MAYO CLINIC LABORATORIES

Test Definition: PEISO

Protein Electrophoresis and Isotype, Serum

Overview

Useful For

Diagnosis of monoclonal gammopathies, when used in conjunction with locally performed serum free light chain studies (performed at client site)

Profile Information

Test Id	Reporting Name	Available Separately	Always Performed
TMAB	Therapeutic Antibody Administered?	No	Yes
TPE	Total Protein	Yes, (Order TP)	Yes
SPE	Protein Electrophoresis	No	Yes
MPTS	M-protein Isotype MALDI-TOF MS, S	Yes, (Order MALD)	Yes

Reflex Tests

Test Id	Reporting Name	Available Separately	Always Performed
IFXED	Immunofixation Delta and Epsilon, S	Yes	No

Testing Algorithm

This test includes total protein, serum protein electrophoresis, and heavy and light chain typing (kappa and lambda).

If a light chain is identified without a corresponding heavy chain during initial testing, immunofixation with IgD and IgE antisera will be performed at an additional charge.

The following algorithms are available:
-Amyloidosis: Laboratory Approach to Diagnosis
-Multiple Myeloma: Laboratory Screening

Special Instructions

- Amyloidosis: Laboratory Approach to Diagnosis
- Multiple Myeloma: Laboratory Screening

Method Name

TPE: Colorimetric, Biuret
SPE: Agarose Gel Electrophoresis
MPTS: Matrix-Assisted Laser Desorption/Ionization-Time of Flight Mass Spectrometry (MALDI-TOF MS)

NY State Available

Yes

Specimen

Specimen Type
Serum

Ordering Guidance
To monitor a patient with an established diagnosis of a monoclonal gammopathy, order TMOGA / Monoclonal Gammopathy, Monitoring, Serum.

Protein electrophoresis alone is not considered an adequate screen for monoclonal gammopathies. When screening a patient or establishing a first-time diagnosis for a monoclonal gammopathy, consider ordering DMOGA / Monoclonal Gammopathy, Diagnostic, Serum instead, which includes free light chain analysis.

Specimen Required
Patient Preparation: Fasting (12 hour) preferred but not required
Container/Tube:
Preferred: Serum gel
Acceptable: Red top
Specimen Volume: 1 mL

Forms
If not ordering electronically, complete, print, and send 1 of the following forms with the specimen:
-Renal Diagnostics Test Request (T830)
-General Request (T239)
-Hematopathology/Cytogenetics Test Request (T726)

Specimen Minimum Volume
0.6 mL

Reject Due To

Gross hemolysis	OK
Gross lipemia	OK
Gross icterus	OK

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Serum	Refrigerated (preferred)	14 days	
	Frozen	14 days	
	Ambient	7 days	

Clinical & Interpretive

Clinical Information

This profile includes total protein, protein electrophoresis, and M-protein isotyping. The serum proteins can be grouped into 5 fractions by protein electrophoresis:
-Albumin, which represents almost two-thirds of the total serum protein
-Alpha-1, composed primarily of alpha-1-antitrypsin (A1AT), an alpha-1-acid glycoprotein
-Alpha-2, composed primarily of alpha-2-macroglobulin and haptoglobin
-Beta, composed primarily of transferrin and complement C3
-Gamma, composed primarily of immunoglobulins (Ig)

The concentration of these fractions and the electrophoretic pattern may be characteristic of diseases such as monoclonal gammopathies, A1AT deficiency disease, nephrotic syndrome, and inflammatory processes associated with infection, liver disease, and autoimmune diseases.

The following algorithms are available:
-Amyloidosis: Laboratory Approach to Diagnosis
-Multiple Myeloma: Laboratory Screening

Reference Values

TOTAL PROTEIN
> or =1 year: 6.3-7.9 g/dL
Reference values have not been established for patients that are <12 months of age.

PROTEIN ELECTROPHORESIS
Albumin: 3.4-4.7 g/dL
Alpha-1-globulin: 0.1-0.3 g/dL
Alpha-2-globulin: 0.6-1.0 g/dL
Beta-globulin: 0.7-1.2 g/dL
Gamma-globulin: 0.6-1.6 g/dL
An interpretive comment is provided with the report.
Reference values have not been established for patients that are <16 years of age.

M-PROTEIN ISOTYPE MALDI-TOF MS, S
No monoclonal protein detected

M-protein Isotype MALDI-TOF MS Flag
Negative

Interpretation

Monoclonal Gammopathies:
-A characteristic monoclonal band (M-spike) is often found on serum protein electrophoresis (SPE) in the gamma globulin region and, more rarely, in the beta or alpha-2 regions. The finding of an M-spike, restricted migration, or hypogammaglobulinemic SPE pattern is suggestive of a possible monoclonal protein. Immunoaffinity purification

followed by matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS) is performed to identify any immunoglobulin heavy and light chains present.
-A monoclonal IgG or IgA of greater than 3 g/dL is consistent with multiple myeloma (MM).
-A monoclonal IgG or IgA of less than 3 g/dL may be consistent with monoclonal gammopathy of undetermined significance (MGUS), primary systemic amyloidosis, early or treated myeloma, as well as a number of other monoclonal gammopathies.
-A monoclonal IgM of greater than 3 g/dL is consistent with macroglobulinemia.
-The initial identification of a serum M-spike greater than 1.5 g/dL on SPE should be followed by MPSU / Monoclonal Protein Study, 24 Hour, Urine.
-The initial identification of an IgM, IgA, or IgG M-spike greater than 4 g/dL, greater than 5 g/dL, and greater than 6 g/dL respectively, should be followed by VISCS / Viscosity, Serum.

After the initial identification of an M-spike, quantitation of the M-spike on follow-up SPE can be used to monitor the monoclonal gammopathy. However, if the monoclonal protein falls within the beta region (most commonly an IgA or an IgM) quantitative immunoglobulin levels may be more a useful tool to follow the monoclonal protein level than SPE. A decrease or increase of the M-spike that is greater than 0.5 g/dL is considered a significant change.

Patients suspected of having a monoclonal gammopathy may have normal serum SPE patterns. Approximately 11% of patients with MM have a completely normal serum SPE, with the monoclonal protein only identified by MALDI-TOF MS. Approximately 8% of MM patients have hypogammaglobulinemia without a quantifiable M-spike on SPE but identified by MALDI-TOF MS. Accordingly, a normal serum SPE does not rule out the disease and SPE should not be used to screen for the disorder. DMOGA / Monoclonal Gammopathy, Diagnostic, Serum which includes MALDI-TOF MS and serum free light chains, should be done to screen if the clinical suspicion is high.

Other Abnormal SPE Findings:
-A qualitatively normal but elevated gamma fraction (polyclonal hypergammaglobulinemia) is consistent with infection, liver disease, or autoimmune disease.
-A depressed gamma fraction (hypogammaglobulinemia) is consistent with immune deficiency and can also be associated with primary amyloidosis or nephrotic syndrome.
-A decreased albumin (<2 g/dL), increased alpha-2 fraction (>1.1 g/dL), and decreased gamma fraction (<1 g/dL) is consistent with nephritic syndrome and, when seen in an adult older than 40 years, should be followed by MPSU / Monoclonal Protein Study, 24 Hour, Urine.
-In the hereditary deficiency of a protein (eg, agammaglobulinemia, alpha-1-antitrypsin [A1AT] deficiency, hypoalbuminemia), the affected fraction is faint or absent.
-An absent alpha-1 fraction is consistent with A1AT deficiency disease and should be followed by a quantitative A1AT assay (AAT / Alpha-1-Antitrypsin, Serum).

Cautions

Very large IgG M-spikes (>4 g/dL) may saturate the protein stain. In these situations, quantitative IgG assays (IGG / Immunoglobulin G [IgG], Serum) should be performed to accurately determine M-spike concentrations to monitor disease progression or response to therapy.

Fibrinogen will migrate as a distinct band in the beta-gamma fraction. Serum specimens from new patients with a beta-gamma band are to be treated with thrombin to ensure complete conversion of fibrinogen.

Hemolysis may augment the beta fraction.

Penicillin may split the albumin band.

Radiographic agents may produce an uninterpretable pattern.

Clinical Reference

1. Mills JR, Kohlhagen MC, Dasari S, et al: Comprehensive assessment of M-proteins using nanobody enrichment coupled to MALDI-TOF mass spectrometry. Clin Chem. 2016;62(10):1334-1344
2. Milani P, Murray DL, Barnidge DR, et al: The utility of mass-fix to detect and monitor monoclonal proteins in the clinic. Am J Hematol. 2017;92:772-779

Performance

Method Description

Total Protein:
Divalent copper reacts in alkaline solution with protein peptide bonds to form the characteristic purple-colored biuret complex. Sodium potassium tartrate prevents the precipitation of copper hydroxide and potassium iodide prevents autoreduction of copper. The color intensity is directly proportional to the protein concentration which can be determined photometrically.(Package insert: TP2 cobas. Roche Diagnostics; V 12.0, 11/2019)

Electrophoresis:
Serum proteins are separated in an electric field according to their size, shape, and electric charge. The separation is performed on agarose gels. The proteins are visualized by staining with acid blue, and the intensity of staining is quantitated by densitometry. Multiplying by the serum total protein (Coomasie blue) converts the percentage of protein in each fraction into serum concentration.(Instruction manual: Helena SPIFE Touch. Helena Laboratories, Corp; 11/2016; package insert: Helena SPIFE Touch SPE Pro 277. Helena Laboratories, Corp; 06/2018)

M-protein Isotype:
M-protein isotype by matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDI-TOF MS) is performed with immunoaffinity purification followed by MALDI-TOF MS analysis. For the immunoaffinity purification, patient serum is applied to 5 separate immunoaffinity resins (CaptureSelect, Life Sciences) specific to immunoglobulin G, A, M, K, and L. Unbound protein is washed away and the isolated immunoglobulins are broken down in to their reduced to separate the heavy and light chains subunits to be analyzed via MALDI-TOF mass spectrometry. The 5 separate spectra from each patient immunopurification are overlaid and investigated for an overabundance of immunoglobulin and immunoglobulin light chain.(Kohlhagen M, Dasari S, Willrich M, et al: Automation and validation of a MALDI-TOF MS (Mass-Fix) replacement of immunofixation electrophoresis in the clinical lab. Clin Chem Lab Med. 2020 Aug 3;59(1):155-163. doi: 10.1515/cclm-2020-0581)

PDF Report

No

Day(s) Performed

Monday through Friday

Report Available
2 to 5 days

Specimen Retention Time
14 days

Performing Laboratory Location
Rochester

Fees & Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their Regional Manager. For assistance, contact Customer Service.

Test Classification
This test was developed, and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information
84155
84165
0077U
86334 (if appropriate)

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
PEISO	Prot Electrophoresis and Isotype, S	In Process

Result ID	Test Result Name	Result LOINC® Value
TPE	Total Protein	2885-2
602837	Albumin	2862-1
602838	Alpha-1 Globulin	2865-4
602839	Alpha-2 Globulin	2868-8
602840	Beta-Globulin	2871-2
602841	Gamma-Globulin	2874-6
602842	A/G Ratio	44429-9
602843	M spike	51435-6
602844	M spike	35559-4
602836	Impression	49296-7
65198	M-protein Isotype MALDI-TOF MS	90990-3

606976	Flag, M-protein Isotype	94400-9
TMAB	Therapeutic Antibody Administered?	98855-0