Increased Serum Protein in an Elderly Debilitated Woman
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CASE DESCRIPTION
An 80-year-old female patient presented in poor general condition, drowsy but responding to verbal commands. Medications given in the emergency room included cefotaxim, ranitidine, and vitamin K. Blood was sent for routine testing; serum total protein was 13.6 g/dL by the biuret method (reference interval, 6.1–7.9 g/dL). On visual inspection, the reaction mixture was brown instead of the usual purple (Fig. 1).

Fig. 1. Usual purple color and brown color due to cefotaxim interference in the reaction mixture for protein estimation by the biuret method.

QUESTIONS
1. What is responsible for the unique appearance of this test solution?
2. What other substance are known to interfere with the biuret method?
3. What precautions should be taken to prevent this interference in blood testing?

The answers are on the next page.
The treating physician indicated that the blood sample was taken from the same femoral line through which cefotaxim had just been administered. Interference due to cefotaxim was confirmed by in vitro experiments (1, 2). It is advisable that blood samples should not be collected from lines used for drug administration.

A sample drawn from the antecubital vein had total protein of 7 g/dL.

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References


News & Views

Circulating Tumor DNA: The Future of Personalized Medicine in Oncology?

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Tissue biopsy has long served as the mainstay of cancer diagnosis, staging, and therapeutic decisions, with its role evolving from simple histologic examination to complex genetic analysis. Despite its utility, biopsy represents only a single time point from a single location, often proving inadequate at fully characterizing a malignancy and its evolution because nearby tissue might contain additional genetic information that would affect staging or treatment. Unfortunately, the invasive nature and inherent selection bias of biopsy limit its usefulness as a real-time monitoring tool. Newer technologies seeking to transcend this shortcoming include analysis of circulating tumor cells and their fragments, such as exosomes and DNA, in peripheral blood. A recent feature in Nature highlights advancements in the detection of circulating tumor DNA (ctDNA) for this purpose (1). This emerging methodology enables sequencing of DNA originating from lysed tumor cells present in a blood sample to follow tumor recurrence and to characterize genetic abnormalities that confer resistance.

Free DNA was first discovered in human circulation during the late 1940s, followed by isolation of tumor-specific genetic material in the 1970s. Yet, ctDNA methods for oncology have since lagged behind applications such as prenatal diagnostics. Challenges that have impeded its development and integration into clinical practice include highly variable, often low, ctDNA concentration in blood, especially in early stage tumors. Fortunately, technologic advancements in target selection and amplification methods as well as sequencing methodologies have facilitated the detection of these minute quantities. The authors describe one methodology, known as BEAMing (beads, emulsions, amplification, and magnetics), which boasts an analytical sensitivity of up to 0.01% using enhanced and highly selective target capture. This exquisite detection capability has allowed researchers to explore the clinical applicability of ctDNA to cancer monitoring. A study published by Diehl et al. (2) showed early evidence of the strong negative predictive value of ctDNA, demonstrating that undetectable ctDNA levels following tumor resection correlate with the absence of tumor recurrence. Further work has confirmed this finding and demonstrated...