

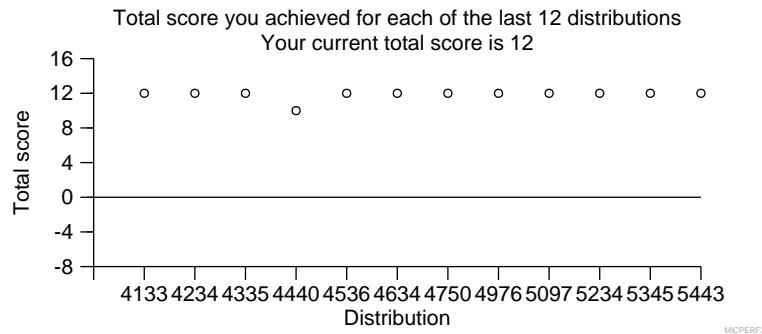
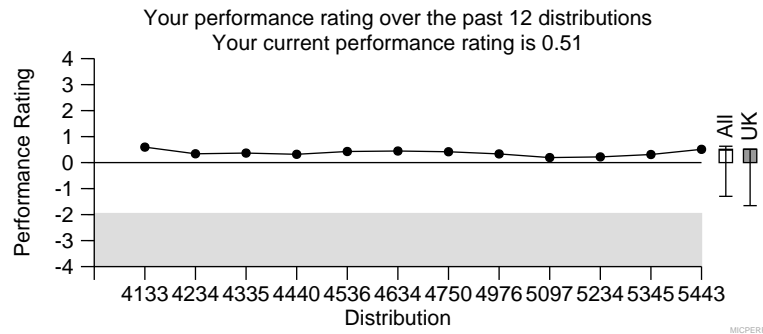
Intended Result	Your Report	Your Score
Specimen 8029 No virus detected	No virus detected	2
Specimen 8030 Enterovirus RNA positive	Enterovirus RNA positive	2
Specimen 8031 VZV DNA positive	VZV DNA positive	2
Specimen 8032 HSV-2 DNA positive	HSV-2 DNA positive	2
Specimen 8033 HSV-1 DNA positive	HSV-1 DNA positive	2
Specimen 8034 Enterovirus RNA positive	Enterovirus RNA positive	2

**Cumulative score information**

Total number of specimens sent to you for **UK NEQAS for Viruses in CSF (molecular)** over the last 2 distributions is 12  
 For these distributions specimen numbers 7718 7719 7720 7721 7722 7723 8029 8030 8031 8032 8033 8034 have been analysed and scored.  
 Number of reports analysed 12  
 Number of specimens reported as not examined (not scored) 0  
 Number of specimens received too late for analysis (not scored) 0  
 Number of specimens for which no report was received (not scored) 0  
 Your cumulative score for these specimens was 24 out of a possible total of 24  
 The mean score calculated from the reports returned by **UK** laboratories was 22.83 (with a standard error of 2.30)

**Performance rating**

Your performance rating for **UK NEQAS for Viruses in CSF (molecular)** (i.e. the number of standard errors by which your cumulative score lies above or below the mean) for **UK** laboratories is 0.51.  
 A performance rating of more than 1.96 standard errors below the mean indicates possible poor performance.  
 Please note your performance rating may alter if other participants' results are amended.  
 No score penalty is incurred for non return of reports. However non return of results may be used as a measure of poor performance.



**Comments:** A total of 138 sets of specimens were distributed with 127 participants returning results.

In the histograms on page 2 and subsequent pages a maximum of 12 methods are displayed: these include the most commonly used methods and the method used in your laboratory indicated by an arrow. The figures in the histograms and those in the overall results tables may differ due to exclusion of methods displayed in the histograms resulting in apparently lower numbers of data sets in the histograms.

- Specimen 8029: A negative specimen**, reported correctly by 98.4% of participants.
- Specimen 8030: Enterovirus RNA (Coxsackie A4) positive**, reported correctly by 81.9% of participants.
- Specimen 8031: VZV DNA positive**, reported correctly by 97.5% of participants.
- Specimen 8032: HSV-2 DNA positive**, reported correctly by 97.5% of participants.
- Specimen 8033: HSV-1 DNA positive**, reported correctly by 95.9% of participants.
- Specimen 8034: Enterovirus RNA (Echovirus 9) positive**, reported correctly by 94.9% of participants.

Please see comments pages 4-6 for more information on this distribution.

**If your laboratory does not test for any of the pathogens included in this EQA scheme please state so in the comments section during results entry to avoid penalisation.**

**Turn around time:** The time taken to report your results was 0-days. This information is provided for your own use and does not form part of your performance assessment.

**Enquiries:** Pre-distribution test results are available should you experience a technical failure and wish to discuss the results. Written enquiries about this distribution should be addressed to Dr Sanjiv Rughooputh at [organiser@ukneqasmicro.org.uk](mailto:organiser@ukneqasmicro.org.uk). For repeat specimens in case of an EQA failure investigation, please request using the web form at <https://ukneqasmicro.org.uk/participant-info/order-repeat-specimens/>.

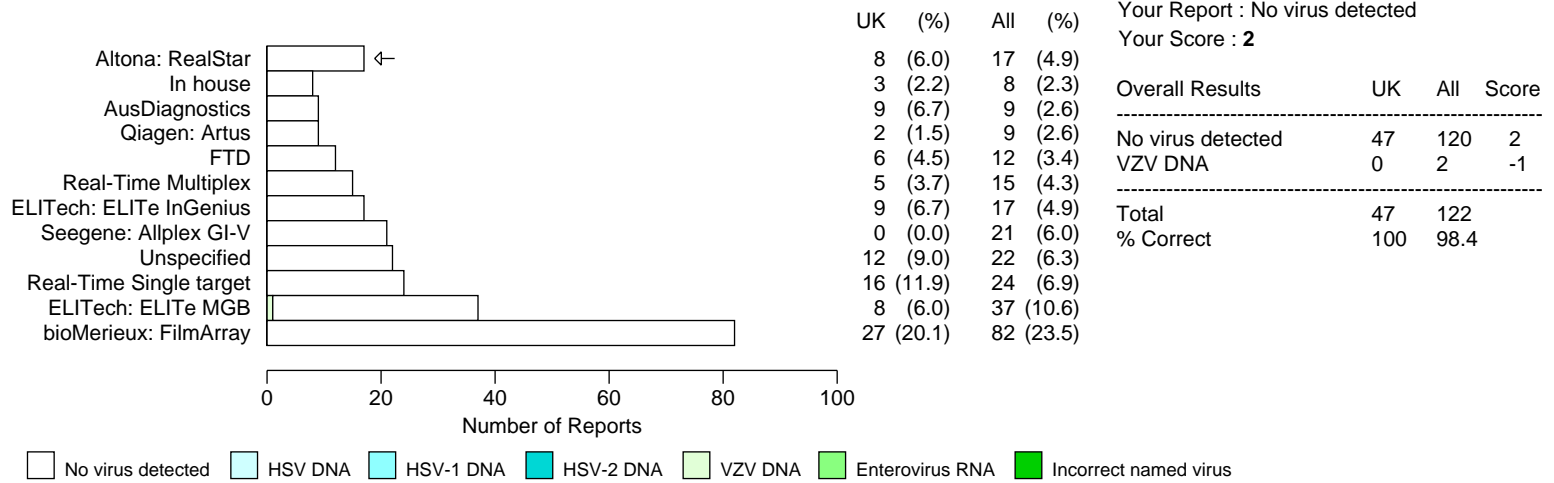
**Acknowledgements:** We would like to thank colleagues at UKHSA Cambridge, University Hospital Southampton and UKHSA Manchester for their kind assistance with pre-distribution testing.

**Report authorised by:** Dr Sanjiv Rughooputh, Scheme Organiser.

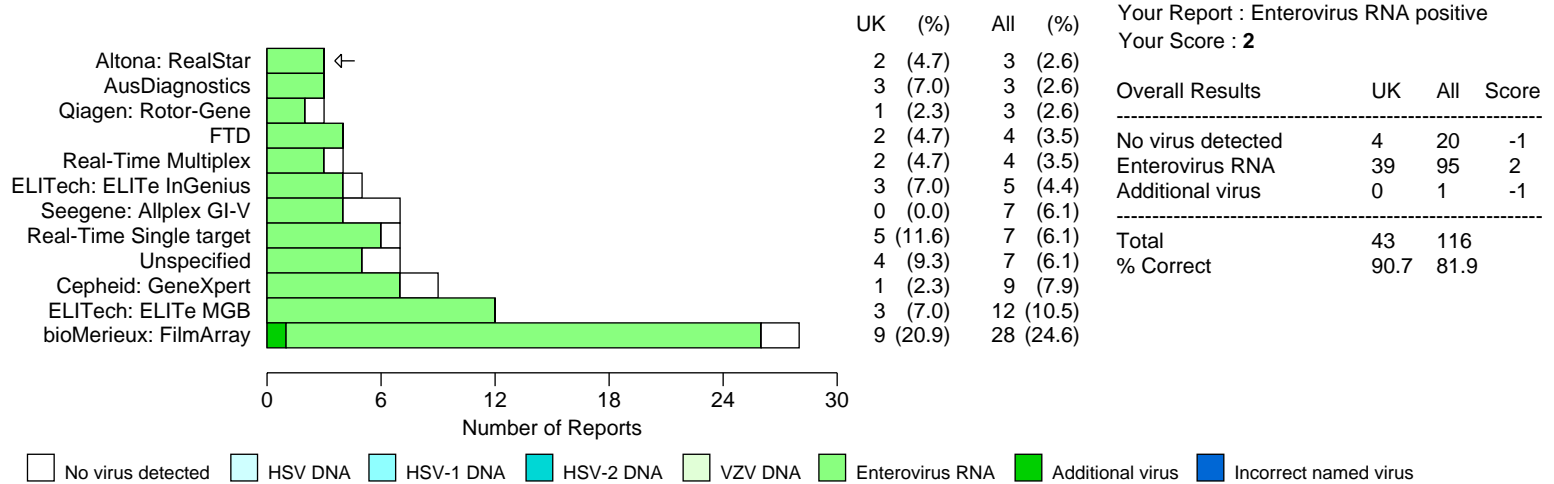


Six specimens of simulated CSF were dispatched with a request for the detection of HSV-1 DNA, HSV-2 DNA, VZV DNA and Enterovirus RNA. Specimen 8029 was negative, consisting of the freeze-drying matrix and HEP-2 cells only. Specimens 8030 and 8034 were positive for Enterovirus RNA (Coxsackie A4 and Echo 9, respectively) with a TCID<sub>50</sub> of  $\sim 10^{-2.77}$  and  $\sim 10^{-3.69}$ , respectively. Specimen 8031 was positive for VZV with a TCID<sub>50</sub> of  $10^{-2.7}$ . Specimen 8032 was positive for HSV-2 with a TCID<sub>50</sub> of  $10^{-4.3}$  and specimen 8033 was positive for HSV-1 with a TCID<sub>50</sub> of  $10^{-4.8}$ .

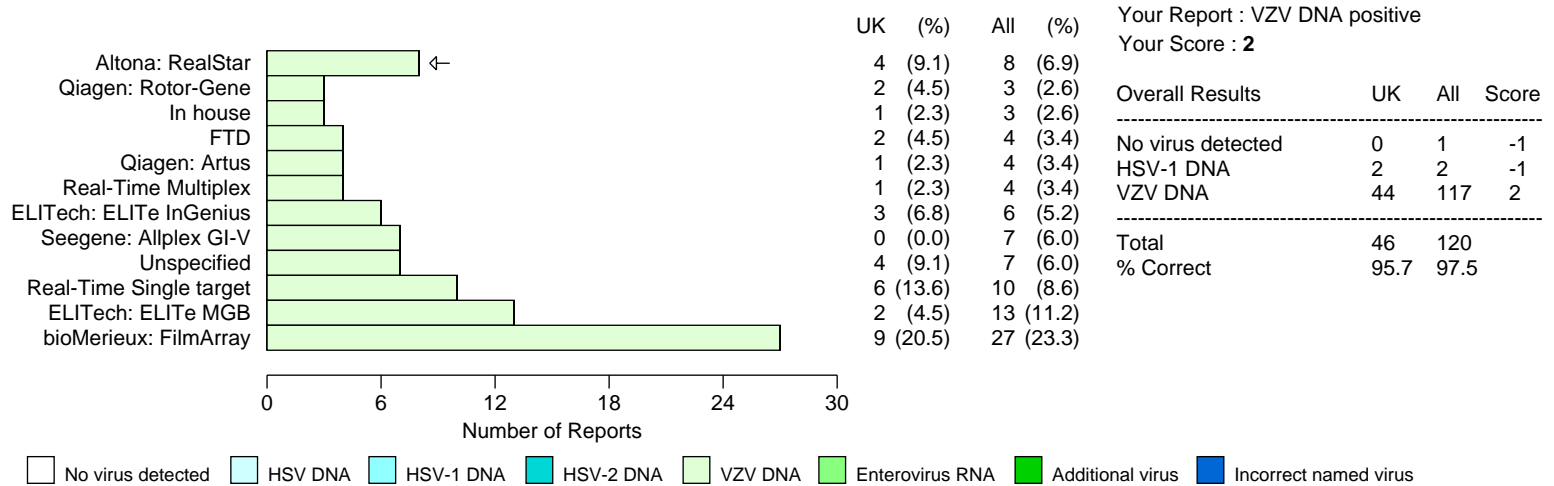
**Specimen : 8029 No virus detected**



**Specimen : 8030 Enterovirus RNA positive (Coxsackie A4)**

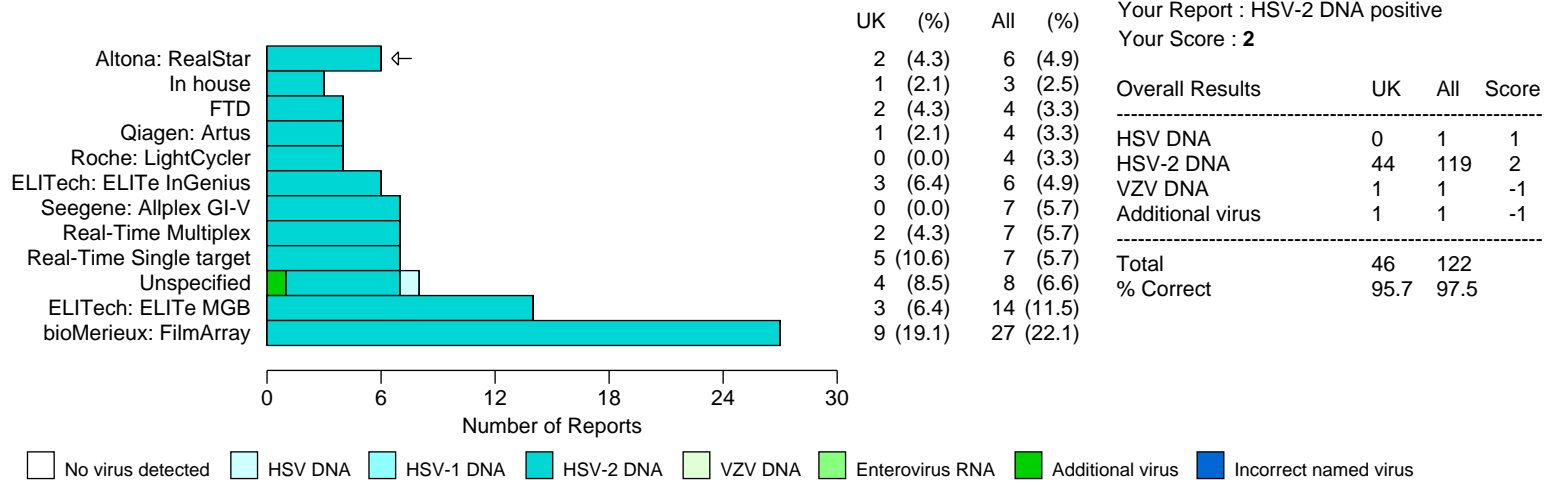


**Specimen : 8031 VZV DNA positive**

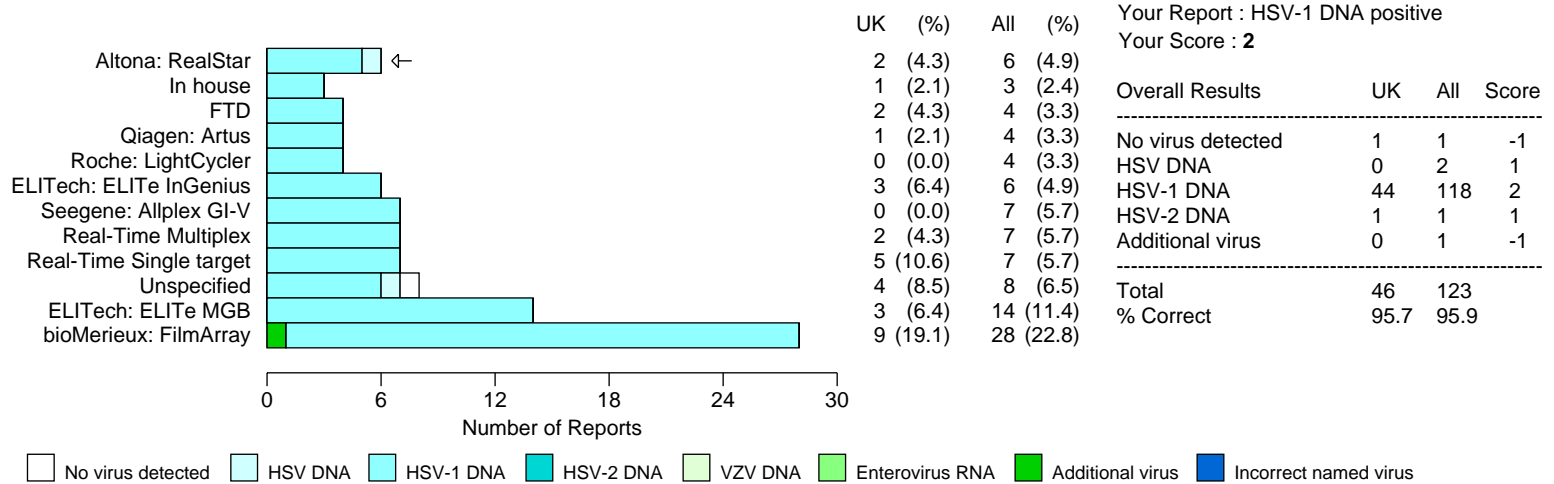


Six specimens of simulated CSF were dispatched with a request for the detection of HSV-1 DNA, HSV-2 DNA, VZV DNA and Enterovirus RNA. Specimen 8029 was negative, consisting of the freeze-drying matrix and HEP-2 cells only. Specimens 8030 and 8034 were positive for Enterovirus RNA (Coxsackie A4 and Echo 9, respectively) with a TCID<sub>50</sub> of  $\sim 10^{-2.77}$  and  $\sim 10^{-3.69}$ , respectively. Specimen 8031 was positive for VZV with a TCID<sub>50</sub> of  $10^{-2.7}$ . Specimen 8032 was positive for HSV-2 with a TCID<sub>50</sub> of  $10^{-4.3}$  and specimen 8033 was positive for HSV-1 with a TCID<sub>50</sub> of  $10^{-4.8}$ .

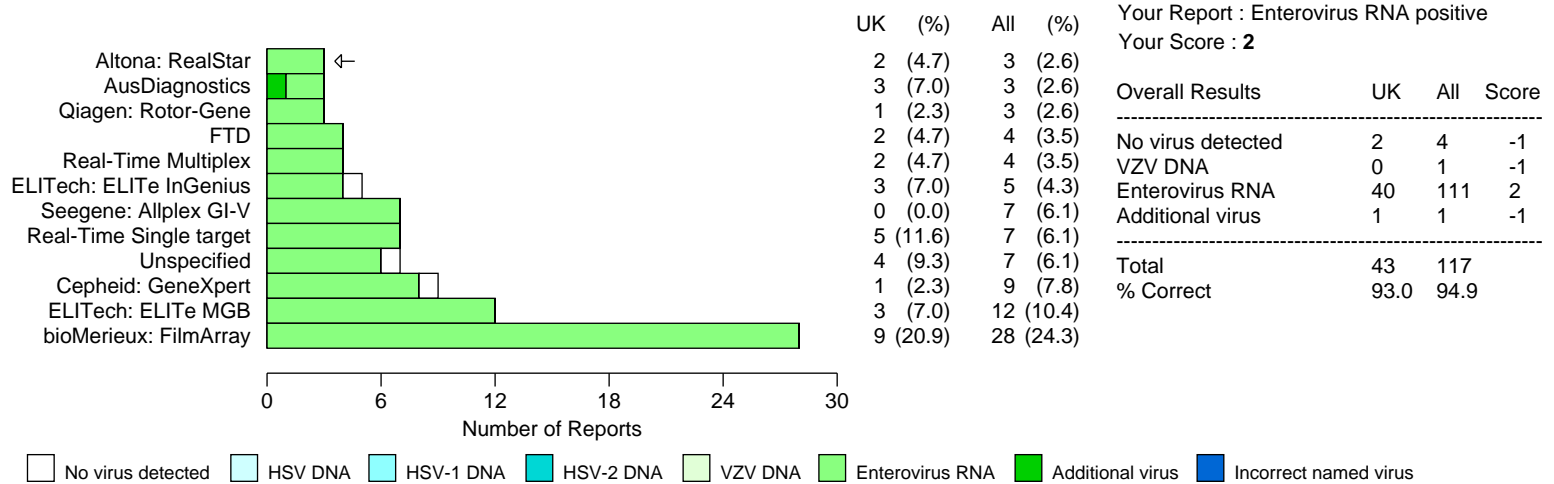
**Specimen : 8032 HSV-2 DNA positive**



**Specimen : 8033 HSV-1 DNA positive**



**Specimen : 8034 Enterovirus RNA positive (Echovirus 9)**



### Comments on distribution 5443

The overall performance in this distribution was excellent with 94.4% of participants reporting the intended results. This is a decline of 4.1% on distribution 5345, where 98.5% of participants reported the intended results.

One hundred and thirty eight sets of specimens were dispatched with 127 participants returning results, representing a return rate of 92.0%, a decline of 0.6% over the previous distribution 5345, where the return rate was 92.6%%.

Enterovirus genus is part of Picornaviridae family and contain several species such as enteroviruses, coxsackieviruses, rhinoviruses, polioviruses, and echoviruses. They are non-enveloped, positive-sense single-stranded RNA viruses with a genome size of approximately 7500 nucleotides.

The name for this genus has been derived due to the tropism that involves the alimentary tract. However, these are viruses have varied pathology, with not all well understood.

They are aetiological agents in a plethora of clinical manifestations such as common colds, poliomyelitis and aseptic meningitis and are the most common causative agents for infections worldwide.

#### **Specimen 8030: Enterovirus (Coxsackie A4)**

Coxsackievirus A4 (CVA4) is a member of the human enterovirus A (HEV-A) species, where most of the infections are subclinical. But they can also case a wide range of clinical manifestations with mild to fatal consequences, such as hand, foot and mouth disease (HFMD), herpangina, acute flaccid paralysis, myocarditis and severe central nervous system symptoms.

CVA4 is one of the most prevalent pathogens associated with HFMD, an acute febrile illness in children, and is also associated with acute localised exanthema, myocarditis, hepatitis and pancreatitis.

#### **Specimen 8034: Enterovirus (Echovirus 9)**

Echoviruses belong to the human enterovirus B (HEV-B) species as part of the genus Enterovirus. There are at least 28 serotypes associated with human infections such as meningitis and are also causative agents for infections of neonates, rashes, respiratory infections, and myocarditis.

Echovirus 9 has been the most prevalent nonpolio enterovirus. Echovirus 9 infection can manifest as nonspecific febrile illness and aseptic meningitis. Exanthem occurs in approximately one third of cases.



The scope of this EQA is to enable participating laboratories to report on the presence or absence of nucleic acid of the following viral pathogens:

**HSV-1 DNA, HSV-2 DNA, VZV DNA and Enteroviruses RNA**

Please visit the link below for more details:

<http://www.ukneqasmicro.org.uk/images/pdf/DOC.0401.pdf>

If you do not test any particular viral pathogen outlined or your kit is limited to only some of them, you may be missing some positive specimens. It is therefore advisable to inform us in advance of the protocol in use in your laboratory and consider any negative result carefully prior to submission of your results.

Participants who did not obtain the intended results are requested to investigate and report the plausible root cause by completing an incident review form (IRF) online within 30 days of this report being published.

Non return of results without a valid reason is considered as poor performance and should also be reported in a similar manner.

IRFs are taken into considerations when poor performance analysis is carried out for the National Quality Assurance Advisory Panel (NQAAP). IRFs can be completed on the following link: <https://ukneqasmicro.org.uk/incident-review-form/>

If you have any queries please email us: [organiser@ukneqasmicro.org.uk](mailto:organiser@ukneqasmicro.org.uk).

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## References

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## End of report

