

FBS26- FBU Report Wording

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1. Scope

- 1.1. The procedures listed below are provided for analysts to use when writing Forensic Biology Unit reports to relay the results and scientifically supported conclusions relative to the testing conducted in as concise a manner as possible.

2. Background

- 2.1. The content of Forensic Biology Unit laboratory reports must conform to the requirements of the Department of Forensic Sciences (DFS) Forensic Science Laboratory (FSL) Quality Assurance Manual, Forensic Biology Unit (FBU) Quality Assurance Manual, the accreditation standards under ISO/IEC 17025:2005, the supplemental standards set by the FSL's accrediting body, and the FBI's Quality Assurance Standards for Forensic DNA Testing Laboratories.

3. Safety

- 3.1. Not applicable

4. Materials Required

- 4.1. Not applicable

5. Standards and Controls

5.1. Not applicable

6. Calibration

6.1. Not applicable

7. Procedures

7.1. In general, FBU reports will contain sections in the following order:

- 7.1.1. Report name (e.g., Report of Examination, Forensic Biology Unit)
- 7.1.2. Case information block
- 7.1.3. Item(s) Submitted
- 7.1.4. Serological Results and Conclusions (as needed)
- 7.1.5. Male Screening DNA Results (as needed)
- 7.1.6. DNA Results, Conclusions and Statistics (as needed)
- 7.1.7. CODIS (as needed)
- 7.1.8. Examination Methods
- 7.1.9. Notes
- 7.1.10. Disposition of Evidence
- 7.1.11. Signature block

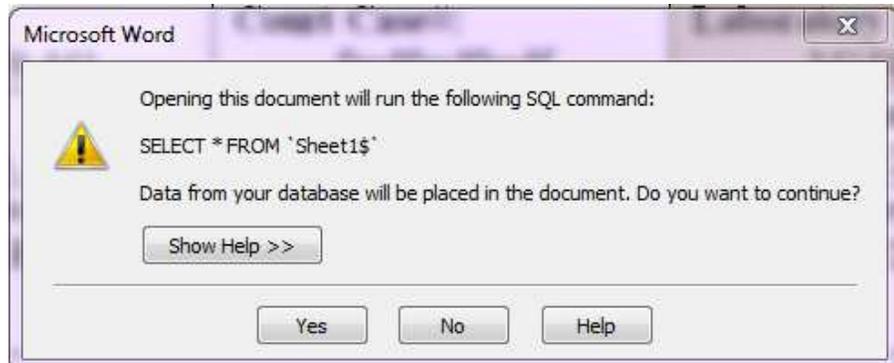
7.2. Report Name

- 7.2.1. Enter the correct type of report; the standard report template is "Report of Examination".
- 7.2.2. If a report is amended, supplemental or a discontinuation of analysis, the report title is appropriately selected to be "Amended Report of Examination", "Supplemental Report of Examination" or "Discontinuation of Analysis".
- 7.2.3. The second line of the report name is "Forensic Biology Unit".
- 7.2.4. The case information block will include the following fields:

MCL#: «MCL_»	CCN#: «CCN_»	Court Case#: «Court_Case»	Laboratory Number: «Lab_Case_»
Offense: «Offense»	Victim(s): «Victim_Name»	Suspect(s): «Suspect_Name»	Incident Date: «Date_of_Offense»
Submitting Agency Name and Address: Metropolitan Police Department 300 Indiana Avenue, NW Washington, DC 20001	Lead Detective: «Detective»	Submission Date: «Lab_Submission_Date»	Report Date: Click here to enter a date.

- 7.2.5. The information in the case information block can either be entered manually or with the use of a mail merge. For mail merge see step 7.2.15.
- 7.2.6. The default for the Submitting Agency Name and Address will be the Metropolitan Police Department. Other agencies may submit evidence as well. When another agency submits evidence, the Submitting Agency Name and address is updated.
- 7.2.7. The MCL#, CCN#, Court Case#, Offense, Victim(s), Suspect(s), Incident Date and Lead Detective fields contain the appropriate information obtained from the submission paperwork.
- 7.2.8. The paperwork may contain variations for each of the fields (for example, the victim name may be spelled several different ways). The Forensic Biology lead or designee will circle which item description/name etc. to use in the report when there are discrepancies.
- 7.2.9. The Laboratory Number is pre-assigned.
- 7.2.10. The Submission Date is the date upon which the evidence was transferred from the Central Evidence Unit (CEU) to the Forensic Biology Unit (FBU).
- 7.2.11. The Report Date is a drop-down feature in which the analyst chooses the calendar date of when the report is composed. If any edits are made, the report date will be updated to reflect the last revision date.
- 7.2.12. If the information is not listed in the submitting paperwork, enter Not listed (i.e. a court case number has not been assigned).
- 7.2.13. A mail merge function can be utilized in which multiple reports can be generated at the same time containing the information needed for the case information block and the Lab submission date under the Item(s) Submitted section.
- 7.2.14. If a manual entry is performed rather than a mail merge, the mail merge fields are deleted and the information is typed in. Proceed to step 7.3
- 7.2.15. To start: copy and paste the required fields from the casework database excel file into the report excel file and save.

- 7.2.16. Open the FBU report template. If the following message appears, click No and proceed to the next step (7.3.17 to continue with the mail merge or if performing manual entry update the appropriate fields and proceed to step 7.3



- 7.2.17. Click on Mailings.
- 7.2.18. Click select Start Mail Merge.
- 7.2.19. Select Letters.
- 7.2.20. Click Select Recipients.
- 7.2.21. Use Existing List.
- 7.2.22. Find the appropriate excel sheet made in section 7.2.15 and open.
- 7.2.23. Click on Sheet1\$.
- 7.2.24. Click OK.
- 7.2.25. Click Finish and Merge.
- 7.2.26. Select Edit Individual documents.
- 7.2.27. Select All.
- 7.2.28. After selecting all, a combined document with all the reports will be produced. Save this document. Individual reports must be separated out by deleting out all other reports and appropriately saving.
- 7.2.29. With the mail merge, the Laboratory#, MCL# and CCN# will also be filled in on the subsequent page(s) of the Report of Examination. Select the drop-down menu in the header to enter the date.

7.3. Item(s) submitted

7.3.1. The following statement will appear under the Item(s) Submitted section:

DFS CEU submitted the following item(s) to the laboratory for analysis:

7.3.2. The following table will be filled out for each evidentiary item that was submitted to the FBU:

<u>Item#</u>	<u>Item Description</u>	<u>Sub-Item#</u>	<u>Sub-Item Description</u>	<u>Examined (Yes/No)</u>
				Select

7.3.2.1. The Item#, Item Description, Sub-Item# and Sub-Item Description are obtained from the submission paperwork and/or evidence packaging.

7.3.2.2. In the Examined column, there is a drop-down menu with the options “Yes” or “No” to indicate whether the item/sub-item was examined.

7.3.2.3. For any unused fields enter “N/A”.

7.3.2.4. For any unused columns, enter “N/A”, do not delete.

7.3.2.5. Delete any unused rows.

7.4. Serological Results and Conclusions

7.4.1. The following table will be filled out for each evidentiary item/sub item that is serologically tested:

<u>Item/Sub-Item#</u>	<u>Item/Sub-Item Description</u>	<u>Blood Results</u>	<u>Semen Results</u>	<u>Processed for DNA</u>
		Select	Select	Select

7.4.2. Enter Item/Sub-Item and Item/Sub-Item Description (at the lowest child level). For example, if a shirt is designated as item 1 and contains stain 1.1, only 1.1 will be listed in the Item/Sub-Item

column and “stain on shirt” will be listed in the Item/Sub-Item Description column.

- 7.4.3. The Blood Results, Semen Results and Processed for DNA columns contain pre-populated statements for possible results. Select the appropriate result from the dropdown.
- 7.4.4. See section 7.4.7 for the Blood results and section 7.4.8 for Semen results.
- 7.4.5. In the Processed for DNA column, make a selection from the dropdown menu to indicate whether the item/sub-item was processed for DNA.
- 7.4.6. If serology was not performed on the case, the entire serology section will be deleted out of the report.
- 7.4.7. Biological Screening results - testing for blood:

<u>Possible Blood Statements</u>	<u>When to Use</u>
Indicated	Positive Phenolphthalein test result
Not detected	Negative Phenolphthalein test result
Inconclusive	Inconclusive Phenolphthalein test result
Not observed using a visual exam	Item/sub-item is visually negative for the presence of blood
Not tested	Test was not performed on item/sub-item

- 7.4.8. Biological Screening results - testing for semen:

<u>Possible Semen Statements</u>	<u>When to Use</u>
Semen confirmed	Positive microscopic exam and a positive p30 test, any AP result, any ALS result
Seminal fluid confirmed	Microscopic negative or not tested, p30 positive, any AP result, any ALS result
Spermatozoa Identified	Positive microscopic exam, p30 negative or not tested, any AP result, any ALS result
No spermatozoa Identified	Negative microscopic exam, p30 not tested, AP not tested, any ALS result
No semen detected	Negative microscopic exam or not tested, negative testing results for AP and/or p30, any ALS results

Seminal fluid indicated but not confirmed	No microscopic exam performed, AP+, p30 negative or inconclusive, any ALS results
Seminal fluid inconclusive	No microscopic exam performed, AP inconclusive and/or p30 inconclusive, any ALS result
Not observed using a visual exam	Item/sub-item is visually negative and/or ALS negative for staining. No other testing was performed
Not tested	Test was not performed on item/sub-item

7.5. Male DNA Screening Results

7.5.1. The following table will be filled out for each evidentiary item/sub-item/stain that is tested for the presence of Male DNA for sexual assault screening or case scenario dependent .

Male DNA Screening Results

<u>Item/Sub-Item/Stain#</u>	<u>Item/Sub-Item/Stain Description</u>	<u>Results</u>	<u>Processed for DNA</u>	<u>Reason Sample not Processed for DNA</u>
		Select	Select	Select

7.5.1.1. Enter Item/Sub-Item/Stain# (at the lowest child level) and Item/Sub-Item/Stain Description (see section 7.4.2 for example).

7.5.1.1.1. Differential extractions should be reported at the fraction level.

7.5.1.1.2. For differentials: at the end of the Item/Sub-Item/Stain Description add (SF) for sperm fraction and (EF) for epithelial fraction.

7.5.1.2. The Results, Processed for DNA and Reason Sample not Processed for DNA columns contain pre-populated statements for possible results.

7.5.1.3. In the Results column, make a selection from the drop-down menu to indicate whether the item/sub-item/stain is Positive (male DNA detected) or Negative (no male DNA detected).

7.5.1.4. In the Processed for DNA column, make a selection from the drop-down menu to indicate whether the item/sub-item/stain was processed for DNA.

7.5.1.5. In the Reason sample not processed for DNA column, make

a selection from the drop-down menu to indicate the reason why the sample was not processed for DNA.

<u>Reason Sample not Processed for DNA</u>	<u>When to Use</u>
Other positive sample(s) selected for further DNA testing	Other male DNA positive sample(s) were processed further
Male DNA indicated; however, high levels of total DNA present	Male DNA to Total DNA is < 1:45
No male DNA detected	The presence of male DNA was not detected
Limited amount of DNA detected, no indication of male	The maximum amount of Total DNA that can entered into an amplification reaction is < 0.041 ng and male DNA was not detected
Limited amount of DNA detected, indication of male	The maximum amount of Total DNA that can entered into an amplification reaction is < 0.041 ng and male DNA was detected
N/A	Sample was processed for DNA

7.5.1.6. If the processing of reference standards is terminated due to the male screening results, the following sentence will remain in the report with the appropriate references listed.

Processing of the following reference standard(s) in this case was/were terminated prior to STR testing due to the human DNA screening results of the evidence:

7.5.1.6.1. If the processing of reference standards was not terminated, the sentence listed above will be deleted out.

7.6. DNA Results, Conclusions and Statistics

7.6.1. Reference samples will be listed first in this section (if present and tested).

7.6.2. If more than one reference sample was tested, the results are listed using the following statement and table:

DNA profiles were obtained from the following reference standards:

Item Number	Name
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7.6.3. If only one reference sample was tested, the result is listed using the following statement and table:

A DNA profile was obtained from the following reference standard:

Item Number	Name

7.6.4. Amplification cut-off samples will be listed next if present.

7.6.5. If the maximum amount of total DNA that could be entered into an amplification reaction is <0.041 ng, the result(s) are listed using the following statement and table:

Human DNA was detected on the following sample(s); however, select from drop-down (it was or they were) insufficient for conducting the STR DNA testing performed in the laboratory:

Item Number	Item Description

7.6.6. For samples that yielded no results during quantitation, the result(s) are listed using the following statement and table:

No human DNA suitable for STR testing was detected on the following sample(s):

Item Number	Item Description

7.6.6.1. If the processing of reference standards is terminated due to the human screening results, the following sentence will remain in the report with the appropriate references listed.

Processing of the following reference standard(s) in this case was/were terminated prior to STR testing due to the human DNA screening results of the evidence:

7.6.6.1.1. If the processing of reference standards was not terminated, the sentence listed above will be deleted out.

7.6.7. DNA Results, Conclusions and Statistics will be listed next if present.

7.6.8. Complete the table listed below for each evidence sample that was processed for STR analysis:

<u>Item/Sub-Item/Stain#</u>	<u>Item/Sub-Item/Stain Description</u>	<u>Mixture Present</u>	<u>Number of Contributors</u>	<u>Reference Name/Item</u>		<u>Interpretation</u>
		Select	Select			Select
Statement:						

7.6.9. Enter in the Item/Sub-Item/Stain# and the Item/Sub-Item/StainDescription at the lowest child level).

7.6.9.1. Differential extractions should be reported at the fraction level.

7.6.9.2. For differentials: at the end of the Item/Sub-Item/Stain Description add (SF) for sperm fraction and (EF) for epithelial fraction.

7.6.10. In the Mixture Present column, make a selection from the drop-down menu indicating “Yes” if a mixture is present, “No” if single source or “N/A” if no results were obtained. See FBS21 (ID+ Interpretation) on how to determine if a mixture is present.

7.6.11. In the Number of Contributors column, make the appropriate selection from the drop-down menu. See FBS21 (ID+ Interpretation) to determine the number of contributors.

<u>Number of Contributors</u>	<u>When to Use</u>
1	Profile is determined to be single source.
2	Profile is determined to be from two contributors.
3	Profile is determined to be from three

	contributors.
4	Profile is determined to be from four contributors.
2 or 3	Profile is determined to be from either two or three contributors and not run in STRmix (neither deconvolved nor LR comparison).
2 or 3, reported as 2	Profile is determined to be from either two or three contributors, the profile was run in STRmix as from both two and three contributors. Two contributors results reported.
2 or 3, reported as 3	Profile is determined to be from either two or three contributors, the profile was run in STRmix as from both two and three contributors. Three contributors results reported.
3 or 4	Profile is determined to be from either three or four contributors and not run in STRmix (neither deconvolved nor LR comparison).
3 or 4, reported as 3	Profile is determined to be from either three or four contributors, the profile was run in STRmix as from both three and four contributors. Three contributors results reported.
3 or 4, reported as 4	Profile is determined to be from either three or four contributors, the profile was run in STRmix as from both three and four contributors. Four contributors results reported.
Uninterpretable-Complexity of mixture	<p>Profile is determined to be from either four or five contributors. OR</p> <p>Profile is determined to be from more than four contributors. OR</p> <p>The number of contributors is not able to be determined due to potential allele sharing, such as in the case of closely related family</p>

	members.
Uninterpretable-Limited data obtained	Not enough data present in profile to determine number of contributors.
N/A	No results obtained.

7.6.12. In the Reference Name/Item column, list each reference that was processed for STR analysis and the respective item number if applicable.

7.6.12.1. If no references are available, type N/A in the Reference Name/Item and Interpretation sections.

7.6.13. In the Interpretation column, select the appropriate interpretation statement from the drop-down menu.

7.6.14. If a qualitative exclusion is made, a likelihood ratio will not be calculated.

7.6.15. A statistical calculation will be performed for all probative inclusionary and inconclusive interpretation statements. Results will be reported to 3 digits.

7.6.16. **Conclusions section for Likelihood Ratios**

7.6.17. For single source samples where there is a probative inclusion for a reference sample, the following statement will be used:

The DNA profile obtained from the evidence item listed above is at least **XXX** times more likely if it originated from **REFERENCE (ITEM #)** than if it originated from an unknown, unrelated individual.”

7.6.18. The likelihood ratio is a numerical value. A likelihood ratio will be generated for every evidence item/sub-item/stain where applicable. If the profiles generated are the same, the overall lowest LR from the three population groups (most conservative) using the 99% 1-sided lower HPD interval will be reported. The Item/Sub-Item/Stain numbers can be entered in the same block along with the corresponding sample description.

7.6.19. For mixtures, if assuming contributor(s), the following statements will be used:

The following individual is expected to be present in the mixture and is an assumed contributor:

Or:

The following individuals are expected to be present in the mixture and are assumed contributors:

7.6.19.1. If a single source sample or mixture with no assumed contributors, this statement will be deleted.

7.6.20. For mixtures where the $LR > 1$, the following statement will be used:

The mixture DNA profile obtained from the evidence item listed above is at least **XXX** times more likely if it originated from REFERENCE, ITEM # and REFERENCE, ITEM # and/or XXX unknown, unrelated individual(s) than if it originated from any assumed contributors and XXX unknown, unrelated individuals.

7.6.21. For mixtures where the $LR < 1$, the following statement will be used:

The mixture DNA profile obtained from the evidence item listed above is at least **XXX** times more likely if it originated from **any assumed contributors and XXX unknown, unrelated individuals** than if it originated from **REFERENCE (ITEM #) and REFERENCE (ITEM #) and/or XXX unknown, unrelated individual(s)**.

7.6.22. For mixtures where the $LR = 0$, the following statement will be used:

REFERENCE (ITEM #) is excluded as a contributor to the evidence item listed above.

7.6.23. For all non-zero LRs, a verbal equivalent statement associated with the LR value will be included and selected from the drop-down menu illustrated below:

This is **Choose an item.** for the following individual(s) to be **Choose an item.** as contributor(s) to the DNA profile obtained from the item listed above: See Notes section for verbal scale.

7.6.24. For mixtures where the $LR = 1.00$, the following statement will be used:

This is equal support for the following individual(s) to be included and excluded as a contributor(s) to the mixture DNA profile obtained from the item listed above:

- 7.6.25. The Statement(s) section of the report is used for the reporting of unknown profiles to include deconvolutions obtained from STRmix.
- 7.6.26. If there are no unknown profiles obtained, the Statement(s) section can be deleted out.
- 7.6.27. If an unknown profile is obtained, select the appropriate statement and delete the remaining statements.

7.7. CODIS

- 7.7.1. One of the two CODIS statements listed below will be included in each report:
 - 7.7.1.1. A CODIS eligible profile was obtained from Item **XXX** and was entered into CODIS to be maintained for routine searching.
 - 7.7.1.2. No CODIS eligible profile(s) were obtained.
- 7.7.2. For non-DNA cases and discontinuation reports, a CODIS statement is not included.

7.8. Examination Methods

- 7.8.1. A list of examination methods used is pre-populated in the report template. All that do not apply should be removed.

7.9. Notes

- 7.9.1. A notes section is included in each report to help with any clarification.
- 7.9.2. If a non-zero likelihood ratio is calculated, a verbal scale is included in this section. See below for full verbal scale published in the Forensic Biology Report. See FBS21 Identifier Plus Interpretation for further explanation of the verbal scale.

Likelihood Ratio Verbal equivalent scale					
1,000,000	<	LR			extremely strong support for the inclusion hypothesis
100,000	<	LR	≤	1,000,000	very strong support for the inclusion hypothesis
10,000	<	LR	≤	100,000	very strong support for the inclusion hypothesis
1,000	<	LR	≤	10,000	strong support for the inclusion hypothesis
100	<	LR	≤	1,000	moderately strong support for the inclusion hypothesis
10	<	LR	≤	100	moderate support for the inclusion hypothesis
1	<	LR	≤	10	limited support for the inclusion hypothesis
1	=	LR			equal support for the inclusion and exclusion hypotheses
1	>	LR	≥	0.1	limited support for the exclusion hypothesis
0.1	<	LR	≤	0.01	moderate support for the exclusion hypothesis
0.01	<	LR	≤	0.001	moderately strong support for the exclusion hypothesis
0.001	<	LR	≤	0.0001	strong support for the exclusion hypothesis
0.0001	<	LR	≤	0.00001	very strong support for the exclusion hypothesis
0.00001	<	LR	≤	0.000001	very strong support for the exclusion hypothesis
0.000001	<	LR			extremely strong support for the exclusion hypothesis

Adapted from *Essential Mathematics and Statistics for Forensic Science* by Craig Adam (2010); pg 289

7.9.3. Any additional information deemed necessary by the analyst will be included in this section of the report.

7.10. Disposition

7.10.1. The following disposition statement will be included in each report: It is FSL policy to return evidence to DFS CEU after the Technical Review. The DNA extracts/substrate remains are returned to the evidence freezer for storage and preservation.

7.11. Signature

7.11.1. At the end of the report, the reporting analyst is required to sign the report. Below the signature, the reporting analyst's name is printed along with his/her title.

8. Sampling

8.1. Not applicable

9. Calculations

9.1. Not applicable

10. Uncertainty of Measurement

10.1. Not applicable

11. Limitations

- 11.1. It is not possible to anticipate the nature of all potential DNA typing results, or the nature of the evidentiary samples from which they may be obtained. These procedures do not exhaust the possible list of the results that may be encountered by the analyst nor the conclusions that the analyst may render based on his/her interpretation of those results. For results not specifically described, conclusion statements should be drafted using statements above that are similar in concept and/or origin, with Technical Leader approval.
- 11.2. Not every situation can, or should, be covered by a pre-set reporting statement. It is important that the analyst follows interpretation criteria for a test when reporting examination results and conclusions.
- 11.3. Any report statements listed herein are intended as a guide only.

12. Documentation

- 12.1. FBU Report of Examination

13. References

- 13.1. ISO/IEC 17025 – General Requirements for the Competence of Testing and Calibration Laboratories, International Organization for Standardization, Geneva, Switzerland (current revision).
- 13.2. ANSI-ASQ National Accreditation Board, Quality Assurance Standards for Forensic DNA Testing Laboratories, (current revision).
- 13.3. National Research Council. The Evaluation of Forensic DNA Evidence, Washington, D.C.: National Academy Press, 1996.
- 13.4. SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories (2010 revision).
- 13.5. LOM02 – Practices for Case Documentation and Report Writing [DCN 1319] (current revision).
- 13.6. FBS21 – Identifiler Plus Interpretation (current revision).
- 13.7. FBS25 – Data Analysis Using STRmix™.

- 13.8. Forensic Science Laboratory Quality Assurance Manual (Current Version).
- 13.9. DFS Departmental Operations Manuals (Current Versions).
- 13.10. FSL Laboratory Operations Manuals (Current Versions).
- 13.11. Forensic Biology Unit Quality Assurance Manual (Current Revision)