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Citadel Health Pty Ltd

Evolution vLab™ Identifiers & Subroutines Guide

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Licensed features: Some **Evolution vLab™** identifiers and subroutines are subject to license and therefore may not be available to all clients. Clients are encouraged to contact Citadel Health if they require additional identifiers or subroutines to be enabled for use.

1. Screen Mask Identifiers

<table>
<tr><th>Identifier</th><th>Description</th></tr>
<tr><td>ACCOUNT</td><td>Billing account</td></tr>
<tr><td>ADM</td><td>Admission Date as entered in billing details</td></tr>
<tr><td>ADMITID</td><td>Admission Identifier as stored in Evolution vLab™</td></tr>
<tr><td>AGE</td><td>Patient’s age, output as a string according to the rules below:
<table>
<tr><th>Age</th><th>Output format</th></tr>
<tr><td>< 50 days</td><td><i>n</i> days</td></tr>
<tr><td>50 days to 6 months</td><td><i>n</i> weeks</td></tr>
<tr><td>6 to 24 months</td><td><i>n</i> months</td></tr>
<tr><td>> 24 months</td><td><i>n</i> years</td></tr>
</table>
AGE is calculated from the patient’s date of birth to the relevant date on the lab number, in the following order of precedence:
1. Collection Date
2. Received Date
3. Requested Date
4. Date lab number was created</td></tr>
<tr><td>BAD_DEBTOR</td><td>Bad Debtor flag</td></tr>
<tr><td>CC_NATA_ACCRED</td><td>Outputs the indication if a Collection Centre is “NATA” accredited as configured for the respective Collection Centre according to the configuration for the Collection Centre.</td></tr>
<tr><td>CLAIMID</td><td>Claim ID</td></tr>
<tr><td>CLINSHORT</td><td>The first 70 characters of the clinical notes</td></tr>
<tr><td>CLINICAL_UNIT</td><td>Patient’s Clinical Unit (Description)</td></tr>
<tr><td>CLINNOTE</td><td>Patient clinical notes</td></tr>
<tr><td>COLLWARD</td><td>Ward of Collection Description</td></tr>
<tr><td>COLLWARD_MNEM</td><td>Ward of Collection Mnemonic</td></tr>
<tr><td>CONFIDENTIAL</td><td>Confidential status as entered at specimen reception</td></tr>
</table>

Identifier	Description
CONS_MOBILE	The mobile number configured for the Consultant against the lab record (`CONSULTANT`); derived from the 'Mobile' field in the Provider configuration.
CONS_PHONE	Consultants Phone number
CONS_PROVIDER_USED	Outputs 'yes' when the episode was billed against the Provider Number for the Consultant on the lab number. Outputs 'no' otherwise.
CONSULTANT	Consultant as entered at specimen reception
CRDATE	Laboratory number creation date, format dd-mmm-yy
CRTIME	Laboratory number creation time, format hh:mm
DIAGNOSIS	Patient's diagnosis code
DNA_PRIORITY	DNA Priority Identifier
DOB	Patient's Date of Birth, format dd-mmm-yyyy
DR_MOBILE	The mobile number configured for the Requesting Doctor against the lab record (`DOCTOR`); derived from the 'Mobile' field in the Provider configuration.
DR_PHONE	Doctor's Phone number
EXTID	External Identification number
FASTING	Fasting status as entered at specimen reception ("yes" or "no"); returns "?" when the fasting status has not been specified.
FINCAT	Patient's Financial Category (Description)
GENETICSEX	Genetic sex of patient as entered at specimen reception
GESTATION	Gestation period as entered at specimen reception
GNAMES	Patient given name only
LL_LABNO	Returns a comma-separated list of the unique tube identifiers for the lab number, i.e. Container IDs and/or **Evolution vLab**™ Unique IDs.
LOCNUM	Requests Location Number/s
LOCNUM_F	Requests Location Number/s with full year YYYY
MEDDATE	Medicare expiry

Identifier	Description
MEDICARE	Medicare number **Note:** For **Evolution vLab**™, the Medicare No field is available for Search (i.e. "Valid For Search Pane" status set to Yes).
MEDPOS	Medicare position
NAME	Patient's full name
NCSR_ID	National Cancer Screening Register (NCSR) Identification
NEHTA_IHI	Individual Healthcare Identifier (IHI)
OPERATION	Medical procedure description
PENSION	Pension number
REQUESTOR_TYPE	Requestor type of the requesting doctor on the current lab episode
SAMPLEP	Sample Period
SAMPLEV	Sample Volume
SEX	Patient's Sex
SPECPRIMSITE	Primary Specimen Site Description
SPECSITE	Specimen Site Description
SPECTYPE	Specimen Type Description
SPECTYPESITE	The Specimen Type (SPECTYPE), Primary Specimen Site (SPECPRIMSITE) and Specimen Site (SPECSITE) Descriptions output as one string, separated by spaces.
SURNAME	Patient's surname only
TM_LAST_ABSC	Last antibody screen
URNO	Patient's UR number
URPREFIX	Patient's UR Prefix (Description)
USER1 **USER2** **USER3** **USER4**	Free text fields (maximum 6 characters each). May be used to capture and display data entered at Specimen Registration.
VUSER	User who performed the final validation

Identifier	Description
VUSERFULL	Full name of user who performed the final validation
WARD	Patient’s ward full description
WARD_MNEM	Patient’s ward mnemonic

2. Transfusion Medicine Screen Mask Identifiers

Identifier	Description
AB_COUNT	Antibody Count as recorded in the lab number/episode
LABTM_SPEC_REQMT	Special requirements, entered at specimen registration
MSBOS	MSBOS for the entered procedure
OBSTETRIC_HIST	Recent pregnancy history from the patient’s UR record (string)
TM_LAST_ABSC	Last Antibody screen (number of days)
TM_PREV_TRANSF	Previous Transfusion history (yes/no)
TM_REC_TRANSF	Recent Transfusion Recent transfer. Relates to Past Transfusion Limit (days) field entry on the Transfusion Options Configuration screen.
TM_SAMPLEXP	Sample Expiry
TM_XMSTATUS	Status of crossmatch, indicates the number of cellular units available to clients
TM_XPLSTAT	Indicates the number of plasma units available to clients
TM_XPTSTAT	Indicates the number of platelets available to clients
TM_XPBSTAT	Indicates the number of batches available to clients
TMBATCH1 to TMBATCH12	Batch number
TMBPROD1 to TMBPROD12	Batch product description
TMBQTY1 to TMBQTY12	Batch product quantity
TMUGP1 to TMUGP70	Unit Group

Identifier	Description
TMUGP1_MNEM to TMUGP70 MNEM	Unit Group Mnemonic
TMULPRD1 to TMULPRD70	Unit product type description (including special requirements)
TMUNIT1 to TMUNIT70	Unit number
TMUPROD1 to TMUPROD70	Unit product type Mnemonic
TMPROD1	Transfusion Medicine Product ordered at Specimen Reception
TMPROD2	Transfusion Medicine Product ordered at Specimen Reception
TMPROD3	Transfusion Medicine Product ordered at Specimen Reception **Note:** Available only when Non Cellular products are enabled.
TMPROD4	Transfusion Medicine Product ordered at Specimen Reception **Note:** Available only when Non Cellular products are enabled.
TMQUANT1	Quantity required, entered at specimen registration
TMQUANT2	Quantity required, entered at specimen registration
TMQUANT3	Quantity required, entered at specimen registration
TMQUANT4	Quantity required, entered at specimen registration
TMU_VTIME[1-n]	Date the unit was crossmatched; format hh:mm dd-mmm-yy
TMU_VUSER1 to TMU_VUSER70	User who validated unit
TMUEXP1 to TMUEXP70	Unit expiry
TMUNIT1 to TMUNIT70	Unit number
TMUNIT1	Units for products, entered at specimen registration (displayed in 'SI' column)
TMUNIT2	Units for products, entered at specimen registration (displayed in 'SI' column)
TMUNIT3	Units for products, entered at specimen registration (displayed in 'SI' column)
TMUNIT4	Units for products, entered at specimen registration (displayed in 'SI' column)

Identifier	Description
TMUPPROD	Unit product Description
TMUSTATUS	Crossmatch status of the Unit
URTM_PHENOTYPES	Patient's phenotype from antibody register
URANTIBODIES	Antibody Count referenced by UR
URGROUP	Patient's UR blood group
URGROUP_MNEM	Patient's UR blood group mnemonic
URTM_SPEC_REQMT	Special requirements, entered into antibody register
URTM_TM_ALERT	Transfusion Medicine Alert Description
XMEXPBP	Batch Allocation Expiry – Calculated by System
XMEXPPL	Plasma Allocation Expiry – Calculated by System
XMEXPPT	Platelet Allocation Expiry – Calculated by System
XMPROD[1-n]	Product Description
XMPROD_MNEM1	Product required, entered at specimen registration (mnemonic)
XMPROD_MNEM2	Product required, entered at specimen registration (mnemonic)
XMQTY1	Quantity required, entered at specimen registration
XMQTY2	Quantity required, entered at specimen registration
XMQTY3	Quantity required, entered at specimen registration
XMQTY4	Quantity required, entered at specimen registration
XMREQD1	Required by time entered at specimen registration
XMREQD2	Required by time entered at specimen registration
XMREQD3	Required by time entered at specimen registration
XMREQD4	Required by time entered at specimen registration

3. Scientific Services Screen Mask Identifiers

Identifier	Description
DNA_PRIORITY	DNA Priority Identifier
SS_ANALYST_FLAG	Flag for whether the User is a State analyst
SS_BATCHREF	Client Batch Reference
SS_BOPNAME	Forensic Biology Operation Name
SS_CLIENT	Client
SS_CLIENT_ABN	Client ABN
SS_CLIENT_ADDR1	Client Address 1
SS_CLIENT_ADDR2	Client Address 2
SS_CLIENT_CNAME	Client Contact name
SS_CLIENT_EMAIL	Client Email Address
SS_CLIENT_FAX	Client Fax Number
SS_CLIENT_MNEM	Client Mnemonic
SS_CLIENT_PHONE	Client Telephone Number
SS_CLIENT_POSTCODE	Client Postcode
SS_CLIENT_PROJECT	Client Project
SS_CLIENT_QUOTE	Client Quote
SS_CLIENT_STATE	Client State
SS_CLIENT_SUBURB	Client Suburb
SS_COPNAME	Forensic Chemistry Operation Name
SS_COURT_DATE	Court Date
SS_CPRIOT	Court Priority
SS_CRICAT	Crime Category
SS_CRMCLS	Crime Class
SS_CSSTAT	Crime Status
SS_DESTROY	Forensic Destruction
SS_NATA_FLAG	Flag for whether the User is a NATA Signatory
SS_NO_ITEMS	Number of Items

Identifier	Description
SS_NSAMPLES	Number of samples in batch
SS_ODF	Offence Date From
SS_ODT	Offence Date To
SS_ORDERNO	Order Number
SS_PKG_DESC	Package Description
SS_PKG_RECDATETIME	Package Received Date and Time
SS_PKG_REQDATE	Package Request Date
SS_POLDAT	Police Due Date
SS_PROGRAM	Program
SS_PROJECT	Project
SS_REPORTING_FLAG	Flag for whether the User is a Reporting analyst
SS_SATCLIENT	Satellite Client Description
SS_SATCLIENT_MNEM	Satellite Client Mnemonic
SS_SUBMITAUTH	Submitting Authority
SS_TEAMS	Team
SS_USER_ACT1 **SS_USER_ACT2** **SS_USER_ACT3** **SS_USER_ACT4** **SS_USER_ACT5** **SS_USER_ACT6** **SS_USER_ACT7** **SS_USER_ACT8**	Legislations/Acts for User (1-8)
SS_USER_EMAIL	User’s Email address
SS_USER_FAX	User’s Fax number
SS_USER_FIRST	First Name of User
SS_USER_FUNCTION	User’s function e.g. Forensic Scientist

Identifier	Description
SS_USER_INST1 **SS_USER_INST2** **SS_USER_INST3** **SS_USER_INST4** **SS_USER_INST5**	User's Institutions (1-5) where qualifications were gained
SS_USER_MIDDLE	Middle Name of User
SS_USER_MEMB1 **SS_USER_MEMB2** **SS_USER_MEMB3** **SS_USER_MEMB4** **SS_USER_MEMB5**	User's Professional Memberships (1-5)
SS_USER_PHONE	User's Phone number
SS_USER_PREF	Preferred First name of User
SS_USER_QUAL1 **SS_USER_QUAL2** **SS_USER_QUAL3** **SS_USER_QUAL4** **SS_USER_QUAL5**	User's Qualification (1-5)
SS_USER_SURNAME	Surname of User
SS_USER_TITLE	Title of the User e.g. Miss, Mrs, Mr.
SS_VENDOR_ADDR	Vendor Address
SS_VENDOR_NAME	Vendor Name

4. Billing Screen and Print Mask Identifiers

Identifier	Description
CONS_PROVIDER_USED	Outputs 'yes' when the episode was billed against the Provider Number for the Consultant on the lab number. Outputs 'no' otherwise.
CONS_PROVIDER	Mnemonic of the Doctor used for Consolidation

CONS_PROVIDER_NUM	Provider number of the Doctor used for Consolidation
CONSULTANT_MNEM	Mnemonic of the Consultant stored on the lab number
CONSULTANT_PROV	Provider number of the Consultant stored on the lab number
CAT_USE_SPEC	Patient Category stored on the lab number value for “Use Specialist” field
T_CONS_PROV_USED	Outputs ‘yes’ when the Schedule Item was billed against the Provider Number for the Consultant on the lab number. Outputs ‘no’ otherwise. Available for use in Billing report masks.

5. Print Mask Identifiers

<table>
<tr><th>Identifier</th><th>Description</th></tr>
<tr><td>ADDRESS</td><td>Patient’s address (including ADDRESSA and ADDRESSB)</td></tr>
<tr><td>ADDRESSA</td><td>First line of patient’s address</td></tr>
<tr><td>ADDRESSB</td><td>Second line of patient’s address</td></tr>
<tr><td>ADMITID</td><td>Admission Identifier as stored in Evolution vLab™</td></tr>
<tr><td>AGE</td><td>Patient’s age, output as a string according to the rules below:
<table>
<tr><th>Age</th><th>Output format</th></tr>
<tr><td>< 50 days</td><td><i>n</i> days</td></tr>
<tr><td>50 days to 6 months</td><td><i>n</i> weeks</td></tr>
<tr><td>6 to 24 months</td><td><i>n</i> months</td></tr>
<tr><td>> 24 months</td><td><i>n</i> years</td></tr>
</table>
AGE is calculated from the patient’s date of birth to the relevant date on the lab number, in the following order of precedence:
Collection Date
Received Date
Requested Date
Date lab number was created</td></tr>
<tr><td>ALERT</td><td>Patient’s Alert Code Description</td></tr>
</table>

Identifier	Description
BAD_DEBTOR	Bad Debtor STRING
CC_NATA_ACCRED	Outputs the indication if a Collection Centre is “NATA” accredited as configured for the respective Collection Centre according to the configuration for the Collection Centre.
CLAIMID	Claim ID
CLINICAL_UNIT	Patient’s Clinical Unit
CLINNOTE	Patient clinical notes
COLLDATE	Specimen collection date, format dd-mmm-yy
COLLSDATE	Specimen collection date, format dd mmm
COLLTIME	Specimen collection time
COLLWARD	Ward of Collection Description identifier
COLLWARD_MNEM	Ward of Collection Mnemonic identifier
CONSULTANT	Consultant as recorded in the lab number/episode
CONS_MOBILE	The mobile number configured for the Consultant against the lab record (`CONSULTANT`); derived from the ‘Mobile’ field in the Provider configuration.
CONS_PROV	Consultant provider number
CONS_PROVIDER_USED	Outputs ‘yes’ when the episode was billed against the Provider Number for the Consultant on the lab number. Outputs ‘no’ otherwise.
CRDATE	Laboratory number creation date, format dd-mmm-yy
CRSDATE	Laboratory number creation date, format dd-mmm
CRTIME	Laboratory number creation time
CRYEAR	Laboratory number creation year
DATE	Current date, format dd-mmm-yy
DEPT	Department of Report Description
DESTADDR	Report destination address
DESTADDRA	Report destination address (line 1)
DESTADDRB	Report destination address (line 2)
DESTADDRC	Report destination address (line 3)

Identifier	Description
DESTNAME	Report destination name (name of recipient)
DIAG	Patient's diagnosis code
DNA_PRIORITY	DNA Priority Identifier
DOB	Date of birth as recorded in the lab number/episode
DOCTOR	Requesting Doctor, format full name
DRADDRESSA	Requesting Doctor's Address Line 1
DRADDRESSB	Requesting Doctor's Address Line 2
DR_MOBILE	The mobile number configured for the Requesting Doctor against the lab record (`DOCTOR`); derived from the 'Mobile' field in the Provider configuration.
DR_PROV	Requesting Doctor's Provider number
DRUNIT	Requesting doctor's Unit
FASTING	Fasting status as entered at specimen reception ("yes" or "no"); returns "?" when the fasting status has not been specified.
EXCOPY1	Extra Doctor Report Copy 1
EXCOPY2	Extra Doctor Report Copy 2
EXCOPY3	Extra Doctor Report Copy 3
EXCOPY4	Extra Doctor Report Copy 4
EXTDRADDR	External Doctor Address
EXTDRADDRA	External Doctor Address Field 1
EXTDRADDRB	External Doctor Address Field 2
EXTDRADDRC	External Doctor Address Field 3
EXTDRNAME	External Doctor name
EXTID	External Identification number
FILE	Patient's unit record number
FINCAT	Patient Category Description
GENETICSEX	Genetic sex of patient as entered at specimen reception
GNAMES	Patient's Given names

Identifier	Description
IDOCTOR	Requesting Doctor, format initial only
LABNO	Laboratory number formatted with hyphens
LABNO_SHORT	Laboratory number without hyphens
TM_LAST_ABSC	Last antibody screen
LCNAME	Patient's full name (lower case)
LL_LABNO	Returns a comma-separated list of the unique tube identifiers i.e. Container IDs and/or **Evolution vLab**™ Unique IDs appropriate to the context. This identifier returns the full list for the lab number unless otherwise stated. **Packing List masks for Evolution vLab™ laboratories** In Packing List request form masks for testing Laboratories configured in **Evolution vLab**™, LL_LABNO instead returns a comma-separated list of only the unique tube identifiers assigned to the request(s) being transferred. **Packing List masks for external laboratories** The unique tube identifiers returned in Packing List masks for external laboratories varies according to configuration. By default LL_LABNO returns all unique tube identifiers against the lab record, excluding those to which no requests are assigned. Where "Column/Output" Lab List Rules are configured against the User List for one or more requests, LL_LABNO returns only the unique tube identifiers to which those requests are assigned. Where one or more of the nominated requests remain unassigned, LL_LABNO returns null for the affected requests, not lab number.
LOCATION	Health Care Facility (Description) entered at Specimen Reception, i.e. patient's hospital location
LOCNUM	Specimen Location Number
LOCNUM_[P]	Specimen Location Number with Location Number Prefix [P]. For example, LOCNUM_B returns the Location Number against the lab record with Prefix 'B', including the Prefix.
MEDDATE	Medicare expiry
MEDICARE	Medicare number

Identifier	Description
MEDPOS	Medicare position
NAME	Patient’s full name (upper case)
NCSR_ID	National Cancer Screening Register (NCSR) Identification
NEHTA_IHI	Individual Healthcare Identifier (IHI)
OBSTETRIC_HIST	Obstetric history
OPERATION	Medical procedure description
OUTPUT_TYPE	The output type or method for the report (e.g. www, fax). Example:

```
if (OUTPUT_TYPE = "www") {
  exit;
}
```

Identifier	Description
PAGER	Pager number for results
PAT_PHONE	Patient’s Phone Number
PENSION	Pension number
PHONE	Phone number for results
POSTCODE	Post code of patient’s address
RADDR1	Lab Group address line 1 as defined in Lab Group configuration details
RADDR2	Lab Group address line 2 as defined in Lab Group configuration details
RDPATHNAME	Lab Group pathologist name as defined in Lab Group configuration details for a department
RDPATHPHONE	Lab Group pathologist name as defined in Lab Group configuration details for a department
RDPATHTITLE	Lab Group pathologist name as defined in Lab Group configuration details for a department
RDSPATHNAMEx	Lab Group pathologist name as defined in Lab Group configuration details for a department +/- section.
RDSPATHPHONEx	Lab Group pathologist name as defined in Lab Group configuration details for a department +/- section.

Identifier	Description
RDSPATHTITLEx	Lab Group pathologist name as defined in Lab Group configuration details for a department +/- section.
RECDDATE	Laboratory number received date, format dd-mmm-yy
RECDTIME	Laboratory received time
REQUESTOR_TYPE	Requestor type of the requesting doctor on the current lab episode.
RFAX	Lab Group fax no. as defined in Lab Group configuration details.
RLABNAME	Lab Group name as defined in Lab Group configuration details
RPATHNAME	Lab Group pathologists name as defined in Lab Group configuration details
RPATHPHONE	Lab Group pathologist phone no. as defined in Lab Group configuration details.
RPATHTITLE	Lab Group pathologist title as defined in Lab Group configuration details
RPCODE	Lab Group postcode as defined in Lab Group configuration details
RPHONE	Lab Group phone no. as defined in Lab Group configuration details
RSTATUS	Interim report status; returns the string "*** Interim Report ***" when the report status is Interim for the lab number concerned. **Note:** This identifier is not supported in equation-based print masks.
RSUBURB	Lab Group suburb as defined in Lab Group configuration details
SAMPLEP	Sample Period
SAMPLEV	Sample Volume
SDATE	Current date, format dd-mmm-yy
SEX	Sex
SLIDE_LOCN	Histology Location number for slide labels
SLIDE_PRIMSPEC	Primary Specimen site for Histology slide labels

Identifier	Description
SPECSITE	Specimen site
SPECTYPE	Specimen type
SPECTYPESITE	The Specimen Type (SPECTYPE), Primary Specimen Site (SPECPRIMSITE) and Specimen Site (SPECSITE) Descriptions output as one string, separated by spaces.
SUBURB	Suburb of patient's address
SURNAME	Patient's Surname
TIME	Current time
TM_LAST_ABSC	Last antibody screen
URAGE	Patient's current age according to the date of birth against the UR record, in the format *n days*, *n months* or *n years* as appropriate.
URCONSULTANT	Patient's current consultant as recorded in the UR record
URDESTNAME	Stores the name of the ward as recorded in the UR record. This identifier gets populated automatically.
URDOB	Patient's current date of birth as recorded in the UR record
URDOCTOR	Patient's current doctor (Description) as recorded in the UR record
URLOCATION	Patient's Health Care Facility (Description) on the UR record
URNO	Patient's unit record number
URWARD	Patient's current Ward
URWARDSITE	Patient's current ward location
USER	User Name/Login Name for the current user. This identifier does not return the configured Full Name.
USER1 **USER2** **USER3** **USER4**	Free text fields of up to 6 characters (can be used to display any data entered at specimen registration)
VUSER	User (final validation)
VUSERFULL	Full name of user (final validation)

Identifier	Description
WARD	Patient's Ward
WARD_MNEM	Patient's Ward Mnemonic
WARDSITE	Location of Ward e.g. unit
YEAR	Current year

6. Transfusion Medicine Print Mask Identifiers

Identifier	Description
AB_COUNT	Antibody Count as recorded in the lab number/episode
LABTM_SPEC_REQMT	Special requirements, entered at specimen registration
MSBOS	MSBOS for the entered procedure
OBSTETRIC_HIST	Recent pregnancy history from the patient's UR record (string)
TM_LAST_ABSC	Last Antibody screen (number of days)
TM_PREV_TRANSF	Previous Transfusion history (yes/no).
TM_REC_TRANSF	Recent Transfusion Recent transfer. Relates to Past Transfusion Limit (days) field entry on the Transfusion Options Configuration screen.
TM_SAMPLEXP	Sample Expiry
TM_XMSTATUS	Status of crossmatch, indicates the number of cellular units available to clients
TM_XPLSTAT	Indicates the number of plasma units available to clients
TM_XPTSTAT	Indicates the number of platelets available to clients
TM_XPBSTAT	Indicates the number of batches available to clients
TMBATCH1 to TMBATCH12	Batch number
TMBPROD1 to TMBPROD12	Batch product description
TMBQTY1 to TMBQTY12	Batch product quantity

Identifier	Description
TMPLEX1 to TMPLEX70	Expiry date for plasma
TMPLPD1 to TMPLPD70	Product description plus modifiers
TMPLPROD1 to TMPLPROD70	Product description for plasma, mnemonic only
TMPROD1	Transfusion Medicine Product ordered at Specimen Reception
TMPROD2	Transfusion Medicine Product ordered at Specimen Reception
TMPROD3	Transfusion Medicine Product ordered at Specimen Reception **Note:** Available only when Non Cellular products are enabled.
TMPROD4	Transfusion Medicine Product ordered at Specimen Reception **Note:** Available only when Non Cellular products are enabled.
TMPTEX1 to TMPTEX70	Expiry date for platelets
TMPTPD1 to TMPTPD70	Product description plus modifiers for platelets
TMPTPROD1 to TMPTPROD70	Product description platelets, mnemonic only
TMQTY1	Quantity required, entered at specimen registration
TMQTY2	Quantity required, entered at specimen registration
TMQTY3	Quantity required, entered at specimen registration
TMQTY4	Quantity required, entered at specimen registration
TMUNIT1	Units for products, entered at specimen registration (Displayed in ‘SI’ column)
TMUNIT2	Units for products, entered at specimen registration (Displayed in ‘SI’ column)
TMUNIT3	Units for products, entered at specimen registration (Displayed in ‘SI’ column)
TMUNIT4	Units for products, entered at specimen registration (Displayed in ‘SI’ column)
TMU_VTIME[1-n]	Date the unit was crossmatched; format hh:mm dd-mmm-yy
TMU_VUSER1 to TMU_VUSER70	User who validated unit
TMUEXP1 to TMUEXP70	Unit expiry

Identifier	Description
TMUGP1 to TMUGP70	Unit Group
TMUGP1_MNEM to TMUGP70 MNEM	Unit Group Mnemonic
TMULPRD1 to TMULPRD70	Unit product type description (including special requirements)
TMUNIT1 to TMUNIT70	Unit number
TMUPPROD	Unit product Description
TMUPROD1 to TMUPROD70	Unit product type Mnemonic
TMUSTATUS	Crossmatch status of the Unit
URTM_TM_ALERT	Transfusion Medicine Alert Description
URTM_PHENOTYPES	Patient’s phenotype from antibody register
URANTIBODIES	Antibody Count referenced by UR
URGROUP	Patient’s UR blood group
URGROUP_MNEM	Patient’s UR blood group mnemonic
URTM_SPEC_REQMT	Special requirements, entered into antibody register
XMPROD[1-n]	Product Description
XMPROD_MNEM1	Product required, entered at specimen registration (mnemonic)
XMPROD_MNEM2	Product required, entered at specimen registration (mnemonic)
XMQTY1	Quantity required, entered at specimen registration
XMQTY2	Quantity required, entered at specimen registration
XMQTY3	Quantity required, entered at specimen registration
XMQTY4	Quantity required, entered at specimen registration
XMREQD1	Required by time entered at specimen registration
XMREQD2	Required by time entered at specimen registration
XMREQD3	Required by time entered at specimen registration
XMREQD4	Required by time entered at specimen registration

7. Scientific Services Print Mask Identifiers

Identifier	Description
SS_ANALYST_STRING	STRING for whether the User is a State analyst
SS_BATCHREF	Client Batch Reference
SS_BOPNAME	Forensic Biology Operation Name
SS_CLIENT	Client
SS_CLIENT_ABN	Client ABN
SS_CLIENT_ADDR1	Client Address 1
SS_CLIENT_ADDR2	Client Address 2
SS_CLIENT_CNAME	Client Contact name
SS_CLIENT_EMAIL	Client Email Address
SS_CLIENT_FAX	Client Fax Number
SS_CLIENT_MNEM	Client Mnemonic
SS_CLIENT_PHONE	Client Telephone Number
SS_CLIENT_POSTCODE	Client Postcode
SS_CLIENT_PROJECT	Client Project
SS_CLIENT_QUOTE	Client Quote
SS_CLIENT_STATE	Client State
SS_CLIENT_SUBURB	Client Suburb
SS_COMMENCED_DATE	Earliest commenced date for the lab
SS_COPNAME	Forensic Chemistry Operation Name
SS_COURT_DATE	Court Date
SS_CPRIOT	Court Priority
SS_CRICAT	Crime Category
SS_CRMCLS	Crime Class
SS_CSSTAT	Crime Status
SS_DESTROY	Forensic Destruction

Identifier	Description
SS_NATA_STRING	STRING for whether the User is a NATA Signatory
SS_NO_ITEMS	Number of Items
SS_NSAMPLES	Number of samples in batch
SS_ODF	Offence Date From
SS_ODT	Offence Date To
SS_ORDERNO	Order Number
SS_PKG_DESC	Package Description
SS_PKG_RECDATETIME	Package Received Date and Time
SS_PKG_REQDATE	Package Request Date
SS_POLDAT	Police Due Date
SS_PROGRAM	Program
SS_PROJECT	Project
SS_REPORT_ANALYST	Analyst for the reported date
SS_REPORTED_DATE	Most recent date for the UR
SS_REPORTING_STRING	STRING for whether the User is a Reporting analyst
SS_SATCLIENT	Satellite Client Description
SS_SATCLIENT_ADDR1	Satellite Client Address 1
SS_SATCLIENT_ADDR2	Satellite Client Address 2
SS_SATCLIENT_CNAME	Satellite Client Contact Name
SS_SATCLIENT_MNEM	Satellite Client Mnemonic
SS_SATCLIENT_PCODE	Satellite Client Postcode
SS_SATCLIENT_STATE	Satellite Client State
SS_SATCLIENT_SUB	Satellite Client Suburb
SS_SATCOPY1	Satellite Client Copy 1
SS_SATCOPY2	Satellite Client Copy 2
SS_SATCOPY3	Satellite Client Copy 3
SS_SATCOPY4	Satellite Client Copy 4

Identifier	Description
SS_SATCOPY5	Satellite Client Copy 5
SS_SATCOPY6	Satellite Client Copy 6
SS_SATCOPY7	Satellite Client Copy 7
SS_SATCOPY8	Satellite Client Copy 8
SS_SUBMITAUTH	Submitting Authority
SS_TEAMS	Team
SS_USER_ACT1 **SS_USER_ACT2** **SS_USER_ACT3** **SS_USER_ACT4** **SS_USER_ACT5** **SS_USER_ACT6** **SS_USER_ACT7** **SS_USER_ACT8**	Legislations/Acts for User (1-8)
SS_USER_EMAIL	User’s Email address
SS_USER_FAX	User’s Fax number
SS_USER_FIRST	First Name of User
SS_USER_FUNCTION	User’s function e.g. Forensic Scientist
SS_USER_INST1 **SS_USER_INST2** **SS_USER_INST3** **SS_USER_INST4** **SS_USER_INST5**	User’s Institutions (1-5) where qualifications were gained.
SS_USER_MIDDLE	Middle Name of User
SS_USER_MEMB1 **SS_USER_MEMB2** **SS_USER_MEMB3** **SS_USER_MEMB4** **SS_USER_MEMB5**	User’s Professional Memberships (1-5)

Identifier	Description
SS_USER_PHONE	User's Phone number
SS_USER_PREF	Preferred First name of User
SS_USER_QUAL1 **SS_USER_QUAL2** **SS_FUSER_QUAL3** **SS_USER_QUAL4** **SS_USER_QUAL5**	User's Qualification (1-5)
SS_USER_SURNAME	Surname of User
SS_USER_TITLE	Title of the User e.g. Miss, Mrs., Mr.
SS_VENDOR_ADDR	Vendor Address
SS_VENDOR_NAME	Vendor Name

8. Billing Print Mask Identifiers

Identifier	Description
ACC_PRINTED	Last line & date the account was printed (i.e. statement)
ACCOUNT	The account number
ADDRESS1	Account address - line 1
ADDRESS2	Account address - line 2
ALERT	Alerts
ALLOCATIONS	Allocations - receipts that have been allocated to an account
BALANCE	Account balances (Charges - Receipts)
C_ADDRESS1	Contact address - line 1
C_ADDRESS2	Contact address - line 2
C_NAME1	Contact name - line 1
C_NAME2	Contact name - line2
C_POSTCODE	Contact address - postcode

Identifier	Description
C_SUBURB	Contact address - suburb
C_TELEPHONE1	Contact telephone number 1
C_TELEPHONE2	Contact telephone number 2
CHARGES	Account charges - total
CONS_PROVIDER	Mnemonic of the Doctor used for Consolidation
CONS_PROVIDER_NUM	Provider number of the Doctor used for Consolidation
CONS_PROVIDER_USED	Consulting Provider Used for Billing
DATE	Current Date (of printing)
INV	Invoice Number
INVPRINTCOUNT	Number of invoices printed
MMYY	UR Creation date in Pos format
MPOS	UR Creation date in decimal format
NAME1	Account name - line 1
NAME2	Account name - line 2
NOTES	Account notes
PATHOLOGIST	Pathologist
POSTCODE	Account address - postcode
RECEIPTS	Account receipts - total
SDATE	Short date i.e. DD MMM, the short for of the current date
SUBURB	Account address - suburb
TELEPHONE 1	Account telephone number 1
TELEPHONE2	Account telephone number 2
TIME	Current Time (of printing)
USER	The identification of the current user, i.e. the person who is printing
VMMYY	UR Veterans date in Pos format
YEAR	Current Year (of printing)
AHS	The Area Health Service

Identifier	Description
BPAY_BIN	Returns the value entered in the **BPay BIN** field in the configuration for the Area Health Service. This identifier may be used where the identifier **AHS** is available.
BPAY_CRN	Returns the BPAY Customer Reference Number (CRN). This identifier may be used where the identifier **INVOICE** is available. The format of the BPAY Customer Reference Number (CRN) is `YYMM[I]C` where `YY` is the two-digit year, `MM` the two-digit month, `[I]` represents the Invoice's number within the cited month (between 1 and 7 digits), and `C` represents the check digit. The portion `YYMM[I]` reflects the Invoice Number in non-alphabetical format. BPAY_CRN returns the CRN as a string in this format. The minimum length for the CRN, and therefore BPAY_CRN, is 6 characters (e.g. 170126) and the maximum length is 12 characters (e.g. 170183886077). This is compliant with BPAY's requirement for CRN values between 2 and 20 characters, and ensures that the CRN visually corresponds to the Invoice Number. **Example:** When the Invoice Number is 17.Jan.2, BPAY_CRN returns the invoice number without the alphabetical characters (17012) plus a check digit suffix, e.g. 170126.
INVOICE	Invoice number

9. Invoices and Invoice Line Items

Identifier	Description
BII_ADDRESS1	Account address - line 1 from the first transaction on the batch invoice
BII_ADDRESS2	Account address - line 2 from the first transaction on the batch invoice
BII_DOB	Patients date of birth from the first transaction on the batch invoice
BII_HCF	Health Care Facility
BII_INVNO	Invoice number from the first transaction on the batch invoice
BII_NAME	Patients name from the first transaction on the batch invoice
BII_POSTCODE	Account address - Postcode from the first transaction on the batch invoice
BII_SUBURB	Account address - suburb from the first transaction on the batch invoice
BII_TELEPHONE1	Account telephone number 1 from the first transaction details on the batch invoice
BII_TELEPHONE2	Account telephone number 2 from the first transaction details on the batch invoice
BII_URNO	MRN number from the first transaction on the batch invoice
DECEASED	Determines if patient has deceased set to “yes” on account
GIVEN	Patients given name from the first transaction on the batch invoice
INITIAL	Patients given name initial from the first transaction on the batch invoice
INV_ACCID_DATE	Date of Accident
INV_ACCNO	Invoice account number
INV_BAL	Outstanding balance on invoice inclusive of GST
INV_BAL_XGST	Outstanding balance on invoice minus the GST component
INV_CATEGORY	Patient category description
INV_CATEGORY	Category name

Identifier	Description
INV_CATGRP	Patient category group description
INV_CLAIM	Insurance claim number
INV_DATE	Invoice date
INV_DOC_NAME	Doctor from the first transaction details on an invoice
INV_DOC_PROV	Doctors provider number from the first transaction details on an invoice
INV_GST_TOTAL	Total GST amount on the invoice.
INV_LABNO	Laboratory number associated with this invoice from the first transaction details on an invoice
INV_LCC	Collection Centre
INV_LCC_NO	Collection Centre License No.
INV_NOTES	Invoice notes
INV_PAY_DUE	Payment due date calculated from the first invoice printed date (or current date if not previously printed), and account type overdue level, if overdue levels are not configured the system will automatically default to 30 days.
INV_PRINTED	First date invoice printed
INV_PROV_NAME	Provider name on the invoice
INV_PROV_PROV	Provider number on the invoice
INV_RDOC_ NAME	Name of requesting doctor from the first transaction details on an invoice
INV_RDOC_PROV	Requesting doctors provider number from the first transaction details on an invoice
INV_REQ_DATE	Request date if present else lab collection date else creation date
INV_REQ_DATE	Request date from the first transaction details on an invoice
INV_SCATEGORY	Patient category mnemonic
INV_SCATEGORY	Category mnemonic
INV_SCATGRP	Patient category group mnemonic
INV_TOTAL	Total amount of invoice

Identifier	Description
INVOICE	Invoice number
MEDICARE	Patients Medicare number from the first transaction on the batch invoice
PATH_NAME	Pathologist name from the first transaction details on an invoice
PATH_PROV	Pathologists provider number from the first transaction details on an invoice
SURNAME	Patients surname from the first transaction on the batch invoice
T_ACCNO	Account number
T_ADJUST_REFERENCE	Adjustment Reference Number
T_ADJUST_TYPE	Adjustment Type
T_AMOUNT	Amount of transaction
T_BALANCE	Balance (for invoices this is amount outstanding)
T_CATEGORY	Category name
T_COLLTIME	Collection Time
T_CONS_PROV	Mnemonic of the Doctor used for Consolidation
T_CONS_PROV_NUM	Provider number of the Doctor used for Consolidation
T_CONS_PROV_USED	Consulting Provider used for Billing (‘Yes’ or ‘No’)
T_CONSULT_PROV	Consultants provider number
T_CONULT_NAME	Consultant name
T_DESC	Transaction description - list of tests (max 20 characters)
T_DESC	Description limited to 20 characters
T_DESC_FULL	Description
T_DETAILS	Transaction details - service date and list of tests (Medicare mnemonic) (max 37 characters)
T_DOC_NAME	Requesting Doctor name
T_DOC_PROV	Requesting Doctor provider number
T_EXEMPTION	Bill exempt - Prints Rule 3 exemption if applied

Identifier	Description
T_INVNO	Invoice number
T_ITEM_DETAILS	Schedule name if present else test description
T_LABNO	Laboratory number
T_LCCNO	Print Mask identifier for including an SCP number on printed invoices.
T_LCCNO_PEI	If transactions lab has a PEI then it's the LCC's NO.
T_NOTES	Transaction notes (max 20 characters)
T_PAT_ADDRESSA	Patient address - line 1
T_PAT_ADDRESSB	Patient address - line 2
T_PAT_GNAMES	Patients given names
T_PAT_NAME	Patients full name
T_PAT_POSTCODE	Patient address - postcode
T_PAT_SUBURB	Patient address - suburb
T_PAT_SURNAME	Patients Suriname
T_PAT_TELEPHONE1	Patient telephone number 1
T_PAT_TELEPHONE2	Patient telephone number 2
T_PATH_NAME	Testing Laboratory's Pathologist Name
T_PATH_PROV	Testing Laboratory's Pathologist Provider Number
T_PROV_NO	Requesting Laboratory's Pathologist Provider Number
T_RECNO	Receipt number
T_REQ_DATE	Request date
T_SCATEGORY	Category mnemonic
T_SCHED_NAME	Description of schedule item
T_SCHED_NO	Schedule number (followed by "A" if patient is an outpatient, "*" if patient is an inpatient or followed by "R" if patient is Rule 3 exempt)
T_SERV_DATE	Service date
T_SERV_TIME	Service time

Identifier	Description
T_TRANS_NO	Transaction number
T_TYPE	Transaction type (e.g. Inv, Rec CR adj)
T_URNO	MRN
T_WARD	Ward
VETERAN	Patients veterans affairs number from the first transaction on the batch invoice

10. Receipts and Receipt Line Items

<table>
<tr><th>Identifier</th><th>Description</th></tr>
<tr><td>M_AMOUNT</td><td>Line item amount</td></tr>
<tr><td>M_BSB_NO</td><td>Line item BSB number</td></tr>
<tr><td>M_PAY_TYPE</td><td>Line item payment type</td></tr>
<tr><td>M_CARD_NO</td><td>Line item credit card number</td></tr>
<tr><td>M_CHEQ_NO</td><td>Line item cheque number</td></tr>
<tr><td>M_DETAILS</td><td>Payment Type. The output varies according to the payment method.
<table>
<tr><th>Payment method</th><th>Output format</th></tr>
<tr><td>Cash</td><td>[paytype]</td></tr>
<tr><td>Credit card</td><td>[paytype] [card number] [card expiry]</td></tr>
<tr><td>Cheque</td><td>[paytype] [cheque number] [BSB] [drawer]</td></tr>
<tr><td>Direct debit</td><td>[paytype]</td></tr>
</table></td></tr>
<tr><td>M_DRAWER</td><td>Line item cheque drawer</td></tr>
<tr><td>M_EXPIRY</td><td>Line item credit card expiry date</td></tr>
<tr><td>M_ITEM_NO</td><td>Receipt line item number</td></tr>
<tr><td>R_BALANCE</td><td>Receipt amount allocated</td></tr>
<tr><td>R_DATE</td><td>Receipt date</td></tr>
<tr><td>R_NOTES</td><td>Receipt notes (max 20 characters)</td></tr>
<tr><td>R_PRINTED</td><td>Date receipts last printed</td></tr>
<tr><td>R_RECNO</td><td>Receipt number</td></tr>
<tr><td>R_TOTAL</td><td>Receipt total</td></tr>
<tr><td>REC_TOTAL</td><td>Receipt total</td></tr>
<tr><td>REC_BAL</td><td>Receipt balance (i.e. unallocated)</td></tr>
</table>

Identifier	Description
REC_NOTES	Receipt notes
REC_DATE	Receipt date
REC_PRINTED	Last date the receipt was printed
REC_CANCEL_TYPE	Cancellation Type
REC_CANCEL_DATE	Cancellation Date
REC_BANK_ACCOUNT	Bank Account Name
RECEIPT	Receipt number

11. GST

Identifier	Description
GST_DATE	Date transaction created
GST_GSTTOTAL	GST amount for the transaction (invoices only)
GST_INVTOTAL	Invoice total
GST_RGST	GST amount of transaction if invoice reversal
GST_RTOTAL	Transaction amount if invoice reversal
GST_WOGST	GST amount of transaction if invoice write off
GST_WOTOTAL	Transaction amount if invoice write off

12. Veterinary Print Mask Identifiers

Identifier	Description
ANIMAL_NAME	Name of animal
BREED	The breed registered with the animal
DE_SEXED	Yes/No whether the animal has been de-sexed

Identifier	Description
LAB_GENFLAG1 **LAB_GENFLAG2** **LAB_GENFLAG3** **LAB_GENFLAG4** **LAB_GENFLAG5** **LAB_GENFLAG6** **LAB_GENFLAG7** **LAB_GENFLAG8**	Generic yes/no field identifier on the laboratory number
LAB_GENNUMBER1 **LAB_GENNUMBER2** **LAB_GENNUMBER3** **LAB_GENNUMBER4** **LAB_GENNUMBER5** **LAB_GENNUMBER6** **LAB_GENNUMBER7** **LAB_GENNUMBER8**	Generic integer field identifier on the laboratory number
LAB_GENSTRING1 **LAB_GENSTRING2** **LAB_GENSTRING3** **LAB_GENSTRING4** **LAB_GENSTRING5** **LAB_GENSTRING6** **LAB_GENSTRING7** **LAB_GENSTRING8**	Generic string field identifier on the laboratory number
OWNER_GIVNAME	Given name of Owner
OWNER_SURNAME	Surname of Owner
SPECIES	Species registered with the animal

Identifier	Description
UR_GENFLAG1 **UR_GENFLAG2** **UR_GENFLAG3** **UR_GENFLAG4** **UR_GENFLAG5** **UR_GENFLAG6** **UR_GENFLAG7** **UR_GENFLAG8**	Generic yes/no field identifier on the UR number
UR_GENNUMBER1 **UR_GENNUMBER2** **UR_GENNUMBER3** **UR_GENNUMBER4** **UR_GENNUMBER5** **UR_GENNUMBER6** **UR_GENNUMBER7** **UR_GENNUMBER8**	Generic integer field identifier on the UR number
UR_GENSTRING1 **UR_GENSTRING2** **UR_GENSTRING3** **UR_GENSTRING4** **UR_GENSTRING5** **UR_GENSTRING6** **UR_GENSTRING7** **UR_GENSTRING8**	Generic string field identifier on the UR number

13. Label Identifiers

<table>
<tr><th>Identifier</th><th>Description</th></tr>
<tr><td>AGE</td><td>Patient’s age, output as a string according to the rules below:
<table>
<tr><th>Age</th><th>Output format</th></tr>
<tr><td>< 50 days</td><td><i>n</i> days</td></tr>
<tr><td>50 days to 6 months</td><td><i>n</i> weeks</td></tr>
<tr><td>6 to 24 months</td><td><i>n</i> months</td></tr>
<tr><td>> 24 months</td><td><i>n</i> years</td></tr>
</table>
AGE is calculated from the patient’s date of birth to the relevant date on the lab number, in the following order of precedence:

Collection Date
Received Date
Requested Date
Date lab number was created
</td></tr>
<tr><td>AHS</td><td>Area Health Service</td></tr>
<tr><td>ALERT</td><td>Patient’s Alert code</td></tr>
<tr><td>CERNERACCNO</td><td>The Cerner Accession Number for the receipted specimen container (collection tube).
<u>Note:</u> This identifier is available when printing labels as part of the eOrder registration workflow, and from the Container Assignment screen.</td></tr>
<tr><td>CERNERACCNOT</td><td>The final 5 digits of the Cerner Accession Number, i.e. the truncated version of CERNERACCNO.
<u>Note:</u> This identifier is available when printing labels as part of the eOrder registration workflow, and from the Container Assignment screen.</td></tr>
<tr><td>COLLDATE</td><td>Specimen Collection Date, format dd-mmm-yy</td></tr>
<tr><td>COLLSDATE</td><td>Specimen Collection Date, format dd mmm</td></tr>
<tr><td>COLLTIME</td><td>Specimen Collection Time</td></tr>
<tr><td>CONSULTANT</td><td>Consultant</td></tr>
<tr><td>CONSULTANT_MNEM</td><td>Consultant (Mnemonic)</td></tr>
<tr><td>CRSDATE</td><td>Laboratory number creation date, format dd-mmm-yy</td></tr>
</table>

Identifier	Description
CRSDATES	Laboratory Number creation date, format dd-mmm
DATE	Current date, format dd-mmm-yy
DIAG	Patient’s Diagnosis code
DOB	Date of Birth
DOCTOR	Requesting Doctor, format full name
DOCTOR_MNEM	Requesting doctor mnemonic
EXTERNALID	External ID
GNAMES	Patient’s Given Names
LABNO	Laboratory Number, format YY/NNNNNN
LABNO_SHORT	Laboratory Number, format NNNNNN
LABNO_SUFFIX	The **Evolution vLab**™ Unique Tube ID for the receipted specimen container (collection tube). **Note:** This identifier is available when printing labels as part of the eOrder registration workflow, and from the Container Assignment screen.
LABORATORY	Laboratory of Testing
LL_LABNO	Outputs the most appropriate specimen identifier for the entity, in the following order of preference: 1. Third-party Container ID Applies to containers receipted via HL7 eOrder. 2. **Evolution vLab**™ Unique Tube ID Applies to manually receipted containers and those subsequently added via the Container Assignment screen. 3. **Evolution vLab**™ Lab Number (short format; no hyphens) Applies when neither a third-party Container ID nor an **Evolution vLab**™ Unique Tube is applicable.
LN_DEPT	Location Number relevant to the Department Mnemonic specified
LOCATION	Health Care Facility (Description) entered at Specimen Reception, i.e. patient’s hospital location

Identifier	Description
LOCATION_MNEM	Health Care Facility (Mnemonic) entered at Specimen Reception, i.e. patient’s hospital location
LOCBLOCKSTAIN	The Location Number (LOCNUM), Specimen Number (SPECNUM), Block Number (BLOCK) and Slide Number (SLIDE) descriptions output as one string, separated by ‘,’.
LOCLAB	Location Number Lab prefix
LOCNB	Location Number, no year or lab prefix
LOCNUM	Specimen Location Number
LOCYR	Location Number year prefix
NAME	Patient’s full name (upper case)
NCSR_ID	National Cancer Screening Register (NCSR) Identification
NEHTA_IHI	Individual Healthcare Identifier (IHI)
RECDDATE	Laboratory Number received date, format dd mmm
RECDTIME	Laboratory Number received time
REQUESTS	All requests on the laboratory record
SDATE	Short date, format dd mmm
SEX	Sex
SLIDE_BLOCKNUM	Block number only for Histology slide labels (Dot matrix)
SLIDE_FRAGS	Histology fragment number for slide labels (Dot matrix)
SLIDE_LEVEL	Histology level number for slide labels (Dot matrix)
SLIDE_LOCN	Histology location number for slide and specimen labels (Barcode & Dot-matrix)
SLIDE_LOCNUMT	Truncated Location Number from the Detailed Histo Table; returns only the Location Number. The Specimen, Block and Slide Numbers are excluded. Histopathology only.
SLIDE_PRIMSPEC	Specimen Type and Site for Histology Specimen Labels (Barcode & Dot matrix)
SLIDE_PROC	Histology detail procedure for slide labels (Dot matrix)

Identifier	Description
SLIDE_SPECBLOCKNUM	Specimen and block number for Histology slide and specimen labels (Dot matrix)
SLIDE_SPECNUM	Specimen number only for Histology slide and specimen labels (Dot matrix)
SLIDE_STAIN	Histology stain for slide and specimen labels (Dot matrix)
SOURCE_TUBE	Returns the most relevant unique container number for the source (parent) tube, similar to the cascading logic for LL_LABNO: 1. Third-party Container ID if it exists; failing that 2. **Evolution vLab**^{TM} Unique ID; failing that 3. **Evolution vLab**^{TM} Lab Number (short format; no hyphens) SOURCE_TUBE is intended for use in aliquot labels. For collection tubes this identifier returns the container's own unique identifier.
SPECSITE	Specimen Site
SPECSITE_MNEM	Specimen Site (Mnemonic)
SPECTYPE	Specimen Type
SPECTYPE_MNEM	Specimen Type (Mnemonic)
SPECTYPESITE	Specimen Type and Site/s
SURNAME	Patient's Surname
T_ITEM_DETAILS	Description of Test / Item Details
T_SCHED_NAME	Description of the Test Name
TMBATCH	Batch Number of Product
TMBPROD	Product Type of Batch Product
TMU_VTIME	Time unit was validated
TMU_VUSER	Mnemonic of user who validated the unit in the XM table
TMUEXP	Expiry time/date of the unit
TMUGP	Unit Blood Group
TMUGP_MNEM	Unit Blood Group Mnemonic
TMUNIT	Unit Number of Transfusion Blood Product

Identifier	Description
TMUPPROD	Primary Product Type of Unit
TMUPROD	Product Type of Unit
TMUPROD_BC1	Outputs the barcode configured in the 1st 'Barcode' field on the Product Configuration screen.
TMUPROD_BC2	Outputs the barcode configured in the 2nd 'Barcode' field on the Product Configuration screen.
TMUSTATUS	Compatibility Status of Blood Product
TUBE_ALIQTUBE	Name of the Aliquot Tube
TUBE_COLLTUBE	Mnemonic for the Sample Container (e.g. EDTA) associated with the receipted specimen container (collection tube). This identifier is available when printing labels as part of the eOrder registration workflow, and from the Container Assignment screen.
TUBE_CONTAINER	The third-party Container ID for the receipted specimen container (collection tube). This identifier is available when printing labels as part of the eOrder registration workflow, and from the Container Assignment screen.
TUBE_COMMENT	Comment, as entered in the Aliquot Processing Rules for this Processing Area
TUBE_LOCN	Location Number of the Aliquot Tube
TUBE_TESTS	The comma-separated list of requests assigned to the receipted specimen container (collection tube). **Note:** This identifier is available when printing labels as part of the eOrder registration workflow, and from the Container Assignment screen.
TUBE_UID	User who printed Aliquot Labels

Identifier	Description
TUBE_NOTES	Container Notes for the receipted specimen container (collection tube), as entered by the user via the Container Notes function on the eOrder Sample Reception screen. **Note:** This identifier is available when printing labels as part of the eOrder registration workflow, and from the Container Assignment screen.
TUBE_VOL	The volume required for the Aliquot Tube
TUBEMINVOL	Minimum volume for the Tube
TUBETYPE	Type of Tube
URAGE	Patient's age on UR record
URDOB	Date of Birth on UR record
URGENCY	Mnemonic of the Urgency (reporting priority) recorded against the lab number. **Note:** This identifier is available when printing labels as part of the eOrder registration workflow, and from the Container Assignment screen.
URGROUP	Patient's Blood Group on UR record
URLOCATION	Patient's Health Care Facility (Description) on the UR record
URLOCATION_MNEM	Patient's Health Care Facility (Mnemonic) on the UR record
URNO	Patient's Unit Record Number
URSEX	Patient's Sex on UR record
URWARD	Patient's Ward on the UR record
URWARD_MNEM	Patient's Ward (Mnemonic) on the UR record
USER	User Name/Login Name for the current user. This identifier does not return the configured Full Name.

Identifier	Description
VSLIDE_LOCNUM	Location Number from the Detailed Histo Table in the format [Lab]`[YY][Location Number]` e.g. AU`17B00233`. Histopathology only. This Identifier was implemented to support the Ventana Vantage workflow solution.
VSLIDE_LOCNUM_SPEC	Location Number and Specimen Number from the Detailed Histo Table, in the format [Lab]`[YY][Location Number];[Specimen Number]` e.g. AU`17B00233;1`. Histopathology only. This Identifier was implemented to support the Ventana Vantage workflow solution.
VSLIDE_LOCNUM_BLK	Location, Specimen and Block Number from the Detailed Histo Table, in the format `[Lab][YY][Location Number];[Specimen Number];[Block Number]` e.g. AU`17B00233;1;2`. Histopathology only. This Identifier was implemented to support the Ventana Vantage workflow solution.
VSLIDE_LOCNUM_SLIDE	Location, Specimen, Block and Slide Number from the Detailed Histo Table, in the format `[Lab][YY][Location Number];[Specimen Number];[Block Number];[Slide Number]` e.g. AU`17B00233;1;2;3`. Histopathology only. This Identifier was implemented to support the Ventana Vantage workflow solution.
VSLIDE_SPEC_BLK	Specimen and Block Number from the Detailed Histo Table, in the format `[Specimen Number].[Block Number]` e.g. `1.2`. Histopathology only. This Identifier was implemented to support the Ventana Vantage workflow solution.
WARD	Patient’s Ward
WARD_MNEM	Patient’s Ward (Mnemonic)

14. Scientific Services Label Identifiers

Identifier	Description
SS_CLIENT	Client
SS_COURT_DATE	Court Date
SS_CPRIOT	Court Priority
SS_CRICAT	Crime Category
SS_CRMCLS	Crime Class
SS_CSSTAT	Crime Status
SS_NSAMPLES	Number of Samples
SS_POLDAT	Police Due Date
SS_PROGRAM	Program
SS_PROJECT	Project

15. Equation Identifiers

Identifier	Description
AB_COUNT	Returns the number of antibodies in the antibody register as a string
ADDRESS	Patient’s address
ADDRESSA	Patient’s address (line 1)
ADDRESSB	Patient’s address (line 2)
ADMITID	Admission Identifier as stored in **Evolution vLab**™

<table>
<tr><th>Identifier</th><th>Description</th></tr>
<tr><td>AGE</td><td>Patient’s age, output as a string according to the rules below:
<table>
<tr><th>Age</th><th>Output format</th></tr>
<tr><td>< 50 days</td><td><i>n</i> days</td></tr>
<tr><td>50 days to 6 months</td><td><i>n</i> weeks</td></tr>
<tr><td>6 to 24 months</td><td><i>n</i> months</td></tr>
<tr><td>> 24 months</td><td><i>n</i> years</td></tr>
</table>
AGE is calculated from the patient’s date of birth to the relevant date on the lab number, in the following order of precedence:

Collection Date
Received Date
Requested Date
Date lab number was created
</td></tr>
<tr><td>AGE_DAYS</td><td>Patient’s age in days</td></tr>
<tr><td>ALERT</td><td>Patient’s Alert (Description)</td></tr>
<tr><td>AN_XXX</td><td>Identifier for the analyser result for Test XXX. These identifiers may only be used in Daemon Equations.
This notation allows differentiation between the identifiers for results received from the analyser and the Evolution vLab™ result field identifiers. For example, when a result for the test HGB (Haemoglobin) is transmitted its identifier is AN_HGB.
The AN_AUTOVAL setting determines how the analyser results are processed. Please refer to the AN_AUTOVAL equation identifier for more information.</td></tr>
</table>

Identifier	**Description**
AN_AUTOVAL	This identifier is available for use in Daemon Equation scripts only. AN_AUTOVAL may be set to 0, 1 or 2. This setting determines how the analyser results are processed by the Daemon Equation. **0** Place all results from the analyser on the Level 1 table in all cases. **1** Accept the results into the patient file (L1 validate) but do not attempt Level 2 validation. **2** Accept the results into the patient file and attempt Level 2 validation. Where possible the relevant results screen(s) for the lab number are Level 2 validated, but otherwise only the populated results are Level 2 validated. Generally the AN_AUTOVAL declaration is made at the beginning of the Daemon script. Please note that unsolicited results from the analyser are placed on the Level 1 table regardless of the AN_AUTOVAL setting. Syntax: `AN_AUTOVAL = 0;`
BAD_DEBTOR	Bad Debtor STRING
CATEGORY	Billing Category Mnemonic for the episode
CC_NATA_ACCRED	Outputs the indication if a Collection Centre is “NATA” accredited as configured for the respective Collection Centre according to the configuration for the Collection Centre.
CLAIMID	Claim ID
CLINICAL_UNIT	Clinical Unit Description
CLINNOTE	Patient’s clinical notes
COLLCENTRE	Returns the Collection Centre (Description). The Collection Centre may be set via Equations via `LAB_COLLC`; refer to the definition for that identifier for more information.
COLLDATE	Specimen collection date, format dd-mmm-yy

Identifier	Description
COLLSDATE	Specimen collection date, format dd mmm
COLLTIME	Specimen collection time
COLLWARD	Ward of Collection Description identifier
COLLWARD_MNEM	Ward of Collection Mnemonic identifier
CONSBILLING	The ‘Billing’ setting configured for the Provider specified in the Consultant field at Registration. The available values are ‘yes’ and ‘no ’. The space character in the ‘no ’ value is intentional and required. This identifier forms part of the Billing by Consultant opt-out functionality. Example of usage:

```
if (CAT_USE_SPEC = "Yes") {
  if (DRPROVIDER) {}
  else if (CONSULTANT_PROV) {
    if (CONSBILLING = "yes") {}
    else FINCAT = "DPP";
  }
  else FINCAT = "DPP";
}
```

CONSULTANT	Consultant Name
CONSULTANT_PROV	Provider number of the Consultant stored on the lab number
CONS_MOBILE	The mobile number configured for the Consultant against the lab record (`CONSULTANT`); derived from the ‘Mobile’ field in the Provider configuration.
CRDATE	Laboratory number creation date, format dd-mmm-yy
CRSDATE	Laboratory number creation date, format dd-mmm
CRTIME	Laboratory number creation time
CRYEAR	Laboratory number creation year
DATE	Current date, format dd-mmm-yy
DEPT	Department of Report
DEPT_MNEM	Department Mnemonic
DESTADDR	Report destination address

Identifier	Description
DESTADDRA	Report destination address (line 1)
DESTADDRB	Report destination address (line 2)
DESTADDRC	Report destination address (line 3)
DESTNAME	Report destination name
DEVICE_MODEL	Model of printer as defined in options field of printer configuration
DIAG	Patient's diagnosis code
DNA_PRIORITY	DNA Priority Identifier (readable)
DNAPRI	DNA Priority Identifier (writeable) This identifier may be used in the REQADD and MODIFY equations to change the DNA Priority on the lab record.
DOB	Patient's Date of Birth
DOCTOR	Requesting doctor, format full name
DOCTOR_MNEM	Doctor Mnemonic
DRADDRESSA	Requesting Doctor's Address Line 1
DRADDRESSB	Requesting Doctor's Address Line 2
DRBILLING	The 'Billing' setting configured for the Provider specified in the Doctor (Req Doctor) field at Registration. The available values are 'yes' and 'no '. The space character in the 'no ' value is intentional and required. This identifier forms part of the Billing by Consultant opt-out functionality. Refer to the description for CONSBILLING for additional context.
DR_FAX	The identifier DR_FAX and function final_validation(0) returns the fax number of the Requesting Doctor's child record. final_validation(0): Returns the time and date of the most recently validated result on a report.
DR_MOBILE	The mobile number configured for the Requesting Doctor against the lab record (`DOCTOR`); derived from the 'Mobile' field in the Provider configuration.
DRPROVIDER	Requesting doctor's Provider number
DRUNIT	Requesting doctor's Unit
EXCOPY1	Extra Doctor Report Copy 1

Identifier	Description
EXCOPY2	Extra Doctor Report Copy 2
EXCOPY3	Extra Doctor Report Copy 3
EXCOPY4	Extra Doctor Report Copy 4
EXTAPA	External APA. Returns the I, R or N STRING from the external APA field in the ward configuration table.
EXTDRADDR	External Doctor Address
EXTDRADDRA	External Doctor Address Field 1
EXTDRADDRB	External Doctor Address Field 2
EXTDRADDRC	External Doctor Address Field 3
EXTDRNAME	External Doctor Name
EXTID	External Identification number
FILE	Patient’s unit record number
FINCAT	Patient Category Mnemonic This identifier may be used in the REQADD and MODIFY equations to change the patient’s Financial Category on the lab record.
GESTATION	Gestational age as entered at specimen registration
GENETICSEX	Genetic sex of patient as entered at specimen reception
GNAMES	Patient’s Given names
HCF	HCF Description
HCF_MNEM	HCF Mnemonic
HCFUND	Health Care Fund Mnemonic
IDOCTOR	Requesting doctor, format initial only
INPATIENT	Inpatient field in the ward configuration table. Returns Y/N.
LAB_COLLC	Collection Centre This identifier may be used in the REQADD and MODIFY Equations to change the Collection Centre on the lab record.
LABNO	Laboratory number formatted with hyphens
LABNO_SHORT	Laboratory number without hyphens

Identifier	Description
LABPEI	PEI (Mnemonic) on the lab record. This identifier may be used in the REQADD and MODIFY equations to change the PEI on the lab record.
TM_LAST_ABSC	Last antibody screen
LCNAME	Patient's full name (lower case)
LOCATION	Health Care Facility (Description) entered at Specimen Reception, i.e. patient's hospital location
LOCATION_MNEM	Health Care Facility (Mnemonic) entered at Specimen Reception, i.e. patient's hospital location
LOCNUM_[P]	Specimen Location Number with Location Number Prefix [P]. For example, LOCNUM_B returns the Location Number against the lab record with Prefix 'B', including the Prefix.
MEDDATE	Medicare expiry
MEDICARE	Medicare number
MEDPOS	Medicare position
MODDATE	Date of last modification of any part of the patient record, format dd-mmm-yy
MODTIME	Time of last modification of any part of the patient record
MSBOS	Medical procedures maximum order
NAME	Patient's full name (upper case)
NCSR_ID	National Cancer Screening Register (NCSR) Identification
NEHTA_IHI	Individual Healthcare Identifier (IHI)
OPERATION	Medical procedure description
PAGER	Pager number for results
PEI	PEI (Description)
PEI_MNEM	PEI (Mnemonic) **Note:** The registration field for PEI can be updated via **Evolution vLab**™ Equation scripts.
PENSION	Pension number
PHONE	Phone number for results
POSTCODE	Post Code of patient's address

Identifier	**Description**
RECDDATE	Laboratory number received date, format dd-mmm-yy
RECDTIME	Laboratory number received time
REG_MESSAGE	This identifier may only be used in the Registration Save script. It allows for the configuration of a custom **Evolution vLab**™ Message prompt (Registration Message) to display when the user attempts to save the Registration screen and specified conditions have not been met, as determined by the script. The configured message should clearly indicate the problem to the user. The episode cannot be saved until the user has corrected the relevant field(s), i.e. it may only be saved when the message is no longer triggered. When REG_MESSAGE is set in the script (see syntax below) the **Evolution vLab**™ Message is automatically triggered under the appropriate conditions upon invocation of the Save [F4] function at Specimen Reception. REG_MESSAGE does not need to be passed to a function for the prompt to work. `REG_MESSAGE = "Example Registration Message";` In the example above, the user would receive an **Evolution vLab**™ prompt containing the message “Example Registration Message”.
REQUESTOR_TYPE	Requestor type of the requesting doctor on the current lab episode.
RLABNAME	Lab Group name as defined in Lab Group configuration details
SAMPLEP	Sample Period
SAMPLEV	Sample Volume
SDATE	Current date, format dd-mmm
SEX	Sex
SPECPRIMSITE	Specimen Primary Site Description
SPECSITE	Specimen Secondary Site Description
SPECTYPE	Specimen Type Description
SPECTYPESITE	The Specimen Type (SPECTYPE), Primary Specimen Site (SPECPRIMSITE) and Specimen Site (SPECSITE) Descriptions output as one string, separated by spaces.

Identifier	Description
STYLE	Style of report as defined in doctor or ward devices table.
STYLE_ID	Style ID of report as defined in doctor or ward devices table.
SUBURB	Suburb of patient's address
SURNAME	Patient's Surname
TIME	Current time
URGENCY	User list entered at the URGENCY field at specimen registration
URGROUP	Blood Group in the antibody register of the UR number
URNO	Patient's unit record number
USER	User Name/Login Name for the current user. This identifier does not return the configured Full Name.
VETERAN	Department of Veteran Affairs (DVA) number
VUSER	User (final validation)
VUSERFULL	Full name of user (final validation)
WARD	Patient's Ward Description
WARD_MNEM	Patient's Ward Mnemonic
WARDSITE	Location of ward eg. unit
YEAR	Current year in the format yyyy

16. Transfusion Medicine Identifiers

Identifier	Description
AB_COUNT	Antibody Count as recorded in the lab number/episode
LABTM_SPEC_REQMT	Special requirements, entered at specimen registration
MSBOS	MSBOS for the entered procedure
OBSTETRIC_HIST	Recent pregnancy history from the patient's UR record (string)
TM_LAST_ABSC	Last Antibody screen (number of days)
TM_PREV_TRANSF	Previous Transfusion history (yes/no).

Identifier	Description
TM_REC_TRANSF	Recent Transfusion Recent transfer. This identifier relates to the Past Transfusion Limit (days) field on the Transfusion Options Configuration screen.
TM_SAMPLEXP	Sample Expiry
TM_XMSTATUS	Status of crossmatch, indicates the number of cellular units available to clients
TM_XPLSTAT	Indicates the number of plasma units available to clients
TM_XPTSTAT	Indicates the number of platelets available to clients
TM_XPBSTAT	Indicates the number of batches available to clients
TMBATCH1 to TMBATCH12	Batch number
TMBPROD1 to TMBPROD12	Batch product description
TMBQTY1 to TMBQTY12	Batch product quantity
TMU_VTIME[1-n]	Date the unit was crossmatched; format hh:mm dd-mmm-yy
TMU_VUSER1 to TMU_VUSER70	User who validated unit
TMUEXP1 to TMUEXP70	Unit expiry
TMUGP1 to TMUGP70	Unit Group
TMUGP1_MNEM to TMUGP70_MNEM	Unit Group Mnemonic
TMULPRD1 to TMULPRD70	Unit product type description (including special requirements)
TMUNIT1 to TMUNIT70	Unit number
TMUPPROD	Unit product Description
TMUPROD1 to TMUPROD70	Unit product type Mnemonic
TMUSTATUS	Crossmatch status of the Unit
URANTIBODIES	Antibody Count referenced by UR
URTM_TM_ALERT	Transfusion Medicine Alert Description

Identifier	Description
URTM_PHENOTYPES	Patient’s phenotype from antibody register
URTM_SPEC_REQMT	Special requirements, entered into antibody register
XMPROD[1-n]	Product Description
XMPROD_MNEM1	Product required, entered at specimen registration (mnemonic)
XMPROD_MNEM2	Product required, entered at specimen registration (mnemonic)
XMQTY1	Quantity required, entered at specimen registration
XMQTY2	Quantity required, entered at specimen registration
XMQTY3	Quantity required, entered at specimen registration
XMQTY4	Quantity required, entered at specimen registration
XMREQD1	Required by time entered at specimen registration
XMREQD2	Required by time entered at specimen registration
XMREQD3	Required by time entered at specimen registration
XMREQD4	Required by time entered at specimen registration

17. Scientific Services Equation Identifiers

Identifier	Description
SS_BATCHREF	Client Batch Reference
SS_BOPNAME	Forensic Biology Operation Name
SS_CLIENT	Client
SS_CLIENT_ABN	Client ABN
SS_CLIENT_ADDR1	Client Address 1
SS_CLIENT_ADDR2	Client Address 2
SS_CLIENT_CNAME	Client Contact name
SS_CLIENT_EMAIL	Client Email Address
SS_CLIENT_FAX	Client Fax Number

Identifier	Description
SS_CLIENT_MNEM	Client Mnemonic
SS_CLIENT_PHONE	Client Telephone Number
SS_CLIENT_POSTCODE	Client Postcode
SS_CLIENT_PROJECT	Client Project
SS_CLIENT_QUOTE	Client Quote
SS_CLIENT_STATE	Client State
SS_CLIENT_SUBURB	Client Suburb
SS_COPNAME	Forensic Chemistry Operation Name
SS_COURT_DATE	Court Date
SS_CPRIOT	Court Priority
SS_CRICAT	Crime Category
SS_CRMCLS	Crime Class
SS_CSSTAT	Crime Status
SS_DESTROY	Forensic Destruction
SS_NO_ITEMS	Number of Items
SS_NSAMPLES	Number of samples in batch
SS_ODF	Offence Date From
SS_ODT	Offence Date To
SS_ORDERNO	Order Number
SS_PKG_DESC	Package Description
SS_PKG_RECDATETIME	Package Received Date and Time
SS_PKG_REQDATE	Package Request Date
SS_POLDAT	Police Due Date
SS_PROGRAM	Program
SS_PROJECT	Project
SS_SATCLIENT	Satellite Client Description
SS_SATCLIENT_MNEM	Satellite Client Mnemonic

Identifier	Description
SS_SATCOPY1	Satellite Client Copy 1
SS_SATCOPY2	Satellite Client Copy 2
SS_SATCOPY3	Satellite Client Copy 3
SS_SATCOPY4	Satellite Client Copy 4
SS_SATCOPY5	Satellite Client Copy 5
SS_SATCOPY6	Satellite Client Copy 6
SS_SATCOPY7	Satellite Client Copy 7
SS_SATCOPY8	Satellite Client Copy 8
SS_SUBMITAUTH	Submitting Authority
SS_TEAMS	Team
SS_VENDOR_ADDR	Vendor Address
SS_VENDOR_NAME	Vendor Name

18. Billing Equation Identifiers

Identifier	Description
CONSULTANT_MNEM	Mnemonic of the Consultant stored on the lab number
CONSULTANT_PROV	Provider number of the Consultant stored on the lab number
CAT_USE_SPEC	Patient Category stored on the lab number value for “Use Specialist” field

19. Batch Functionality Identifiers

Identifier	Description
DNABATCHNO	Batch number
DNABATCHTYPE	Batch type
DNABAUTO	DNA batch auto assign (yes or no)
DNABATCHUSER	User who created the batch
DNABATCHDATE	Batch creation date
DNABSEQUSER	User who performed the sequence check
DNABSEQDATE	Sequence check date
DNAWELL	DNA grid position id or well id

20. General Identifiers

The identifiers below may be used in conjunction with Request, Histology, Epidemiology, Transfusion Medicine and Billing Identifiers.

Identifier	Description
ACCOUNT	Account number
ADMDATE	Admission Date
ADMITNO	Admission number (or Campus encounter number)
AGE	Patient’s age (number of days) For autodumps, AGE is calculated from the patient’s date of birth to the relevant date on the lab number, in the following order of precedence: 1. Collection Date 2. Date lab number was created
AHS	Area Health Service
BED	Bed Number
CAT	Category
CATG	Category Group
CLIN_UNIT	Clinical Unit Mnemonic
CLINICAL_UNIT	Clinical Unit Description

Identifier	Description
COLLCENTRE	Collection Centre
COLLDATE	Date of Specimen Collection
COLLDATETIME	Date and Time of Collection
CONSPROVIDER	Consultant Provider Number
CONSULTANT	Consultant
CONSULTANTG	Consultant Group
CRDATE	Creation Date, format YYYYMMDD;HH:MM
DISDATE	Discharge date
DOB	Date of Birth, format YYYYMMDD
DOCTOR	Doctor
DOCTORG	Doctor Group
EPISODE	Episode Number for this patient
ETHNICITY	Patient Ethnicity
EXTID	External ID
GENETICSEX	Genetic sex of patient as entered at specimen reception
GESTATION	Gestational age of the patient
GIVENNAMES	Patient Given Names
HCF	Health Care Facility (mnemonic)
HCFG	Health Care Facility Group
HCFUNDSTAT	Health Care Fund Status
HCFUND	Health Care Fund Mnemonic
HCFUNDID	Health Care Fund Number
HCFUNDLVL	Health Care Fund Level
HCFUNDNAME	Health Care Fund Description
HL7_OBR4_1	Returns the OBR4.1 value (Request Mnemonic)
HL7_OBR4_2	Returns the OBR4.2 value (Request Description)
LABCR	Laboratory, where the record was created

Identifier	Description
LABCRG	Laboratory Group, where the record was created
LABNO	Laboratory Number (short format; no hyphen)
LABTEST	Testing laboratory
MEDICARE	Medicare Number
MRN	Medical Record Number
NAME	Patient Name in the format Surname, Given Name e.g. Smith, John
OPERATION	Medical procedure description
PEI	PEI Category on the Lab Number
PENSION	Pension Number
RECDATE	Received Date
REQDATE	Requested Date
SERVICEDATE	Service Date
SEX	Patient gender: (M/F/O/I/U/A)
SHIFT	Workshift
SPECDETAIL1	Specimen Details 1
SPECDETAIL2	Specimen Details 2
SPECDETAIL3	Specimen Details 3
SPECDETAIL4	Specimen Details 4
SPECIMEN	Specimen Type
SPECIMENID	Specimen Mnemonic
SPECPRIM	Primary Specimen Site
SPECSITE	Secondary Specimen Site
SPECTYPESITE	Specimen Type and Primary Site
SURNAME	Patient Surname
URGENCY	Urgency
URNO	Unit Record Number

Identifier	Description
USER1 **USER2** **USER3** **USER4**	Free text, user-definable data fields
VETERAN	Veterans' Affairs (DVA) Number
WARD	Ward
WARDCOLL	Ward of Collection
WARDCOLLG	Ward of Collection Group
WARDCOLLIO	Collection ward inpatient or outpatient status.
WARDG	Ward Group
WARDIO	Inpatient or Outpatient ward status.
WARD_HL7TYPE	Outputs the contents of the "HL7 Type" field in the configuration for the Ward.

21. Request Identifiers

These identifiers may be used in conjunction with General Auto Report Identifiers. They may not be used in conjunction with Histology, Epidemiology Transfusion Medicine or Billing Auto Report Identifiers.

Identifier	Description
REQ_ADDON	Previous request, registered >= 5 mins prior to this request. Outputs 'yes' or 'no'.
REQ_ADDONREQD	Subsequent request registered at Specimen Registration >= 5 mins after this request. Outputs 'yes' or 'no'.
REQ_DEPT	Request Test Department
REQ_LAB	Request Test Lab
REQ_METHOD	Request Test Method (i.e. most prevalent testing method for the request)
REQ_ORDERED	Time request was ordered (Results in two fields being created, 1 for time 1 for date, delimited as per configuration)
REQ_ORDERUSER	Username of person who ordered request

Identifier	Description
REQ_RECDATE	Displays the date/time a specimen has been accepted via the Specimen Receive List.
REQ_REQUEST	One individual orderable request per line
REQ_RETESTFAIL	Retest interval failure, returns if retest interval over-ridden.
REQ_SECTION	Registering Section
REQ_TAT	Turn Around Time – Measured in Minutes (Calculated from time of order to validation)
REQ_TATFAILED	TAT failure – Yes, if fails turn around time
REQ_TESTLAB	Majority testing laboratory for the request (if no result remains blank)
REQ_TESTUSER	Username of person who processed / validated request
REQ_VALIDATED	Time of validation (Results in two fields being created, 1 for time 1 for date, delimited as per configuration)
REQ_WORKPOINTS	Workload points as per test/panel configuration
TEST_DEPT	Test department
TEST_METHOD	Testing method
TEST_NAME	Test Name
TEST_REQLAB	Requesting laboratory
TEST_SECTION	Test section
TEST_TESTLAB	Testing laboratory
TEST_WORKPOINTS	Work points allocated to the test

22. QC Identifiers

These identifiers may be used in conjunction with the General Identifiers. They may not be used with Request, Histology, Epidemiology or Billing identifiers.

Identifier	Description
QC_ANALYSER	Analyser the QC was received from
QC_EXPIREDATE	Expiry date of the QC Lot
QC_LOT	Lot number of the QC material
QC_NAME	Mnemonic of the QC material
QC_STARTDATE	Start date for the QC lot number
QC_SUPPLIER	Supplier of the QC material
QC_USERID	User that created the QC material
QCT_ANNOTATION	Annotations on the QC point
QCT_CV	Cumulative variance for the QC material
QCT_DATE	Date the QC was performed
QCT_HIGH	Upper limit of the QC material
QCT_LOW	Lower limit of the QC material
QCT_MEAN	Mean value for the QC lot
QCT_MEAN2SDT-	Value of mean – 2 standard deviations for the QC lot
QCT_MEAN2SDT+	Value of mean + 2 standard deviations for the QC lot
QCT_POINTS	Number of QC points in the lot
QCT_STATUS	Status of the QC point
QCT_STDDEV	Standard deviation for the QC lot
QCT_TARGET	Target value for the QC material
QCT_TEST	Mnemonic of the Test the QC material was performed for
QCT_TSDEV	Target standard deviation for the QC material
QCT_USERID	User id of the person who accepted (or last modified) the QC point
QCT_VALUE	Value of the QC point

23. Transfusion Medicine Identifiers

These identifiers may be used in conjunction with the General Identifiers. They may not be used with Request, Histology, Epidemiology or Billing identifiers.

Identifier	Description
TM_ALERT	Transfusion alert stored on the patient's UR or lab record
TM_CMV	CMV status of a product
TM_COLLDATE	Collection date of the product
TM_DATE	Date and time of the audit of Transfusion Medicine Event
TM_DIAGNOSIS	Sign Out Diagnosis
TM_ENTEREDDATE	Manually entered date and time of the transfusion information by the user
TM_EVENT	Unit/Batch events including “Transferred” events I.e. crossmatched, dispatched
TM_EVENT_LOC	The location associated with a given Transfusion Medicine event, such as where the product was dispatched to.
TM_EXPDATE	Expiry date of the product
TM_FILTERED	Filtered Status of a product
TM_GROUP	Blood Group i.e. O Neg with Haemolysins
TM_IRRADIATED	Irradiated status of a product
TM_LAB	Laboratory at which the transaction occurred
TM_LOCATION	Ward/location where the product was despatched to
TM_MSBOS	MSBOS as referenced at Specimen Reception
TM_PRIMGROUP	Primary Blood Group i.e. O Neg for a given product
TM_PRIMPRODUCT	Primary Product i.e. FFP, Packed Cells
TM_PROCEDURE	Sign Out Procedure
TM_PRODUCT	Unit/Batch product (Mnemonic) e.g. RCSML
TM_QTY	Amount of product involved in a given event, eg. X2 products despatched
TM_SHELF	Shelf life of the product
TM_TRANS	Non-cellular products that have been allocated and transfused. Records limited to those that have been allocated. A 'yes' will appear at the end of the record if it has been transfused. (May not be used in conjunction with TM_XMTRANS).

Identifier	Description
TM_UNITNO	Unit/batch number of product
TM_USER	User who validated the crossmatch
TM_WARD	Ward products were dispatched to
TM_WASHED	Washed status of a product
TM_XMTRANS	Cellular Products which have been crossmatched and transfused. Records limited to those that have been crossmatched and that are cellular products only. A ‘yes’ will appear at the end of the record if it has been transfused.

24. Billing Identifiers

These identifiers may not be used in conjunction with Request, Histology, Epidemiology, Transfusion Medicine or General Auto Report Identifiers.

Identifier	Description
BT_ACCOUNT	Account Number
BT_ADDRESS	Address
BT_ADJUSTREF	Adjustment Reference Number
BT_ADJUSTTYPE	Adjustment Type
BT_AMOUNT	Amount
BT_BALANCE	Balance
BT_C1	MBS Column Number
BT_C2	MBS Column Number
BT_C3	MBS Column Number
BT_C4	MBS Column Number
BT_C5	MBS Column Number
BT_C6	MBS Column Number
BT_C7	MBS Column Number
BT_C8	MBS Column Number
BT_CAT	Billing category

Identifier	Description
BT_CATG	Financial Class Group
BT_CCG	Cost Centre Group
BT_CHARGEABLE	Chargeable
BT_COLLCENTRE	Collection Centre
BT_COMPANY	Company
BT_CONSULTANT	Consultant
BT_COSTCENTRE	Cost Centre
BT_DATE	Invoiced date (YYYYMMDD)
BT_DEPT	Department
BT_DOCTOR	Doctor
BT_FACFEE	Facility %
BT_HCF	Health Care Facility
BT_HCFG	HealthCare Facility Group
BT_HDATE	Invoiced date in hours and minutes
BT_INVNO	Invoice Number
BT_ITEM	Item Number
BT_ITEMDESC	Item Description
BT_LAB	Laboratory
BT_LABNO	Laboratory Number
BT_NAME	Patient Name
BT_PATHOLOGIST	Pathologist (Specialist)
BT_PEI	PEI category of the request
BT_PROVIDER	Pathologist Provider Number
BT_RECNO	Receipt Number
BT_REQDATE	Requested Date
BT_SERVDATE	Service Date
BT_TEST	Requests

Identifier	Description
BT_TRANSNO	Transaction Number
BT_USER	User Id
BT_WARD	Ward
BTEST_ITEMNO	MBS Item No.
BTEST_REQ	Request
GST_DATE	Date transaction created
GST_GSTTOTAL	GST amount for the transaction (invoices only)
GST_INVTOTAL	Invoice total
GST_RGST	GST amount of transaction if invoice reversal
GST_RTOTAL	Transaction amount if invoice reversal
GST_WOGST	GST amount of transaction if invoice write off
GST_WOTOTAL	Transaction amount if invoice write off

25. Scientific Services Identifiers

These identifiers may be used in conjunction with the General Identifiers. They may not be used with Request, Histology, Epidemiology or Billing identifiers.

Identifier	Description
BAD_DEBTOR	Bad Debtor STRING
SS_BATCHREF	Client Batch Reference
SS_BOPNAME	Forensic Biology Operation Name
SS_CLIENT	Client
SS_CLIENT_ABN	Client ABN
SS_CLIENT_ADDR1	Client Address 1
SS_CLIENT_ADDR2	Client Address 2
SS_CLIENT_CNAME	Client Contact name
SS_CLIENT_EMAIL	Client Email Address
SS_CLIENT_FAX	Client Fax Number

Identifier	Description
SS_CLIENT_MNEM	Client Mnemonic
SS_CLIENT_PHONE	Client Telephone Number
SS_CLIENT_POSTCODE	Client Postcode
SS_CLIENT_PROJECT	Client Project
SS_CLIENT_QUOTE	Client Quote
SS_CLIENT_STATE	Client State
SS_CLIENT_SUBURB	Client Suburb
SS_COPNAME	Forensic Chemistry Operation Name
SS_COURT_DATE	Court Date
SS_CPRIOT	Court Priority
SS_CRICAT	Crime Category
SS_CRMCLS	Crime Class
SS_CSSTAT	Crime Status
SS_DESTROY	Forensic Destruction
SS_NO_ITEMS	Number of Items
SS_NSAMPLES	Number of samples in batch
SS_ODF	Offence Date From
SS_ODT	Offence Date To
SS_ORDERNO	Order Number
SS_PKG_DESC	Package Description
SS_PKG_RECDATETIME	Package Received Date and Time
SS_PKG_REQDATE	Package Request Date
SS_POLDAT	Police Due Date
SS_PROGRAM	Program
SS_PROJECT	Project
SS_SATCLIENT	Satellite Client Description
SS_SATCLIENT_MNEM	Satellite Client Mnemonic

Identifier	Description
SS_SUBMITAUTH	Submitting Authority
SS_TEAMS	Team
SS_VENDOR_ADDR	Vendor Address
SS_VENDOR_NAME	Vendor Name

26. Microbiology Epidemiology Identifiers

These identifiers may be used in conjunction with the General Identifiers. They may not be used with Request, Histology, Transfusion Medicine or Billing identifiers.

Identifier	Description
MICRO_AB	Antibiotic
MICRO_ABRES	Antibiotic Result: outputs configured result i.e. ‘s’ or ‘n’
MICRO_ORG_CAT	Organism Category
MICRO_ORG_GENUS	Genus
MICRO_ORG_ID	Identifies the organism to its corresponding position on screen. E.g. org1, org2, org3 etc.
MICRO_ORG_PRIMARY	Primary Organism
MICRO_ORG_PRIMGRP	Primary Group

27. Histology Identifiers

These identifiers may be used in conjunction with General Auto Report Identifiers. They should not be used in conjunction with Request, Epidemiology, Transfusion Medicine or Billing Auto Report Identifiers.

Identifier	Description
SLIDE_BLKPOINTS	Block workload points
SLIDE_BLKTYPE	Block Type
SLIDE_DEPT	Prefix of Location No
SLIDE_GROSS	Gross Procedure

Identifier	Description
SLIDE_LOCNUML	Full location number including level id
SLIDE_NBLOCK	Number of blocks on episode
SLIDE_NSLIDE	Number of slides on episode
SLIDE_NSPEC	Number of specimens in the Histo Table for the lab record
SLIDE_PRIMSPEC	Primary specimen site
SLIDE_PROC	Detail Procedure
SLIDE_PROCPOINTS	No. of detail procedure workload points
SLIDE_RECUT	Recut (y/n)
SLIDE_SECSITE_1	Secondary site on this slide 1
SLIDE_SECSITE_2	Secondary site on this slide 2
SLIDE_SPECIMEN	Specimen type on this slide
SLIDE_SPROC	Special Procedure
SLIDE_STAIN	Stain
SLIDE_STAINPOINTS	Workload points for a stain

28. Definable Screen Layout Identifiers

Identifier	Description
ABALERT	Antibody Alert
ACCADDR1	Account address 1
ACCADDR2	Account address 2
ACCDATE	Accident date
ACCGNAME	Account Given Name
ACCNAME	Account Name.
ACCOUNT	Billing Account
ACCPCODE	Account Postcode
ACCSUBURB	Account Suburb
ADDRESS1	Patient Address Line 1

Identifier	Description
ADDRESS2	Patient Address Line 2
ADMITID	Admission ID
ADMITTED	Admission Date
AHS	Area Health Service
ALERT	Patient's alert code
ALIAS_GNAME1	Alias Given Name 1
ALIAS_GNAME2	Alias Given Name 2
ALIAS_GNAME3	Alias Given Name 3
ALIAS_GNAME4	Alias Given Name 4
ALIAS_GNAME5	Alias Given Name 5
ALIAS_NAME1	Alias Surname 1
ALIAS_NAME2	Alias Surname 2
ALIAS_NAME3	Alias Surname 3
ALIAS_NAME4	Alias Surname 4
ALIAS_NAME5	Alias Surname 5
ASSIGNMENT	Medclaim assignment
BAD_DEBTOR	Bad Debtor STRING
BED	Bed Number (string)
BEDXX	Bed Number (integer)
BILL_OVERRIDE	Billing Override indicator (STRING); outputs yes/no. This setting is used to override the "Conflicting categories on this day" and "Same date of request already billed" Exceptions.
BLOODGRP	Patient blood group
CATEGORY	Billing Category
CLAIMID	Claim Number
CLINICAL_SHORT	Clinical Unit Mnemonic
CLINICAL_UNIT	Clinical Unit as recorded in the lab number/episode

Identifier	Description
CLINUNIT	Clinical Unit referenced by UR (mnemonic)
COLLCENTRE	Collection Centre (mnemonic)
COLLECT_STRING	Collected status as entered in Order Entry Screen.
COLLECT_ON	Required collection date as entered in Order Entry Screen.
COLLECTED	Specimen collection date, format dd-mmm-yy
COLLECTORID	Collector ID (string)
CONFIDENTIAL	Confidential Status
CONS_PHONE	Consultant’s Phone Number
CONS_PROVIDER_USED	Outputs ‘yes’ when the episode was billed against the Provider Number for the Consultant on the lab number. Outputs ‘no’ otherwise.
CONSADDRESSA	Doctor Address Line 1 from Doctor configuration for the Consultant
CONSADDRESSB	Doctor Address Line 2 from Doctor configuration for the Consultant
CONSULTANT	Consultant
DIAGNOSIS	Patient’s Diagnosis code
DISCHARGED	Discharged Date
DNA_SAMPLETYPE	DNA Sample Type
DOB	Date of birth
DOCTOR	Requesting Doctor
DR_PHONE	Doctor’s Phone Number
DRADDRESSA	Doctor’s Address Line 1
DRADDRESSB	Doctor’s Address Line 2
EPISODE	Episode Number for the patient
EVOCLINNOTES	Clinical Notes (**Evolution vLab**TM Registration screens only).
EVOORDERNOTES	Ordering Notes (**Evolution vLab**TM Registration screens only).

Identifier	Description
EVOURNOTES	Create a new UR Note for the lab's UR (**Evolution vLab**™ Registration screens only).
EVOSPECNOTES	Create a new Specimen Note for the lab episode (**Evolution vLab**™ Registration screens only).
EVOEXCOPIES_[1-10]	Copy Doctor 1-10 (**Evolution vLab**™ Registration screens only). * Note: For the Extra Copies Identifiers up to 10 distinct extra copy fields can be configured.
EVOEXCOPIES_DEST_[1-10]	Copy Doctor destination (**Evolution vLab**™ only). * Note: For the Extra Copies Identifiers up to 10 distinct extra copy fields can be configured. This identifier is display only and cannot be used to create an editable field.
ETHNICITY	Patient ethnicity
EXCOPIES	Extra copy
EXEMPT	Bill Exempt (yes/no)
EXTERNALID	External ID
FASTING	Fasting
FUND	Bill fund
FUNDLEVEL	Bill fund level
FUNDNO	Fund number
FUNDSTAT	Bill fund status
GENETICSEX	Genetic sex of patient as entered at Specimen Registration
GESTATION	Gestation
GIVNAME	Patient Given Name
HCFDOCTOR	Requesting Doctor (limited to HCF entered)
HCFWARD	Ward
HCFWARDCOLL	Ward of Collection
LABNO	Laboratory number
TM_LAST_ABSC	Last antibody screen

Identifier	Description
LOCATION	Health Care Facility (Description) entered at Specimen Reception, i.e. patient's hospital location
MEDICARE	Medicare Number
MEDDATE	Medicare expiry
MEDPOS	Medicare position
MRN	Medical Record Number
MSBOS	MSBOS for the entered procedure
NAME	Patient's Full Name
NEHTA_IHI	Individual Healthcare Identifier (IHI)
PAGER	Doctor Pager Number
PAT_PHONE	Phone number of patient
PEI	PEI
PENSION	Pension number
PHONE	Phone number for results
POSTCODE	Postcode
PREGNANCY	Pregnancy Status
PREVTRANSF	Previous transfer (yes/no)
PSITE	Specimen Primary Site
RACK	Specimen rack locations
RECEIVED	Time of Laboratory record registration
RECPREG	Recent pregnancy (yes/no)
REQUESTED	Date of Request
SAMPLE_PERIOD	Sample Period
SAMPLE_VOLUME	Sample Volume
SEX	Sex
SITE	Secondary Specimen Site
SPECDETAIL1	Specimen Details 1
SPECDETAIL2	Specimen Details 2

Identifier	Description
SPECDETAIL3	Specimen Details 3
SPECDETAIL4	Specimen Details 4
SPECIAL_FEE	Special fee for laboratory, excluding GST where applicable
SPECIMEN	Specimen Type
SPECIMENID	Specimen Identification Number
SPECREQMT	Transfusion special requirement
SUBURB	Suburb
SURNAME	Patient Surname
TESTS	Allows for entry of requested tests and panels **Note:** Superseded by identifiers REQUEST1 to REQUEST [n] in **Evolution vLab**^{TM}.
TMALERT	Transfusion Alert
TMPROD1	Transfusion Product 1
TMPROD2	Transfusion Product 2
TMQUANT1	Transfusion Product Quantity 1
TMQUANT2	Transfusion Product Quantity 2
TMREQDATE	Required date (Transfusion)
URGENCY	Urgency Status as entered at Specimen Registration, Fast Registration or Order Entry
URNO	Patient’s Unit Record Number
USER_RECEIVED	Time of receipt in laboratory as entered at specimen registration
USER1 **USER2** **USER3** **USER4**	Free text, user-definable fields (maximum 6 characters each)
WARD	Patient’s Ward
WARDCOLL	Patient’s Ward of Collection

29. Scientific Services Definable Screen Identifiers

Identifier	Description
DNA_PRIORITY	Priority for DNA lab
SS_BATCHREF	Batch reference number
SS_BOPNAME	Forensic Biology Operation Name
SS_CLIENT	Client
SS_CLIENT_ABN	Client ABN
SS_CLIENT_ADDR1	Client Address 1
SS_CLIENT_ADDR2	Client Address 2
SS_CLIENT_CNAME	Client Contact Name
SS_CLIENT_EMAIL	Client Email Address
SS_CLIENT_FAX	Client Fax Number
SS_CLIENT_MNEM	Client Mnemonic
SS_CLIENT_PHONE	Client Phone Number
SS_CLIENT_POSTCODE	Client Postcode
SS_CLIENT_PROJECT	Client Project
SS_CLIENT_QUOTE	Client Quote
SS_CLIENT_STATE	Client State
SS_CLIENT_SUBURB	Client Suburb
SS_COPNAME	Forensic Chemistry Operation Name
SS_COURT_DATE	Court Date
SS_CPRIOT	Priority
SS_CRICAT	Crime Category
SS_CRMCLS	Crime Class
SS_CSSTAT	Crime Status
SS_DESTROY	Forensic Destruction
SS_NO_ITEMS	Number of Items
SS_NSAMPLES	Number Of Samples In Batch

Identifier	Description
SS_ODF	Offence Date From
SS_ODT	Offence Date To
SS_ORDERNO	Order Number
SS_PKG_DESC	Package Description
SS_PKG_RECDATETIME	Package Received Date and Time
SS_PKG_REQDATE	Package Request Date
SS_POLDAT	Police Due Date
SS_PROGRAM	Program
SS_PROJECT	Project
SS_SATCLIENT	Satellite Client Description
SS_SATCLIENT_CNAME	Satellite Client Contact Name
SS_SATCLIENT_MNEM	Satellite Client Mnemonic
SS_SUBMITAUTH	Submitting Authority
SS_TEAMS	Team
SS_VENDOR_ADDR	Vendor Address
SS_VENDOR_NAME	Vendor Name
SS_SATCLIENT_ADDR1	Satellite Client Address 1
SS_SATCLIENT_ADDR2	Satellite Client Address 2
SS_SATCLIENT_SUB	Satellite Client Suburb
SS_SATCLIENT_STATE	Satellite Client State
SS_SATCLIENT_PCODE	Satellite Client Postcode

30. Veterinary Definable Screen Identifiers

Identifier	Description
ANIMAL_NAME	Name of animal
BREED	The breed registered with the animal
DE_SEXED	Yes/No whether the animal has been de-sexed

Identifier	Description
LAB_GENFLAG1 **LAB_GENFLAG2** **LAB_GENFLAG3** **LAB_GENFLAG4** **LAB_GENFLAG5** **LAB_GENFLAG6** **LAB_GENFLAG7** **LAB_GENFLAG8**	Generic yes/no field identifier on the laboratory number
LAB_GENNUMBER1 **LAB_GENNUMBER2** **LAB_GENNUMBER3** **LAB_GENNUMBER4** **LAB_GENNUMBER5** **LAB_GENNUMBER6** **LAB_GENNUMBER7** **LAB_GENNUMBER8**	Generic integer field identifier on the laboratory number
LAB_GENSTRING1 **LAB_GENSTRING2** **LAB_GENSTRING3** **LAB_GENSTRING4** **LAB_GENSTRING5** **LAB_GENSTRING6** **LAB_GENSTRING7** **LAB_GENSTRING8**	Generic string field identifier on the laboratory number
OWNER_GIVNAME	Given name of Owner
OWNER_SURNAME	Surname of Owner
SPECIES	Species registered with the animal

Identifier	Description
UR_GENFLAG1 UR_GENFLAG2 UR_GENFLAG3 UR_GENFLAG4 UR_GENFLAG5 UR_GENFLAG6 UR_GENFLAG7 UR_GENFLAG8	Generic yes/no field identifier on the UR number
UR_GENNUMBER1 UR_GENNUMBER2 UR_GENNUMBER3 UR_GENNUMBER4 UR_GENNUMBER5 UR_GENNUMBER6 UR_GENNUMBER7 UR_GENNUMBER8	Generic integer field identifier on the UR number
UR_GENSTRING1 UR_GENSTRING2 UR_GENSTRING3 UR_GENSTRING4 UR_GENSTRING5 UR_GENSTRING6 UR_GENSTRING7 UR_GENSTRING8	Generic string field identifier on the UR number

31. Definable Table Identifiers

Identifier	Description
ABALERT	Antibody Alert
ABC	Display the result for the Test with Mnemonic ABC
ABC[1]	Display the most recent historical result for the Test with Mnemonic ABC

<table>
<tr><th>Identifier</th><th>Description</th></tr>
<tr><td>ABC[2]</td><td>Display the second most recent historical result for the Test with Mnemonic ABC</td></tr>
<tr><td>ABC[3]</td><td>Display the third most recent historical result for the Test with Mnemonic ABC</td></tr>
<tr><td>ABC[4]</td><td>Display the fourth most recent historical result for the Test with Mnemonic ABC</td></tr>
<tr><td>ACCAMOUNT</td><td>Total amount ($) of outstanding invoices on the account</td></tr>
<tr><td>ACCPHONE1</td><td>Account phone number 1</td></tr>
<tr><td>ACCPHONE2</td><td>Account phone number 2</td></tr>
<tr><td>ACCTYPE</td><td>Account Type (Mnemonic)</td></tr>
<tr><td>AGE</td><td>Patient’s age, output as a string according to the rules below:
<table>
<tr><th>Age</th><th>Output format</th></tr>
<tr><td>< 50 days</td><td><i>n</i> days</td></tr>
<tr><td>50 days to 6 months</td><td><i>n</i> weeks</td></tr>
<tr><td>6 to 24 months</td><td><i>n</i> months</td></tr>
<tr><td>> 24 months</td><td><i>n</i> years</td></tr>
</table>
AGE is calculated from the patient’s date of birth to the relevant date on the lab number, in the following order of precedence:
Collection Date
Date lab number was created</td></tr>
<tr><td>AHS</td><td>Area Health Service</td></tr>
<tr><td>ALERT</td><td>Patient’s Alert code</td></tr>
<tr><td>ASSIGNMENT</td><td>Medclaim Assignment</td></tr>
<tr><td>BAD_DEBTOR</td><td>Bad Debtor STRING</td></tr>
<tr><td>BALANCE</td><td>Total monies owed</td></tr>
<tr><td>BED</td><td>Patient’s Bed Number</td></tr>
<tr><td>BLOODGROUP</td><td>Patient’s Blood Group</td></tr>
<tr><td>CATEGORY</td><td>Patient’s Billing Category</td></tr>
</table>

Identifier	Description
CCPM_INITIALS	Patient's initials, i.e. first character from the Given Name and first character from the Surname. May only be used in Definable Tables for CCPM screens.
CCPM_TESTS	Outputs the tests configured in the CCPM configuration table. May only be used in Definable Tables for CCPM screens.
CDATEONLY	Specimen Collection Date only
CLAIMID	Claim ID
CLINICAL_UNIT	Patient's Clinical Unit
COLLCENTRE	Collection Centre
COLLECTED	Specimen Collection Time and Date, format hh:mm dd-mmm-yyyy
CONPHONE	Consultant's phone number
CONPROV	Consultant's Provider number
CONSNAME	Outputs the Consultant's title and full name
CONS_PROVIDER_USED	Outputs 'yes' when the episode was billed against the Provider Number for the Consultant on the lab number. Outputs 'no' otherwise.
CONSULTANT	Consultant (Mnemonic)
CREATED	Laboratory Number creation date, format dd-mmm-yy
CREDITS	Amount of Receipts
CURRENT	$ Amount of Receipts
CYTO_RES	Lists of all the PAP code results for the Laboratory Number
DEBTAGE	The number of days since the creation of earliest outstanding invoice
DEPTREQS	Requests belonging to the Department; used with a Department-specific Daysheet. The request(s) returned by this identifier in a User List may be customised by configuring "Column/Output" Lab List Rules against the User List in question
DIAGNOSIS	Patient's Diagnosis code

Identifier	Description
DNA_PRIORITY	Priority for DNA lab
DOB	Date of birth, format dd-mmm-yyyy
DOCTOR	Requesting Doctor (Mnemonic)
DOCNAME	Outputs the Doctor’s title and full name
DRPHONE	Requesting Doctor’s telephone number
DRPROV	Requesting Doctor’s Provider number
ENQSTATUS	Enquiry Status
ETHNICITY	Patient Ethnicity
EXTERNALID	External Specimen ID
GENETICSEX	Genetic sex of patient as entered at Specimen Registration
GROSS	Gross Procedure Mnemonic
HCF	Health Care Facility
INVDATE	Creation date of earliest outstanding invoice for the Account
INVNUMBER	Comma separated list of outstanding invoice numbers (up to 10). The system outputs “.............” where more than 10 exist.
LABNO	Laboratory number formatted with a hyphen
LABNO_SHORT	Laboratory number formatted without a hyphen
LASTCOLL	Date of last specimen collection
LEVEL1	Monetary value of invoices that equate to what is configured for this level for the account, e.g. 30 days
LEVEL2	Monetary value of invoices that equate to what is configured for this level for the account, e.g. 60 days
LEVEL3	Monetary value of invoices that equate to what is configured for this level for the account, e.g. 90 days

LL_LABNO	Outputs the most appropriate specimen identifier(s) for the entity, in the following order of preference: 1. Third-party Container ID Applies to containers receipted via a HL7 eOrder. 2. **Evolution vLab**™ Unique Tube ID Applies to manually receipted containers and those subsequently added via the Container Assignment screen. 3. **Evolution vLab**™ Lab Number (short format; no hyphens) Returned when neither a third-party Container ID nor an **Evolution vLab**™ Unique Tube ID is applicable. **System Lists** In Definable Tables for **System Lists** the identifier returns only the specimen identifier(s) associated with the request in question. **Packing/Receive Lists for Evolution vLab™ laboratories** In Packing/Receive Lists for testing Laboratories configured in **Evolution vLab**™ `LL_LABNO` returns only the specimen number(s) relevant to the request(s) being transferred, i.e. the third-party Container ID or **Evolution vLab**™ Unique Tube ID as appropriate for each request. In the absence of any receipted containers this identifier returns the lab number. "Column/Output" Lab List Rules override this standard functionality, as described below for User Lists. **User Lists** By default, this identifier returns the appropriate unique identifier for each container receipted against the laboratory record. In the absence of any receipted containers this identifier returns the lab number. Where "Column/Output" Lab List Rules are configured against the User List for one or more requests, `LL_LABNO` returns only the unique tube identifiers to which those requests are assigned. Where one or more of the nominated requests remain unassigned, `LL_LABNO` returns null for the affected requests, not lab number. In this context the identifier returns the lab number only in

Identifier	Description
	the absence of any receipted containers for all of the nominated requests. The identifier `WS_LL_LABNO` is recommended for use in the Definable Tables for Worksheets **Note:** Unique Tube IDs for Aliquots are excluded for some clients.
LL_LABNOPACK	This identifier is available for use in Definable Tables for Packing and Receive Lists. The identifier and its cascading logic is equivalent to that of the `LL_LABNO` identifier. **Packing/Receive Lists for Evolution vLab™ laboratories** In Packing/Receive Lists for testing Laboratories configured in **Evolution vLab™** `LL_LABNOPACK` returns only the specimen number(s) relevant to the request(s) being transferred, i.e. the third-party Container ID or **Evolution vLab™** Unique Tube ID as appropriate for each request. **Packing Lists for external laboratories** The logic for `LL_LABNOPACK` in external Packing Lists is consistent with that of `LL_LABNO` in the Definable Tables for User Lists. Please refer to the **User Lists** section in the definition for `LL_LABNO`, above.
LOCATION	Health Care Facility (Description) entered at Specimen Reception, i.e. patient's hospital location
LOCNUM[Mnemonic]	Location number relevant to the specified Department (Mnemonic)
MEDDATE	Medicare expiry
MEDPOS	Medicare Position
NAME	Patient's Full Name **Definable Tables for Worksheets** **Note:** This identifier outputs the patient's name for pathology specimens or QC Material for QC entries, as appropriate, similar to WS_NAME. The QC name is derived from the 'Material' field for the QC Material configured against the Worksheet.
NEHTA_IHI	Individual Healthcare Identifier (IHI)

Identifier	Description
NBLOCK	Block Number
NOTES	Clinical Notes
NSLIDE	Slide Number
NSPEC	Number of specimens in the Histo Table for the lab record
PAP_STATUS	Status of record within user list i.e. deleted, transferred, accepted or on hold
PENSION	Pension number
RACK_POS	Specimen Rack Positions
RDATEONLY	Received Date Only, format dd-mmm-yyyy
RECEIVED	Received Time and Date
REQPACKING	Returns a comma-separated list of the requests appropriate to the Packing or Receive List. This identifier is only supported in Packing/Receive Lists for Laboratories configured in **Evolution vLab**™ . The Definable Table for Packing Lists to external (non-**Evolution vLab**™) sites must instead be configured with the `REQUESTS` identifier. The request(s) returned by this identifier may be customised by configuring “Column/Output” Lab List Rules against the User List in question. **Note:** On the Packing List screen this identifier excludes requests for which the configured Default Test Lab (Def Test Lab) does not match the Laboratory the requests are being referred to. This may be observed when requests are added to the Packing List via a Test Processing Rule.
REQ_STATUS	Request Status
REQUESTS	Returns a comma-separated list of the ordered requests (Tests and/or Panels) for the lab record. The request(s) returned by this identifier may be customised by configuring “Column/Output” Lab List Rules against the User List in question.
REQUESTOR_TYPE	Requestor Type of the Requesting Doctor on the current lab episode

Identifier	Description
REQUIRED	Required Time
RFIMAGE	Indication of presence of request form image, format Y or N
SEX	Sex, format (F,M,A,I,U,O)
SLIDENO	Slide Number **<u>Note:</u>** Available for use in Daysheets only.
SLIDETYPE	Specimen Type **<u>Note:</u>** Available for use in Daysheets only.
SNOMEDCODES	Snomed Codes
SPECDETAIL1	Specimen Detail 1 – Additional free text specimen detail description
SPECDETAIL2	Specimen Detail 2 – Additional free text specimen detail description
SPECDETAIL3	Specimen Detail 3 – Additional free text specimen detail description
SPECIMEN	Specimen Type
SPECPRIM	Primary Specimen Site
SPECSITE	Specimen Site
SPECTYPESITE	Specimen Type and Primary Site and Specimen Site
STATUS	Status of record within User List, i.e. deleted, transferred, accepted or on hold
SLIDESTATUSUSER	User configured status for the Histology recut worksheet
TM_ALERT	Transfusion Medicine Alert
TRANSFUSED	Transfused status as recorded in Transfusion details at Specimen Registration
TUBE_LOCN	Aliquot Location Number for Worksheets
U_EXP	Unit expiry date
U_GP	Unit Group
U_PROD	Unit Product Type
U_DESC	Unit Product Description

Identifier	Description
U_QTY	Quantity of Product allocated
ULISTTEST	Mnemonic(s) for the Request(s) belonging to the User List (comma-separated)
UNIT	Unit Number
URGENCY	Urgency Status as entered at Specimen Registration
URNO	Patient's Unit Record Number
USER1	Outputs contents of the USER1 field, which may be configured as part of the Specimen Registration screen (maximum 6 characters)
USER2	Outputs contents of USER2 free text field, which may be configured as part of the Specimen Registration screen (maximum 6 characters)
USER3	Outputs contents of USER3 free text field, which may be configured as part of the Specimen Registration screen (maximum 6 characters)
USER4	Outputs contents of USER4 free text field, which may be configured as part of the Specimen Registration screen (maximum 6 characters)
UTUBEID	When the entry in the Definable Table references a specific container, this identifier outputs the appropriate unique identifier for that container. When the entry in the Definable Table references a lab number, this identifier outputs a comma-separated list of the unique tubes recorded against the lab number. This includes collection tubes (Tube/Container Assignment screen) and Aliquots. The containers returned by this identifier may be customised by configuring "Column/Output" Lab List Rules against the User List in question. Where this identifier returns a lab number it is output in the 'short' format, i.e. without hyphens.
VETDATE	Veteran Expiry
VETERANS	Veteran Affairs Number
VUSER	User who validated the entry
WARD	Patient's Ward (Mnemonic)

Identifier	Description
WARDCOLL	Ward in which the specimen was collected
WS_LABNO	Laboratory number formatted with hyphens
WS_LABNO_SHORT	Laboratory number formatted without hyphens
WS_LL_LABNO	This identifier is available for use in the Definable Tables for Worksheets. Outputs the most appropriate specimen identifier(s) for the Worksheet entry (Test), in the following order of preference: 1. Third-party Container ID Applies to containers receipted via a HL7 eOrder. 2. **Evolution vLab**™ Unique Tube ID Applies to manually receipted containers and those subsequently added via the Container Assignment screen. 3. **Evolution vLab**™ Lab Number (short format; no hyphens) Applies when neither a third-party Container ID nor an **Evolution vLab**™ Unique Tube ID is applicable. The identifier returns only the Container IDs and Unique Tube IDs associated with the Test in question, or the orderable Panel containing the Test when the Test is not explicitly ordered.
WS_NAME	Laboratory number, name of QC or calibrator in a worksheet. Used only where QC is configured on the worksheet.
WS_POS	Position number of the entry in the worksheet
WS_REALLOCATE_R_SHORT	Outputs the first letter of the reason for reallocation, e.g. D, R, P or Blank
WS_REALLOCATE_R_LONG	Outputs the description of the reason for reallocation in full, e.g. Dilution
WS_STATUS	Status of the worksheet
XM_M1	Crossmatch method 1
XM_M2	Crossmatch method 2
XM_M3	Crossmatch method 3

Identifier	Description
XM_M4	Crossmatch method 4
XM_ST	Compatibility status
XMREQD	Required by date entered in Transfusion Details at specimen reception
XMREQUESTS	Product type (Quantity) as entered in Transfusion details at Specimen Reception

32. Aged Debtor Identifiers

Identifier	Description
ACCOUNT	Billing Account
ACCTYPE	Account Type (Mnemonic)
ACCADDR1	Account Address 1
ACCADDR2	Account Address 2
ACCPHONE1	Account phone number 1
ACCPHONE2	Account phone number 2
ACCAMOUNT	Total amount ($) of outstanding invoices on the account
ACCSUBURB	Account Suburb
AHS	Area Health Service
CATEGORY	Billing Category Mnemonic for the episode
DEBTAGE	The number of days since the creation of earliest outstanding invoice
DOB	Date of birth
INVNUMBER	Comma separated list of outstanding invoice numbers (up to 10). The system outputs “.............” where more than 10 exist.
INVDATE	Creation date of earliest outstanding invoice for the Account

Identifier	Description
LEVEL1	Monetary value of invoices that equate to what is configured for this level for the account, e.g. 30 days
LEVEL2	Monetary value of invoices that equate to what is configured for this level for the account, e.g. 60 days
LEVEL3	Monetary value of invoices that equate to what is configured for this level for the account, e.g. 90 days
NAME	Patient name
POSTCODE	Postcode of patient's address
SRVDATE	Service Date

33. Scientific Services Definable Table Identifiers

Identifier	Description
SS_BATCHREF	Batch reference number
SS_BOPNAME	Forensic Biology Operation Name
SS_CLIENT	Client
SS_CLIENT_ABN	Client ABN
SS_CLIENT_ADDR1	Client Address 1
SS_CLIENT_ADDR2	Client Address 2
SS_CLIENT_CNAME	Client Contact Name
SS_CLIENT_EMAIL	Client Email Address
SS_CLIENT_FAX	Client Fax Number
SS_CLIENT_NMEM	Client Mnemonic
SS_CLIENT_PHONE	Client Phone Number
SS_CLIENT_POSTCODE	Client Postcode
SS_CLIENT_PROJECT	Client Project
SS_CLIENT_QUOTE	Client Quote
SS_CLIENT_STATE	Client State

Identifier	Description
SS_CLIENT_SUBURB	Client Suburb
SS_COPNAME	Forensic Chemistry Operation Name
SS_COURT_DATE	Court Date
SS_CPRIOT	Priority
SS_CRICAT	Crime Category
SS_CRMCLS	Crime Class
SS_CSSTAT	Crime Status
SS_DEPT_LIST	Comma separated list of department mnemonics
SS_DESTROY	Forensic Destruction
SS_NO_ITEMS	Number of Items
SS_NSAMPLES	Number Of Samples In Batch
SS_ODF	Offence Date From
SS_ODT	Offence Date To
SS_ORDERNO	Order Number
SS_PKG_DESC	Package Description
SS_PKG_RECDATETIME	Package Received Date and Time
SS_PKG_REQDATE	Package Request Date
SS_PKG_STATUS	Package Status
SS_POLDAT	Police Due Date
SS_CPRIOT	Priority
SS_PROGRAM	Program
SS_PROJECT	Project
SS_SATCLIENT	Satellite Client Description
SS_SATCLIENT_MNEM	Satellite Client Mnemonic
SS_SATELLITE_MNEM	Satellite client Menom
SS_SUBMITAUTH	Submitting Authority
SS_TEAMS	Team

Identifier	Description
SS_VENDOR_ADDR	Vendor Address
SS_VENDOR_NAME	Vendor Name

34. Definable Registration Output Identifiers

Identifier	Description
ABALERT	Antibody alert
ACCADDR1	Account Address 1
ACCADDR2	Account Address 2
ACCDATE	Accident date
ACCGNAME	Account Given Name
ACCNAME	Account Name
ACCOUNT	Billing Account
ACCPCODE	Account Postcode
ACCSUBURB	Account Suburb
ADDRESS1	Patient Address Line 1
ADDRESS2	Patient Address Line 2
ADMITID	Admission ID
ADMITTED	Admission Date
AHS	Area Health Service
ALERT	Patient’s Alert code
ALIAS_GNAME1	Alias Given Name 1
ALIAS_GNAME2	Alias Given Name 2
ALIAS_GNAME3	Alias Given Name 3
ALIAS_GNAME4	Alias Given Name 4
ALIAS_GNAME5	Alias Given Name 5
ALIAS_NAME1	Alias Surname 1
ALIAS_NAME2	Alias Surname 2

Identifier	Description
ALIAS_NAME3	Alias Surname 3
ALIAS_NAME4	Alias Surname 4
ALIAS_NAME5	Alias Surname 5
ASSIGNMENT	Medclaim Assignment
BAD_DEBTOR	Bad Debtor STRING
BED	Patient's Bed Number (string)
BEDXX	Bed Number (integer)
BLOODGRP	Patient's Blood Group
CATEGORY	Billing Category
CLAIMID	Claim ID
CLINICAL_SHORT	Clinical Unit (Mnemonic)
CLINICAL_UNIT	Clinical Unit
CLINUNIT	Clinical Unit
COLLCENTRE	Collection Centre
COLLECTED	Specimen collection date, format dd-mmm-yy
COLLECT_STRING	Collected status as entered in Order Entry Screen
COLLECT_ON	Required collection date as entered in Order Entry Screen
CONFIDENTIAL	Confidential Status
CONSADDRESSA	Doctor Address Line 1 from Doctor configuration for the Consultant
CONSADDRESSB	Doctor Address Line 2 from Doctor configuration for the Consultant
CONSULTANT	Consultant
CONS_PHONE	Consultant's Phone Number
DIAGNOSIS	Patient's Diagnosis code
DISCHARGED	Discharged Date
DNA_PRIORITY	Priority for DNA lab
DNA_SAMPLTYPE	DNA Sample Type

Identifier	Description
DOB	Patient's Date of Birth
DOCTOR	Requesting Doctor, format full name
DRADDRESSA	Requesting Doctor's Address Line 1
DRADDRESSB	Requesting Doctor's Address Line 2
DR_PHONE	Doctor's Phone Number
EPISODE	Episode Number for the patient
ETHNICITY	Patient Ethnicity
EXEMPT	Bill Exempt (yes/no)
EXTERNALID	External ID
FASTING	Fasting
FUND	Bill Fund
FUNDLEVEL	Bill Fund Level
FUNDNO	Fund Number
FUNDSTAT	Bill Fund Status
GESTATION	Gestation (number of weeks)
GIVNAME	Patient Given Name
HCFDOCTOR	Requesting Doctor (limited to HCF entered)
HCFWARD	Ward
HCFWARDCOLL	Ward of Collection
LABNO	Laboratory number formatted with hyphens
TM_LAST_ABSC	Last antibody screen
LOCATION	Health Care Facility (Description) entered at Specimen Reception, i.e. patient's hospital location
LOCNUM_1 to LOCNUM_20	Location Number 1-20
MEDDATE	Medicare expiry
MEDICARE	Medicare Number
MEDPOS	Medicare Position

Identifier	Description
MRN	Medical Record Number
MSBOS	MSBOS for the entered procedure
OPERATION	Medical procedure description
ORDER_NUMBER	Order Number
PAGER	Pager number for results
PAT_PHONE	Patient's Phone Number
PEI	PEI Description
PENSION	Pension number
POSTCODE	Postcode of patient's address
PREGNANCY	Pregnancy Status
PREVTRANSF	Previous transfer (yes/no)
PSITE	Specimen Primary Site
RECEIVED	Time of Laboratory record registration
RECPREG	Recent pregnancy (yes/no)
RECTRANSF	Recent transfer. Relates to Past Transfusion Limit (days) field entry on the Transfusion Options Configuration screen.
REQUEST1 to REQUEST[n]	Request Mnemonic 1 through Request Mnemonic [n], where [n] is 48 or 72 according to licensing.
REQUESTED	Date of Request
REQUEST_DESC1 to REQUEST_DESC[n]	Request Description 1 through Request Description [n], where [n] is 48 or 72 according to licensing.
REQUEST_NAME1 to REQUEST_NAME[n]	Request Display Name 1 through Request Display Name [n], where [n] is 48 or 72 according to licensing.
SAMPLE_PERIOD	Sample Period
SAMPLE_VOLUME	Sample Volume
SEX	Sex
SITE	Secondary Specimen Site
SPECDETAIL1	Specimen Details 1
SPECDETAIL2	Specimen Details 2

Identifier	Description
SPECDETAIL3	Specimen Details 3
SPECDETAIL4	Specimen Details 4
SPECIAL_FEE	Special fee for laboratory, excluding GST where applicable
SPECIMEN	Specimen Type
SPECIMENID	Specimen Identification Number
SPECREQMT	Transfusion special requirement
SS_BATCHREF	Batch reference number
SS_BOPNAME	Forensic Biology Operation Name
SS_CLIENT	Client
SS_CLIENT_ABN	Client ABN
SS_CLIENT_ADDR1	Client Address 1
SS_CLIENT_ADDR2	Client Address 2
SS_CLIENT_CNAME	Client Contact Name
SS_CLIENT_EMAIL	Client Email Address
SS_CLIENT_FAX	Client Fax Number
SS_CLIENT_NMEM	Client Mnemonic
SS_CLIENT_PHONE	Client Phone Number
SS_CLIENT_POSTCODE	Client Postcode
SS_CLIENT_PROJECT	Client Project
SS_CLIENT_QUOTE	Client Quote
SS_CLIENT_STATE	Client State
SS_CLIENT_SUBURB	Client Suburb
SS_COPNAME	Forensic Chemistry Operation Name
SS_COURT_DATE	Court Date
SS_CPRIOT	Priority
SS_CRICAT	Crime Category
SS_CRMCLS	Crime Class

Identifier	Description
SS_CSSTAT	Crime Status
SS_DESTROY	Forensic Destruction
SS_NO_ITEMS	Number of Items
SS_NSAMPLES	Number Of Samples In Batch
SS_ODF	Offence Date From
SS_ODT	Offence Date To
SS_ORDERNO	Order Number
SS_PKG_DESC	Package Description
SS_PKG_RECDATETIME	Package Received Date and Time
SS_PKG_REQDATE	Package Request Date
SS_POLDAT	Police Due Date
SS_PROGRAM	Program
SS_PROJECT	Project
SS_SATCLIENT	Satellite Client Description
SS_SATCLIENT_ADDR1	Satellite Client Address 1
SS_SATCLIENT_ADDR2	Satellite Client Address 2
SS_SATCLIENT_MNEM	Satellite Client Mnemonic
SS_SATCLIENT_PCODE	Satellite Client Postcode
SS_SATCLIENT_STATE	Satellite Client State
SS_SATCLIENT_SUB	Satellite Client Suburb
SS_SUBMITAUTH	Submitting Authority
SS_TEAMS	Team
SS_VENDOR_ADDR	Vendor Address
SS_VENDOR_NAME	Vendor Name
SUBURB	Suburb
SURNAME	Patient Surname
TMALERT	Transfusion Alert

Identifier	Description
TMPROD1 to TMPRODx	Transfusion products 1-2. **Note:** Transfusion products 3-4 available when Non Cellular products are enabled.
TMQUANT1	Transfusion Product Quantity 1
TMQUANT2	Transfusion Product Quantity 2
TMREQDATE	Required date (Transfusion)
URGENCY	Urgency Status as entered at Specimen Registration, Fast Registration or Order Entry
URNO	Patient's Unit Record Number
USER1 **USER2** **USER3** **USER4**	Free text, user-definable fields (maximum 6 characters each)
USER_RECEIVED	Time of receipt in laboratory as entered at Specimen Registration
VETDATE	Veteran Expiry
VETERANS	Veteran Affairs Number

35. Extended Enquiry Identifiers

Identifier	Description
ACCOUNT	Patient account number
ADDRESS	Patient address
AGE	Patient's age (number of months)
AHS	Area Health Service Mnemonic
ALERT	Alert Code recorded on laboratory record
ALLTESTS	All requests on laboratory record
BED	Patient's bed number
BILLC	Billing value with coning (y/n)
BILLNC	Billing value without coning (y/n)

Identifier	Description
CATEGORY	Patient Category
CLIN_UNIT	Clinical Unit Mnemonic
CLINICAL_UNIT	Clinical Unit Mnemonic
COLLECTED	Collection date and time
CONSULTANT	Consultant recorded on laboratory record
COPIES	Mnemonic of all Extra Copies Doctors on laboratory record
CREATED	Creation date and time of laboratory record
CWARD_UNIT	Clinical Unit Mnemonic from the ward configuration based on the collection ward
DEPARTMENT	Department that owns the test
DIAGNOSIS	Diagnosis Code recorded on laboratory record
DOB	Patient Date of Birth
DOCTOR	Requesting Doctor recorded on laboratory record
ETHNICITY	Patient’s ethnicity
EXTID	External Identifier
GENETICSEX	Genetic sex of patient as entered at specimen reception
GESTATION	Patient’s gestational age
HCFUND	Health Care Fund Mnemonic
HCFUNDID	Health Care Fund Membership Number
LABCREATED	Laboratory (Mnemonic) in which the laboratory record was created
LABNO	Laboratory Number
LOCATION	Health Care Facility (Description) entered at Specimen Reception, i.e. patient’s hospital location
LOCNUM_?	Location Number where ? is department prefix
LONGTESTS	Tests requested (not truncated)
MEDICARE	Patient Medicare Number
NAME	Patient name
PEI	Patient Episode Initiator (Mnemonic)

Identifier	Description
PENSION	Pension Number
POSTCODE	Postcode
RECDATE	Received Date
REQDATE	Requested Date
SERVICEDATE	Date of service
SEX	Patient sex
SHIFT	Workshift
SPECDETAIL1	Specimen Details 1
SPECDETAIL2	Specimen Details 2
SPECDETAIL3	Specimen Details 3
SPECDETAIL4	Specimen Details 4
SPECIMEN	Specimen Type
SPECIMENID	Specimen ID (number)
SPECSITE	Specimen Primary Site and Specimen Site (comma separated)
STORAGE_POS	Storage position in rack, including the name of the rack
TESTS	Tests requested
URG	Urgency
URNO	Patient UR or MRN
USER1 **USER2** **USER3** **USER4**	User-defined free text fields
VETERAN	Department of Veteran’s Affairs number
WARD	Ward Mnemonic recorded on laboratory record
WARD_HL7TYPE	Displays the “HL7 type” field stored in WARDS configuration
WARD_UNIT	Clinical Unit Mnemonic from the ward configuration based on the lab ward
WARDCOLL	Ward of specimen collection

Identifier	Description
XXX	Any Test where XXX represents the **Evolution vLab**™ Test Mnemonic

36. Scientific Services Extended Enquiry Identifiers

Identifier	Description
BAD_DEBTOR	Bad Debtor STRING
DNA_PRIORITY	Priority for DNA lab
SS_BATCHREF	Batch reference number
SS_CLIENT	Client
SS_CLIENT_ABN	Client ABN
SS_CLIENT_ADDR1	Client Address 1
SS_CLIENT_ADDR2	Client Address 2
SS_CLIENT_CNAME	Client Contact Name
SS_CLIENT_EMAIL	Client Email Address
SS_CLIENT_FAX	Client Fax Number
SS_CLIENT_MNEM	Client Mnemonic
SS_CLIENT_PHONE	Client Phone Number
SS_CLIENT_POSTCODE	Client Postcode
SS_CLIENT_PROJECT	Client Project
SS_CLIENT_QUOTE	Client Quote
SS_CLIENT_STATE	Client State
SS_CLIENT_SUBURB	Client Suburb
SS_COURT_DATE	Court Date
SS_CPRIOT	Priority
SS_CRICAT	Crime Category
SS_CRMCLS	Crime Class
SS_CSSTAT	Crime Status
SS_NO_ITEMS	Number of Items

Identifier	Description
SS_NSAMPLES	Number Of Samples In Batch
SS_PKG_DESC	Package Description
SS_PKG_RECDATETIME	Package Received Date and Time
SS_PKG_REQDATE	Package Request Date
SS_POLDAT	Police Due Date
SS_PROGRAM	Program
SS_PROJECT	Project
SS_SATCLIENT	Satellite Client Description
SS_SATCLIENT_MNEM	Satellite Client Mnemonic
SS_SUBMITAUTH	Submitting Authority
SS_VENDOR_ADDR	Vendor Address
SS_VENDOR_NAME	Vendor Name

37. GSI & GII Identifiers

Identifier	Description
BAD_DEBTOR	Client Bad Debtor STRING
GSI_MODE	Export/import mode
GSI_REGSTATUS	Whether or not lab has been saved by GSI
LAB_BED	Bed number
LAB_CLINNOTES	Clinical notes
LAB_CLINUNIT	Clinical unit
LAB_COLLC	Collection centre
LAB_COLLDATE	Lab collection date
LAB_COLLECTED	Collection date
LAB_COLLTIME	Collection time
LAB_CONSULTANT	Consultant
LAB_DIAGNOSIS	Diagnosis

Identifier	Description
LAB_DNAPRIORITY	DNA priority
LAB_DOB	Date of Birth
LAB_DOCTOR	Doctor/requesting officer
LAB_EPISODE	Episode
LAB_EXTID	External id
LAB_FASTING	If the tests required fasting
LAB_FINCAT	Financial category
LAB_GESTATION	If the tests required gestation
LAB_LOCATION	Lab location
LAB_PEI	PEI
LAB_PRIMSITE	Primary site
LAB_REQDATE	Lab request date
LAB_SEX	M/F/O/I/U/A
LAB_SITE	Lab site
LAB_SPECDET1	Spec detail
LAB_SPECDET2	Spec detail
LAB_SPECDET3	Spec detail
LAB_SPECDET4	Spec detail
LAB_SPECID	Specimen site
LAB_SPECIMEN	Specimen
LAB_URGENCY	Urgency
LAB_USER1	User
LAB_USER2	User
LAB_USER3	User
LAB_USER4	User
LAB_USERREC	User received
LAB_WARD	Patient ward

Identifier	Description
LAB_WARDCOLL	ward collection
QPS_REGSTATUS	Whether or not to lab has been saved by QPS
SS_CLIENT_ABN	Client ABN
SS_CLIENT_ADDR1	Client Address 1
SS_CLIENT_ADDR2	Client Address 2
SS_CLIENT_EMAIL	Client Email Address
SS_CLIENT_POSTCODE	Client Postcode
SS_CLIENT_PROJECT	Client Project
SS_CLIENT_QUOTE	Client Quote
SS_CLIENT_SUBURB	Client Suburb
SS_NO_ITEMS	Number of Items
SS_PKG_DESC	Package Description
SS_PKG_RECDATETIME	Package Received Date/Time
SS_PKG_REQDATE	Package Request Date
SS_SATCLIENT	Satellite Client
SS_SUBMITAUTH	Submitting Authority
SS_VENDOR_ADDR	Vendor Address
SS_VENDOR_NAME	Vendor Name
UR_ADDRESS1	Address 1
UR_ADDRESS2	Address2
UR_ALERT	Alert
UR_DOB	Date of Birth
UR_ETHNICITY	Ethnicity
UR_FINCAT	Financial category
UR_GNAME	Given name
UR_NAME	Surname
UR_POSTCODE	Postcode

Identifier	Description
UR_SEX	F/M/I/U/O/A
UR_SSBATCHREF	Batch reference number
UR_SSBOPNAME	Forensic Biology Operation Name
UR_SSCLIENT	Client
UR_SSCLIENTPROJECT	Client Project
UR_SSCLIENTQUOTE	Client Quote
UR_SSCOPNAME	Forensic Chemistry Operation Name
UR_SSCPRIOT	Number priority
UR_SSCRICAT	Crime Category
UR_SSCRISP	Crisp UR
UR_SSCRMCLS	Crime Class
UR_SSCSSTAT	Crime Status
UR_SSDESTROY	Forensic Destruction
UR_SSNOITEMS	Number of Items
UR_SSODF	Offence from date
UR_SSODT	Offence to date
UR_SSORDERNO	Order no
UR_SSPKGDESC	Package Description
UR_SSPKGRECDATETIME	Package Received Date and Time
UR_SSPKGREQDATE	Package Request Date
UR_SSPOLDAT	Police Due Date
UR_SSPROGRAM	Program
UR_SSPROJECT	Project
UR_SSSAMPLES	Samples
UR_SSSATCLIENT	Satellite Client
UR_SSSUBMITAUTH	Submitting Authority
UR_SSTEAMS	Teams

Identifier	Description
UR_SSVENDORADDR	Vendor Address
UR_SSVENDORNAME	Vendor Name
UR_SUBURB	Suburb
XML_ID	Internal identifier assigned to the current element in the XML document
XML_LABEL	Tag name for the current element
XML_LINES	Number of children under the current element in the XML document
XML_VALUE	Data associated with the current element in the XML document. It is the element Content.

38. Mathematical Subroutines

Subroutine Syntax	Description
abs(x)	Converts x to its absolute value
exp(x)	Calculates the value of “e” raised to the power of x
int(x)	Converts x to an integer
ln(x)	Calculates the natural logarithm of x
log(x)	Calculates the logarithm to base ten of x
max(a,b)	Calculates the maximum value of a & b
min(a,b)	Calculates the minimum value of a & b
pow(y,x)	Calculates the value of y raised to the power of x
rnd(x,y)	Rounds of the value of x to y significant figures
sqrt(x)	Calculates the square root of x
whole(x)	Round x to the nearest whole number

39. Data Subroutines

Subroutine Syntax	Description
accept(XXX)	Accepts the results for the test or panel. XXX represents a single test or all test within a panel.
add_antibiotics(TEST)	Triggers the addition of antibiotic nominations to the sensitivity panel(s) for the organism Test passed to it (TEST, e.g. ORG1 or UORG1). This function is not required when the organism is populated after the sensitivity panels have been ordered against the lab number. Example:

```
if (UOR1V = 'YES')
{
  add_request(ORG);
  if (!test_ordered(SENS1))
  {
    add_request(SENS1);
    add_request(SENS2);
    add_request(SENS3);
    add_antibiotics(UORG1);
  }
  if (aoc) add_request(ABX);
}
```

add_request(“TEST”)
 	
add_request(PANEL)
	Add the specified request to the current episode, where “TEST” represents a Test mnemonic and PANEL represents a Panel mnemonic. This subroutine cannot be used in the Registration Save Equation.
	
	The inverted commas are only required when passing a Test mnemonic to the function.
	
	Example for Test Haemoglobin:
	
	`add_request(“HBG”);`
	
	Example for Panel Full Blood Count:
	
	`add_request(FBC);`

an_program(“XXX”)	Sends a message to the specified analyser to program the request on the instrument. “XXX” represents a hardware device configured in the devices table.

Subroutine Syntax	Description
atof("string")	Converts an ascii string to a floating point value n = atof("23.54") returns n = 23.54
atoi("string")	Converts an ascii string to an integer n = atoi("15") returns n = 15
ccom_expand("CCOM")	Expands a coded comment into a variable or test result field. The comment must be the mnemonic of a configured coded comment and enclosed within quotation marks.
ccom_search(x,'abc')	The syntax is: ccom_search(x,y) or ccom_search(x,'abc') x represents the entity being searched y represents a variable containing the string being searched Where y is to contain a Code Comment, the ccom_expand() function should be used to expand the Comment into the variable, prior to passing the variable to ccom_search() 'abc' represents the literal string (abc) being searched Note: This function returns true when the string (y or 'abc') is found in the string x and does not have a limit for string length.

Subroutine Syntax	Description
check_delta(result,test,A,P)	Returns a value indicating the delta check status if the result indicated were inserted into the specified test. Returns: 0 if normal 1 if high -1 if low 2 if greater than critical high -2 if less than critical low "A" can be used to define an absolute value above or below (-A) the defined delta check range "P" can be used to define a percentage above or below (-P) the defined delta check range
check_refrange(result,test,A,P)	Returns a value indicating the reference range status if the result indicated were inserted into the specified test. Returns: 0 if normal 1 if high -1 if low 2 if greater than critical high -2 if less than critical low "A" can be used to define an absolute value above or below (-A) the defined reference range "P" can be used to define a percentage above or below (-P) the defined reference range
days_add(date,days)	Returns a date the number of days forward from the specified date field. Both system dates and test results can be used as the date field.
days_difference(date1,date2)	Returns the difference in days between two dates. This can be combined with a loadhistorical routine to calculate the date a test was last performed. e.g. days_difference(COLLDATE,COLLDATE[1])
delta(TEST)	Returns true (1) if the test has a delta STRING.

Subroutine Syntax	Description
duplicate_count(“XXX”)	This function is only available for STKS and STARRSED analysers For the STKS this function returns the number of times the WBC, RBC and HGB results have been received from the analyser for this specimen. For the STARRSED this function returns the number of times the ESR result has been received from the analyser. In both cases, the number returned is a combination of the number of times lab results have been received and the number of times the specific results have been received n = duplicate_count("STKS"); Returns n = 9003; This means that the analyser sent results for this specimen 3 times and that 9 (9 * 1000) results for WBC, RBC and HGB were received.

<table>
<thead>
<tr><th>Subroutine Syntax</th><th>Description</th></tr>
</thead>
<tbody>
<tr>
<td>eorder_copyto()</td>
<td>
<p>Returns integer 1 when the Extra Copies table contains one or more eOrder-derived entries without a Device specified. No parameters are passed to this function.</p>
<p>This function is likely to be used in combination with <code>is_eorder()</code> and <code>REG_MESSAGE</code>.</p>
<p>Example usage:</p>
<pre>
if (is_eorder()) {
  if (eorder_copyto()) REG_MESSAGE =
'Copy Doctor exists without device';
}
</pre>
<p>Evolution vLab™ Doctors added to the Extra Copies table are not subject to this function.</p>
<p>This script is designed to alert users to the presence of eOrder-derived incomplete free text data on the Extra Copies screen, and to enforce completion of the necessary details. The user has the option of populating the Device or selecting an Evolution vLab™ Doctor to replace the free text information. The system administrator should ensure the Device sub-table is configured appropriately for each Doctor.</p>
</td>
</tr>
<tr>
<td>eorder_count()</td>
<td>Returns number of eOrders (in ward/UR) as an integer.</td>
</tr>
</tbody>
</table>

Subroutine Syntax	Description
eorder_string(number, type)	Returns the specified field from the eOrder as a string. Type is the field required and number is the *n*th eOrder. This function is typically used in iterating code to return a specified field from each of the available eOrders. The 'number' passed to eorder_string() is an integer variable, iterating from 0 (the first available eOrder) through to eorder_count() – 1 (the last eOrder). Valid values for type are: 0 Order Code 1 Order Description 2 Order Number 3 Specimen Type 4 Scheduled collection date/time 5 Priority 6 Clinical Notes 7 Returns the string 'ADD ON' if the eOrder is an add-on, or a blank string otherwise. 8 Creation Date/Time (from HL7 field OBR-36.1) 9 Third-party Accession Number (full) 10 Truncated third-party Accession Number (last 5 digits)
ftoa(nnn.nn)	Converts a floating point number to a string. This function may be used in equations, print masks, general masks and batch analyser masks.
get_previousbatch(batch type, request, labno)	Outputs the previous batch number in equations and masks. batch type = Mnemonic of required configured batch type request = Mnemonic of Request (Test/Panel) labno = LabNo required
get_storage_info(labno)	Returns a string that contains the storage information for a laboratory number. It includes the rack name, row and column (if any). This function may be used in equations and masks.

Subroutine Syntax	Description
get_unique_tube(mode, index)	Returns a string containing either container number or tube type. Index is the *n*th tube. This function is typically used in iterating code to return the container number or tube type for each unique tube on the lab number. The 'index' passed to get_unique_tube() is usually an integer variable, iterating from 0 (for the first tube) through to unique_tube_count() – 1 (for the last tube). Valid options for mode: 1 Third-party Container ID 2 **Evolution vLab**TM Container Type 3 Container Notes
is_eorder()	Returns integer 1 when an eOrder exists on the current lab record. No parameters are passed to this function. Please refer to `eorder_copyto()` in this section for an example of usage.
itoa(nnnnnn)	Converts an integer to a string. This function may be used in equations, print masks, general masks and batch analyser masks.
lab_processed(labno)	Allows the GSI equation to check if the laboratory record has been processed before (in the same equation run). The use of this function eliminates the need to cycle through all the previous lines of the import file over and over during the equation run.
lis_testcount(n)	Returns the number of tests with unsuppressed results. n refers to the number of tests from beginning not to include.
lis_testlist(n,p)	Prints a list of tests on the lab number. n refers to the number of tests from beginning not to include. P refers to the number of tests after n to included.

Subroutine Syntax	Description
listcount(list)	Returns the total number of items in the specified list. The list must have the format “{A}{B}{C}” but it may be a test list or a list of other items; it need not contain valid test codes. The function disregards all tlist codes such as 'o' and 'r'.
listelement(n,tlist)	Returns a string of the first n items in the specified list. The list must have the format “{A}{B}{C}” but it may be a test list or a list of other items; it need not contain valid test codes. The function disregards all tlist codes such as 'o' and 'r'. For example: tlist = “{NA}{K}{CL}{CRE}{UREA}”; str = listelement(3,tlist); returns str = “NA,K,CL”
loadcumulative(n,tlist)	Loads n cumulative results for the tests listed in the test list. Test lists should be in the format “{TESTA}{TESTB}” This subroutine includes both validated and unvalidated results and includes the current episode. A maximum of 500 episodes at a time can be load with this function call.
loadhistorical(n,tlist)	Loads n historical results for the tests listed in the test list. Test lists should be in the format “{TESTA}{TESTB}” This subroutine will only return level 2 validated results. The current record is not included in the number of results to be loaded. A maximum of 500 episodes at a time can be load with this function call.

Subroutine Syntax	Description
loadlabrecs(number, sort, tlist)	Load results that are not required to be validated or resulted; so that these results can be used for result computations. Provide flexibility to sort loaded results by collected, received or registered date Addresses the limitations in the current load historical and load cumulative subroutines and can be used in all system equations including screen masks, print masks, Request Add, Registration Save, Modify, Validate, Analyser daemon, level 1 and Generic System Interface (GSI). **Parameters:** number (int)= number of records to be loaded sort (int) = 0 - Collected Date 1 - Registered Date 2 - Received Date 3 - External Id 4 - Reverse Collected Date 5 - Reverse Registered Date 6 - Reverse Received Date 7 - Reverse External Id tlist (string) = List of tests to filter labs by The recommended maximum number of records to load is 50 records.
mins_difference(time1,time2)	Calculates the difference in minutes between two times. **Note:** this assumes that both times are on the same date.
remove_request(XXX)	Removes the specified test or panel from the current episode.

Subroutine Syntax	Description
report_validated(XXX)	Returns 1 when there are no unvalidated results populated in the report for printing, including any cumulative results included in the report. To accurately reflect the report status this function must be called towards the end of the print mask, once the report is populated with all of its results. This function does not utilise any arguments (parameters). However, the parsing algorithm used by **Evolution vLab**™ requires a placeholder argument, represented by 'XXX'. For example, some clients use 0: `report_validated(0);` **Note:** Should this function be called at the start of the report mask script, prior to inclusion of any results, it will return the value 1. This is because there are no unvalidated results present (in actuality, no results at all). Should this function be called part-way through the report mask, when some but not all of the results have been included, the value returned will be accurate at that point in the construction of the report, but may not reflect the desired outcome.
result_allow(TEST,result)	Allow the specified result for the specified test

Subroutine Syntax	Description

suppress_output(n)	This function is suppress_output(n), where n is 1 or 0.
	
	When the argument 1 is passed, **Evolution vLab**™ suppresses the output of all content to the report.
	
	When the argument 0 is passed, **Evolution vLab**™ does not suppress the output and therefore all output subroutines populate the report normally.
	
	This function is designed to be used as part of an encapsulating script for all report masks, in combination with some custom variables for tracking and a while statement to produce two 'iterations' of the report.
	
	Example:
	suppress_output(1);
	printpass - 0;
	while (printpass < 2)
	{
	/* existing print mask body goes here */
	printpass - printpass + 1;
	suppress_output(0);
	}
	
	Masks such as XHEAD do not require this encapsulation and should be left unchanged. They are called within the while statement as shown above.
	
	For the first iteration the report is 'built' by the mask but the outputs are suppressed from populating the report. This iteration allows the script to establish details such as the total page count and the validation status for the entire report.
	
	The second iteration actually generates the report.
	
	Note: Citadel Health recommends that the existing print masks be reviewed to remove any script elements or methodologies that are no longer required.

Subroutine Syntax	Description
result_count(tlist)	Returns the number of items in the specified test list (tlist) calculated after the tlist codes (e.g. ‘o’, ‘r’) have been applied. The test list must have the format “{TEST1}{TEST2}”. **Example:** tlist0 = “{TEST1}{TEST2}{TEST3}{TEST4}{TEST5}”; tlist1 = “o{TEST1}{TEST2}{TEST3}{TEST4}{TEST5}”; tlist2 = “r{TEST1}{TEST2}{TEST3}{TEST4}{TEST5}”; Lab number 8000-1234: • TEST1, TEST2 and TEST3 ordered • Only TEST1 resulted result_count(tlist0) -> returns 5 result_count(tlist1) -> returns 3 result_count(tlist2) -> returns 1
result_disallow(TEST,result)	Disallows a result for the specified tests. A result of 0 disallows all result for the specified test.
result_match(test1,result1,test2, result2)	Returns true if both tests have the corresponding result
retest_interval(XXX)	Returns true if the specified test/panel has a retest interval over-ride.
strcasecmp(a,b)	Returns “0” if string a matches string b, case insensitive
strcmp(a,b)	Returns “0” if string a is identical to string b
strfind(x,”a,b,c,d”)	Returns true if string a or b or c or d is found in string x
strlen(a)	Returns the number of characters in string *a*. The parameter *a* must be a string. Test mnemonics are not strings and therefore may be not be passed to this function.
strsearch(x,"abcd")	Returns true when “abcd” is found in string x. This function supports strings up to 250 characters in length.
substring(a,b,x)	Returns substring of a, which is x characters long starting at character b. The first position in the string is 1.

Subroutine Syntax	Description
suppress_output(x)	When the argument 1 is passed, **Evolution vLab**™ suppresses the output of all content to the report. When the argument 0 is passed, **Evolution vLab**™ does not suppress the output and therefore all output subroutines populate the report normally. This function is designed to be used as part of an encapsulating script for all report masks, in combination with some custom variables for tracking and a while statement to produce two 'iterations' of the report.
test_check_status(STRING,TEST)	Checks for the presence of the greater than (>) and/or less than (<) STRING against the Test result, where `STRING` is an integer indicating the STRING type and `TEST` is the Test mnemonic. The function returns `0` when the specified `STRING` is not present against the Test result, and returns `1` when the STRING is present. Supported values for the `STRING` argument are: `1` Check for the less than (<) STRING. `2` Check for the greater than (>) STRING. `3` Check for the less than (<) and greater than (>) STRING. Checking for the greater than and/or less than STRING may be desirable as part of scripted calculations involving the Test result.
test_loadvalue(XXX)	Loads the value for the specified Test, where XXX represents the Test Mnemonic. Applications for this function include setting a user-defined variable to the Test value. For example: myvar = test_loadvalue(TEST);

Subroutine Syntax	Description

test_modified(XXX)	Checks whether the result for the specified Test (XXX) has been modified on the lab number. XXX represents the Test Mnemonic.
	Returns 1 when the Test has been modified and 0 (zero) otherwise. When the specified Test is not present on the lab number the function returns 0.
	Example:
	if (test_modified(NA) = 1) {
	/* desired code */
	}

test_ordered(XXX)	Returns true when the specified test or panel (XXX) is present on the specimen registration screen for the current episode. This function returns false when the Test passed to it has been manipulated by a Test Processing Rule. For example, when Test ‘B’ is configured as the Actual Request for Test ‘A’, test_ordered(A) and test_ordered(B) would each return false. This does not apply to Panels subject to Test Processing Rules.
test_result(XXX)	Returns true if the specified Test or Panel contains results.
test_validated(XXX)	Returns true if the Test or Panel is Level 2 validated.
testing_lab(XXX) = “LAB”	Returns true if the testing lab of the test matches the lab specified Testing lab must use the configured mnemonic and be enclosed within quotation marks.
testing_method(XXX) = “METHOD”	Returns true if the specified test was tested using the specified testing method. The METHOD must use the configured mnemonic and be enclosed by quotation marks. The test method must be defined either via the test/panel configuration or via the test processing rules.

Subroutine Syntax	Description
testlist_item(tlist,n)	Allows common code to be placed in a loop, allowing processing of each item in a test list, rather than duplicating sections for each item. This function can be used for GSI and in normal equations. This function returns the testID n = test element required
testres_encode(test,”result”,n,p)	Encodes the result into the specified test. The result must be a configured test result mnemonic and enclosed within quotation marks n refers to the required starting char of the result p refers to the required number of chars of the result. n = 0 - start p = 0 all chars will be included.
unique_tube_count()	Returns the number of containers receipted to the lab number (as an integer).

validate(XXX)	Validates the specified Test or Format Panel (XXX). Please note that the function does not support the validation of Panels that are not Format Panels.
	For example, where the orderable Panel LFT is its own Format Panel, the following function call will validate the results in that Panel:
	`validate(LFT);`
	However, where the orderable Panel LFT has the Format Panel XBGEN, ‘XBGEN’ should instead be passed as the argument to the validate() function, as follows:
	`validate(XBGEN);`

40. Reporting Subroutines

Subroutine Syntax	Description
add_extra_copy(n,destination)	Adds “n” extra copies for the specified destination to specimen registration extra copy details. The destination can either be: 1. Doctor mnemonic 2. Free text When inserting a free text extra copy the syntax is “copy to name^address^device mnemonic” and must be enclosed within quotation marks

Subroutine Syntax	Description

cumpageno(page)	Returns the cumulative report page number according to the value supplied for `page`.
	Valid options for `page`:
	`0`: Returns the page number in the cumulative report sequence.
	`1`: Returns the page number for the final page in the cumulative report sequence
	In combination, these two values for page facilitate cumulative report page numbering in the style 'x of y'
	Page numbers are returned as strings and are calculated based on the number of columns per page and the results loaded by the `loadcumulative` function, which must be called prior to this subroutine.
	Example of usage:
	`n = loadcumulative(ncols,tlist);`
	`pageno= cumpageno(0);`
	Example of page numbers returned:
	When cumulative report is first generated:
	First page: `cumpageno(0)` returns '1', `cumpageno(1)` returns '1' (1 of 1).
	When additional lab records are appended to the report and a second page is generated:
	First page: `cumpageno(0)` returns '1', `cumpageno(1)` returns '2' (1 of 2).
	Second page: `cumpageno(0)` returns '2', `cumpageno(1)` returns '2' (2 of 2).
	Later when a third page is generated:
	First page: `cumpageno(0)` returns '1', `cumpageno(1)` returns '3' (1 of 3).
	Second page: `cumpageno(0)` returns '2', `cumpageno(1)` returns '3' (2 of 3).
	Third page: `cumpageno(0)` returns '3', `cumpageno(1)` returns '3' (3 of 3).

Subroutine Syntax	Description
date_to_words(XXX)	Converts a date field to verbose format. For example 09/09/2005 would be converted to 9th September 2005.
document_repaginate(string,linesperpage)	Repaginates the results entered into a word document. Should be used after the result_format or result_format_images subroutines.
getlines(string,startline,nlines)	Returns a String of the lines required. String refers to the string to analyse. Startline refers to the line to start from. nlines refers to the max number of lines required.
HL7_OBR4_1	General Mask identifier introduced to facilitate Secure Messaging Header and Footer configuration. Returns the OBR4.1 value (Request Mnemonic).
HL7_OBR4_2	General Mask identifier introduced to facilitate Secure Messaging Header and Footer configuration. Returns the OBR4.2 value (Request Description).
image_height(n)	Returns the height of the nth image loaded from the images_load routine
image_output(n,x,y,size)	Outputs the *n*th image loaded via the images_load() subroutine. The *x* and *y* values determine position of the image, with the top left corner of the image at coordinates (x,y). The *size* is the magnification factor; specify 1.0 to output the image without adjusting its size. 0.5 produces a half-size image and 2.0 doubles the size of the image.

Subroutine Syntax	Description
image_text(n,text)	Returns details for the *n*th image loaded via the images_load() subroutine. Valid values for `text` are: 0 Returns the image number 1 Returns the image description Request form images do not possess an image description; please specify 0 for images of that type.
image_width(n)	Returns the width of the *n*th image loaded via the images_load() routine.

Subroutine Syntax	Description

images_load(type,key,generation,"imagetype",0)	Loads the images specified via the parameters described below. The function is most often used in combination with the output_image() subroutine.
	type
	Determines whether the images are loaded from the UR record (i.e. across all lab numbers for the UR Number) or only the specified lab number. Specify 0 for UR record or 1 for lab number.
	key
	The cumulative array index for the lab number. Specify 0 for the current lab record. This value is referenced only when the *generation* parameter is set to 1.
	generation
	Determines the lab number from which the image is loaded. Specify 1 to load the image from the lab record specified by the key parameter, or 0 for the current lab record. When 0 is specified the *key* parameter is ignored.
	"imagetype"
	Determines whether the images are loaded from the Request Forms or Images tab for the lab number(s). This parameter must be enclosed in double quotation marks. Specify the Mnemonic of the desired Image Type (Administration > Image Storage > Types) to load images of that Type stored in the Images tab for the lab record(s). Specify a null value i.e. "" to load the images from the Request Forms tab for the lab record(s).
	status
	Determines whether only annotated images or all images are loaded. Specify 0 for annotated images and 1 for all images.
	Example usage:
	images_load(1,1,0,"",0);
	image_output(0,1,1,1.0);

Subroutine Syntax	Description
include_mask("MASK")	Includes the specified mask into the current mask. **Note:** This function can be used a maximum of 512 times per mask. Masks cannot be included in summary reports.
interim_repsum(XXX)	Posts an interim summary report for the specified panel.

nata_accred(test)	Outputs the indication if a test is "NATA" accredited as configured for the respective test, lab group, date according to the configuration for the function.
	Example
	if (nata_accred(KEAMPA))
	output_text(36,1,7,0,0,"Y");
	else
	output_text(36,1,7,0,0,"N");
	if (nata_accred(KEWCAF)=0)
	output_text(0,2,7,0,0,"NATA Accreditation does not apply to the performance of this services");

outcum_audittest(page,x,y,down,font,size,orientation)	Outputs a list of test mnemonics according to the parameters given. Page defines the page number to output data for. Down defines the number of audits to display per page. Orientation defines the direction the page is output in: 0 = Vertical (Advancing on the Y axis) 1 = Horizontal (Advancing on the X axis)

Subroutine Syntax	Description
outcum_audittext(page,x,y,down,font,size,orientation)	Outputs a list of audit text according to the parameters given. Page defines the page number to output data for. Down defines the number of audits to display per page. Orientation defines the direction the page is output in: 0 = Vertical (Advancing on the Y axis) 1 = Horizontal (Advancing on the X axis)
outcum_audituser(page,x,y,down,font,size,orientation)	Outputs a list of users according to the parameters given. Page defines the page number to output data for. Down defines the number of audits to display per page. Orientation defines the direction the page is output in: 0 = Vertical (Advancing on the Y axis) 1 = Horizontal (Advancing on the X axis)
outcum_highprec(page,x,y,across,down,font,size, xfont,xsize,just,tlist)	Outputs a list of high precisions according to the parameters given. Page defines the page number to output data for. Across defines the number of labs across a page. Down defines the number of tests down a page. The parameters xfont and xsize allow the user to configure a different font and size of the test names if the current result is outside the configured range. Justification uses the standard justification options. Test lists should be in the format “{TEST1}{TEST2}” and can be prefixed by the standard test list functions.

Subroutine Syntax	Description
outcum_lowprec(page,x,y,across,down,font,size, xfont,xsize,just,tlist)	Outputs a list of low precisions according to the parameters given. Page defines the page number to output data for. Across defines the number of labs across a page. Down defines the number of tests down a page. The parameters xfont and xsize allow the user to configure a different font and size of the test names if the current result is outside the configured range. Justification uses the standard justification options. Test lists should be in the format "{TEST1}{TEST2}" and can be prefixed by the standard test list functions.
outcum_pagecount(across,down,tlist)	Calculates and returns the total number of pages required to output loaded labs. Across defines the number of labs across a page. Down defines the number of tests down a page. Test lists should be in the format "{TEST1}{TEST2}" and can be prefixed by the standard test list functions.

Subroutine Syntax	Description
outcum_refrange(page,x,y,across,down,font,size,xfont, xsize,just,tlist)	Outputs a list of reference ranges according to the parameters given. Page defines the page number to output data for. Across defines the number of labs across a page. Down defines the number of tests down a page. The parameters xfont and xsize allow the user to configure a different font and size of the test names if the current result is outside the configured range. Justification uses the standard justification options. Test lists should be in the format “{TEST1}{TEST2}” and can be prefixed by the standard test list functions.
outcum_results(page,x,y,across,down,font,size,xfont,xsize,just, format,tlist)	Outputs a list of results according to the parameters given. If a given test does not exist on a lab, then ‘—‘ will be output. Page defines the page number to output data for. Across defines the number of labs across a page. Down defines the number of tests down a page. The parameters xfont and xsize allow the user to configure a different font and size of the test names if the current result is outside the configured range. Justification uses the standard justification options. Format is used to format the display of test results. Test lists should be in the format “{TEST1}{TEST2}” and can be prefixed by the standard test list functions.

Subroutine Syntax	Description
outcum_testmethod(page,x,y,across,down,font,size,xfont,xsize,just,tlist)	Outputs a list of testing methods according to the parameters given. Page defines the page number to output data for. Across defines the number of labs across a page. Down defines the number of tests down a page. The parameters xfont and xsize allow the user to configure a different font and size of the test names if the current result is outside the configured range. Justification uses the standard justification options. Test lists should be in the format "{TEST1}{TEST2}" and can be prefixed by the standard test list functions.
outcum_testname(page,x,y,across,down,font,size,xfont,xsize,just,mode,tlist)	Outputs a list of test names according to the parameters given. Page defines the page number to output data for. Across defines the number of labs across a page. Down defines the number of tests down a page. The parameters xfont and xsize allow the user to configure a different font and size of the test names if the current result is outside the configured range. Justification uses the standard justification options. Mode is used to determine which test name to output: 0 = Full description 1 = Mnemonic 2 = Alias 3 = Display name Test lists should be in the format "{TEST1}{TEST2}" and can be prefixed by the standard test list functions.

Subroutine Syntax	Description
outcum_units(page,x,y,across,down,font,size,xfont,xsize,just,tlist)	Outputs a list of units according to the parameters given. Page defines the page number to output data for. Across defines the number of labs across a page. Down defines the number of tests down a page. The parameters xfont and xsize allow the user to configure a different font and size of the test names if the current result is outside the configured range. Justification uses the standard justification options. Test lists should be in the format “{TEST1}{TEST2}” and can be prefixed by the standard test list functions.
output_accreditation	Outputs the “Full Name” of the Accreditation as configured for the respective test, lab group, and date according to the configuration for the function. The complete parameters are: output_accreditation(x axis postion,y axis position,font/colour code, point size,justification string,test or tlist) Example: output_accreditation(45,10,0,0,0,tlista) Note: If the Test Accreditation, NATA is configured as No an “*” is displayed at the start of the output of the Test Name.

Subroutine Syntax	Description
output_barcode(x,y,dx1,dx2,dy,rotation,type,data)	Formats and outputs a barcode rather than a numeric string. The x and y co-ordinates represent the bottom left corner of the barcode. dx1 represents the width of the thin bands and dx2 represents the thickness of the thick bands of the barcode dy id the height of the barcode Rotation determines the orientation of the barcode. Valid values are: 0 No rotation is applied to the barcode before output (horizontal orientation). 90 The barcode is rotated 90 degrees to the right for output (vertical orientation). Valid barcode types are: 1 = Interleaved 2 of 5 2 = Interleaved 2 of 5 with check digit 6 = Code 128

Subroutine Syntax	Description
output_box(x,y,width,height,linewidth, lineintensity,fill)	Draws boxes and lines according to the parameters given. This subroutine is available for use in print masks only. The x and y co-ordinates represent the bottom left corner of the box or line. Width and height determine the size of the box. A height of 0 draws a horizontal line; a width of 0 draws a vertical line. Linewidth is number between 0 and 1, with 0 giving the thinnest line and 1 giving the thickest line. Lineintensity is a number between 0 and 1, with 0 giving the faintest line and 1 giving a solid line. A value of “-” produces no line at all. Fillvalue determines the fill intensity of the box. A value of 0 gives a solid black fill and value of 1 gives blank fill. **Note:** The line width and line intensity may not be rendered in the online preview (via Shift Insert) exactly as they appear in the printed report.

Subroutine Syntax	Description
output_control(x)	Allows the user to send commands to the printer. Valid controls include: 0 – Designates the middle tray of HP laser jet printer 1 - Designates the lower tray of HP laser jet printer 2 - Designates no tray of HP laser jet printer is to be used 3- Designates the upper tray of HP laser jet printer 4 – Designates print is to be on the reversed side of the page for duplex printing “ showpage “ – transfers the current page to the printer and begins a new page. The quotation marks and spaces before and after the control are necessary. For postscript printers only. “ \033&IOH ” - transfers the current page to the printer and begins a new page for PCL printers only. The quotation marks and spaces before and after the control are necessary “ 180 rotate “ – Designates the print format is to be rotated 180 degrees. Useful in duplexed reports. The quotation marks and spaces before and after the control are necessary. “ 602 -844 translate “ – Converts the report to a landscape format. The quotation marks and spaces before and after the control are necessary

Subroutine Syntax	Description
output_cumgraph(x,y,width,height,test,0,0,0)	Formats and outputs a graph of results displayed as points with the reference range represented as a solid line. Must be used in conjunction with the loadcumulative subroutine. The number of points displayed will be determined by the load size of the loadcumulative. The x and y co-ordinates represent the bottom left corner of the graph. Width and height determine the output size of the graph. The three zeros at the end of the routine are place holders and are not currently used.
output_cumrefrange(x,y,font,size,xfont,xsize, justification,test_list)	This subroutine can only be used in conjunction with the loadcumulative subroutine Formats and outputs the reference range(s) for a given test code or group of test codes according to the parameters given. The reference range printed will be those applicable to the most recent laboratory record. Font codes are given at the end of this section. The parameters xfont and xsize allow the user to configure a different font and size of the reference range if the current result is outside the configured reference range. Justification uses the standard justification options listed at the end of this section.

Subroutine Syntax	Description
output_cumresults(x,y,font,size,xfont,xsize, justification,format,generation,test_list)	This routine can only be used after the loadcumulative subroutine. Outputs a single or list of results according to the parameters given. Font codes are given at the end of this section. The parameters xfont and xsize allow the user to configure a different font and size of the results if the current result is outside the configured reference range. Justification uses the standard justification options listed at the end of this section. Format is used to format the display of the test results, valid format codes are given at the end of this section. Generation is used as an index to determine which result is to be output, and is used in cumulative reporting. If the generation is entered as “n” the system will output the nth previous result. A value of zero outputs the oldest result. Test lists should be in the format “{TEST1}{TEST2}” and can be prefixed by the standard test list functions listed in the next section of this document.

Subroutine Syntax	Description
output_document(x,y,font,size,justification,test, linesperpage,currentpage,startingpage)	Outputs a Word document onto a print mask. This function must be used in combination with result_format(), which performs the formatting. The document_repaginate() function is optional, should repagination be required. The **test** parameter should be a variable containing the formatted Word report for the appropriate text. Passing a Test code instead will produce an unformatted report. The **justification** parameter must include an uppercase W, which may coexist with another justification code. Example: “80.420wW”, including the quotation marks. Suggested usage: 1. Set a variable to the output of the result_format() subroutine. 2. Pass this variable to document_repaginate(), if required. Update the variable to contain the output of document_repaginate(). 3. Pass the variable to output_document().
output_email(x,y,font,size,colour,”email”, ”text”)	Outputs a hyperlink to an email address for use in the **Evolution vLab**™ Clinical Viewer browser or via Shift-F1 report viewing. Colours should be selected using HTML colour palates. The default colour is blue. The url should be in an email format Eg: username@xxx.xx.xx Text refers to the “clickable” text to be displayed if used in **Evolution vLab**™ Clinical Viewer.

Subroutine Syntax	Description
output_eps("file.ps",x,y,xscale,yscale,rotation)	Outputs an electronic version of the postscript file of a print mask file.ps = filename xscale = magnification (float) ie; 2.0 = double size yscale = magnification (float) ie: 1.0 = ½ size rotation = 0-360 (degree of rotation required.
output_guideline	Outputs the "Guideline" text (0) or the guideline "Value" (1) according to the configuration for the function of the Mode/6th identifier parameter for the respective test, date, and specimen. The complete parameters are: output_guideline(x axis position,y axis postion,font/colour code,point size,mode,justification string,test or tlist) Example: output_guideline(45,20,0,0,1,0,test or test list) will output the guideline Value. Example: output_guideline(45,20,0,0,0,0,test or test list) will output the guideline Text.
output_highprec(x,y,font,size,xfont,xsize, justification, tlist)	Formats and outputs the high precision limit for a given test code or group of test codes according to the parameters given. Font codes are given at the end of this section. The parameters xfont and xsize allow the user to configure a different font and size of the reference range if the current result is outside the configured reference range. Justification uses the standard justification options listed at the end of this section.

Subroutine Syntax	Description
output_hlseven("XXX") OR output_hl7("XXX")	Formats and sends results according to the HL7 configuration for the specified HL7 feed. Both routines shown perform the same function, however some versions of the UNIX operating system will not allow the numerical 7 in the subroutine and will cause equation errors. It is recommended that the word seven be used in the subroutine.
output_lowprec(x,y,font,size,xfont,xsize, justification, tlist)	Formats and outputs the low precision limit for a given test code or group of test codes according to the parameters given. Font codes are given at the end of this section. The parameters xfont and xsize allow the user to configure a different font and size of the reference range if the current result is outside the configured reference range. Justification uses the standard justification options listed at the end of this section.
output_ncidd_xml() No parameters required	Formats DNA results in a QHHSSA specified format, and is designed for use in DNA analysers. Stores file to configured directory.
output_panelname	Outputs the panel display name according to the configuration for the function. Example: output_panelname(45,1,7,0,7,0,0,3,0,test or test list)

Subroutine Syntax	Description
output_raw(“string”)	Outputs a string and converts certain string sequences to the raw values. The string sequences are :- \r - converts to CR (Carriage return) \s - Converts to STX (start of text) \e - converts to ETX (end of text) \f - Converts to FF (form feed) \t - Converts to TAB \n - Converts to LF (line feed) output_raw("The quick brown fox\r\n"); returns "The quick brown fox<CR><LF>"
output_rawimage(x,y,width,height,"file.tif",0)	Allows the output of images and logos on reports. The x and y co-ordinates represent the bottom left corner of the image. Width and height determine the size of the image output. The image files must be in TIF format and cannot exceed 1MB in size. The file must be provided to Citadel Health. The last parameter is set to 0.
output_refrange(x,y,font,size,xfont,xsize, justification,tlist)	Formats and outputs the reference range(s) for a given test code or group of test codes according to the parameters given. Font codes are given at the end of this section. The parameters xfont and xsize allow the user to configure a different font and size of the reference range if the current result is outside the configured reference range. Justification uses the standard justification options listed at the end of this section.

Subroutine Syntax	Description
output_results(x,y,font,size,xfont,xsize, justification,format,generation,tlist)	Outputs a single or list of results according to the parameters given. Font codes are given at the end of this section. The parameters xfont and xsize allow the user to configure a different font and size of the results if the current result is outside the configured reference range. Justification uses the standard justification options listed at the end of this section. Format is used to format the display of the test results; valid format codes are given at the end of this section. Generation is used to determine which result is to be output, and is used in cumulative reporting. If the generation is entering as “n” the system will output the nth previous result. A value of zero outputs the current result. Test lists should be in the format “{TEST1}{TEST2}” and can be prefixed by the standard test list functions listed at the end of this section.

Subroutine Syntax	Description
output_sensitivities(x,y,fontsize,dx1,dx2,dy,style,n, generation,0)	Formats and output the sensitivities for each organism. dx1 is the distance between the output of the organism name and the first antibiotic dx2 is the distance between each antibiotic dy is the distance between organisms Style determines the style of the output of the antibiotic. Valid styles are: 0 = mnemonic of antibiotic 1 = Full name at 42 degree angle 2 = Full name at 42 degree angle with dividing lines 10 = mnemonic of antibiotics on the x-axis with the organism on the y axis n is the number of columns (only applicable if the style is 10). The default value is 6. Generation determines which previous result to output when used in conjunction with a loadhistorical subroutine. Zero outputs the current results. Last parameter set to 0.
output_signature(x,y,height,width,user)	Outputs the user's signature from image file configured in the user configuration screen.
output_sigtext(x,y,font,size,just,text)	Outputs content as significant text, according to the parameters given. Significant text is referenced by **Evolution vLab**™ when determining whether a given report has changed since it was last issued to **Evolution vLab**™ Clinical Viewer. In the event that a significant change is detected, **Evolution vLab**™ updates **Evolution vLab**™ Clinical Viewer accordingly. The argument `text` accepts a literal string encapsulated in quotation marks, such as "This is my text", a Test Mnemonic, system variable or user-defined variable. The argument `just` accepts a standard justification option; refer to section 50 Justification. The argument `font` accepts a font code; refer to section 53 Font Parameter.

Subroutine Syntax	Description
output_testmethod()	Outputs a single or list of test methods according to the parameters given.
output_testname(x,y,font,size,xfont,xsize, justification,mode,generation,tlist)	Outputs a single or list of test names according to the parameters given. Font codes are given at the end of this section. The parameters xfont and xsize allow the user to configure a different font and size of the test names if the current result is outside the configured reference range. Justification uses the standard justification options listed at the end of this section. Mode is used to determine which test name to output: 0 = Full description 1 = Mnemonic 2 = Alias 3 = Display name Generation is not used. Test lists should be in the format "{TEST1}{TEST2}" and can be prefixed by the standard test list functions listed at the end of this section.
output_text(x,y,font,size,just,text)	Outputs text according to the parameters given. The argument `text` accepts a literal string encapsulated in quotation marks, such as "This is my text", a Test Mnemonic, system variable or user-defined variable. The argument `just` accepts a standard justification option; refer to section 50 Justification. The argument `font` accepts a font code; refer to section 53 Font Parameter.
output_tm_alert(0)	Outputs the transfusion medicine alert as a string

Subroutine Syntax	Description
output_units(x,y,font,size,xfont,xsize, justification,test_list)	Formats and outputs the units for a given test code or group of test codes according to the parameters given. Font codes are given at the end of this section. Justification uses the standard justification options listed at the end of this section. The parameters xfont and xsize allow the user to configure a different font and size of the units if the current result is outside the configured reference range.
output_url(x,y,font,size,colour,”url”,”text”)	Outputs a hyperlink to a url for use in the **Evolution vLab**™ Clinical Viewer browser or shift-F1 result viewing. Colours should be selected using HTML colour palates. The default colour is blue. The url should be in the format http://www.myurl.com Text refers to the “clickable” text to be displayed if used in **Evolution vLab**™ Clinical Viewer.
pdf_version(“labno”, “test”)	Outputs the highest pdf version number for the test on the lab number
remove_extra_copy(“destination”) OR remove_extra_copy(doctor)	If double quotes are used it moves the extra copies from the destination If double quotes are not used it moves the extra copies from the doctor
result_format(TEST,generation,linewidth)	Formats results that have been entered via a Word document. It can be used without another word document routine if the result is a text. It cannot be used with a tlist. Generation is used to output the nth previous result when used in conjunction with a loadhistorical subroutine. Zero outputs the current result. Linewidth sets the maximum number of characters per line.

Subroutine Syntax	Description
result_format_images(TEST,generation, linewidth)	Formats results that have been entered via a Word document and retains any images included in the word document. . It can be used without another word document routine if the result is a text. It cannot be used with a tlist. Generation is used to output the nth previous result when used in conjunction with a loadhistorical subroutine. Zero outputs the current result. Linewidth sets the maximum number of characters per line.

send_sms(number,device,message)	Generates an SMS text message. The function accepts three arguments:
	`number`
	The telephone number. This may be specified as a mobile number enclosed in quotation marks e.g. `"0400123456"`, or via a string variable or appropriate identifier such as `DR_MOBILE` or `CONS_MOBILE` without quotation marks.
	`device`
	The Mnemonic of the Hardware Device for transmission of the SMS. This may be specified as directly in quotation marks e.g. `"SMS"`, or via a string variable.
	`message`
	The content (body) of the message. This may be specified directly in quotation marks e.g. "Report available" or via a string variable or identifier.
	Examples:
	`send_sms(DR_MOBILE,"SMS","Message text");`
	`send_sms("0400123456","SMS",mytext);`
	SMS transmissions are recorded in the Specimen Audit with Event description `SMS Sent [Mobile Number]`, e.g. ‘SMS Sent 0400123456’.

strlines(string)	Returns the number of lines in a given string. Must be used after the result_format subroutines.

Subroutine Syntax	Description
strmklower(string)	Converts the given string to lower case. This function can be used in equations, print masks, general masks and batch analyser masks.
strmkupper(string)	Converts the given string to upper case
testres_expand(“test”)	Expands a test result mnemonic out to the description. This function can be used in equations, print masks, general masks and batch analyser masks.
validate_user(format,test)	Returns the user details that last validated the specified test Valid formats are: 0 – user id 1 – full name Use in combination with the output_text subroutine.

41. Workflow Subroutines

Subroutine Syntax	Description
listinsert(“LIST”)	Inserts the episode to the specified list. The list mnemonic must be within inverted commas.
listinsert_test(”LIST”,TEST)	Inserts the specified test/panel to the specified list. The list mnemonic must be within inverted commas. The list can be specified to be at a particular site entering the list mnemonic as LIST~LAB
listremove(“LIST”)	Removes the episode from the specified list. The list mnemonic must be within inverted commas.

42. GSI Subroutines

This function runs in minimal time and does not impact negatively on memory.

Subroutine Syntax	Description
allocate_labno()	No parameters. Allocate and return a lab number. A maximum combination of 1000 Lab No and/or UR No records can be allocated.
allocate_urno("ur_prefix")	ur_prefix is the prefix of the UR number. The number portion of the UR is returned as determined by the next number that can be allocated for that UR prefix. The prefix must have increment set to yes. A maximum combination of 1000 Lab No and/or UR No records can be allocated.
associate_crisp(ur_number)	Associates ur_number to currently opened LAB and UR records. Create UR record for ur_number if it doesn't already exist.
fetch_labur(urno, labno)	Gets the lab and UR record for the urno (UR number) and the labno (lab number) passed and creates them if necessary.
gsi_error_log(line_number, line_field_number, error_msg)	Add error_msg string to the gsi log. Line_number is the line where the error occurred and the field_number is the field in the line where it occurred
gsi_status(adding,updating, labno, urno)	Updates the GSI status of how many labs have been added/updated. For this labno and this urno, it updates the status as to whether the lab and UR record (indicated by the arguments labno and urno respectively) were added or updated. The arguments adding and updating can either be 1 or 0 to indicate whether the lab and UR supplied were added to the system or whether they've been updated in the system respectively. They should not both be 1 and they shouldn't both be 0 at the same time.

Subroutine Syntax	Description
lab_processed(labno)	Allows the GSI equation to check if the laboratory record has been processed before (in the same equation run). The use of this function eliminates the need to cycle through all the previous lines of the import file over and over during the equation run.
loadlabrecs(number, sort, tlist)	Allows the GSI equation to specify the number of records to load, up to all available records on a UR number. **Parameters:** number (int)= number of records to be loaded sort (int) = 0 - Collected Date 1 - Registered Date 2 - Received Date 3 - External Id 4 - Reverse Collected Date 5 - Reverse Registered Date 6 - Reverse Received Date 7 - Reverse External Id tlist (string) = List of tests to filter labs by The recommended maximum number of records to load is 50 records.
splitstr_count(string, delimeter)	Returns the number of times it could split the string passed in based on the delimeter; returns the number of times the delimeter occurs.
splitstr_get(string, delimeter, position)	Returns the string from position in string when split by delimeter. If an invalid position then an empy sting is returned.

Subroutine Syntax	Description
test_resultstring(testid, return_type, str_length)	Expands the test identifier given. The testid is the test mnemonic and the return_type is a number which indicates whether or not to just return the short result (0) or to return the full result (1). Str_length is a number which indicates the maximum string length to be returned.
decode-string(“FORMAT”,”STRING”)	If the “FORMAT” is the word ”CRISP” the return will be the CRISP number without the prefix If the “FORMAT” is “LABNO” it will return the lab number from the string passed If the “FORMAT” is “URNO” it will return the UR number from the string passed If the “QPS_DATE” where the date is in the format “dd/mm/yyyy” it will return the numerical date

43. GII Subroutines

Subroutine Syntax	Description
stripchars(*string1, string2*)	This subroutine will look in *string1* for characters specified in *string2* and remove them. Example: string1=' 46831-6971' and string2=' -'. When function is run string1 will contain '468316971'

Subroutine Syntax	Description
fetch_lab(*labno*)	This subroutine will get a lab record, if it already exists, and load it for use. Will return 0 if lab record not found, 1 if it is found and loaded.
test_on_lab(*test*)	This subroutine will check to see if a test exists on a lab record. This will return a 0 if the test is not on the lab record, 1 if it is. The *test* passed in can be a standard test identifier, CA or CA[1], or can be a string name/mnem/alias of the test, 'CA'.
get_xml_info(*id, line*)	This subroutine will fill in the 'XML_' identifiers with details on the requested information.

44. Billing Subroutines

There are a few specialised subroutines needed to output an invoice, as outlined below.

Subroutine Syntax	Description
bill_mline_set(x,line,font,size,justification,IDENTIFIER);	This is used to output the billing items on the body of the invoice. It defines where each piece of information will print. This subroutine allows output of billing line items on multiple lines. A line value of "0" will print the information on every line of the invoice body A line value of "1" will only print the information on the 1st line; similarly a value or "2" will only output the information on the 2nd line, etc. Subsequent sections of this Chapter outline Justification options, Postscript Font Codes and Font Size guidelines.
bill_line_set(x,font,size,justification,IDENTIFIER);	Performs the same function as bill_mline_set, except that all of the data is output on one line. Subsequent sections of this Chapter outline Justification options, Postscript Font Codes and Font Size guidelines.

Subroutine Syntax	Description
bill_gen_inv_text(lines_per_page);	Calculates the number of pages an invoice will require. For example: `total_pages = bill_gen_inv_text(lines_per_page);` where total_pages and lines_per_page are user-defined variables. lines_per_page is the total number of lines available in the invoice body and should be set to an integer. It is necessary to make the returned value an integer using the "int" subroutine (e.g. total_pages = int(total_pages);)
output_inv_body(lines_per_page,y,current_line,fontsize);	Outputs the invoice line items. For example: `more = output_inv_body(lines_per_page,y,current_line,fontsize);` Where current_line and lines_per_page are user defined variables, and y represents the y axis position. This subroutine should be used within a while loop (i.e. while more > 0), when there are no more lines to output the system returns a value of zero. Font size guidelines are provided in a subsequent section of this document.

45. Import Analyser Mask Subroutines (Batch Functionality)

The Import Analyser mask receives the result file and handles it as a very large string. The delimiter and line terminator are specified in the Analyser configuration. Specific batch functionality subroutines are required for this to work, as outlined below.

Subroutine Syntax	Description
get_file_lines();	Returns the number of lines in the file as an integer. This provides the stopping point for the equation's looping through the lines in the file.
count_line_fields(line);	Returns the number of fields in the given line, where line is the line number.
get_line_field(line, field);	Returns a string value of that line and field number, where line is the line number and field is the field number in the text file.

Subroutine Syntax	Description
add_dna_string(format, value, result);	This function is used to construct each 'entry' for the DNA results. An 'entry' is a field which could either be a result type field or an allele type field. Format is the format of that string entry; this value is treated as a string. Format arguments are listed below: "LABNO" - Must be a lab number stored as a string "URNO" - Must be a valid UR number stored as a string "DNAWELL" - Must be a valid DNA well entry. When invalid this field is set to 0. "TEST" - Must be a valid test/panel mnemonic for this batch. "DNA_PRIORITY" - Must be a valid DNA priority (1-3) otherwise this field is set to 0. "TESTNAME" - Must be string value of test or allele name e.g. "D18" (can also be the alias) "TESTTYPE" - Says whether or not this is an allele or test. If omitted it will be assumed it is a test. "INTRES" - Will convert to a string, formatted as an integer. "STRRES" - Will store the string value. "FLOATRES" - Will convert to a string, formatted as a floating point value. (6 decimals) Value will be the string of whatever you're building, and must be a string. Result is whether or not it is a result field, and takes the value 0 (not a result field) or 1 (it IS a result field). There is no real need to set result to anything but 1.

Subroutine Syntax	Description

add_dna_entry(format, lineno, fieldno, result);	Works similarly to add_dna_string(), only instead of adding a string value it will grab exactly what is in the lineno and fieldno you specify.
	The code:
	`add_dna_entry(format, lineno, fieldno, result);`
	is reasonably equivalent to:
	`thing = get_line_field(line, field);` or
	`thing = "0.95";`
	`add_dna_string(format, thing, result);`
	The format argument is identical to that for add_dna_string(). Refer to the list provided for add_dna_string().

build_dna_entry();	This function takes the DNA entry you have constructed using add_dna_string() and/or add_dna_entry(). This will insert the result or value and clear out the DNA structure for you to construct the next field.

Subroutine Syntax	Description
apply_stringency(lower,upper);	This function is used to apply staff matching functionality to the imported results. It is entered at the very end of the mask. With this function, all of the imported profiles are compared to the staff profile table and STRINGged when the number of matches falls between the minimum (lower) and maximum (upper) amounts specified. This STRING is present in the DNA batch details screen after importing the results. lower is the minimum number of alleles to match upper is the maximum number of alleles to match

Using add_dna_entry(), add_dna_string() and build_dna_entry()

For each mask these functions will be handled slightly differently.

These 3 functions are what build each of the results on the SF7 DNA profile screen. The first two functions construct the DNA entry and once that entry has been built, it is inserted with `build_dna_entry().`

For example, this code inserts the CTB value for the Quantifiler mask:
`add_dna_string("LABNO",labno,1);` - Specifies what lab number it goes to.
`add_dna_string("TEST",request,1);` – Specifies the orderable (e.g. 9PLEX)
`add_dna_string("DNAWELL",well,1);` - Specifies the DNA well
`add_dna_string("TESTNAME","CTB",1);` - Specifies the test name for this result
`add_dna_entry("FLOATRES",cnt,4,1);` - Adds in the result on line `cnt`, field 4 as a floating point result.
`build_dna_entry();` - builds the entry.

Here is an example of code that inserts the D7 result for Genotyper:
`add_dna_string("LABNO",labno,1);`
`add_dna_string("TEST",request,1);`
`add_dna_string("TESTNAME","D7",1);`
`add_dna_string("TESTTYPE","ALLELE",1);` - Says D7 is an allele type field.
`add_dna_entry("STRRES",cnt,12,1);` - Adds in the result on line `cnt`, field 12 as a string.
`build_dna_entry();`

You will notice the D7 has a TESTTYPE line, whereas the CTB field does not. This is because the D7 is a configured allele rather than a traditional result field. Omit this testtype line if you do not want the result to be treated as an allele.

Result fields vs. Allele fields:
A result field is a configured test in **Evolution vLab**™ , while an allele is configured through the allele configuration table.

An allele result will be transferred to the 9PLEX or COFIL screen using the SF6 function, going into the 9PLA01, 9PLA02, 9PLA03 etc fields down the left hand side of the screen.

A result field is a field that is on the same panel, which will save like any other test field when doing the SF6 save profile function. So if you have SV1 non-allele results and you perform a SF6 Save Profile, the result will go into the SV1 field on the 9PLEX page rather than the 9PLA01, 9PLA02 etc fields.

46. Export Analyser Mask Subroutines

Export analyser masks construct the platemap file used by the robots. The platemap file is a plain text file detailing information about the samples present. This information can include well designation, dilution volume information and ordered request.

Subroutine Syntax	Description
load_dnabatch(0);	This behaves like the loadcumulative() function, only it will load all of the lab numbers in the current DNA batch. This is to be used at the top of every export analyser mask (does not work in modify equations). E.g. LABNO[1] specifies the first lab number in the batch. You can also grab results for these lab numbers this way, such as REQDAT[i] or CSCI[i] if required.

build_string(value, STRING, separator, count);	*value* can be a string or identifier for a string such as LABNO.
	
	STRING indicates what separator will follow the text in the file.
	Possible STRING values include:
	0 – None
	1 – Field separator (as specified in the analyser configuration)
	2 – Line terminator (as specified in the analyser configuration)
	3 – User defined separator.
	
	separator is used to specify the user defined separator if 3 is set for the ‘STRING’ value, otherwise this value should be “”.
	The separator can be anything including - \n for line feed, \t for tab, \r for carriage return.
	\\ will output a single backslash - \.
	
	count specifes how many time the separator will appear, for example, if the separator is set to “*” and count to 5 then “*****” will separate this field.
	
	Example:
	`build_string("The Lab Number ",1,"",1);`
	`build_string(LABNO[i],3," ",1);`
	`build_string(" is in batch",2,"",1);`
	`build_string(DNABATCHNO,0,"",1);`
	
	will output:
	`The Lab Number 123456789 is in batch`
	`BLDEXT20060101_01`

Subroutine Syntax	Description
dna_test(index);	This function is used to determine what test is ordered for that lab number in the batch. This is since each lab number can have different orderables on the same batch. Example: dna_test(1); will return the ordered test (such as 9PLEX) for LABNO[1]
dna_wflow_result(index, format panel, orderable, profile result);	This function is used to grab results directly from the profile results page. This is mainly used to obtain the dilution volumes, since these figures aren't on any result screen. *index* - specifies the lab number index on the batch *format panel* - specifies which screen to select result from, this will usually be \9PLEX or COFIL, this value is not in inverted commas. *orderable* - specifies which column to retrieve results from. You may have several results for the same allele on the SF7 profile results screen, so this is where you specify which set of results to look at (not in inverted commas). *profile result* – this specifies the actual field to grab the value from, such as "TV1". This value must be in inverted commas. Examples:

dna_wflow_result(index, format panel, orderable, profile result);

```
stest = dna_test(cnt);
if (stest = "NCLRF") {
   stest1 =
dna_wflow_result(cnt,\9PLEX,NCLRF,"SV1");
   stest2 =
dna_wflow_result(cnt,\9PLEX,NCLRF,"TV1");
   stest3 =
dna_wflow_result(cnt,\9PLEX,NCLRF,"SV2");
   stest4 =
dna_wflow_result(cnt,\9PLEX,NCLRF,"TV2");
}
build_string(stest1,1,"",1);
build_string(stest2,1,"",1);
build_string(stest3,1,"",1);
build_string(stest4,1,"",1);
```

The code above will grab the TV1, TV2, SV1, SV2 values on the SF7 screen with NCLRF results, provided a NCLRF is ordered. These values will then be added into the platemap file.

47. Auto-validation Mask Subroutines

The auto-validation mask works much like daemon equations, where an accept STRING is set. This mask executes after the analyser mask, but before the modify equations. In this mask, you can perform if statements on allele or test results.

Each field is prefixed with 'AN_'. The accept STRING can be set with AN_ACCEPT = 0; or AN_ACCEPT = 1;

This means you can do the following:

```
if (AN_CTB > 40) {
   AN_ACCEPT = 0;
} else {
   AN_ACCEPT = 1;
}
```

Subroutine Syntax	Description
add_dna_wflow(panel, columntest, rowtest);	This function is typically used in the auto-validation equation, but can also be used in the modify or request add equations. This function will allow you to add a blank row or column to the SF7 profile history screen. The first parameter 'panel' is the format panel of the SF7 screen you are using, such as 9PLEX or COFIL. The 'columntest' value is the header of the column you want to add, or add a row to. The 'rowtest' value is the header of the row you want to add. Say you wanted to add an SV1 row to the 9PLEX column on the 9PLEX profile history screen then you would use the following: `add_dna_wflow(\9PLEX,\9PLEX,SV1);` If you just wanted to add an extra column such as for a rework as it is added through the auto-validation equation you would use the following: `add_dna_wflow(\9PLEX,AMP1CW,0);` That would add a column entitled 'AMP1CW' on the 9PLEX results history screen.

48. Image Annotation Subroutines

Evolution vLab™ allows the System Administrator to tailor the display of image annotations in print masks either in the printed report or **Evolution vLab**™ Clinical Viewer . The following is a list available and an explanation of their usage.

Subroutine Syntax	Description
annotate_load e.g.: **number = annotate_load(type,which);**	This is the first of the annotation functions to use. If type = 0 it will load the UR image, If type= 1 it loads the lab image which: determines the previous result when used in conjunction with the load historical sub routine. This argument indicates how many of the images you want from the URNO or laboratory number as selected in the type parameter.. To get the images for the single lab associated with the report you would use annotate_load(1,0). The value returned is the number of images associated with your selection.
annotate_select e.g. **resultstr =annotate_select(imageindex);**	This function is used to identify which of the images found by the annotate_load function is to be considered. This function will, as well as selecting the image, have the annotations read, deciphered and arranged for processing. **Imageindex:** this argument indicates which image of the number of returned images from the `annotate_load` function is to be processed. **resultstr:** The returned string is one of: `""` there are no annotations on this image `"1"` there are annotations on this image `"?"` Unable to locate the requested image i.e out of range of indexes.
annotate_text e.g. **resultstr = annotate_text(whatstr);**	This function is used to extract strings to facilitate the output and annotation of the image selected with the selection function. The following values may be supplied as the argument.

Subroutine Syntax	Description
annotate_value () e.g. **resultvalue= annotate_value("NUMBER");**	This function is used to extract values to facilitate the output and annotation of the image selected with the previous function. The following values may be supplied as the argument. **"NUMBER"** returns the image identifier **"WIDE"** the width of the image **"HIGH"** the height of the image **"LSIZE"** the annotation line thickness **"COLOUR"** the colour of the line **"TSIZE"** the text size **"ZOOM"** the zoom factor for the current annotation **"X1"** the horizontal component of the first point **"Y1"** the vertical component of the first point **"X2"** the horizontal component of the second point **"Y2"** the vertical component of the second point **"DESCRIPTION"** the description associated with the image **"IMAGETYPE"** the image type associated with the image **"IMAGENO"** the image number associated with the image **"ANNOTATION_FIRST"** returns "1" if there is an annotation, else "". **"TYPE"** the type of annotation (see table below) **"TEXT"** the text with the current annotation **"FONT_COLOUR"** the colour of the current text **"TEXT_ANGLE"** the angle for the current text **"ANNOTATION_NEXT"** returns "1" if there are more annotations, and advances if so See the "Type of Annotations" table immediately below for more information.

Type of Annotations

TYPE	LSIZE	COLOUR	X1	Y1	X2	Y2	TEXT	TSIZE	ZOOM	FONT_COLOUR	TEXT_ANGLE
"T"	N/A	N/A	Yes	Yes	N/A	N/A	Yes	Yes	Yes	Yes	N/A
"F"	Yes	Yes	Yes	Yes	Yes	Yes	N/A	N/A	N/A	N/A	N/A
"L"	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
"P"	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	N/A
"C"	Yes	Yes	Yes	Yes	Yes	Yes	N/A	N/A	N/A	N/A	N/A
"E"	Yes	Yes	Yes	Yes	Yes	Yes	N/A	N/A	N/A	N/A	N/A

Each annotation is basically a line, a piece of text or both.
The **"T"** is a piece of text which appears horizontally on the image.
The **"F"** is one segment of the freehand line.
The **"L"** is a straight line. Associated with this line is a possible piece of text, which has to be places parallel to the line.
The **"P"** is a line with an arrowhead at one end, and a piece of text (possibly) at the other.
The **"C"** is a box.
The **"E"** is an ellipse.

The ZOOM value indicates the percentage zoom which was in effect when the annotation was made. You can use this to decide to shrink the specified text size if this is desired.

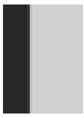
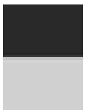
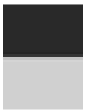
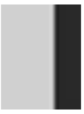
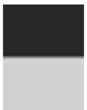
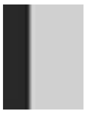
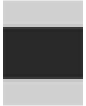
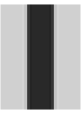
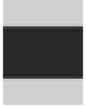
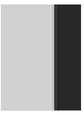
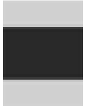
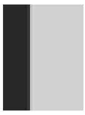
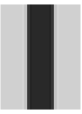
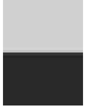
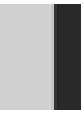
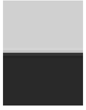
Subroutine Syntax	Description
annoteimage_output e.g. **y=annoteimage_output(num,left,bot,wide,high,positioning,mode);** *Note: previously used output_annoteimage is now obsolete. Please convert all instances of this equation used in existing print masks to the* ***annoteimage_output***	Causes the output of the specified image where placed, and includes the annotations as specified. The first parameter "**num**" is the number for the image. The next four parameters, "**left, bot, wide, high**" specify a rectangular area in which the picture is to be placed. The picture will be scaled so that no dimension of the image will exceed the specified height and width. This means that on occasion the picture will not fill the full width or height. The question arises as to where in the specified rectangle the picture is to appear. Note that if the picture exactly fills the specified rectangular region, then this discussion is not relevant. Assuming there is not an exact fit, the sixth parameter "**positioning**" is used to determine how the picture appears in

the rectangle. This has been detailed below using example pictures which have extreme aspect rations. The area will be a grey rectangle; the picture will appear as a black rectangle. Refer to the Figure below.

The mode argument details the scaling of the annotations. An annotation was performed by a user at a particular zoom factor. The output picture will be further zoomed by the fitting of the picture to the rectangle desired. The section below indicates how this mode is used.

Mode	**Meaning**
0	Do not emit any annotations.
1	Scale line widths and font sizes from the annotation zoom factor to the 1/1 image, then scale line widths and font sizes to the display area. Minimum font size is 6 points.
2	Scale line widths and font sizes to the display area. Minimum font size is 6 points.
3	Scale line widths and font sizes from the annotation zoom factor to the 1/1 image. Minimum font size is 6 points.
4	Do no scale line widths and font sizes. Minimum font size is 6 points.
5	Scale down only, line widths and font sizes from the annotation zoom factor to the 1/1 image, then scale down only, line widths and font sizes to the display area. Minimum font size is 6 points.
6	Scale down only, line widths and font sizes to the display area. Minimum font size is 6 points.
7	Scale down only, line widths and font sizes from the annotation zoom factor to the 1/1 image. Minimum font size is 6 points.
x0	Do not emit any annotations. X indicates the value selected for the minimum font size.
x1	Scale line widths and font sizes from the annotation zoom factor to the 1/1 image, then scale line widths and font sizes to the display area. X indicates the value selected for the minimum font size

	x2 Scale line widths and font sizes to the display area. Minimum font size is x points. x3 Scale line widths and font sizes from the annotation zoom factor to the 1/1 image. Minimum font size is x points. x4 Do not scale line widths and font sizes. Minimum font size is 6 x points. x5 Scale down only, line widths and font sizes from the annotation zoom factor to the 1/1 image, then scale down only, line widths and font sizes to the display area. Minimum font size is x points. x6 Scale down only, line widths and font sizes to the display area. Minimum font size is x points. x7 Scale down only, line widths and font sizes from the annotation zoom factor to the 1/1 image. Minimum font size is x points. **Note**: It is envisaged that the most useful mode is 1, although for good printers 41 is recommended and for crude printers 81 is recommended.

Positioning	**tall**	**wide**
0 (top left)		
1 (top centre)		
2 (top right)		
3 (centre left)		
4 (centre centre)		
5 (centre right)		
6 (bottom left)		
7 (bottom centre)		
8 (bottom right)		

Note: that the value returned from this function is the bottom value of where the picture has been placed. This can be used to determine the maximum bottom value for positioning of other things under the picture or pictures output. For example, passing a bottom value of 50, and a positioning of 0, 1, or 2, would return the bottom value of the picture which might be 400 for a wide but short picture. Further output could then continue from 380, say, rather than leaving a large white space.

49. Format Codes

Format codes are used to format the display of Test results. The supported values are described in the table below.

Test results are displayed in “expanded” form (equivalent to format code “e”) by default in screen masks, and in “short” form (i.e. mnemonic) by default in report masks. The “e” and “m” codes should be used as appropriate where the default behaviour is not desired.

With the exception of code “m”, the following format codes are available for use in the following functions:

- output_results()
- output_cumresults()
- outcum_results()
- output_fullcum()

Code	Description
“e”	Outputs Test results in expanded format. For coded and coded comment Test results (Formats ‘C’ and ‘CC’) the expanded form is the Description. Test results with Format Tx.*y* require this format code to appear in report masks.
“m”	Outputs the Mnemonic for coded and coded comment Test results (Formats ‘C’ and ‘CC’). This Format Code is ignored for all other (non-coded) Test results, and synoptic results (Synoptic set to ‘yes’). This format code is available for use in the following functions: • output_results() • output_cumresults() • outcum_results()
“O”	Disables reference range STRINGging.
“r”	Enables reference range STRINGging.
“R”	Enables reference range STRINGging and offsets the STRING on printouts.
“T”	Outputs T/F when a test is ordered but not resulted or validated. It is necessary to use the 'o' output with the test list.
“w”	Produces colour coding in online view of report.

50. Justification

Justification is used to achieve right and left justified and centred output. The supported values are described in the table below.

Code	Description
"c"	Centre
"O"	Left justification
"r"	Right justification
"v"	Vertical output, where the default is horizontal output.
"w"	Text field width, where "70.300w" denotes output 70 characters on a line of 300 points width.
"xC"	Setting of colour, where x denotes the numeric colour code.
"xR"	Rotation, where x denotes the number of degrees characters are to be rotated from the vertical position.
"xS"	Spread, where x denotes the number of characters for the spread of text.
"xt"	Truncation, where x denotes the number of characters before which text is truncated

51. Postscript Font Codes

Evolution vLabTM supports the following font codes for use in reporting functions.

Code	Font
0	Helvetica
1	Helvetica Bold
2	Helvetica Italic
3	Helvetica Bold Italic
4	Courier
5	Courier Bold
6	Courier Italic

Code	Font
7	Courier Bold Italic

52. Font (Point) Size Guidelines

Postscript Point Sizes
Point size governs the physical size of output characters and typically ranges between 7 and 36, with a value of 10 producing 'readable' text. Font (point) size 10 is commonly used for body text.

Dot Matrix Point Sizes
Two-point sizes are available for dot matrix text: These are 0, which produces readable text as displayed and 11, which produces expanded text.

53. Font Parameter

The **font** parameter passed to the output subroutines described in this document allows the specification of text style and colour.

The following font parameter codes are available for use in **Evolution vLab**^{TM}.

Code	Text colour and style
0	Black, plain
1	Black, plain
2	Yellow, bold
3	Black, plain
4	Blue, bold
5	Blue, bold
6	Blue, bold
7	Black, plain
8	Black, plain
9	Black, plain
10	Red, bold
11	Red, bold

Code	Text colour and style
12	Yellow, bold
13	Black, plain
14	Red, bold
15	Red, bold
16	Black, plain

Some output subroutines in **Evolution vLab**™ support an enhanced font parameter. For the following output functions the font parameter has been enhanced to provide greater flexibility in the styling of text:

output_sigtext
output_text
outcum_audituser
outcum_auditdate
outcum_audittest
outcum_auditlabg
outcum_audittext
outcum_auditlab
output_cumresults
output_results
outcum_results

The syntax for the enhanced font parameter is:

“n,#xxxxxx”

where *n* is the font style:

1	(plain text) or
2	(bold text)

and #*xxxxxx* is a valid 6-digit hexadecimal (hex) colour code. The hash symbol (#) and quotation marks must be included. Do not include any spaces.

Any valid 6-digit hex colour code may be used.

For example, “2,#00CC00” would produce bold, bright green text.

Refer to http://www.w3schools.com/html/html_colornames.asp for more hex colours.

Default font and colour may be applied by **Evolution vLab**™ where the font parameter is not otherwise defined.

The following table indicates the default, system-determined colours.

Colour	Usage
Black	Default text and results within reference range
Yellow	Results outside reference range
Red	Results in critical range
Pink	Results that failed a delta check
Blue	Lab Use Only and Suppressed results

Note: Refer to Appendix A for **AUSLAB** Font Parameter codes.

54. Test lists

A test list (tlist) is a list of Test mnemonics nominated for use in the script. Test lists may be used as a parameter in many **Evolution vLab**™ subroutines.

Syntax:

```
tlista = "{WBC}{HBG}{RBC}";
```

55. tlist Codes

Designated characters can prefix the test list to modify the output format, filter the list according to certain criteria and improve tlist efficiency. For example, the code `l` (lowercase L) filters the tlist to include only the Tests which have been ordered.

These prefixes may only be included at the beginning of the test list; entering these codes within the tlist renders the whole list invalid.

When a tlist containing a code prefix is passed to an **Evolution vLab**™ subroutine, generally the subroutine will only apply itself to the filtered Tests, i.e. excluding any Tests that have been omitted. However, where a subroutine ignores the tlist code this is stated in the description for the subroutine in this Guide, e.g. see `listcount()` and `listelement()`.

Syntax:

```
tlista = "l{WBC}{HBG}{RBC}";
```

tlist Code	Description	Effect
`h`	Lowercase H	Output the list of tests horizontally across the page.

tlist Code	Description	Effect
`l`	Lowercase L	Removes tests which have not been ordered.
`O`	Uppercase O	Leaves blank line(s) for tests not requested. Tests designated “lab use only” are omitted.
`o`	Lowercase O	Removes tests which have not been ordered. Tests designated “lab use only” are omitted.
`R`	Uppercase R	Leaves blank line(s) for tests without a result. Tests designated “lab use only” are omitted.
`r`	Lowercase R	Removes tests without a result from test list. Tests designated “lab use only” are omitted.
`Z`	Uppercase Z	Leaves blank line(s) for tests with 'zero' result. Tests designated “lab use only” are omitted.
`z`	Lowercase Z	Removes tests with a 'zero' result from the test list. Tests designated “lab use only” are omitted.

56. tlist Numbers

Numbers between the Tests cause **Evolution vLab**TM***’s*** output functions to skip that number of coordinates when postscript printing.

Syntax:

```
tlista = “{WBC}10{RBC}10{PLT}”;
```

57. Evolution vLab^{TM} Scripting Language (ASL) – Control Statements

Statement Syntax	Description
exit	Exits the **Evolution vLab**^{TM} script, thus terminating the Equation or mask at that point. This statement is particularly useful in the Daemon and Level 1 Equations for analysers. The `exit` statement should *not* be used in the system Equations (Modify, Validate, Request Remove, Request Add or Accept). Exit statements are not required at the end of **Evolution vLab**^{TM} Scripts; the scripts cease automatically when the end is reached. Examples:

```
if (AN_ABC) > -1.0) exit;

if (PLT[1] = "*") {
  AVCODE = AVCODE + "J";
  listinsert("SYODP");
  exit;
}

if (WBC > 25.0)
  exit;
```

58. Appendix A - AUSLAB Font Parameter Codes

The following font parameter codes are available for use in **AUSLAB**.

Code	Text colour and style
0	Green Light
1	Grey Medium
2	Grey Dark
3	Grey Light
4	Yellow Dark

Code	Text colour and style
5	Yellow Medium (STRINGs results outside reference range)
6	Yellow Light
7	Green Dark (Default for text and results within ranges)
8	Green Medium
9	Green Light
10	Red Dark
11	Red Medium (STRINGs results in critical range)
12	Purple
13	Orange (STRINGs results that have failed delta checking)
14	Cyan (STRINGs results that are for Lab Use only)
15	Blue Light
16	Black

59. Version control

The following changes are made to this document:

Version	Revised by	Authorised by	Change	Date Approved
4	T. Zafrin	T. Nightingall	• Product branding and trademark updated: ▪ **EVOLUTION** to **Evolution vLab**^{TM} ▪ **AUSLAB** to **Evolution vLab**^{TM} ▪ **AUSCARE** to **Evolution vLab**^{TM} Clinical Viewer • Section 54 updated and **AUSLAB** Font Parameter moved to Section 58 Appendix A. • Template updated.	30/07/2022