

Monoclonal Protein Identification

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|--|---|-------|------|------|----------|--|-------|------|--|----|
| Accreditation Status: | UKAS Schedule of Accreditation | | | | | | | | | |
| Date Scheme started: | 1993 | | | | | | | | | |
| Clinical Applicability: | Diagnosis of monoclonal gammopathy in serum and urine | | | | | | | | | |
| Analytes: | Total serum protein, Albumin, IgG, IgA, IgM, free light chains (Kappa, Lambda and ratio), urine total protein & Monoclonal Component identification and Quantitation (SER/019) | | | | | | | | | |
| Units for Reporting: | Isotype of heavy and light chain together with the concentration of monoclonal protein in g/L. Serum free light chains in mg/L | | | | | | | | | |
| Samples Distributed: | Liquid format. Normal and pathological human serum and urine Each distribution will contain a serum sample and a urine sample, they should be considered as separate requests for investigation. It should NOT BE ASSUMED that they emanate from the same patient | | | | | | | | | |
| Number of Distributions per year: | 6 | | | | | | | | | |
| Number of Samples per Distribution: | 2 (1 urine and 1 serum) | | | | | | | | | |
| Frequency of Distributions: | Every two months as outlined in the Distribution Schedule | | | | | | | | | |
| Schedule of Analysis: | Data entry is via the web for the submission of results. Data analysis is commenced 21 days after sample dispatch. Late returns are accepted and will contribute to the laboratory's cumulative performance statistics | | | | | | | | | |
| Data Analysis: | Whilst the programme will analyse participant's isotype identification and monoclonal quantitation, the returns will require data on total serum protein, albumin, IgG, IgA, IgM (and urine total protein). This latter information will not be formally analysed as it is covered in other EQA programmes but will be of value in the recognition of analytical or isotype identification problems Chosen Coefficient of Variation: 29% for FLC Chosen Coefficient of Variation: 14% for Monoclonal Component Quantitation | | | | | | | | | |
| Performance Scoring: | MI Scoring - The qualitative elements of electrophoresis and isotype identification MRVIS - Assessment of the monoclonal quantitation and free light chains | | | | | | | | | |
| Criteria of Performance: | The qualitative elements of electrophoresis and isotype identification are assessed by MI scoring over a running analytical window of 6 Distributions (12 months) <table><tr><td>Good</td><td>OMIS</td><td>Zero</td></tr><tr><td>Adequate</td><td></td><td>1 - 2</td></tr><tr><td>Poor</td><td></td><td>>2</td></tr></table> | Good | OMIS | Zero | Adequate | | 1 - 2 | Poor | | >2 |
| Good | OMIS | Zero | | | | | | | | |
| Adequate | | 1 - 2 | | | | | | | | |
| Poor | | >2 | | | | | | | | |

Poor Performance

For the monoclonal component and serum Free Light Chain quantitation, laboratory performance is assessed in relation to the MRVIS over a running analytical window of 6 Distributions.

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| Ideal | MRVIS | <50 |
| Good | | 50 - 100 |
| Adequate | | 101 - 200 |
| Poor | | >200 or SDBIS >200 |

Persistent Poor Performance:

Defined as being in the Poor Performance category for two or more successive Distributions