal Year	FY	$4.00			None.
Genesis Go Live Date	gen_begin_dt	MMDDYY			None.
Patient Gender	GENDER_D	$1.00			None.
HCDP - Enrolled	HCDP	$3.00			None.
HCDP - Assigned	HCDP_ASGN	$3.00			None.
Inpatient Indicator	INPT	$1.00			None.
Patient IPI	IPI	$10.00			None.
Patient Name	NAME	$61.00			None.
Patient Marital Status	MARITAL	$1.00			None.
Medicare Eligibility	MEDICARE_FLAG	$40.00			None.
MEPRS 1-Level Code	MEPR1	$1.00			None.
MEPRS 2-Level Code	MEPR2	$2.00			None.
MEPRS 3-Level Code	MEPR3	$3.00			None.
MEPRS4 Code, Ordering	MEPRS_CD	$4.00			None.
MHS Genesis Flag	MHS_GENESIS_FLAG	N(8)			None.
Medical Record Number	MRN	$40.00			None.
MTF	MTF	$4.00			None.
Enrollment MTF	MTF_ENR	$4.00			None.
Enrollment MTF Branch of Service	MTF_ENR_SVC	$1.00			None.
Enrollment MTF T17 Region	MTF_ENR_T17_REG	$2.00			None.
Enrollment MTF T3 Region	MTF_ENR_T3_REG	$2.00			Hide. Not populated as of Jan 2025.
Tmt MTF Parent of Record	MTF_PARENT_REC	$4.00			None.
Tmt MTF Military Service	MTF_SVC	$1.00			None.
Tmt MTF T17 Region	MTF_T17_REG	$2.00			None.
Tmt MTF T3 Region	MTF_T3_REG	$2.00			Hide. Not populated as of Jan 2025.
Date Time Order Local	ORDER_DT_TM_LOCAL	DATETIME			None.
Orders Secondary Key	ORDER_SK	$100.00			None.
MHS Genesis Test Ordered Description	ORDERABLE_DISP	$100.00			None.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Parent MTF Name	ORGANIZATION_NAME	$40.00			None.
Person Association Reason Code	PARC	$2.00			None.
Parent Event SK	PARENT_EVENT_SK	$100.00			None.
Patient Age	PATAGE	N(8)			None.
PATCAT Code	PATCAT	$40.00			None.
Patient Date of Birth	PATDOB	YYMMDDN			None.
Primary Care Manager (PCM) ID	PCM_ID	$18.00			None.
Primary Care Manager (PCM) Type	PCM_TYPE	$1.00			None.
MHS Genesis Person ID	PERSON_SK	$100.00			None.
Patient Privilege Code	PRIVILEGE	$1.00			None.
Personnel Completing EDIPN	PRSNL_COMPL_EDIPN	$10.00			None.
Personnel Completing HIPAA Taxonomy	PRSNL_COMPL_HIPAA	$10.00			None.
Personnel Completing Name	PRSNL_COMPL_NAME	$61.00			None.
Personnel Completing MD Flag	PRSNL_COMPL_MD_FLAG	N(8)			None.
Personnel Completing NPI	PRSNL_COMPL_NPI	$100.00			None.
Personnel Non-Physician Ordering EDIPN	PRSNL_ORD_EDIPN	$10.00			None.
Personnel Non-Physician Ordering HIPAA Taxonomy	PRSNL_ORD_HIPAA	$10.00			None.
Personnel Non-Physician Ordering Name	PRSNL_ORD_NAME	$61.00			None.
Personnel Non-Physician Ordering MD Flag	PRSNL_ORD_MD_FLAG	N(8)			None.
Personnel Non-Physician Ordering NPI	PRSNL_ORD_NPI	$100.00			None.
Patient Race	RACE	$1.00			None.
~~Reason for Test~~	~~REASON_FOR_TEST~~	~~$250~~	-	-	~~None.~~
Patient Relationship to Sponsor	REL	$1.00			None.

Variable Name	SAS Name	Format	PI-EDW 2.4 Field	MIP Redshift 3.0 Field	Business Rule
Sponsor ID	SPONSSN	$9.00			None.
Sponsor Service	SPONSVC	$1.00			None.
Patient SSN	SSN	$9.00			None.
Sponsor Service, Aggregate	SVCAGG	$1.00			None.
TPR Eligibility Flag	TPR	$1.00			None.
MTF Display Name	UNIT_DISPLAY	$45.00			None.
MTF Name	UNIT_NAME	$100.00			None.
Beneficiary Zip Code	ZIP_D	$5.00			None.
Beneficiary T5 Region	BEN_T5_REG	$2.00			T5_REG from DMIS ID Index OR OMNI-Cad based on matching FY and appropriated field. Populated FY23+.
Enrollment T5 Region	MTF_ENR_T5_REG	$2.00			T5_REG from DMIS ID Index, based FY and ENRDMIS Populated FY23+.
Treatment DMIS ID T5 Region	MTF_T5_REG	$2.00			T5_REG from DMIS ID Index, based FY and TXDMIS Populate FY23+.

VIII. EXCLUSIONS

Here are the conditions required to exclude and/or remove records from the MHS GENESIS General Laboratory Results file. If any of the following conditions are met, either delete the record or output to an error file.

If the primary key is missing or zero.

IX. SPECIAL OUTPUTS

This file serves as the input to the MIP Core MHS GENESIS Laboratory Results table. In accordance with Technical Data Standards, the data should be made available to users with the same file names, field names and formats as the source data, with underscores replacing spaces in the names, if desired. The MIP core MHS GENESIS Laboratory Results table should be updated at the same cadency of the M2 file and row counts should be validated against the MDR Export transmittals.