

Public Comment Deadline: March 28, 2022

ASB Standard 078, Standard for Training in Forensic Autosomal Short Tandem Repeat (STR) Data and Y-STR Data Interpretation and Comparison

#	Section	Revised Section	Type of Comment (E-Editorial, T-Technical)	Comments	Proposed Resolution	Final Resolution
59	General		T	The standard seems a little backward looking.	Provide more guidance on probabilistic thinking instead of emphasizing categorical conclusions.	Reject. Section 4.2.2.2 d) 3) covers probabilistic genotyping appropriate for this document.
76	General throughout document (specifically noted: 4.2.1 a, d; 4.2.2; 4.2.2.2 b, c, d; 4.3.1; 4.3.4; 4.4.1; 4.4.2; 4.4.3)		E	the stated requirements only cover interpretation but not comparison; critical to include both in the requirements for this standard	add "and comparison" to "interpretation" throughout the document; and please do search to see if it goes anywhere else that I missed catching	Accept
40	1		E	"This standard defines the minimum requirements to be met in a forensic DNA analyst training program for autosomal and Y-STR data interpretation and comparison. This standard excludes training for DNA sequencing." Inasmuch as DNA sequencing can be used to generate "autosomal and Y-STR data," the standard either does not fully define minimum requirements for interpretation of STR data. Or maybe it excludes sequence data as STR data, but the scope and limitations of the standard could be stated more clearly. The standard omits many other topics as well.	If the standard is limited to training in the interpretation of STR profiles as determined by PCR and capillary electrophoresis, that should be stated directly in the scope section..	Accept with modifications. Added "including the derivation of STR profiles from DNA sequencing data"
41	1		T	The standard does not discuss how to present the interetations in legal proceedings and does not address any other legal training for analysts. At least the former limitation should be noted in the statememntn of scope.	Note that the standard does not discuss how to present the interetations in legal proceedings.	Reject, presentation in legal proceedings in out of scope for this standard. Standard 154, : Standard for Training on Testimony for Forensic Biology
60	1		T	The current document is primarily a checklist of topics that must be covered in a training program, with little to no specificity regarding the substance of the training in each area. The document also does not address training in common sources of error or human factors in the interpretation of DNA data. The statement of scope needs to be clear that compliance with this standards does not ensure that the content of a training program is adequate.	Revise the Scope to clarify that this document defines a minimal list of training areas and topics that must be addressed in a training program. It does not address the substance of the required training within each topic area.	Accept with modifications. Changed "defines" to "outlines"
61	3		T	Many of the definitions in Section 3 conflate the actual (ground truth) properties of a DNA sample or a PCR reaction with the observed characteristics or patterns of peaks commonly associated with those DNA properties. A major human factors concern in any scientific training is training analysts to maintain a clear distinction between what they observe and what they infer based on those observations.	Draft definitions need to be reviewed and revised as need to clarify which terms refer to an underlying property of a DNA sample, molecular events in a PCR reaction, etc., and which terms refer to observable features of an electropherogram or analytical procedure. Suggested revisions for individual terms (below) are offered as examples, but we recommend that subject area experts review the definitions for all terms and revise as needed to address the general concern.	Reject, no proposed resolutions were provided. Modifications made to definitions based on other comments received. This provided clarification.
71	3.1		E	"a" in front of STR should be "an"	change "a" to "an"	Reject, a is grammatically correct
5	3.2		E	unneeded comma	remove comma after "or"	Accept with modifications, removed comma before "or"
72	3.2		E	commas around "or breakdown" and after "or" may not be necessary	consider deleting extra commas	Accept with modifications, removed comma before "or"

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62	3.3		T	The proposed definition of "drop in" is unclear and potentially misleading. "Allelic peaks" is not defined, but appears to refer to peak on an electropherogram that correspond in size to the potential alleles at a particular locus. The proposed definition describes "drop in" as an observed difference between repeated amplifications of the same DNA sample (non-reproducible peaks). However, the term "drop in" is typically described as a type of PCR artifact, referring to a peak that does not accurately reflect amplification of an allele present in the original DNA sample. This standards needs to define whether "drop in" refers to an actual mismatch between the original DNA template and the PCR products, or to whether a peak is reproducible.	Clarify whether the term refers to the actual correspondence of electropherogram peaks to alleles in a DNA sample, or to occurrence of the same peaks in two PCR reactions. Define whether "allelic peaks" refers to any peak that corresponds in size to an expected allele, or to peaks that actually result from amplification of an allele present in the original sample.	Accept with modification, removed the word "allelic" Note: this definition is not in the OSAC lexicon
42	3.4		E	"Drop-out" is defined as "Failure of an otherwise amplifiable allele to produce a signal above analytical threshold because the allele was not present or was not present in sufficient quantity in the aliquot that underwent PCR amplification." Not present where? The allele had to be present somewhere to be "otherwise amplifiable." I would seem that the only thing one can say is that an allele is not present in sufficient quantity to be detected. The insufficient quantity could be zero, or it could be greater than zero.	Define "drop-out" as "The failure of an otherwise amplifiable allele to produce a signal above a desired threshold because the allele was not present in sufficient quantity in the aliquot that underwent PCR amplification."	Reject, this definition was copied from the OSAC lexicon
63	3.4		T	The proposed definition of "drop out" conflates an inference regarding the original DNA ("otherwise amplifiable allele") with an inferred mechanism (insufficient quantity of DNA) to explain an observation (absence of an expected allele from an electropherogram). Training in DNA interpretation needs to emphasize the distinction between observations, interpretations, and molecular mechanisms.	Need to clarify whether "drop out" refers to a failure to detect an allele that was present in the original DNA sample (one potential interpretation of PCR results), or to observations that could support such an interpretation (very small sample, DNA degradation, etc).	Reject, this definition was copied from the OSAC lexicon
43	3.5		T	"Inclusion is defined as "A conclusion for which an individual cannot be excluded as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other); a statement of inclusion does not confirm that an individual is a source of the DNA." OSAC has asked that "conclusion" not be used in standards.	Define "inclusion" as "A determination that a specific individual cannot be excluded as a source of some or all of the DNA in a sample."	Reject, this definition was copied from the OSAC lexicon
44	3.5		E	"Inclusion is defined as "A conclusion for which an individual cannot be excluded as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other); a statement of inclusion does not confirm that an individual is a source of the DNA." But an individual whose DNA is in the sample may not have "contributed" it. It may have been taken surreptitiously.	Define "inclusion" as "A determination that an individual cannot be excluded as a source of one of all of the DNA in a sample."	Reject, this definition was copied from the OSAC lexicon
45	3.5		T	"Inclusion is defined as "A conclusion for which an individual cannot be excluded as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other); a statement of inclusion does not confirm that an individual is a source of the DNA." The dictionary definition of "confirm" (Merriam-Webster) is "to make firm or firmer: strengthen." Surely an inclusion strengthens a source hypothesis—it is probative of identity. It is not neutral in its implications. It confirms rather than disconfirms the hypothesis that the named individual is indeed the source of some or all of the DNA in the sample.	Define "inclusion" as "A determination that an individual cannot be excluded as a source of some of all of the DNA in a sample." If further discussion of the implications of an inclusion is necessary (which is doubtful), add that "An inclusion is not conclusive proof of the presence of the individual's DNA in the sample because of the risk of error in ascertaining the alleles and the possibility that other individuals could not be excluded."	Reject, this definition was copied from the OSAC lexicon

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46	3.6		E	"Inconclusive" is defined as "A statement provided as the conclusion when testing results are insufficient or lacking in quality and/or quantity, as defined by the laboratory, for comparison purposes; the data are inadequate to draw any meaningful conclusions." The phrase "testing results are insufficient" is unclear. Insufficient in what respect other than quality or quantity?	Define "inconclusive" as "a determination that the samples or the test results are inadequate to draw any meaningful conclusions." (?) (Of course, OSAC has decreed that the word "conclusions" cannot be used in standards, but it seems appropriate here.)	Reject, this definition was copied from the OSAC lexicon
73	3.6		E	this definition is from the OSAC lexicon, but different from the one in Standard 139 [A determination that no conclusion (i.e., inclusion or exclusion) can be drawn from the comparison of reference data to evidentiary data. This could also result from statistical analyses that fail to provide sufficient support for an inclusion or exclusion.]	suggest replacing with the definition from 139, which is more comprehensive, and for consistency within DNA standards	Reject, this definition was copied from the OSAC lexicon
64	3.7		T	Need to clarify. The proposed definition refers to "the act of interfering" with DNA synthesis. In the context of PCR training, the relevant distinction is an active interference with the DNA polymerase by components of the test specimen vs other processes that can result in poor amplification (insufficient template DNA, inactive enzyme, instrument errors, etc).	Clarify what type of interference the term refers to and/or the context in which it is relevant to this training. Possible revision: interference with a DNA polymerase chain reaction by materials present in a specimen.	Accept with modification: Active interference with or prevention of the synthesis of DNA during the polymerase chain reaction (PCR).
6	3.8		E	"types" vague	change "types" to "alleles" (or genotype)	Reject, this definition was copied from the OSAC lexicon
47	3.8		E	The section defines "match" implicitly rather than explicitly, as "When used in a DNA testing report, a match refers to genetic profiles that show the same types at all loci tested in common; a match statement does not confirm that an individual is the source of the DNA." Why the restriction to reports? Does the word have a different meaning in testimony?	Define "match" as "The condition in which two STR profiles have exactly the same alleles at each locus."	Reject, this definition was copied from the OSAC lexicon
48	3.8		T	The characterization of a match ("a match statement does not confirm that an individual is the source of the DNA") is not a part of the definition, and it is inconsistent with the dictionary definition of "confirm" (Merriam-Webster) as "to make firm or firmer: strengthen." Surely a match strengthens a source hypothesis. It is not neutral in its implications. It is probative of identity. It disconfirms rather than disconfirms the hypothesis that the named individual is indeed the source of some or all of the DNA in the sample.	Define "match" as "The condition in which two STR profiles have exactly the same alleles at each locus." If it is necessary to add remarks (which is doubtful), one could say that "Like an inconclusive, a match is not conclusive proof of the presence of the individual's DNA in the sample because of the risk of error in ascertaining the alleles and the possibility that other individuals have matching alleles."	Reject, this definition was copied from the OSAC lexicon
49	3.9		T	"Mixture" is defined as "DNA typing results originating from two or more individuals." However, a mixture is a state of the world--a combination of DNA molecules from more than one individual in the same sample. A low-level mixture may not produce results that would let an analyst recognize it as a mixture, but it is mixture nevertheless.	Define "mixture" as "A combination of DNA from two or more individuals in the same sample."	Reject, this definition was copied from the OSAC lexicon
65	3.9		T	A DNA mixture generally refers to the (ground truth) fact that a DNA sample contains DNA from two or more individuals. The proposed definition converts the term to refer to the results of a PCR amplification, electropherogram, and assignment of genotypes based on an interpretation of those results. This conflates the analyst's conclusions with the ground truth being investigated.	Revise the definition to maintain a clear distinction between an actual mixture (DNA from two or more sources) and laboratory results and analysis that might lead an analyst to infer the presence of a mixture.	Reject, this definition was copied from the OSAC lexicon
50	3.10		E	"Mutation" is defined as "A change in DNA sequence; an alteration or change of an allele at a particular locus resulting in genetic inconsistency between a biological or cellular parent and offspring." The phrase "genetic inconsistency" is obscure. What makes the mutated allele "inconsistent"? How can there be an alteration that is not a change? How can there be a change other than a change in the sequence? Deletions, insertions, and substitutions all change the sequence of base-pairs within an STR allele.	Define "mutation" as "a change in the sequence of base-pairs in a genome. Mutations can consist of insertions, deletions, or substitutions of base pairs."	Reject, this definition was copied from the OSAC lexicon

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51	3.11	Now 3.12	T	"Peak height ratio" is defined as "The relative ratio of two peaks at a given locus in a diploid heterozygous single-source sample." The ratio is a simple ratio, not a relative ratio (which would be a ratio of ratios).	Define "peak height ratio" as the ratio of the heights of two peaks in an electropherogram."	Reject, adopted OSAC lexicon definition
52	3.11	Now 3.12	T	"Peak height ratio" is defined as "The relative ratio of two peaks at a given locus in a diploid heterozygous single-source sample." The peaks do not have to represent two alleles in a sample from a single individual.	Define "peak height ratio" as the ratio of the heights of two peaks in an electropherogram."	Reject, adopted OSAC lexicon definition
66	3.11	Now 3.12	T	"Peak height ratio" refers to an observed feature of a DNA electropherogram, the ratio of the heights of two peaks. Determining whether the sample represents DNA from a single diploid individual who is heterozygous at that locus is an interpretation, which may be based on the peak height ratios. This conflates observations and interpretations or assumptions.	Peak height ratio: the ratio in height between two peaks on a DNA electropherogram. (If there are specific situations in which peak height ratios should or should not be used for analysis, a separate term is needed.)	Accept with modification, adopted OSAC lexicon definition
53	3.13	Now 3.15	E	"Stochastic threshold" is defined as "The peak height value in a DNA profile above which it is reasonable to assume that, at a given locus, allelic drop-out of a sister allele in a heterozygous pair has not occurred in a single source DNA sample." Is not a DNA profile the so-called genotype, which in the case of STR profiling is a list of the alleles at each locus?	Change "DNA profile" to "electropherogram."	Accept with modification, adopted OSAC lexicon definition
67	3.13	Now 3.15	T	"Stochastic threshold" is defined as a peak height "above which it is reasonable" to make certain assumptions. This conflates the operating determination of a threshold with the goal of choosing threshold that balances the risks of type I or type II errors when the threshold is applied in an analysis.	Revise the definition to distinguish the procedure or statistical criteria for defining a threshold from the policy goal of choosing a reasonable threshold for analysis.	Reject, adopted OSAC lexicon definition
68	3.14	Now 3.16	T	Need to clarify whether "stutter" refers to a biochemical process (a DNA polymerase either skips over or inserts repeated elements due to strand slippage) or to an observation that might be interpreted as an artifact based on that process (peaks one or two repeat units smaller or larger than expected alleles).	"Stutter" in molecular biology refers to the enzymatic process. "Stutter peaks" or "stutter pattern" might refer to a set of criteria that might be interpreted as artifacts because they can be explained by stutter.	Reject, adopted OSAC lexicon definition
74	3.15	Now 3.16	E	suggest an insertion for additional clarity	suggest inserting "the DNA profile of" between "in " and "one individual"	Reject, this definition was copied from the OSAC lexicon
17	4.1		T	The statement, "Based upon the laboratory procedures, some of the requirements in this section may be omitted from the training program" is vaguely worded.	Either delete or reword to be clearer, i.e. " The laboratory's training program shall include all requirements applicable to the work conducted by the laboratory and by the individual in training." (I borrowed and modified that language from Standard 022 4.2.2.)	Accept
22	4.1		E	Section 4.1 is different than in previously ASB published training standards.	Make this section as consistent as possible with other training standards.	Accept, added wording similar to standard 023
30	4.1		E	This section does not match 4.1 in previously published training standards.	Make all sections consistent throughout all training standards.	Accept
69	4.1		T	Section 4.1 provides a general authorization to omit "required" content from a training program "based upon the laboratory procedures. This guts any meaning to the claimed scope of "minimum" training requirements.	Delete 4.1 or provide specific criteria for omitting specific training requirements.	Accept
75	4.1		E	This statement only covers methods that are not relevant to the laboratory but should also include portions of testing conducted in the laboratory that the analyst is not being trained in. More inclusive language is suggested.	suggest replacing with "Some of the requirements in this standard may not be applicable depending on the types of DNA testing procedures used in the laboratory and/or the testing to be conducted by the analyst being trained. "	Accept with modification " The laboratory's training program shall include all requirements applicable to the work conducted by the laboratory and by the individual in training."
18	4.2		T	Cognitive bias is included in Std 022 but should be emphasized here as it relates to interpretation and comparison.	Add cognitive bias and effect on interpretation and comparison to knowledge based portion of training.	Accepted with modification to 4.2.1 (f) "literature on the effects of cognitive bias in decision-making processes associated with forensic DNA analysis. "

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23	4.2.1		E	This section is missing a paragraph that was in previously ASB published training standards.	Make this section as consistent as possible with other training standards.	accept with modification, the standard was made consistent with published standards to the extent possible
31	4.2.1		E	Missing a paragraph that is in previously published training standards.	Make all sections consistent throughout all training standards.	accept with modification, the standard was made consistent with published standards to the extent possible
77	4.2.1 b		T	This probably needs more clarity such that the laboratory must define the "relevant" validation studies.	maybe change to something like "all of the validation studies relied upon by the laboratory to support the development of the interpretation and comparison protocol"	Reject, the working group feel that b. plus c. covers the same requirements succinctly
55	4.2.1(e)		E	"At a minimum, the knowledge-based portion of the training program shall require review of the following: ... e) applicable literature as assigned by the trainer." Subsection (e) is vacuous. It does not prescribe any minimum.	Delete (e)	Reject, retained language consistent with published standard 23 and others
54	4.2.2		E/T	What are "interpretation parameters"? It seems to be a technical phrase, but is not defined anywhere in the standard, and it does not seem to refer to the parameters of a statistical model.	Define "interpretation parameters" in § 3.	Accept with modification, changed "parameters" to "criteria"
70	4.2.2		T	Section 4.2 is essentially a checklist of topics the should be covered in training; 4.2.2 provides some general guidance on what should be covered for each topic. Missing from this section is an emphasis on the importance of training that addresses human factors and the potential effects of human judgment at each step in DNA analysis. At a minimum, training under each topic in section 4.2.2 should include awareness of results or conditions that increase the potential for error or misinterpretation and sources of uncertainty at each step in any analysis.	Add a sentence addressing human factors and an emphasis on sources of error as a training focus, e.g.: Training shall address the role of human judgment, sources of uncertainty, and conditions that increase the potential for error at each step in DNA analysis and interpretation.	Accept with modification, "The training shall also address documentation requirements of decisions made during the interpretation and comparison process, to include a basic understanding of the risks of bias and potential for human error." added to 4.2.2
78	4.2.2		E	Laboratories should be laboratory's	change "laboratories" to "laboratory's"	Accept
79	4.2.2		E	the last sentence seems to be missing context as it applies to some of the topics	Suggest modifying to: The training shall include, at minimum, the application of the following topics to data interpretation and comparison listed in 4....	Reject, redundant to previous sentence
19	4.2.2.2		T	Sources of error, including false positives and false negatives should be part of knowledge based training. Additionally, effect of different assumptions (i.e. what if you misspecify NOC; what if you are off on mixture ratio) on interpretation and comparison should be emphasized.	Add wording to 4.2.2.2(d): how assumptions affect interpretation and conclusions. Add e) to 4.2.2.2: sources of false positives and false negatives	Reject, addressed in 4.2.2.2 d. 1) / Reject, outside the scope of this standard - addressed in standard 081
80	4.2.2.2		T	requirement is missing offscale data, data above detection threshold (saturation)	add offscale data; data above detection threshold	Accept with modification, added to 4.2.2.2 a) 7) "off-scale STR data" and added definition in 3.11
7	4.2.2.2a 6		E	"pref and dif amp" not defined	Define in section 3	Partial Accept, added definition for preferential amplification. Removed differential from 6)
8	4.2.2.2a 7		E	"microvariant" not defined	Define in section 3	Accept with modification. Defined Variant Allele and changed "microvariant" to "variant allele" in 7)
81	4.2.2.2 d) 2) v)		T	unclear how one would audit the "etc." part of the requirement	delete "etc"	Accept
20	4.2.2.2(d)(3)(iii)		T	what is a foreign component? Contamination? Any other contributor not major or minor?	Define foreign component or add note explaining it.	Accept " (i.e., alleles not belonging to an assumed contributor) " added
82	4.2.2.2 e		T	there is minimal context to this requirement	perhaps modify by adding something like "Use of the following terms in reports, oral communications and testimony for the"	Reject, covered under standard 080
1	4.2.2.2, e ii)		T	Unclear how the word 'consistent' differs from the word 'match', if at all	Consider putting a definition for 'consistent' or making this clarification in Terms & Definitions section or removing 'consistent' from 4.2.2.2, e ii)	Reject, covered under standard 080
33	4.2.2.2.vi		E	Data too limited/complex is redundant to 4.2.2.3 a and b	remove from 4.2.2.2.vi	Accept with modification, changed 4.2.2.2 a) 8) "data too limited and/or too complex"

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34	4.2.2.2.4.iii		E	Statistics are covered in separate training standard.	remove from list.	Reject, intentional inclusion as a component of prob gen data interp
32	4.2.2.2.d		T	NOC, conditioning and ratios are not considered to be "limitations". These are considerations to be used during mixture interpretation and not limitations.	List these as separate requirements in 4.2.2.2.c and remove from limitations section.	Accept with modification , changed "limitations" to "Considerations" in d); added e) "limitations of mixture interpretation and comparison" as a new section
24	4.2.2.2d		T	Conditioning, NOC and ratios are not considered to be limitations.	Move these as separate requirements in 4.2.2.2c	Accept with modification , changed "limitations" to "Considerations" in d); added e) "limitations of mixture interpretation and comparison" as a new section
9	4.2.2.2d2i		E	comma missing	add comma after (first) "stutter" (stutter, including....)	Reject, section was removed due to redundancy to 4.2.2.2a
10	4.2.2.2d2iii		E	awkward phrase ("on")	consider adding "the effect of allele sharing on..." or similar	Reject, section was removed due to redundancy to 4.2.2.2a
11	4.2.2.2d2v		E	semicolon at end is inconsistent	make consistent with others	Reject, section was removed due to redundancy to 4.2.2.2a
12	4.2.2.2d2vi		E	period at end is inconsistent	make consistent with others	Reject, section was removed due to redundancy to 4.2.2.2a
25	4.2.2.2vi		E	Data too limited/complex is already listed under 4.2.2.3 a and b	Remove this section since it is already listed in 4.2.2.3.	Accept
13	4.2.2.3a		E	period at end is inconsistent	make consistent with others	Reject, section was removed and added to 4.2.2.2.a.8
15	4.3.1		E	I think this is a typo because there isn't a 4.12 in this document. I think this was intended to be 4.2.	Replace "4.12" with the clause that was intended.	Accept with modification. The section numbers were removed for simplification
26	4.3.1		E	4.12 should be 4.3.2-4.3.4	Change 4.12 to 4.3.2-4.3.4	Accept with modification. The section numbers were removed for simplification
35	4.3.1		E	Typo "4.12"	This should be 4.3.2-4.3.4	Accept with modification. The section numbers were removed for simplification
3	4.3.2		Technical/Clarification requested	Clarification requested if this is intended to be an observation of the procedure or requirement of the trainee to read the procedure. Based on the note, it seems to be observation, but with practice exercises.	The trainee shall observe the procedure from a seasoned analyst.	Accept with modification, added "observation with a trained analyst."
27	4.3.2		E	The Note is not used in previously published ASB training standards.	Make this section as consistent as possible with other training standards.	Accept
36	4.3.2		E	This note is not listed as a note in other published training standards.	Make consistent throughout all training standards.	Accept
83	4.3.2		E	It's unclear how a protocol can be observed and this requirement monitored in an audit	Suggest changing to "the use of the protocol..." or "the application of the protocol to DNA data..." or some similar language	Accept
4	4.3.4		Technical/Clarification requested	Clarification requested regarding manual and automated methods. I am assuming this is referring to binary vs. probabilistic genotyping, but in our laboratory we use these terms for manual vs automated platform amplification.	The number and quality of samples interpreted by the trainee shall include the binary and/or probabilistic methods, as applicable.	Accept with modification, "The number and quality of samples interpreted by the trainee shall include manual data review and automated data analysis methods, as applicable, including all validated software programs in use by the laboratory, as applicable."
84	4.3.4		T	in the last sentence, the requirement only covers results, but should also include interpretation and comparison of the results and their conclusions	add ", interpretation and comparison of the results and conclusions" to the end of the last sentence; could also consider deleting the word "results" since that is covered under the technology based standards and not directly applicable here	Accept with modification, deleted "and to produce reliable and accurate results"

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16	4.4		T	The results of competency testing should be easily available.	Add a 4.4.4 that requires competency results to be easily accessible: "The results of competency testing for the analyst(s) involved in the case should be made available to all stakeholders."	Reject, Competencies are considered personnel records by many laboratories and are subject to agency specific policies. Competencies can be provided upon subpoena
21	4.4		T	The competency test should be performed on sample(s) representative of the range, type, complexity encountered in casework. Standard 022, 4.3.2(a)(2) does contain a requirement that a practical test on a lab's analytical procedure be performed on samples representative of the range, type, and complexity typically analyzed by the lab but that requirement is important enough to be repeated here.	Add language: "Practical competency tests shall include samples representative of the range, type, and complexity typically analyzed by the laboratory."	Accept, with modification - language added to 4.4.3: Samples representative of the range, type, and complexity for which the trainee will be authorized to interpret shall be included in the practical competency test.
37	4.4.1		E	Missing title of document for ASB 022	Add "Standard for Forensic Training DNA Analysis Training Programs"	Accept
85	4.4.1 & 4.4.2		E	knowledge-based or knowledge based?	use hyphen (or not) consistently	Accept
28	4.4.2		E	4.12 should be 4.2.	Change 4.12 to 4.2	Accept with modification. The section numbers were removed for simplification
29	4.4.2		E	This section is different than in previously ASB published training standards.	Make this section as consistent as possible with other training standards.	Accept with modification, also made changes to 4.4.3 for consistency
38	4.4.2		E	This section does not match 4.4.2 in previously published training standards.	Make all sections consistent throughout all training standards.	Accept with modification, also made changes to 4.4.3 for consistency
39	4.4.2		E	Typo "4.12"	This should be 4.2	Accept with modification. The section numbers were removed for simplification
56	4.4.2		T	The section "Knowledge-based Competency" states that "The trainee shall successfully complete a knowledge-based test covering the critical information obtained during the training of forensic autosomal and Y-STR data interpretation protocol(s). The format of the test(s) shall be at the discretion of the DNA technical leader or comparable authority. The test(s) shall cover, at a minimum, the topics outlined under 4.12." Beyond the minimum required topics, the section gives no guidance. What does "format" refer to: paper and pencil versus computerized? Essay versus multiple choice? Open-book versus book? Should the same test be given to all trainees?	Either delete the sentence "The format of the test(s) shall be at the discretion of the DNA technical leader or comparable authority." or list the permissible formats. Add something about the level of difficulty that the test must have.	Accept, sentence deleted
86	4.4.2		E	incorrect requirement number stated (no 4.12)	correct requirement number	Accept with modification. The section numbers were removed for simplification
2	4.4.3		T	Last sentence: "All types of samples..." is unnecessarily strict and vague at the same time.	Consider changing to less prescriptive and slightly more specific wording like "A representation of the range of sample types..."	Accept, with modification: Samples representative of the range, type, and complexity for which the trainee will be authorized to interpret shall be included in the practical competency test.
57	4.4.3		T	The section states "The trainee shall successfully complete a practical competency test covering each of the forensic autosomal and Y-STR data interpretation protocol(s) for which he or she will be independently authorized. All types of samples for which the trainee will be authorized to interpret shall be included in the practical competency test." How should the test be administered? Must it be same for all trainees? How difficult should it be? What level of performance is "successful"?	Develop this section in more detail to provide sufficient guidance.	Reject, this level of detail can be determined by the laboratory and/or technical leader
14	Bibliography		E	Hyphen (-) between page numbers	These should be n-dashes (–), not hyphens	Accept.
58	Bibliography		T	The bibliography seems dated and scattered -- particularly if it is supposed to include training in PGS! The readings associated with each topic in the body of the standard should be identified in the pertinent sections. That would greatly assist anyone seeking to create a training program.	Eliminate the bibliography and provide a list of recommended readings (classic or modern) on each required topic within the each topic section or subsection.	Reject, please provide specific changes as appropriate

#	Section	Revised Section	Type of Comment (E-Editorial, T-Technical)	Comments	Proposed Resolution	Final Resolution
87	Bibliography		E	this document relies heavily on validation studies and protocol	suggest adding Standard 018, 020 and 040 to the Bibliography	Partial accept, added standard 40. Bibliography is not intended to be all-inclusive
47	4.4 (comment brought over from comments on Draft Standard 091 for consistency)	4.4.1	T	This section should require that the criteria for passing a competency test be documented and established in advance.	Add a requirement that the criteria for passing should be documented and established in advance.	Accept, requirements added to 4.4.1 for all training standards

Deadline of Submission of Comments: 10-Jul-23

Document Number: ANSI/ASB Std 078

Document Title: Standard for Training in Forensic Autosomal Short Tandem Repeat (STR) and Y-STR DNA Data Interpretation and Comparison

#	Section	Type of Comment (E-Editorial, T-Technical)	Current Document Wording	Comments	Proposed Resolution	Final Resolution
	Forward	E	The aim is to provide a framework for quality training that will result in consistency in the forensic DNA community.	changed for consistency across training documents	The aim is to provide a framework for quality training resulting in consistency within a laboratory and in the forensic DNA community.	Accept
49	General	T		The standard seems a little backward looking.	Provide more guidance on probabilistic thinking instead of (or at very alongside) emphasizing categorical conclusions.	Reject. The CB adjudicated this comment in round 01 and voted to approve the previous resolution.
16	keywords	E	training, interpretation, mixture deconvolution, comparison, DNA standard, autosomal STR, Y-STR	remove mixture interpretation	It isn't a focus of this training document, maybe for a mixture standard, but not for a training document broadly on interpretation	Reject. Comment too vague. The CB cannot make assumptions about what wording the commenter would like to propose.
33	1	T		The standard does not discuss how to present the interpretations in legal proceedings and does not address any other legal training for analysts. This limitation should be noted in the statement of scope. The scope should also note that legal training documents have been added to the bibliography. We recommend adding LTG legal training guidance doc, found at https://sites.google.com/nist.gov/osac/osac-units/legal-task-group?authuser=0 , to the bibliography. Unfortunately, none of the DNA training docs include any specifics about legal training, even Std 022. The subcommittee should take this opportunity to correct that with this doc	Note in the scope that the standard does not discuss how to present the interpretations in legal proceedings. However, a guidance document regarding legal training is referenced in the bibliography.	Reject. A similar comment was adjudicated in round 01 and the CB voted to approve the following resolution: presentation in legal proceedings in out of scope for this standard. Standard 154, : Standard for Training on Testimony for Forensic Biology
18	3.3	T	Allele peak Peak(s) in an electropherogram that are not reproducible across multiple independent amplification events.	This definition is incorrect in that it fails to distinguish several phenomena that are conceptually distinct (sporadic contamination of 1 or 2 alleles that are not reproducible; artifacts of the PCR or CE process; an allele from a true contributor to a sample pre-extract which only shows up say in 1 of 3 amplifications because it is a low level profile and the allele has dropped out of the other two amps. The edit removing "allelic" only confounds this problem. It really seems like a hard phenomenon to define. A possible suggestion: "Presence of one or two spurious alleles only in a profile; these alleles are not reproducible across multiple independent amplifications; also theory of same to explain 1-2 alleles not belonging to known contributor in a profile " Maybe include a cite to DNA Commission.	Drop in definition is inconsistent with the scientific literature. From Draft NIST Mixture Foundation Review: " 385 Allele drop-in: allele peak(s) in an electropherogram (EPG) that are not reproducible across multiple 386 independent amplification events; also, a hypothesis/postulate for the observation of one or more 387 allelic peaks in an electropherogram that are inconsistent with the assumed/known contributor(s) to a 388 sample"; Michael D. Coble & Jo-Anne Bright, <i>Probabilistic genotyping software: An overview</i> , FSI Int'l Genetics Vol. 38 (2019) "Drop-in is the presence of low amounts of DNA within a profile that are not inherent to the DNA extract.". DNA Commission of ISFG, <i>Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods</i> (2012): ". In this context, we distinguish between drop-in and contamination. The latter term specifically describes more than two or more alleles that come from a single individual. Conversely, drop-in alleles come from different individuals. The distinction is important, because the assumption of independence enables the use of the product rule to multiply drop-in probabilities, whereas this is novalid if the events are dependent." At 681.	Reject, the suggested definition is specific to probabilistic genotyping and the WG feels it is not the most appropriate definition for this training document. The definition used in standard 078 is based on that from 2010 Fundamentals book by John Butler.
22	3.4	E		above analytical	above the analytical	Accept.
34	3.5	T		"Inclusion is defined as "A conclusion for which an individual cannot be excluded as a potential contributor of DNA obtained from an evidentiary item based on the comparison of known and questioned DNA profiles (or multiple questioned DNA profiles to each other); a statement of inclusion does not confirm that an individual is a source of the DNA." OSAC has asked that "conclusion" not be used in standards.	Define "inclusion" as "A determination that a specific individual cannot be excluded as a source of some or all of the DNA in a sample."	Reject. This section was not part of the redline, therefore not open for comment in this round.

#	Section	Type of Comment (E-Editorial, T-Technical)	Current Document Wording	Comments	Proposed Resolution	Final Resolution
35	3.6	E		"Inconclusive" is defined as "A statement provided as the conclusion when testing results are insufficient or lacking in quality and/or quantity, as defined by the laboratory, for comparison purposes; the data are inadequate to draw any meaningful conclusions." The phrase "testing results are insufficient" is unclear. Insufficient in what respect other than quality or quantity?	Define "inconclusive" as "a determination that the samples or the test results are inadequate to draw any meaningful conclusions." (Of course, OSAC has decreed that the word "conclusions" cannot be used in standards, but it seems different in kind and appropriate here.)	Reject. This section was not part of the redline, therefore not open for comment in this round.
36	3.8	E		The section defines "match" implicitly rather than explicitly, as "When used in a DNA testing report, a match refers to genetic profiles that show the same types at all loci tested in common; a match statement does not confirm that an individual is the source of the DNA." Why the restriction to reports? Does the word have a different meaning in testimony?	Define "match" as "The condition in which two genetic profiles show the same types at all loci tested in common."	Reject with modification. "match" has been deleted from the document and the terms.
21	3.8 & 4.2.2.2	T	use of word match	I thought the community was moving away from the word "match"--though the definition in 3.8 appropriately makes clear that a match does not equate to "is the source of"		Accept with modification. Comment vague with no proposed resolution. "match" has been deleted from the document and the terms.
37	3.9	T		"Mixture" is defined as "DNA typing results originating from two or more individuals." However, a mixture is a state of the world--a combination of DNA molecules from more than one individual in the same sample. A low-level mixture may not produce results that would let an analyst recognize it as a mixture, but it is mixture nevertheless.	Define "mixture" as "A combination of DNA from two or more individuals in the same sample; a mixture with low level components may not be recognized as such based on the detected results"	Reject. This section was not part of the redline, therefore not open for comment in this round.
38	3.10	E		"Mutation" is defined as "A change in DNA sequence; an alteration or change of an allele at a particular locus resulting in genetic inconsistency between a biological or cellular parent and offspring." The phrase "genetic inconsistency" is obscure. What makes the mutated allele "inconsistent"? How can there be an alteration that is not a change? How can there be a change other than a change in the sequence? Deletions, insertions, and substitutions all change the sequence of base-pairs within an STR allele.	Define "mutation" as "a change in the sequence of base-pairs in a genome. Mutations can consist of insertions, deletions, or substitutions of base pairs."	Reject. This section was not part of the redline, therefore not open for comment in this round.
39	3.11	T		"Data produced when the emitted fluorescence from the PCR products being measured saturates the detector in an electropherogram". This is confusingly worded, sounds like the electropherogram has a detector	Change to: "Data produced when the emitted fluorescence from the PCR products being measured saturates the detector in an electrophoretic device" (or, in a capillary electrophoresis instrument, or genetic analyzer...)	Accept with modification, it was corrected to read "Data produced when the emitted fluorescence from the PCR products being measured saturates the detector; may result in flat-topped peaks in an electropherogram for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak." This definition was obtained from NIST STRbase.
50	3.11	E	Data produced when the emitted fluorescence from the PCR products being measured saturates the detector in an electropherogram; may result in flat-topped peaks for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak.	Data produced when the emitted fluorescence from the PCR products being measured saturates the detector during capillary electrophoresis in an electropherogram; may present on the electropherogram as a result in flat-topped peak for an STR allele and pull-up peak(s) in one or more color channels corresponding to the off-scale peak.	provide clarity in the definition (e.g., the detector is not in the electropherogram); generally results in a single flat-topped peak per allele (changed to singular)	Accept with modification, it was corrected to read "Data produced when the emitted fluorescence from the PCR products being measured saturates the detector; may result in flat-topped peaks in an electropherogram for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak." This definition was obtained from NIST STRbase.
6	3.11	E	may result in flat-topped peaks for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak	may result in flat-topped peaks for STR alleles and pull-up peaks in one or more color channels that is the same size of the STR allele peak	removing the ending takes a portion of the term out of the definition, adding additional wording clarifies where to expect the pull-up peak	Accept with modification, it was corrected to read "Data produced when the emitted fluorescence from the PCR products being measured saturates the detector; may result in flat-topped peaks in an electropherogram for STR alleles and pull-up peaks in one or more color channels corresponding to the off-scale peak." This definition was obtained from NIST STRbase.

#	Section	Type of Comment (E-Editorial, T-Technical)	Current Document Wording	Comments	Proposed Resolution	Final Resolution
7	3.11	T	Data produced when the emitted fluorescence from the PCR products being measured saturates the detector in an electropherogram	Unsure	I do not feel like this definition captures all the reasons for off-scale data, such as bacterial contamination which can produce a peak and it isn't on scale	Reject with modification. Comment too vague. The CB cannot make assumptions about what wording the commenter would like to propose. Definition was revised based on other comments.
1	3.12	T		I haven't seen any forensic biology laboratories calculating PHR using way 1. The second calculation method is the most common (i.e. shortest peak/tallest peak * 100%) and should be listed as number 1.	Consider switching ways 1) and 2).	Accept
23	3.12	E		divided by the taller peak.	divided by the taller peak height.	Accept
40	3.12	T		"Peak height ratio" is defined as "The relative ratio of two peaks at a given locus in a diploid heterozygous single-source sample." The ratio is a simple ratio, not a relative ratio (which would be a ratio of ratios).	Define "peak height ratio" as "The ratio of the heights of two peaks at a given locus in an electropherogram". (please not that our recommended definition is more concordant with textbook definitions (e.g. Butler, Fundamentals)	Reject with modification. The CB adjudicated this comment in round 01 and voted to approve the previous resolution. Separate modifications were made based on comments #1 and #23
41	3.13	T		Preferential amplification. This includes a definition of preferential amplification <i>within</i> a locus; why is there no definition of amplification efficiency between loci, i.e. locus specific amplification efficiency, a concept used in PGS	Add locus specific amp efficiency, as well as other prob gen concepts that are missing from this document	Reject, the community accepted definition is specific to within a locus. Imbalance across loci resulting in a sloping profile is usually caused by degradation. Under standard 4.2.2.2, a) 9), "other considerations (...imbalance observed between loci)" was added.
10	3.13	T	A situation where one allele of a heterozygous pair at a locus is amplified by PCR with greater efficiency than the other allele	Unsure	This definition does not account for preferential amplification of smaller loci versus larger loci.	Reject, the community accepted definition is specific to within a locus. Imbalance across loci resulting in a sloping profile is usually caused by degradation. Under standard 4.2.2.2, a) 9), "other considerations (...imbalance observed between loci)" was added.
42	3.15	E		"Stochastic threshold" is defined as "The peak height value in a DNA electrophoretic profile above which it is reasonable to assume that, at a given locus, allelic drop-out of a sister allele in a heterozygous pair has not occurred in a single source DNA sample" It's nonsensical to say a stochastic threshold is a peak height value in a profile. If you develop no profile from a sample, the stochastic threshold still exists (there would be no alleles above the analytical or stochastic threshold).	Change to "The stochastic threshold is a peak height value, measured in RFUs, above which it is reasonable to assume... "	Accept with modification, "commonly measured in RFUs" added to definition
24	3.16	E		doesn't make sense	clarify	Reject. Comment too vague. The CB cannot make assumptions about what wording the commenter would like to propose.
9	3.17	T	The detection of three alleles in one individual at a particular short tandem repeat (STR) locus	The detection of three alleles in one individual at a particular autosomal short tandem repeat (STR) locus	to be very clear in where trialleles occur since this is an autosomal and Y-STR document	Reject with modification. This definition was not part of the redline, therefore not open for comment in this round. For simplicity an editorial modification was made: the written out "short tandem repeat" was deleted and "STR" remains.
43	3.18	T		"Variant allele. A non-standard form of an allele due to a point mutation, an insertion or a deletion relative to other commonly seen alleles." Confusingly written, b/c insertions and deletions are types of point mutation. Also, to the extent a point mutation is commonly considered an insertion, deletion or substitution of a single nucleotide, and mutations that result in variant alleles could plausibly come from deletion or insertion from a small number, but more than one nucleotide, is the "point mutation" part necessary?	Cut "point mutation" and just say "A non-standard form of an allele due to insertion or deletion of nucleotide base(s) relative to commonly seen alleles"	Reject with modification. a point mutation is not the same as an insertion or deletion. Modification made based on comment #8
8	3.18	T	A non-standard form of an allele due to a point mutation, an insertion or a deletion relative to other commonly seen alleles	A form of an allele not represented on the allelic ladder due to a point mutation, an insertion or a deletion relative to other commonly seen alleles.	the term 'non-standard' would mean that there are standard alleles, where this varies between allelic ladders which varies between previously identified variants.	Accept with modification. Definition changed to "A form of an allele due to an insertion or a deletion relative to other commonly seen alleles."
44	4.1	E		"The laboratory's training program shall include all requirements applicable to the work conducted by the laboratory and by the individual in training."	Insert "to be" before "by the individual in training" (presumably the scope of what that person does before they are fully trained is limited)	Reject, this wording is consistent across all the training documents

#	Section	Type of Comment (E-Editorial, T-Technical)	Current Document Wording	Comments	Proposed Resolution	Final Resolution
11	4.2.1c	E	literature used to support validation	literature used to support validation studies and reporting	I feel like this is vague, does it refer to the literature used to conduct the validation and write the report, the literature referenced in the report? More similar to how 4.2.1d is worded	Reject. This section was not part of the redline, therefore not open for comment in this round.
12	4.2.1e	E	applicable literature as assigned by the trainer.	applicable literature as assigned by the trainer;	change period to semicolon	Accept.
25	4.2.2	E		(such as mixtures with number of	(such as mixtures with numbers of	Accept
51	4.2.2	E	last line: ...in 4.2.2.1 through 4.2.2.3	4.2.2.1 through 4.2.2.2	there is no section 4.2.2.3	Accept. Revised to 4.2.2.2.
2	4.2.2.1	T		The internal PCR control (IPC) may be considered a positive control, but it's important to classify it separately, especially since it may differ from kit to kit.	Add "internal PCR controls" to the list.	Reject. This section was not part of the redline, therefore not open for comment in this round.
3	4.2.2.2	T		"[A]llele sharing" may be more suitable under 4.2.2.2(d)	Remove 4.2.2.2(a)(7) and put it under 4.2.2.2(d)	Accept, became 4.2.2.2 d) ii)
26	4.2.2.2	E		punctuation within lists not consistent	make consistent	Accept. ASB Staff will clean fix.
13	4.2.2.2	E	Consistency in semicolons, commas, and periods are needed throughout			Accept. ASB Staff will clean up punctuation.
45	4.2.2.2	T		"Data suitable for interpretation and/or comparison" ... "(a) factors in data interpretation" ... "(8) data too limited and/or too complex" This section is confusingly structured. It shouldn't be titled "Data suitable for interpretation" if one of the concepts included is "data is too limited and/or complex". Also, "data too limited and/or complex" feels tacked on at the end. Shouldn't it precede all of the stuff on interpretation, since it involves data deemed unsuitable for interpretation/comparison?	EITHER add a section before this section called "Data unsuitable for interpretation and comparison", with subsections for "data too limited" and "data too complex" (with sub-subsections on what makes profiles too limited or complex), OR change the title of this section to "Data suitability for interpretation and/or comparison" and lead off with data suitability determination, before getting into interpretation issues	Accept, 4.2.2.2 changed to "Data suitability..."
19	4.2.2.2(a)(2)	T	2) artifacts (i) drop out/drop in	Make Drop-out and drop-in their own number under (a) factors in DNA interpretation (i.e. make drop out and drop in number 2); remove them from artifacts	drop out and drop in are not artifacts	Accept. Moved to it's own item
52	4.2.2.2 a) 2) i)	T	drop-in/drop-out	delete "drop out" here and move below as a separate number still under 4.2.2.2 a)	drop out is NOT an artifact	Accept. Moved to it's own item
53	4.2.2.2 d)	E	::	delete extra ; at the end	two ::	Accept. ASB Staff will clean up punctuation.
4	4.2.2.2(d)	E		There's an extra semicolon.	Remove extra semicolon.	Accept. ASB Staff will clean up punctuation.
5	4.2.2.2(d)(iii)	T		This is also known as "mixture ratios" or "mixture proportions". It would be useful to define mixture ratio or proportion and provide calculation methods (similar to how peak height ratio was define).	Specify the term "mixture ratio" or "mixture proportion" and define it with suggested calculations.	Reject. This section was not part of the redline, therefore not open for comment in this round.
46	4.3.1	E		"At a minimum, the practical portion of the training program shall include the observation of a trained analyst performing the processes at least once or until clearly understood 4.3.2 with exercises representative of the range, type, and complexity..." Confusingly redlined, is this whole sentence suppose to be in 4.3.2?	Move the part of the sentence in 4.3.1 to 4.3.2	Accept with modification, revised paragraph based on multiple comments
54	4.3.1	E	The laboratory's training program shall provide...to obtain the skills for forensic...STR data interpretation and comparison protocols(s) used by the laboratory	The laboratory's training program shall provide...to obtain the skills for <i>the use of the laboratory's</i> forensic...STR data interpretation and comparison protocols(s) used by the laboratory	words missing	Accept with modification, revised paragraph based on multiple comments
55	4.3.2	E	...at least once or until clearly understood with exercises...	...at least once or until clearly understood, with exercises...	added comma for better ease of reading	
20	4.3.2	E	4.3.2 Practical with exercises shall berepresentative of the range, type, and complexity of routine casework or database samples processed by the laboratory.	double check to ensure it is a sentence--maybe reinsert Practical and delete "with"	may just be the redline aking the flow look confusing but doesn't seem to be a sentence	
27	4.3.2	E		4.3.2 not needed	delete "4.3.2" as it does nt appear to be a new item in the list, and renumber	Reject, CB feels the numbering is necessary for clarity
47	4.3.3	T		"At a minimum, the practical portion of the training program shall include hands-on exercises representative of the range, type, and complexity of routine casework..." Needs some guidance as to what this means, ala other OSAC docs	Add a parenthetical "(e.g. considering number of contributors, template input, allele sharing, degradation)"	Reject, consistent with language in QAS, training topics are detailed in 4.2

#	Section	Type of Comment (E-Editorial, T-Technical)	Current Document Wording	Comments	Proposed Resolution	Final Resolution
56	4.3.3	E	...samples processed by the laboratory that include using the laboratory's own data	samples processed by the laboratory using current testing methods.	unclear what is meant by "laboratory's own data" and how that differs from "samples processed by the laboratory" so advise deleting that language. Also not in 4.3.2.	Accept
28	4.4.2	E		the quality controls steps	the quality control steps	Accept (4.4.2 c) extra "s" deleted
14	4.4.2b	E	the function of the reagent controls used in forensic autosomal and Y-STR data interpretation and comparison	the purpose and function of the controls used in forensic autosomal and Y-STR data interpretation and comparison	function is the way an object accomplishes its purpose, the purpose is the intended or ultimate goal of an object - both should be captured in the competency test; remove the word reagent since that is not defined, this generalizes all controls that may be interpreted	Accept
15	4.4.2c	E	the quality controls steps	the quality control steps	remove plural form of 'controls'	Accept (4.4.2 c) extra "s" deleted
17	4.4.2 & 4.4.3	E		ISO/IEC 17025 requires a laboratory define what "successfully complete" means. A lot of labs miss this.	"The trainee shall successfully complete (as defined by the laboratory's policy) a..." OR Add a "NOTE The laboratory must define how they determine what "successfully complete" means.	Accept with modification (as defined by the laboratory's policy) added to 4.4.2 and 4.4.3. sentence structure edited for consistency across all training documents.
32	4.4.3	E		For the following language "a) properly and accurately execute forensic autosomal and Y-STR data interpretation and comparison protocol(s)", the difference between properly and accurately is unclear/not defined/	either define the difference or delete the word properly	Accept "Properly" removed from 4.4.3 a)
57	4.4.3	E	...for which the trainee will be authorized to interpret shall be included...	...for which the trainee will be authorized to interpret <i>and compare</i> shall be included...	the comparison aspect of the training is missing from this statement	Accept "and compare" added to 4.4.3
58	4.4.3 c)	E	...and software used in the laboratory for forensic...interpretation and comparison protocol(s);	<i>properly and accurately</i> operate relevant equipment, instrumentation, and software used as stated in the laboratory <i>protocol(s)</i> for forensic...interpretation and comparison protocol(s);	working awkward and confusing, and align with a) ; also, what's the difference between equipment and instrumentation - just keep equipment or instruments?	Accept with modification "accurately" and "as stated in the laboratory's protocol for "added to 4.4.3 c) Instruments are used for measuring, equipment is a tool with a specific purpose, not always used for measuring. Both words are necessary to cover all operations in the laboratory.
59	Annex A 6)	E	Butler, John	Butler, J	correction	Accept
60	Annex A 7)	E	Dror, et al.	Dror, I., et al.	correction	Accept
61	Annex A general	E	formatting/spacing needs correcting		inconsistent spacing	Accept. ASB Staff will clean up layout.
48	Bibliography	T		The bibliography seems dated and scattered (other than the OSAC standards and Butler's textbook (2015), there is nothing on this list post 2011. I.e. it predates the rise of complex DNA interpretation (and lessons learned). It's particularly problematic given this training is intended to cover PGS. The readings associated with each topic in the body of the standard should be identified in the pertinent sections. That would greatly assist anyone seeking to create a training program.	Eliminate the bibliography and provide a list of recommended readings (classic or modern) on each required topic within the each topic section or subsection. Whether or not the bibliography is kept, add references related to PGS. Include more recent literature re: mixture interpretation challenges . Include reference to LTG guidance on legal training (found at found at https://sites.google.com/nist.gov/osac/osac-units/legal-task-group?authuser=0).	Reject with modification, recommended LTG reference is not publicly available. ASB 018 referenced as 1) in bibliography
29	ref 3]	E		vol.1	vol. 1	Accept
30	ref list	E		inconsistent use of et al.	make consistent (e.g. if three or more authors in the list)	Accept - ASB staff to clean up formatting
31	ref 9]	E		article title is capitalised	make sentence case	Accept - ASB staff to clean up formatting

Deadline of Submission of Comments: 13-Oct-25

Document Number: ASB Std 078

Document Title: Standard for Training in Forensic Autosomal Short Tandem Repeat (STR) and Y-STR DNA Data Interpretation and Comparison

Comment #	Text Line # (s)	Document Section	Type of Comment	Current Document Wording	Proposed Revision	Revision Justification	For Working Group and Consensus Body use only, not to be completed by commenter.
			E-Editorial T-Technical				Final Resolution
1		Foreword	E	minimum requirements	delete minimum	we voted to delete minimum from the Scope; should also be deleted from the Foreword	Accept
2		3.11	T	The relative ratio of two peaks at a given locus. Mathematically, the ratio may be calculated in two ways: 1) The shorter peak (or area) divided by the taller peak height (or area). This is commonly expressed as a percentage. 2) The peak height (or area) of the longer length allele divided by the peak height (or area) of the shorter length allele.	The relative ratio of two peaks at a given locus. The shorter peak (or area) divided by the taller peak height (or area). This is commonly expressed as a percentage.	Supporting documentation could not be located showing that labs (US, Canada, European) currently use this inverse method. It results in a value larger than 100%. Also, consider removing the parenthesis for the word area. If peak or area can be used, the parenthesis doesn't seem necessary.	Reject: The standard gives two options and both are correct
3	99	4.2.1		minimum	delete "At a minimum,"	we voted to delete minimum from the Scope; should also be deleted here; if the requirement is met, it's irrelevant if there is more that was required in their program	Accept
4	121	4.2.6		minimum	delete "At minimum,"	we voted to delete minimum from the Scope; should also be deleted here; if the requirement is met, it's irrelevant if there is more that was required in their program	Accept
5	177	4.3.2	E	minimum	delete "At a minimum,"	we voted to delete minimum from the Scope; should also be deleted here; if the requirement is met, it's irrelevant if there is more that was required in their program	Accept
6		4.3.2	E	At a minimum, the practical portion of the training program shall include the observation of a trained analyst performing activities representative of the range, type, and complexity of DNA data from routine casework or database samples processed by the laboratory, at least once or until clearly understood.	At a minimum, the practical portion of the training program shall include the observation of a trained analyst performing activities representative of the range, type, and complexity of DNA data from routine casework or database samples processed by the laboratory, at least once or until demonstration by the trainee that the material is completely and clearly understood.	A trainee could clearly understand the material but not be able to demonstrate that they understand. It is important add demonstrate to this section.	Reject: The demonstration is accomplished with the competency portion. Additionally 4.3.4 discusses the trainee's ability to demonstrate.
7	181	4.3.3	E	minimum	delete "At a minimum,"	we voted to delete minimum from the Scope; should also be deleted here; if the requirement is met, it's irrelevant if there is more that was required in their program	Accept
8		4.4.3 c	E	accurately operate relevant equipment, instrumentation, and software as stated in the laboratory's protocol for forensic autosomal and Y-STR data interpretation and comparison protocol(s);	accurately operate relevant equipment, instrumentation, and software as stated in the laboratory's autosomal and Y-STR interpretation and comparison protocol(s)	Cleaner sentence for the modification	Accept
9		Bibliography d		http://media.wix.com/ugd/4344b0_da25419ba2dd4363bc4e5e8fe7025882.pdf	use reference to swg website for the up to date version	this link takes you to an outdated version of this document	Accept
10		Bibliography	E		add NIST Mixture Foundational review; Butler, J.M., et al. (2024) DNA Mixture Interpretation: A NIST Scientific Foundation Review. (National Institute of Standards and Technology, Gaithersburg, MD), NIST IR 8351. https://doi.org/10.6028/NIST.IR.8351; https://nvlpubs.nist.gov/nistpubs/ir/2024/NIST.IR.8351.pdf (sent 16 2025)	very important document for DNA data interpretation and comparison	Accept
11			T	none	Requirement to review and evaluate comparison of evidence profile data to elimination databases	This is a critical component of data interpretation and comparison that is not present in this document. Perhaps add a requirement under Quality Control Indication (2.6.1) or under 4.2.6.2 somewhere.	Reject: Not part of the redlined portion

Deadline of Submission of Comments: 11-May-26

Document Number: ASB Std 078

Document Title: Standard for Training in Forensic Autosomal Short Tandem Repeat (STR) and Y-STR DNA Data Interpretation and Comparison

Comment #	Text Line # (s)	Document Section	Type of Comment	Current Document Wording	Proposed Revision	Revision Justification	For Working Group and Consensus Body use only, not to be completed by commenter.
			E-Editorial T-Technical				Working Group Resolution
1			Ballot Comment	Just a suggestion for section 5 Conformance. As written, it is unclear if the second to last word "this" refers to standard 078 or to ANSI/ASB Std. 022. If it's referring to standard 078, I'd suggest wording it as follows: ...the laboratory shall meet the requirements outlined in this document as well as those in Section 5 of..."			Reject, wording is consistent with other training documents.