STEC EQA-13 2024-2025

Dear Participant,

Welcome to the thirteenth External Quality Assessment (EQA-13) scheme for typing of STEC in 2024-2025.

NOTE: New virulence gene esta (STa).
If you are using WGS, please read the WGS part of the submission protocol thoroughly before starting your analysis. This year, you are required to use a specific strain/sequence when reporting allele differences/SNP distances.

Please note that most of the fields must be filled in before the submission can be completed. You can write any comments at the end of the form. If you have any questions, please feel free to contact us at ecoli.eqa@ssi.dk.

To begin, please fill in your country, laboratory name, and LAB_ID.

The available options in this participation form include:

- Provide your email to receive a link with your answers. The email containing the link will be sent after pressing "Finish" on the last slide of the survey.
- Open the windows in full screen for the best survey format.
- If the survey is closed before completion, your answers will be saved, and you can return to the survey using the same link.

Note: After pressing "Finish," you will not be able to review your results.

1. Country

(1) □ Australia

(2) □ Austria

(3) □ Belgium

(4) □ Bulgaria

(5) □ Canada

(6) □ Croatia

(7) □ Czech Republic

(8) □ Denmark

(9) □ Estonia

(10) □ Finland

(11) □ France

(12) □ Germany

(13) □ Greece

(14) □ Hungary

(15) □ Iceland

(16) □ Ireland

(17) □ Italy

(18) □ Israel

(19) □ Latvia

(20) □ Lithuania

(21) □ Luxembourg

(22) □ Malta

(23) □ México

(24) □ Montenegro

(25) □ New Zealand

(26) □ Norway

(27) □ Paraguay

(28) □ Poland

(29) □ Portugal

(30) □ Romania

(31) □ Scotland, UK

(32) □ Slovakia

(33) □ Slovenija

(34) □ South Africa

(35) □ Spain

(36) □ Sweden

(37) □ The Netherlands

(38) □ Turkey

(39) □ United Kingdom

(40) □ United States of American

2. Institute name _____

3. Laboratory name _____

4. Laboratory ID _____

Consisting of country code (two letters) Lab ID on the vial e.g DK_SSI

5. E-mail	_____

6. STEC EQA-13 Strain ID´s

Please enter the isolate ID(4 digits)

We recommend to print this page out!
To have the overview of isolate ID's and isolate No. 1-12, it will make the work easier.

Strain1	_____
Strain2	_____
Strain3	_____
Strain4	_____
Strain5	_____
Strain6	_____
Strain7	_____
Strain8	_____

Strain9	_____
Strain10	_____
Strain11	_____
Strain12	_____

7. Serotyping and virulence gene determination of STEC

8. Submitting results

(1) □ Submit serotyping/virulence gene determination results

(2) □ Did not participate in the serotyping or virulence determination part(s) – Go to 21

9. Submitting results - Serotyping

(1) □ Both O group and H type – Go to 10

(2) □ Only O Group – Go to 10

(3) □ Only H type – Go to 12

(4) □ Did not participate in serotyping – Go to 14

10. Results for serotyping (O Group)
please type the number of O Group by using (1-188)
Non Typable: 7777, Rough: 8888, Not done: 9999

O Group

Strain1	_____
Strain2	_____
Strain3	_____
Strain4	_____
Strain5	_____
Strain6	_____
Strain7	_____
Strain8	_____
Strain9	_____
Strain10	_____

Strain11	_____
Strain12	_____

11.Please specify the method used:
Phenotypic or molecular (PCR based, WGS based)

	Phenotypic	PCR based	WGS based
Method:	(1) ☐	(2) ☐	(3) ☐

12. Results for serotyping (H Type)
please type the number of H Type by using (1-56)
H-: 6666, Non Typable: 7777, Not done: 9999

H Type

Strain1	_____
Strain2	_____
Strain3	_____
Strain4	_____
Strain5	_____

Strain6	_____
Strain7	_____
Strain8	_____
Strain9	_____
Strain10	_____
Strain11	_____
Strain12	_____

13. Please specify the method used:
Phenotypic or molecular (PCR based, WGS based)

	Phenotypic	PCR based	WGS based
Method:	(1) ☐	(2) ☐	(3) ☐

14. Submitting results - Virulence gene determination

(1) □ Submit Virulence gene determination data (*eae*, *aggR*, *esta* (STa), stx1, stx2 or subtyping)

(2) □ Did not participate in the Virulence gene determination *eae*, *aggR*, *esta* (STa) stx1a, stx2 or subtyping). – Go to 21

15. Please specify the method used for the virulence gene determination (incl. subtyping):

	WGS – Go to 17	Other – Go to 16
Method:	(1) □	(2) □

16. If another method is used please describe in detail your method:

_____

_____

17. Results for Virulence gene determination
please use 1 for detected and 0 for not detected, Not done: 9999

	eae	***aggR***	***esta* (STa)**	**stx1**	**stx2**
Strain1	_____	_____	_____	_____	_____
Strain2	_____	_____	_____	_____	_____
Strain3	_____	_____	_____	_____	_____
Strain4	_____	_____	_____	_____	_____

Strain5	_____	_____	_____	_____	_____
Strain6	_____	_____	_____	_____	_____
Strain7	_____	_____	_____	_____	_____
Strain8	_____	_____	_____	_____	_____
Strain9	_____	_____	_____	_____	_____
Strain10	_____	_____	_____	_____	_____
Strain11	_____	_____	_____	_____	_____
Strain12	_____	_____	_____	_____	_____

18. Submitting results - subtyping results

(1) □ Submit subtyping data

(2) □ Did not participate in subtyping – Go to 21

19. Results for subtyping

Subtyping of stx1, select variant (stx1a, stx1c, stx1d)

All isolates have to be subtyped regardless of the results of the initial screening. "Not done/ND" will by default be evaluated as an incorrect result.

	stx1a	stx1c	stx1d	stx1a; stx1c	stx1a; stx1d	stx1c; stx1d	Negative	ND
Strain1	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain2	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain3	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain4	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain5	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain6	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain7	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain8	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain9	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain10	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐
Strain11	(1) ☐	(2) ☐	(3) ☐	(4) ☐	(5) ☐	(6) ☐	(7) ☐	(8) ☐

Strain12	(1) ☐		(2) ☐		(3) ☐		(4) ☐		(5) ☐			(6) ☐		(7) ☐			(8) ☐											

20. Subtyping of stx2 select variant (stx2a, stxb, stx2c, stx2d, stx2e, stx2f, stx2g)
All isolates have to be subtyped regardless of the results of the initial screening.
"ND" will by default be evaluated as an incorrect result.

	stx2a	stx2b	stx2c	stx2d	stx2e	stx2f	stx2g	stx2a; stx2b	stx2a; stx2c	stx2a; stx2d	stx2a; stx2e	stx2a; stx2g	stx2b; stx2c	stx2b; stx2d	stx2b; stx2g	stx2c; stx2d	stx2c; stx2e	stx2c; stx2g	stx2d; stx2e	stx2d; stx2g	stx2e; stx2f	stx2a; stx2b; stx2c	stx2a; stx2c; stx2d	stx2b; stx2c; stx2d	stx2a; stx2b; stx2c; stx2d	Negative	ND
Strain1	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐
Strain2	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐
Strain3	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐
Strain4	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐
Strain5	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐
Strain6	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐
Strain7	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐

Strain8	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□
Strain9	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□
Strain10	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□
Strain11	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□
Strain12	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□	□

21. Submitting Cluster results

(1) □ Cluster analyses based on PFGE and/or WGS

(2) □ Did not participate in the Cluster part – Go to 116

22. Submitting Cluster analysis results

(1) □ Cluster analysis based on PFGE – Go to 23

(2) □ Do not wish to submit any cluster results based on PFGE analysis – Go to 26

23. Cluster analysis based on PFGE data

24. Please list the ID for the isolate included in the cluster of closely related isolate detected by PFGE results (bands >33 kb):
please use semicolon (;) to separate the ID´s

_____

25. XbaI - Total number of bands (>33kb) in a cluster strain

_____

26. Submitting Cluster results

(1) □ Cluster analysis based on WGS data – Go to 27

(2) □ Do not wish to submit any cluster results based on WGS data – Go to 116

27. Cluster analysis based on WGS data

28. Please select the analysis used to detect the cluster using WGS
The results of the cluster detection can only be reported once (main analysis). If more than one analysis is performed please report later in this submission

(1) □ SNP based – Go to 30

(2) □ Allele based – Go to 37

(3) □ Other – Go to 29

29. If another analysis is used please describe in detail your approach (including: assembler, number of loci, variant caller, read mapper or reference ID ect.)

- Go to 44

_____
_____
_____
_____
_____
_____

30. Please report the used SNP-pipeline
(reference if publicly available or in-house pipeline)

_____

31. Please select the approach used for the SNP analysis

(1) □ Reference based – Go to 32

(2) □ Assembly based – Go to 35

32. Reference genome used:
Preferable use EQA strain0018 (downloaded sequences) as reference. Otherwise indicate Multi-locus Sequence Type (e.g. ST8) and identification of the used reference.

_____

33. Please indicate the read mapper used
(e.g. BWA, Bowtie2)

_____

34. Please indicate the variant caller used
(e.g. SAMtools, GATK)

_____

35. Please indicate the assembler used
(e.g. SPAdes, Velvet)

_____

36. Please specify the variant caller used
(e.g. NUCMER)

_____

37. Please select tools used for the allele analysis

(1) □ BioNumerics – Go to 39

(2) □ SeqSphere – Go to 39

(3) □ Enterobase – Go to 39

(4) □ Other – Go to 38

38. If another tool is used please enter here:

_____

39. Please indicate allele calling method:

(1) □ Assembly based and mapping based – Go to 40

(2) □ Only assembly based – Go to 40

(3) □ Only mapping based – Go to 41

40. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

41. Please select scheme used for the allele analysis

(1) □ Applied Maths (wgMLST) – Go to 43

(2) □ Applied Maths (cgMLST/Enterobase) – Go to 43

(3) □ Enterobase (cgMLST) – Go to 43

(4) □ Other – Go to 42

42. If another scheme (e.g. in-house) is used, please give a short description

_____
_____
_____
_____

_____
_____

43. Please report the number of loci in the used allelic scheme

_____
_____
_____
_____
_____
_____

Cluster detected by analysis on data derived from WGS

On this page you have to report the results for the cluster detected by the selected analysis (e.g. SNP based). If another additional analysis (e.g. allele based or another SNP based analysis) is performed please report results later, but you will not be asked to submit the ID´s for isolates in the cluster detected with the additional analysis.

44. Please list the ID for the strains included in the cluster of closely related strains detected by WGS: please use semicolon (;) to separate the ID´s
This includes the 12 test strains and the 8 provided sequences (20 in total). For the provided sequences write the numbers like: 0013, 0014, 0015, 0016 ect.

_____
_____
_____
_____
_____
_____

45. Report the ID, part of the cluster (yes/no), and SNP distance/allele difference

Please use 9999 for not analyzed

	ID	Cluster (Yes/No)	AD/SNP
Strain1	_____	❍ (Yes) ❍ (No)	_____
Strain2	_____	❍ (Yes) ❍ (No)	_____
Strain3	_____	❍ (Yes) ❍ (No)	_____
Strain4	_____	❍ (Yes) ❍ (No)	_____
Strain5	_____	❍ (Yes) ❍ (No)	_____
Strain6	_____	❍ (Yes) ❍ (No)	_____
Strain7	_____	❍ (Yes) ❍ (No)	_____
Strain8	_____	❍ (Yes) ❍ (No)	_____
Strain9	_____	❍ (Yes) ❍ (No)	_____
Strain10	_____	❍ (Yes) ❍ (No)	_____
Strain11	_____	❍ (Yes)	_____

		❍ (No)		
Strain12	_____	❍ (Yes) ❍ (No)	_____	

46. For each ID report: part of the cluster (yes/no), QC status (A/B/C), QC comment and SNP distance/allele difference

QC status:
Please select the QC status that fits with your assessment of the strain
A = Acceptable quality, B = Quality only acceptable for outbreak situations (less good quality), C = Not acceptable quality - strain not analyzed

Distance:
Please use 9999 for not analyzed

	Cluster (Yes/No)	**QC (A/B/C)**	**QC comment**	**AD/SNP**
Strain0013	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0014	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0015	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0016	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0017	❍ (Yes) ❍ (No)	❍ (A) ❍ (B)	_____	_____

		❍ (C)		
Strain0018	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0019	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____
Strain0020	❍ (Yes) ❍ (No)	❍ (A) ❍ (B) ❍ (C)	_____	_____

47. (Optional) Would you like to add additional information for the strains? e.g. serotype or sequence type (ST)

(1) ❍ Yes

(2) ❍ No – Go to 48

	Serotype	**Subtype**	**Sequence type (ST)**
Strain1	_____	_____	_____
Strain2	_____	_____	_____
Strain3	_____	_____	_____
Strain4	_____	_____	_____
Strain5	_____	_____	_____

Strain6	_____	_____	_____
Strain7	_____	_____	_____
Strain8	_____	_____	_____
Strain9	_____	_____	_____
Strain10	_____	_____	_____
Strain11	_____	_____	_____
Strain12	_____	_____	_____
Strain0013	_____	_____	_____
Strain0014	_____	_____	_____
Strain0015	_____	_____	_____
Strain0016	_____	_____	_____
Strain0017	_____	_____	_____

Strain0018	_____	_____	_____
Strain0019	_____	_____	_____
Strain0020	_____	_____	_____

48. Would you like to add results performed with another additional analysis on the data derived from the WGS?
e.g. if SNP based results are submitted you can also report allele based results or results from a second SNP analysis

(1) □ Yes – Go to 49

(2) □ No – Go to 86

49. Please select the additional analysis used on data derived from WGS

(1) □ SNP based – Go to 51

(2) □ Allele based – Go to 58

(3) □ Other – Go to 50

50. If another analysis is used please describe in detail your approach (including: assembler, number of loci, variant caller, read mapper or reference ID ect.)

_____
_____
_____
_____
_____
_____

51. Please report the used SNP-pipeline
(reference if publicly available or in-house pipeline)

_____

52. Please select the approach used for the SNP analysis

(1) □ Reference based – Go to 53

(2) □ Assembly based – Go to 56

53. Reference genome used: (preferable use EQA strain0018, downloaded sequences as reference). Otherwise indicate Multi-locus Sequence Type (e.g. ST8) and isolate ID

_____

54. Please indicate the read mapper used (e.g. BWA, Bowtie2)

_____

55. Please indicate the variant caller used (e.g. SAMtools, GATK)

_____

56. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

57. Please specify the variant caller used (e.g. NUCMER)

_____

58. Please select tool used for the allele analysis

(1) □ BioNumerics – Go to 60

(2) □ SeqSphere – Go to 60

(3) □ Enterobase – Go to 60

(4) □ Other – Go to 59

59. If another tool is used please list here:

_____

60. Please indicate allele calling method:

(1) □ Assembly based and mapping based – Go to 61

(2) □ Only assembly based – Go to 61

(3) □ Only mapping based – Go to 62

61. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

62. Please select scheme used for the allele analysis

(1) □ Applied Maths (wgMLST) – Go to 64

(2) □ Applied Maths (cgMLST/Enterobase) – Go to 64

(3) □ Enterobase (cgMLST) – Go to 64

(4) □ Other – Go to 63

63. If another scheme (e.g. in-house) is used, please give a short description

_____
_____
_____
_____
_____
_____

64. Please report the number of loci in the used allelic scheme

_____
_____

_____
_____
_____
_____

65. Additional analysis on data derived from WGS

66. Results for an additional cluster analysis.
Reporting allele differences /SNP distances to strain0018 (as downloaded sequence) (e.g. SNP or Allele based)
Please use 9999 for not analysed

	Distance/difference (e.g. SNP/allele) to the strain0018 (downloaded sequence)
Strain1	_____
Strain2	_____
Strain3	_____
Strain4	_____

Strain5	_____
Strain6	_____
Strain7	_____
Strain8	_____
Strain9	_____
Strain10	_____
Strain11	_____
Strain12	_____

Strain0013 (as downloaded sequence)	_____
Strain0014 (as downloaded sequence)	_____
Strain0015 (as downloaded sequence)	_____
Strain0016 (as downloaded sequence)	_____
Strain0017 (as downloaded sequence)	_____
Strain0018 (as downloaded sequence)	_____
Strain0019 (as downloaded sequence)	_____
Strain0020 (as downloaded sequence)	_____

67. Would you like to add results performed with a third analysis on the data derived from the WGS?
e.g. if SNP based results are submitted you can also report allele based results or results from a second SNP analysis

(1) □ Yes – Go to 68

(2) □ No – Go to 86

68. Please select the third analysis used on data derived from WGS

(1) □ SNP based – Go to 70

(2) □ Allele based – Go to 77

(3) □ Other – Go to 69

69. If another analysis is used please describe in detail your approach (including: assembler, number of loci, variant caller, read mapper or reference ID ect.)

_____
_____
_____
_____
_____
_____

70. Please report the used SNP-pipeline
(reference if publicly available or in-house pipeline)

_____

71. Please select the approach used for the SNP analysis

(1) □ Reference based – Go to 72

(2) □ Assembly based – Go to 75

72. Reference genome used:(preferable use EQA strain0018, downloaded sequences as reference) Otherwise indicate Multi-locus Sequence Type (e.g. ST8) and isolate ID

_____

73. Please indicate the read mapper used (e.g. BWA, Bowtie2)

_____

74. Please indicate the variant caller used (e.g. SAMtools, GATK)

_____

75. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

76. Please specify the variant caller used (e.g. NUCMER)

_____

77. Please select tool used for the allele analysis

(1) □ BioNumerics – Go to 79

(2) □ SeqSphere – Go to 79

(3) □ Enterobase – Go to 79

(4) □ Other – Go to 78

78. If another tool is used please enter here:

_____

79. Please indicate allele calling method:

(1) □ Assembly based and mapping based – Go to 80

(2) □ Only assembly based – Go to 80

(3) □ Only mapping based – Go to 80

80. Please indicate the assembler used (e.g. SPAdes, Velvet)

_____

81. Please select scheme used for the allele analysis

(1) □ Applied Maths (wgMLST) – Go to 83

(2) □ Applied Maths (cgMLST/Enterobase) – Go to 83

(3) □ Enterobase (cgMLST) – Go to 83

(4) □ Other – Go to 82

82. If another scheme (e.g. in-house) is used, please give a short description

_____
_____
_____
_____
_____
_____

83. Please report the number of loci in the used allelic scheme

_____
_____
_____
_____
_____
_____

84. Third analysis on data derived from WGS

85. Results for the third cluster analysis. Reporting allele differences /SNP distances to strain0018 (as downloaded sequence) (e.g. SNP or Allele based) Please use 9999 for not analysed

	Distance/difference (e.g. SNP/allele) to the strain0018 (downloaded sequence)
Strain1	_____
Strain2	_____
Strain3	_____
Strain4	_____
Strain5	_____
Strain6	_____
Strain7	_____
Strain8	_____
Strain9	_____
Strain10	_____

Strain11	_____
Strain12	_____
Strain0013 (as downloaded sequence)	_____
Strain0014 (as downloaded sequence)	_____
Strain0015 (as downloaded sequence)	_____
Strain0016 (as downloaded sequence)	_____
Strain0017 (as downloaded sequence)	_____
Strain0018 (as downloaded sequence)	_____
Strain0019 (as downloaded sequence)	_____
Strain0020 (as downloaded sequence)	_____

86. Additional questions to the WGS part

87. Where was the sequencing performed

(1) □ In own laboratory

(2) □ Externally

88. Protocol used to prepare the library for sequencing:

(1) □ Commercial kits – Go to 89

(2) □ Non-commercial kits – Go to 91

89. Please indicate name of commercial kit:

_____

90. If relevant please list deviation from commercial kit shortly in few bullets:

_____
_____
_____
_____
_____
_____

91. For non-commercial kit please indicate a short summary of the protocol:

_____
_____
_____
_____
_____
_____

92. The sequencing platform used

(1) □ Ion Torrent PGM – Go to 94

(2) □ Ion Torrent Proton – Go to 94

(3) □ Ion S5 XL System – Go to 94

(4) □ Ion Genestudio S5 system – Go to 94

(5) □ Genome Sequencer Junior System (454) – Go to 94

(6) □ Genome Sequencer FLX System (454) – Go to 94

(7) □ Genome Sequencer FLX+ System (454) – Go to 94

(8) □ PacBio RS II – Go to 94

(9) □ PacBio RS – Go to 94

(10) □ HiScanSQ – Go to 94

(11) □ HiSeq 1000 – Go to 94

(12) □ HiSeq 1500 – Go to 94

(13) □ HiSeq 2000 – Go to 94

(14) □ HiSeq 2500 – Go to 94

(15) □ HiSeq 4000 – Go to 94

(16) □ Genome Analyzer Iix – Go to 94

(17) □ MiSeq – Go to 94

(18) □ MiSeq Dx – Go to 94

(19) □ MiSeq FGx – Go to 94

(20) □ ABI SOLiD – Go to 94

(21) □ NextSeq – Go to 94

(22) □ MinION (ONT) – Go to 94

(23) □ Mini Seq Illumina – Go to 94

(24) □ Other – Go to 93

93. If another platform is used please list here:

_____

94. Criteria used to evaluate the quality of sequence data.

In this section you can report criteria used to evaluate the quality of sequence data. Please first reply on the use of 5 selected criteria, which were the most frequently reported by in previous EQAs.

Next you will be asked to report 5 **additional** criteria of your own choice.

For each criteria please also report the threshold or procedure used to evaluated the current criteria.

95. Did you use confirmation of species to evaluate the quality of sequence data?

(1) □ Yes

(2) □ No – Go to 97

96. Procedure used to evaluate confirmation of genus:

_____

97. Did you use coverage to evaluate the quality of sequence data?

(1) □ Yes

(2) □ No – Go to 99

98. Procedure or threshold used for coverage:

_____

99. Did you use Q score (Phred) to evaluate quality of sequence data?

(1) □ Yes

(2) □ No – Go to 101

100. Threshold or procedure used to evaluate Q score (Phred):

_____

101. Did you use genome size to evaluate the quality of sequence data?

(1) □ Yes

(2) □ No – Go to 103

102. Procedure or threshold used for genome size:

_____

103. Did you evaluate the number of good cgMLST loci?

(1) □ Yes

(2) □ No – Go to 105

104. Threshold or procedure used to evaluate the number of good cgMLST loci:

_____

105. ONLY list additional information related to other criteria used to evaluate the quality of sequence data.

Please list up to 5 additional criteria (e.g. N50, read length, contamination)

106. Other criteria used to evaluate the quality of sequence data - additional criteria 1:

_____

107. Threshold or procedure used to evaluate the additional criteria 1:

_____

108. Other criteria used to evaluate the quality of sequence data - additional criteria 2:

_____

109.Threshold or procedure used to evaluate the additional criteria 2:

_____

110. Other criteria used to evaluate the quality of sequence data - additional criteria 3:

_____

111. Threshold or procedure used to evaluate the additional criteria 3:

_____

112. Other criteria used to evaluate the quality of sequence data - additional criteria 4:

_____

113. Threshold or procedure used to evaluate the additional criteria 4:

_____

114. Other criteria used to evaluate the quality of sequence data - additional criteria 5:

_____

115. Threshold or procedure used to evaluate the additional criteria 5:

_____

116. Comment(s):
e.g. remarks to the submission, the data analyses or the laboratory methods

_____
_____
_____
_____
_____
_____

117. Please remember to upload your raw reads to the sFPT site:

https://sit-ftp.statens-it.dk/

Code: EQA_STEC13_upload

Have you remebered to upload your raw reads?

(1) ❍ Yes

118. You have reached the end of the reporting scheme.

Please note that when you select "Yes" and "Next", your results will be automatically submitted and the reporting form will be locked.

If you wish to change your answers, use "Previous" to navigate backwards.

Upon completion, you will receive a link with your answers.

(1) □ Yes

Thank you for your participation

Thank you for filling out the Submission form for the STEC EQA-13.

For questions, please contact ecoli.eqa@ssi.dk or phone +45 3268 8341

Remember to press "Finish" to complete submission.

After submission you will recieve a confirmation email with a link to the answers. We highly recommend to save this email.

Important: After pressing "Finish" you will no longer be able to edit or print your information.