1. Hair Evidence
    - If a DNA case record is being made and a DNA packet is being sent for DNA testing by the serologist then add a comments in the DNA case record Items that are being sent for trace only and put your full name and date
    - Do not use sticky note to tape out panties
        i. If you see a hair on panties, send entire item
        ii. If you see a single hair on a swab, place the hair on a sticky note
    - Check for fiber request **BEFORE** you begin analysis on an item. If there is a fiber request, send to trace **FIRST**
    - If there is no Trace record:
        i. If there are not inclusionary results to all suspects, create record and send hairs
        ii. If there are inclusionary results to all suspects, send hairs back
    - If there is a Trace hair record, send hairs to Trace

2. Workbook Packaging Page-
    - Make sure initials are filled in
    - Put a space between each case
    - Items should be listed in numerical order and alphabetical order
    - Change the number of containers as applicable
    - List all packaging except for slides/smears and tube generated by trace for hairs
        i. Not required to list things such as swab protectors, swab caps, etc.
    - Include all items in the analyst's possession (associated with case record), to include sub-items created by analyst
        i. If the entire item is not being analyzed, indicate "not analyzed"
        ii. Individual/additional contents of items, slides/smears, etc. may be indicated as "not analyzed" here (e.g. "smear not analyzed")
        iii. If it is unclear based on the item, scenario, or other info as to why an item is "not analyzed", then it needs to be noted
    - If extracts are submitted/present:
        1. Only need to list the container item
        2. In the notes section, indicate which extracts used
        3. If dried, indicate volume re-constituted to
    - Sexual assault kit should be sub-itemed as follows:
        – Known standards (blood or saliva)
        – Vaginal
        – Rectal
        – Oral
        – Panties
        – Other
        – Hairs
    - Any packaging notes will be placed here (examples)
        i. Serology notes may be added; these notes include KM+, sperm quant
        ii. Multiple items within one package
        iii. If no packaging exits (i.e. item created and consumed) state created and consumed

3. Workbook Serology Page-
    - Order of tests
        i. Blood
            1. Visual (with aid of ALS)

2. KM
3. RSID

ii. Semen
1. Visual (with aid of ALS)
2. AP
3. Micro
4. RSID

- List test QC(s) performed and if they worked properly (only need to be listed once)
- If the initial QC fails
  i. Rerun the sample and test. If the subsequent QC passes then indicate in comments area: initial QC didn't pass; controls and sample rerun"
  ii. Put subsequent QC results in the QC check area with worked properly populated in the box.
- In Description column:
  i. Describe # of swabs or articles
  ii. Brief description; such as blue shirt or pants covered in sand indicate all items contained within
  iii. Staining that may be present
  iv. Any other notes as appropriate
  v. If multiple articles contained in one item, list each article in the area
  1. If not all objects examined in the item, select "not analyzed"
- Date, test choice and results columns - Enter date test was performed, test choice, and results (only need one date per item unless tests performed on multiple days)
  i. If swabbing for epis, select "epi collection".
- Areas column:
  i. Indicate all areas tested with a number as well as multiple items present.
  ii. Do not need to list area if a swab
  iii. "Smear" if from kit
  iv. For condoms -Outside is area 1. Inside is area 2
- Comments box: this area is used for description of results (examples)
  i. Weak KM
  ii. Cutting/swabbings taken for DNA
  iii. Epis seen
- Indicate any sub-items taken (add created sub-items to packaging page)

4. Workbook Extraction Page-
   - Initials should be filled in
   - Nomenclature for negative extraction controls:
     i. NegH for hairs
     ii. NegQ for Questions
     iii. NegSP for sperm fractions
     iv. NegNS for non-sperm fractions
     v. NegK for Knowns
     vi. NegB for Bones/Teeth
     vii. NegF1 for Direct to DNA "non-sperm fractions"
     viii. NegF2 for Direct to DNA "sperm fractions"
   - Samples Column
     i. List all items and negatives for all cases that will be batched (and extracted) together. Leave a space between each case.
     ii. All controls and samples will be written with the full case number#Item number

iii. List each case together, starting with negative and then associated items (e.g., NegQ, 1, 2, NegNS, 3NS, 4NS, NegSP, 3SP, 4SP, NegK, 5, 6)

- Fill out time, date, robot and extraction type for all samples
- Every attempt should be made to keep samples in the same order throughout quant, amp and CE
- Notes (examples):
  i. Consumption notes for each item (may be listed on serology page for start to finish case)For items that consist of swabs or cuttings, indicate how much of sample was used and/or remains (eg. ~1/2 of two swabs used, stained portion of swab used, half of cutting used staining remains)
  ii. For items that are swabbed, indicate how many swabs taken and used (eg. One swab taken and consumed)
  iii. For items that are cut, indicate cutting taken and consumed
  iv. For cigarette butts, indicate approximate amount of filter taken
  v. Note if a sample needs to be combined/concentrated; indicate final volumes (indicate corresponding negative)
  vi. If a sample needs multiple tubes for extraction, note the # of tubes used as well as the # of additional Neg tubes used
  vii. Any additional notes as needed (e.g., swabbing/cutting taken)
- NO packaging notes should be placed on this page

5. Workbook QIAcube data-
   - Fill in initials(add initials for all analysts batching together)
   - All controls and samples will be written with the full case number#Item number
   - Fill in instrument name
   - Fill in date

6. Workbook Quant data-
   - Fill in initials (add initials for all analysts batching together)
   - All controls and samples will be written with the full case number#Item number
   - Print standards, NTC, and all cases from batch (should typically be sorted by sample name)
   - Notes:
     i. List any standard curve points that are deleted
     ii. Note if entire run isn't used
     iii. If any samples are diluted prior to quant
     iv. Any additional samples of yours that are added to a new batch at quant
   - Dilution worksheet(s): Do Not add NTC to the printed table
   - Note: if the entire run fails or standard curve does not pass, a new setup sheet is only required if the sample setup changes
   - If a sample quantity states "Use Above" on the dilution sheets, the sample shall be copied into the appropriate section

7. Workbook Amplification data-
   - Make sure initials are filled in (add initials for all analysts batching together)
   - Add the thermal cycler number
   - Nomenclature for negative amp: NegAmp
   - All controls and samples will be written with the full case number#Item number
   - Notes:

i. Only dilution notes needed are 1:5, 1:10, etc.
ii. Any additional samples of yours that are added to a new batch at amp

8. Workbook 3500 data-
    - Make sure initials are filled in (add initials for all analysts batching together)
    - Add the plate name (At a minimum, name contains one analyst's initials and date)
    - Any additional samples of yours that are added to a new batch at CE
    - Runs should typically be set up with ladder (e.g. Well A1), followed by 2800M (e.g. Well A2), NegAmp (e.g. Well A3), then controls and samples (additional ladder, 2800M and NegAmp may be added to run if necessary)
    - 2800M and NegAmp are only required to be present one time in a plate setup
    - All controls and samples will be written with the full case number#Item number
    - Casework Table should be printed in descending column order (ie Al, Bl, Cl) by run (this will start the egram PDF)
        i. Use an * to mark samples that need additional processing and add why the processing is needed. Eg sample reinjected to confirm OL
        ii. Put any notes about run/items directly under table (not in footer)
    - Egrams should be printed with all dye colors, to include sizing standard, in descending column order per run
    - The samples will be printed in descending column order by run
    - If entire run is being reinjected do not generate a new CE set up; new CE set ups will be for re-setups only
    - OL and microvariant data: Call the allele prior to printing and print the size table immediately after the egram (if multiple samples contain the same microvariant, one sizing table with all associated samples may be printed after the last applicable egram)
    - Negative Raw Data should be printed in column order by run

9. FA
    - Main tab-Choose a Type of Analysis

10. Results/Report-
    - Results tab-
        i. for serology only cases use the serology results tab to write report
        ii. for Cases with both serology results and DNA results use the DNA results tab to write the report
        iii. for DNA only cases use the DNA results tab to write the report
    - Items should be reported numerically unless items with similar results are combined (it is not required to combine all similar results)
    - For each item(s), the appropriate result wording and stats (as applicable) will be cut and placed into the box.
        i. Stats values shall be listed to 3 significant figures. If value is between 1,000 and 9,999, the entire value is listed (e.g., 1,111 listed as 1,110)
    - Popstats PDF: no comments need to be added to this box other than the items that are reflected in this stat.
    - List only the names (and Item #s) for the known standards. Do not state the type of sample that the standard is coming from.
    - Results Section Statement order (where applicable)
        i. Previous technology statement

ii. Any Items that are not examined
iii. The no chemical analysis statement
iv. DNA extraction statement
    1. Fill in question sample #s extracted along with the names and item #s of knowns
    2. Indicate standards as eliminations in this paragraph only. ie. "known standard from John Smith (Item 1, elimination standard)". In item results, do not indicate "elimination standard".
    3. Alternate standards should be listed as swabbing/cutting from ___ (Item _; used as alternate standard for ____) in this paragraph only. In item results, list as "alternate standard from ___ (Item _)."
v. Samples previously examined statement
vi. Standards not suitable statement
vii. Item results
    1. For cases with both serology and DNA results, combine results under the same Item header in report
    2. If main item has body fluid testing and sub-items are collected and tested for DNA, list Main item under a header and then list sub-items under a new header

- Swabbing/cutting will be placed in the item description (as appropriate)
- Differential samples will only be combined with other differential samples, if both fractions of each sample can be combined
- Differential samples will be reported under one Item header (do not list the fractions), not as separate items, with the Fraction 1/non-sperm fraction being reported first
- The stats will be reported in a block format not a paragraph format
- For the CODIS statement, add the item number(s) for any samples being entered
    i. Spell out fraction 1/sperm fraction/non-sperm fraction/major profile for Item etc.
    ii. If no samples being entered, indicate no samples being queried
    iii. For subsequent reports with no additional items being queried, statement shall be changed to no "new" items

11. Disposition/Result page-
    - Enter appropriate disposition for each item
        i. For items being transferred directly to another Scientist, the name to whom the item is being transferred and the date of transfer does not need to be noted
    - Check Human Remains button as appropriate
    - For any disposition statement not automatically populated, the appropriate statement shall be manually typed
    - The Disposition will be included as necessary:
        i. Previously returned items
        ii. Cross referenced items
        iii. Consumed items
        iv. Items going to other sections
        v. Items retained for DNA
        vi. Items going back to the agency

vii. DNA container note (extracts/slides)
viii. Bone note

12. Allele Call Tables-
    - Every attempt should be made to print tables in the same order as egrams
    - The following are examples of notations for call table (where appropriate)
        i. If ArmedXpert is not used for mixture deconvolution, denote reason on table (e.g. greater than 4:1). If a sample is put into ArmedXpert (other than the exceptions listed below), add note to see ArmedXpert (do not mark minor).
        ii. Major/no major
        iii. Assumed number of contributors/ unknown number of contributors
        iv. Imbalance noted at loci if it affects assumptions in interpretation (do not put the % imbalance calculation in)
        v. Loci used for stats
            1. For unresolved mixtures and derived contributors/minors, state type of RMP (eg. mRMP, rRMP, uRMP) used at each locus
            2. For single source profiles (to include major profiles), state mRMP or "allele, any" at loci with possible dropout; however, this is not required
            3. It is not necessary to make a note for single source profiles (to include major profiles) with no alleles in stochastic to state RMP at all
            4. If stats are performed differently than what is on the allele table after comparison to knowns, make this note on the stats page
        vi. If sample is INC, state reason (eg. due to dropout, at least 4 contributors, unknown number of contributors, <5 areas for stats)
    - For unknowns
        i. List a brief description of the evidence
        ii. Indicate non-sperm/sperm fraction/fraction 1/fraction 2 (as applicable)
    - For knowns, do not list the type of sample.
    - For alternate standards, list the item description and (alt stnd from ___)
    - For multiple CE runs, only the sample that was re-processed must have the corresponding CE run date listed
    - Note if OL alleles are not going to be verified

13. ArmedXpert Data-
    - "Green sheets" are required for any sample analyzed using Armedxpert except:
        i. single source samples when only stats are being performed
        ii. samples containing a major or multiple major (no reference is being applied) with less than 5 minor alleles and only stats need to be performed
        iii. 4 person mixtures approved by TL do not require green sheets
    - If a major is called at a locus, all minor alleles shall be present on the armedxpert allele table for the corresponding locus except:
        1. if in a 3 person mixture, you have a called major and have deduced a 2nd contributor but at some areas the minor cannot be confidently assigned to the 2nd or 3rd contributor

14. Other
    - If a sample has to be re-concentrated the note will be placed in the workbook on the corresponding sheet where the re-concentration is noted. (if it is noted at the quant step the note will be made on the quant setup page)
    - Note the corresponding control that is being re-concentrated with the sample in the same area
    - DNA extracts description shall have the item #s listed out ("through" may be used).
    - You can combine items in the notes, FA and report to state items 1 through 10 as long as there are no sub-items as part of that set and the items are in complete sequential order. Sub-items can also be combined as long as they are in complete sequential order. If items are combined, the word "through" must be spelled out (dashes are not permitted).
    - If multiple unknown profiles are present within a case, they should be qualified numerically. Separate unknowns from male unknown profile and numerically number each if possible.
    - Workstation will be added to the worksheet but no QC information will be added to individual pages within FA. If a different lot # was used than what is in the workstation, note the information on the corresponding Workbook page
    - Any re-processing of samples at any step (except for CE setup only) will have a DNA workbook file with a note on the appropriate setup sheet indicating the additional sample added and a batch verification will be performed. If the re-processing is added to another analyst(s) batch, the workbook will start from the re-processing step. If the re-processing is performed with your new batch, the workbook will start from the beginning.
    - All workbook related raw files (i.e. QAS, eds) shall be placed into all case record object repositories at the time the batch review is requested.
    - DNA extract containers shall be made and assigned to the case record at the time the record is prepared for tech review.
    - Allele call tables from previous case records shall be added to new case records when additional comparisons are being performed.
    - For cases that stop at quant, do not include the amp or CE QAS files or the stats reference and expected results files in the OR.

15. Making case records for DNA and YSTRs
    i. Use sequence code 71 for sexual assault kit
    ii. Use sequence code 80 for everything else
    iii. Count items and negatives and place in parentheses in case record notes
    iv. Use DNA exam type
    v. If possible YSTR case, denote "Y?" in case record notes
    vi. If creating a case record for YSTRs, choose YSTR as exam type. Put a note in the case record comments section to indicate which samples need further testing.

Case Object Repository (use the following nomenclature):

Allele Call Table(s) Knowns
Allele Call Table(s) Unknowns (to include Armedxpert tables)
Armedxpert data (mixture/green pages)
Armedxpert project
Biology Workbook (through ce setup)
Biology Workbook verification
CE Negative Raw Data
CE date (zip folder) group by CE set up
CODIS (file prior to tech)
CODIS upload (including employee search and SDIS)
CV Last name year
Egrams (including casework table and ILS)
GMIDX (ser file)
Item (for pictures)
Kit papers Item
QAS Amp
QAS CE
QAS Quant
Quant eds
Serology workbook
Stats
Stats Reference and Expected Results (may be part of workbook)

Notes
-for multiple runs for egrams, GMIDX, negative raw data, CE runs, CODIS, QAS files, eds files, DNA workbook, Armedxpert data list dates but if ran on same day label with numbers 1, 2, etc.
-for emails and other objects with multiple files list date
-for omitted pages in a file, print just the omitted page as a separate document with an appropriate name that explains what it is.
-for corrections to existing pages, check out the file, make corrections and check in the new file with the same name.
- if you are only performing an additional CE injection eg. reset up or reinjection, no batch verification is required for that work, this will be responsibility of the tech/combined admin reviewers. However the nomenclature for that file will contain CE setup_reinject