

Root Cause Analysis Using Pinnacle 21 Validation Reports: How to Improve End-to-End Programming Process

Aakar Shah, Nektar Therapeutics; Tracy Sherman, Efficacy Consulting Group Inc.

ABSTRACT

As reviewers adjudicate Pinnacle 21 validation reports to address the quality of submission activities, further analysis can uncover underlying process-related issues which cause those findings in the first place. Even a single Pinnacle 21 validation report can identify underlying shortcomings. However, if you are part of large pharmaceutical company or have access to a large number of Pinnacle 21 validation reports, it can help you analyze various trends and improve all aspects of the current programming process. In this paper, we will discuss how to analyze Pinnacle 21 validation reports, categorize findings in various buckets such as Data Collection and Cleaning, SDTM Process, ADaM Process, e-Submission Process, Internal Stakeholder Management and External Stakeholder Management, and how to subsequently use root cause analysis to find and address end-to-end programming process improvement.

INTRODUCTION

According to The American Society for Quality, a root cause is defined as a factor that causes a nonconformance and should be permanently eliminated through process improvement. The root cause is the core issue that sets in motion the entire cause-and-effect reaction that ultimately leads to the problem. Root Cause Analysis (RCA) is defined as a collective term that describes a wide range of approaches, tools and techniques used to uncover causes of problems.

The statistical programming team is one of the core groups of a pharmaceutical and/or medical device organization responsible for high quality and efficient submissions to regulatory agencies, with the goal of faster treatments to patients. Programmers work within stringent and evolving requirements and standards set by multiple regulatory agencies. We work in a highly regulated and competitive industry. To produce high quality deliverables, your underlying process must be error-proof. To produce efficient deliverables, your underlying process must have “lean” principles focusing on value added stream, waste elimination and continuous improvement.

The statistical programming group is a fast-paced working environment involved in answering adhoc requests from different stakeholders in addition to the typical study and submission work. Such work is sometimes outsourced or in transition from outsourced to insource or vice versa or performed inhouse with limited resources. Sometimes a dedicated resource is not assigned to oversee all these moving parts. Sometimes a process is also not set up to collect and analyze quality and efficiency related metrics within statistical programming group. Such metrics are necessary to achieve operational excellence. As a result, you will notice similar quality or efficiency related findings occurring repetitively across studies.

There are many concepts and tools available in the market which a statistical programming group uses to improve overall quality and efficiency. In this paper, we will focus on the use of Pinnacle 21 Enterprise (P21) validation reports to improve end-to-end programming process. If you have a large supply of P21 validation reports, you can compile all the reports and perform trend analysis and prioritize process improvement related to high impact or most frequent findings. If you are part of a small pharmaceutical company and have access to very few P21 validation reports, you can still perform the analysis and improve your process. Once you address all findings from your current P21 validation reports, we strongly suggest to performing this analysis routinely.

Remember, the key is ongoing evaluation followed by continuous improvement of your current programming process that will produce higher quality deliverables with increased efficiency and therefore delivering faster treatments to patients. We highly recommend setting up a process improvement team led by the statistical programming group and involving members from various functional groups within clinical development department to oversee the root cause analysis activities.

HOW TO PREPARE FOR META-ANALYSIS OF PINNACLE 21 VALIDATION REPORTS

To prepare for meta-analysis of the P21 validation reports, you will need to save all the SDTM validation reports from P21 into a new folder and all the ADaM validation reports into a separate directory. A simple macro can be used to read all the reports in single folder, count the number of validation reports, append all the data taken from the details worksheets and creates a SAS® dataset used for the meta-analysis. For our analyses, we named the worksheets with the STUDYID as the first part of the input filename. This STUDYID can be further used to break down the meta-analysis by study. See APPENDIX 1 for the full SAS code. Please note that for our analysis, we added root cause classification values in column Category manually. However, you can create a metadata of Category and Rule ID and automate the population of the column for future analysis.

SDTM ROOT CAUSE ANALYSIS FINDINGS

Using the SAS dataset created above, the information from all the Details worksheets of the SDTM P21 validation reports, overall tables for the number and description of FDA and PMDA Rejects, Errors and Warnings are produced.

Table 1 shows summary of the FDA and PMDA SDTM reject criteria for all the P21 validation reports. The most frequent FDA reject criteria was 'Missing define.xml file' that is categorized as an electronic submission process issue. Sample SAS code to produce the summary tables is included in APPENDIX 2.

Reject Criteria				
(SDTM Pinnacle 21 Validation Reports)				
Category	Rule ID	Message	FDA (N=20)	PMDA (N=20)
d	DD0101	Missing define.xml file	20	0
b	SD1115	Missing TS dataset	18	0
a, b	SD0064	Subject is not present in DM domain	0	7
d	DD0006	Missing required 'ItemDef' value	0	5
d	DD0006	Missing required 'ProtocolName' value	0	5

Table 1 Summary of FDA/PMDA Reject Criteria for SDTM. Category a=Data Collection and Cleaning; b=SDTM Process; c=ADaM Process; d=e-Submission Process; e=Internal Stakeholder Management; f=External Stakeholder Management

Table 2 shows the summary of the FDA and PMDA SDTM error criteria with the most frequent finding of 'FDA Expected variable EPOCH not found', classified as a SDTM process issue.

Error Criteria				
(SDTM Pinnacle 21 Validation Reports)				
Category	Rule ID	Message	FDA (N=20)	PMDA (N=20)
b	SD1077	FDA Expected variable EPOCH not found	20	0
b	SD1112	Missing TA dataset	0	20
b	SD1113	Missing TE dataset	0	20
b	SD1115	Missing TS dataset	0	20
a	SD0009	No qualifiers set to 'Y', when AE is Serious	15	0
a	SD0013	AESTDTC is after AEENDTC	2	2
a	SD0035	Missing value for CMDOSU, when CMDOSE, CMDOSTXT or CMDOSTOT is provided	5	5
b	SD0051	Inconsistent value for VISIT within VISITNUM	6	0
f	SD9999	Dataset RELRECLR class not recognized	1	1

Table 2 Summary of FDA/PMDA Error Criteria for SDTM

Table 3 shows the summary of the FDA and PMDA SDTM warning criteria with the most frequent finding being 'No Treatment Emergent info for Adverse Event'. This was categorized as a SDTM process issue.

Warning Criteria				
(SDTM Pinnacle 21 Validation Reports)				
Category	Rule ID	Message	FDA (N=20)	PMDA (N=20)
b	SD1097	No Treatment Emergent info for Adverse Event	20	0
b	SD1141	No Treatment Emergent info for Adverse Event	0	20
b	SD1140	PMDA Expected variable EPOCH not found	0	20
b	SD1082	Variable length is too long for actual data	0	15
a	SD0009	No qualifiers set to 'Y', when AE is Serious	0	18
a	SD0026	Missing value for LBORRESU, when LBORRES is provided	15	15
a	SD0082	Exposure end date is after the latest Disposition date	18	18
a, b	SD1201	Duplicate records in AE domain	10	10
f	SD0063	SDTM/dataset variable label mismatch	10	10
f	SD1078	Permissible variable with missing value for all records	8	8
f	SD1083	Missing AEDY variable, when AEDTC variable is present	7	7
b	SD1023	VISIT/VISITNUM values do not match TV domain data	5	5
a, b	SD0070	No Exposure record found for subject	6	6
e	CT2002	LBSTRESU value not found in 'Unit' extensible codelist	10	10

Table 3 Summary of FDA/PMDA Warning Criteria for SDTM

ADAM ROOT CAUSE ANALYSIS FINDINGS

The process for SDTM can be duplicated using the P21 validation reports for ADaM. Table 4 shows a small sample of the ADaM FDA and PMDA reject findings with the most frequent being the 'Missing define.xml file'. It was categorized as an electronic submission process issue.

Reject Criteria				
(ADaM Pinnacle 21 Validation Reports)				
Category	Rule ID	Message	FDA (N=20)	PMDA (N=20)
d	DD0101	Missing define.xml file	20	0
c	AD0178	ANL01FL value is not Y or null	0	4
c	AD0178	ANL02FL value is not Y or null	0	4
c	CT2001	SEX value not found in 'Sex' non-extensible codelist	0	2
c	AD0005	ADTH30FL value is not Y, N or null	0	4

Table 4 Summary of FDA/PMDA Reject Criteria for ADaM

Table 5 and Table 6 shows a small sample of the ADaM FDA and PMDA error and warning findings respectively with the most frequent being the 'Variable label mismatch between dataset and ADaM standard. Note that this issue is considered as an error for FDA evaluation and as a warning for PMDA evaluation.

Listings are then generated for the most frequent issues. As show in Listing 1, the message 'ADTH30FL values is not Y, N or null' is coming from Study XYZ-001 and XYZ-002 and two other studies not shown here. The description of RuleID AD0005 is displayed in the footnote and can be important to include when discussing with the process improvement team.

Error Criteria				
(ADaM Pinnacle 21 Validation Reports)				
Category	Rule ID	Message	FDA (N=20)	PMDA (N=20)
f	AD0018	Variable label mismatch between dataset and ADaM standard	18	0
f	AD0047	Required variable is not present	18	18
c	AD0141	Inconsistent value for PARAM within a unique PARAMCD	11	11
c	AD0124	Inconsistent value for PARCAT1 within a unique PARAMCD	7	7
c	AD0124	Inconsistent value for PARCAT2 within a unique PARAMCD	5	5
a	AD0196	Required AEBODSYS value is null	7	7
a	AD0196	Required AEDECOD value is null	7	7
c	AD0256	USUBJID value does not exist in the ADaM ADSL domain	4	4
c	AD1011	Secondary variable AVISITN is populated but its primary variable AVISIT is not populated	4	0
c	AD0019	COMPLFL subject-population flag value is null	4	4
d	DD0060	Define.xml/CDISC variable Label mismatch	0	3
c	AD0151	Inconsistent value for CRIT1 within a unique PARAMCD	3	3
d	SD0054	Variable in define.xml is not present in the dataset	0	2

Table 5 Summary of FDA/PMDA Error Criteria for ADaM

Warning Criteria				
(ADaM Pinnacle 21 Validation Reports)				
Category	Rule ID	Message	FDA (N=20)	PMDA (N=20)
c	AD0018	Variable label mismatch between dataset and ADaM standard	0	18
d	SD0054	Variable in define.xml is not present in the dataset	0	5
d	SD0061	Domain referenced in define.xml but dataset is missing	6	0

Table 6 Summary of FDA/PMDA Warning Criteria for ADaM

PMDA Reject RuleID AD0005				
(ADaM Pinnacle 21 Validation Reports)				
Study	Dataset	Variables	Values	Message
XYZ-001	ADSL	ADTH30FL	Unknown	ADTH30FL value is not Y, N or null
		DRUG1FL	Unknown	DRUG1FL value is not Y, N or null
			No	
			Not Reported	
			Yes	
XYZ-002	ADSL	DRUG2FL	Unknown	DRUG2FL value is not Y, N or null
		MONTH1FL	M	MONTH1FL value is not Y, N or null
		MONTH3FL	M	MONTH3FL value is not Y, N or null
		MONTH6FL	M	MONTH6FL value is not Y, N or null
		WEEK1FL	M	WEEK1FL value is not Y, N or null
		WEEK2FL	M	WEEK2FL value is not Y, N or null

Rule: A variable with a suffix of FL must have value that is Y, N or null (exception 1: RFL, PFL, ABLFL, ANLzzFL. Exception 2: Population flags COMPLFL, FASFL, ITTFL, PPROTFL, SAFFL, RANDFL, ENRFL cannot be null and at least 1 must be included in ADSL).

Listing 1 PMDA Reject RuleID AD0005 for ADaM

Sample SAS code to produce the listings by RuleID is included in APPENDIX 3.

ROOT CAUSE ANALYSIS: DATA COLLECTION AND CLEANING

P21 validation findings categorized as “a” in above tables are attributed to data collection and cleaning. CRF design plays an important part in efficiency and quality of data collection. Data should be collected in the form of CDISC controlled terminology as much as possible. The use of a text box should be minimized or eliminated in the CRF. You may consider running P21 validation check on SDTM created using dummy data before database activation to check CDISC compliance and adjust CRF design accordingly.

We highly recommend using prescription approach in SDTM and ADaM development where define.xml is created upfront just after database activation and before datasets are created and then being used as a tool to check quality of incoming data and assist data management group with data cleaning (Shah and Sherman, 2018).

Findings related to RuleID SD0009 (No qualifiers set to 'Y', when AE is Serious) were because of the lack of synchronization between the electronic data collection (EDC) system and the safety database. A process was developed to automate periodic comparison of both databases, issue queries for any mismatches and copy data to an EDC raw dataset for the matched record.

Findings related to RuleID SD0013 (AESTDTC is after AEENDTC) were attributed to two root causes: lack of data cleaning for last minute entries between the latest dry run, final data extraction and date imputation rule. A process was developed to ensure such findings such as these were not repeated.

ROOT CAUSE ANALYSIS: SDTM PROCESS

P21 validation findings categorized as “b” in above tables are attributed to SDTM process. Legacy SDTM process included creation of DM domain first followed by rest of the domains. Trial design domains were considered as a submission activity and were created at the end at the time of submission. During P21 validation review, we found mismatches between the IE and TI domain, and mismatches between Visit/Visitnum variables in comparison with the TV domain. A re-designed SDTM process was developed to ensure a streamlined domain creation in the order of TS, TE, TA, TV, TI, DM, SV, SE followed by rest of the domains. We believe that trial design domains should be created first and used as input to the rest of the SDTM domains and that should not be considered a submission-only activity.

One curious case we found was of a subject that was present in SUPP domain but not in the main domain. Root cause for this problem was how the data cut algorithm was applied. Data cut algorithm was applied after the split of SUPP domain from main domain. A proper data cut algorithm process was developed because of such findings.

ROOT CAUSE ANALYSIS: ADAM PROCESS

P21 validation findings categorized as “c” in above tables are attributed to ADaM process inefficiencies. Findings related to RuleID AD0178 (ANL01FL value is not Y or null) were because of legacy process which allowed different values other than what is required by ADaM IG. A process was developed because of such findings to assign appropriate flag variable values. ANLzzFL should be either “Y” or null. Other variables with suffix FL should have values “Y”, “N” or null.

Several findings were related to CRIT variables RuleID AD0151 (Inconsistent value for CRIT1 within a unique PARAMCD). ADaM standard specifications were adjusted so that such findings never occur in future.

ROOT CAUSE ANALYSIS: E-SUBMISSION PROCESS

P21 validation findings categorized as “d” in above tables are attributed to e-submission process. In legacy process, creation of define, P21 validation report, and creation of reviewer’s guide were considered as submission activities. If the goal of the organization is to deliver high quality submission in shortest possible duration, then this legacy process will not work.

Findings related to RuleID DD0006 (Missing required 'ItemDef' value), DD0101 (Missing define.xml file), DD0060 (Define.xml/CDISC variable Label mismatch), SD0054 (Variable in define.xml is not present in the dataset) are because of the legacy process.

As a result, dedicated e-submission group was created to find efficiency in end-to-end programming process with focus on global submissions. This group oversaw merging submission components into day to day programming work.

A process was developed to have a single document for both programming specifications and define specifications for both SDTM and ADaM. Reviewer's guide development was started in the beginning of programming process, not in the end. Define.xml was created in the beginning of the programming process before datasets development. P21 validation reports were run routinely. They were no longer considered as just "submission" activities.

A limited duration team was created to establish process around Study Data Standardization Plan (SDSP) to enhance submission focus from the beginning of drug development process for the whole organization.

ROOT CAUSE ANALYSIS: INTERNAL STAKEHOLDER MANAGEMENT

P21 validation findings categorized as "e" in above tables are attributed to internal stakeholder management. Statistical programming group is a service group and must collaborate with all other functional group within the organization.

We noticed ORRES for IETEST was truncated abruptly for text longer than 200 character. A process was developed as a result to collaborate with statistician and clinicians to re-word certain text to fit the length. Certain findings related to RuleID CT2002 (LBSTRESU value not found in 'Unit' extensible codelist) were because of the text box within CRF form.

In legacy process identical units written multiple way (e.g. Once, 1 a day, 1 time a day etc.) were kept as-is. A process was developed to apply controlled terminology to all unit variations in collaboration with statistician and clinicians.

A training plan was developed to train not only statistical programming team but also other members of biometrics and clinical development team including clinicians, project managers to help them familiarized with CDISC, e-Sub and other necessary trainings based on these findings.

ROOT CAUSE ANALYSIS: EXTERNAL STAKEHOLDER MANAGEMENT

P21 validation findings categorized as "f" in above tables are attributed to external stakeholder management. As significant number of studies were outsourced, time to time CRO standards differ from company's internal standards. CROs were also using P21 community version which is different from company's P21 enterprise version.

A process was developed to direct CROs upfront on communications on several topics: Change in data standards to align with internal standards, expectations for e-submission activities, resolution for P21 findings, frequency of dry run etc. A decision was made to check work performed by CRO internally using P21 Enterprise version.

As previously mentioned a process was developed to implement SDSP to manage data standard expectation with the FDA.

CONCLUSION

Through the use of root cause analysis using inputs of Pinnacle 21 generated validation reports, we can uncover underlying process-related programming issues contributing to inferior quality and decreased efficiency of programming deliverables. These issues can be analyzed and categorized into various buckets such as Data Collection and Cleaning, SDTM Process, ADaM Process, e-Submission Process, Internal Stakeholder Management and External Stakeholder Management. Summary tables and listings of the FDA and PMDA reject, errors and warnings by these categories can be shared within statistical

programming group and with the applicable cross functional team members and can contribute towards process improvement and SDTM/ADaM/e-submission related trainings. Once you resolve the current set of findings and improve the identified processes, move forward to analyze the next round of findings. This analysis will be part of your continuous improvement of the end-to-end programming process.

REFERENCES

The American Society for Quality. 2019. "What is Root Cause Analysis?" Accessed June 1, 2019. <https://asq.org/quality-resources/root-cause-analysis>

Shah, Aakar and Sherman, Tracy, 2018. Doctor's 'Prescription' to Re-engineer Process of Pinnacle 21 Community Version Friendly ADaM Development. PharmaSUG 2019 Conference Proceedings. Paper DS-15.

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CONTACT INFORMATION

Your comments and questions are valued and encouraged. Contact the author at:

Name: Aakar Shah
Enterprise: Nektar Therapeutics
E-mail: AShah@nektar.com

Name: Tracy Sherman
Enterprise: Efficacy Consulting Group, Inc.
E-mail: shermantracy@gmail.com

APPENDIX 1

```
%macro ms_import_details(location=);

    filename _dir_ "&location.";

    data filenames(keep=fname);
        handle=dopen( '_dir_' );
        if handle > 0 then do;
            count=dnum(handle);
            do i=1 to count;
                fname=subpad(dread(handle,i),1,10);/* extract first 10 letters */
                fname=tranwrd(fname,'-V','');
                output filenames;
            end;
        end;
        rc=dclose(handle);
    run;

    filename _dir_ clear;

    proc sort data=filenames;
        by fname;
    run;
```

```

** Build a series of macro variables by combining study name 'studnam' and
left aligned value of _n_. Create a macro variable, fnams, for the number of
filenames in the directory **;

data _null_;
  set filenames end=eof;
  call symput("studnam"||left(_n_),trim(fname));
  if eof then do;
    call symput("fnams",strip(_n_));
  end;
run;

%put fnams = ***&fnams***;
%put studnam = ***&studnam1 &studnam2***;

** Import all worksheets based on the number of files (&fnams) **;
%do i=1 %to &fnams;

  filename source "&location/&&studnam&i-Validation-Report.xlsx" encoding
= "utf-8" lrecl=32767;

  proc import datafile=source out=ds&i dbms=xlsx replace;
    sheet="Details";
    getnames=no;
  run;

** format the columns and remove rows with no data or column names **;
data ds&i.a;
  length studyid $10 num 8. Dataset $40 Record Count 8. Variables
$200 Values $300 RuleID $7 PublisherID $12 Message Category $200
FDA $7 PMDA $7;
  set ds&i;
  studyid="&&studnam&i";
  num=&i;
  if a='' or a='Pinnacle 21 Enterprise Validation Report' or a='Issue
Details' or a='Dataset' then delete;
  Dataset=a;
  Record=b;
  Count=c;
  Variables=d;
  Values=e;
  RuleID=f;
  PublisherID=g;
  Message=h;
  Category=i;
  FDA=j;
  PMDA=k;
  keep studyid num dataset variables values ruleid publisherid
message category fda pmda;
run;

** Add attributes to the first file to have the maximum variable lengths **;
%if &i=1 %then %do;
  data allods;
    length studyid $10 num 8. Dataset $40 Record Count 8. Variables

```

```

    $200 Values $300 RuleID $7 PublisherID $12 Message Category $200 FDA $7
    PMDA $7;
    studyid=''; num=.; Dataset=''; Record=.; Count=.; Variables='';
    Values=''; RuleID=''; PublisherID=''; Message=''; Category='';
    FDA=''; PMDA='';
    run;
%end;

** Append worksheets into one dataset, allods **;
proc append base=allods data=ds&i.a force nowarn;
run;

%end;

%mend ms_import_details;

** Sample macro call **;
%import_details(location=%str(//programming/p21report));

```

APPENDIX 2

```

%macro tab(id=,crit=);
options mprint symbolgen;
proc format;
    value col
        1 = 'FDA'
        2 = 'PMDA' ;
    value reject
        1 = "Number of studies with &crit criteria";
run;

*-----*
* Processing Section *
*-----*

data master1;
set allods; ** from ms_import_details macro above **;
fda=lowercase(fda);
pmda=lowercase(pmda);
if fda="&crit" or pmda="&crit";
if fda = "&crit" then do;
    col=1;
    output;
end;
if pmda = "&crit" then do;
    col=2;
    output;
end;
format col col.;
run;

proc sort data=master1;
by studyid col;
run;

```

```

data master1;
  set master1;
  by studyid col;
  if first.col then reject=1;
  format reject reject.;
run;

proc sort data=adamin.alldata out=allstud (keep=studyid) nodupkey;
  by studyid;
run;

data allstud;
  set allstud;
  col=1;
  output;
  col=2;
  output;
  format col col.;
run;

proc sort data=allstud;
  by studyid col;
run;

data master;
  merge master1 allstud;
  by studyid col;
run;

proc sort data=master;
  by RuleID message;
run;

** Standard summary stat macros for N and PCT **;
%denom(data=master, ptvar=studyid, colvar=col);
%ptsum(var=ruleid, order=2, stat= N PCT, denom=col, dec=0,sortby=F);
%ptsum(var=ruleid message,order=2,stat= N PCT,denom=col, dec=0, sortby=F);

data all;
  set all; ** from stat macros above **;
  if linlabel ne 'Missing';
run;

** Add ordering variable **;
data ord;
  set all;
  ord=max(input(pctx1,8.),input(pctx2,8.));
  keep ruleid ord;
run;

proc sort data=ord;
  by descending ord ruleid;
run;

data ord;
  set ord;
  num=_n_;

```

```

run;

proc sort data=ord;
  by ruleid;
run;

proc sort data=all;
  by ruleid;
run;

data ord2;
  merge all ord;
  by ruleid;
run;

proc sort data=ord2;
  by order descending ord ruleid message;
run;

data all;
  set ord2;
  by order descending ord ruleid message;
  statord1=put(num,8.);
  statord2=put(1000+_n_,8.);
run;

*-----*
* Output Section - use standard reporting macro for table (%tablerpt) *
*-----*

%tablerpt(flabeled=RuleID/Message);

%mend tab;

** Call macro to produce a table for rejects, errors and warnings **;
%tab(id=adam_reject,crit=reject);
%tab(id=adam_err,crit=error);
%tab(id=adam_warn,crit=warning);

APPENDIX 3

%macro listit(ruleid=);

*-----*
* Processing Section *
*-----*

data master1;
  set all; ** from macro in Appendix 1 **;
  if ruleid=upcase("&ruleid");
run;

proc sort data=master1;
  by studyid dataset variables values;
run;

```

```

data master1;
  set master1;
  by studyid dataset variables values;
run;

*****;
* create page numbering and insert blank lines if needed *;
*****;
data all;
  set master1;
  ps=19;
  pageno=ceil(_n_/ps);
  call symput('tpages',put(pageno,3.));
run;

proc sort data=all;
  by pageno studyid dataset variables message;
run;

data final(keep=pageno studyid dataset variables values message category fda
pmda);
  set all;
  by pageno studyid dataset variables message;

  if not first.pageno then do;
    if not first.studyid then do;
      studyid = ' ';
      category = ' ';
      fda = ' ';
      pmda = ' ';
    end;
    if not first.dataset then do;
      dataset = ' ';
    end;
    if not first.variables then do;
      variables = ' ';
    end;
    if not first.message then do;
      message= ' ';
    end;
  end;
  output;

  if last.studyid then do;
    array va(*) studyid dataset variables values message category fda pmda ;
    do i = 1 to dim(va);
      va(i) = ' ';
    end;
    output;
  end;
run;

*****;
** Output          **;
*****;

%titles;

```

```

ods escapechar='^';
ods tagsets.rtf style=basic file="&listings./rtf/&pgmid..rtf" ;
ods listing close;
title;

options nodate nonumber nobyline;
proc report data = final split = '~' missing nowindows
  style(report)={outputwidth=100% just=left}
  style(header)={bordertopwidth=0.24pt bordertopcolor=black} ;
  by pageno;

  column (pageno studyid dataset variables values message);

  define pageno      / order order=internal noprint;
  define studyid    / display "StudyID" style={cellwidth=0.50in just=center
rightmargin = .5em};
  define dataset    / display 'Dataset' style={cellwidth=0.50in just=center};
  define variables  / display "Variables" style={cellwidth=1in leftmargin =
1em just=left};
  define values     / display 'Values' style={cellwidth=2.5in leftmargin = 1em
just=left};
  define message    / display 'Message' style={cellwidth=3.0in leftmargin =
1em just=left};

  * pagination;
  break after pageno / page;

  *titles and footnotes;
  %listing;

run;
quit;
ods tagsets.rtf close;

%mend listit;

**Reject**;
%listit(ruleid=ad0005);

```