(95% confidence interval, 0.98–1.05), and the constant bias of −0.2 mmol/L (−0.53 to −0.05) is acceptable. As also shown in Fig. 1, the difference between the two methods is independent of leukocyte concentration up to at least 450×10^9 cells/L. White cells, which interfere during spectrophotometric measurement of Hb on automated hematology analyzers, are ultrasonically lysed in the co-oximeter of the blood gas analyzer. This together with the turbidity correction on the ABL analyzer *(4)* explains why leukocytosis does not influence Hb measurements on the ABL. The bias between the hemiglobincyanide method and the ABL is independent of Hb concentration and leukocyte count; it thus may be attributable to differences in standardization.

In conclusion, Hb measurements on an ABL 700 series blood gas analyzer in samples with a leukocyte count that may interfere with Hb measurements on automated hematology analyzers are in good agreement with the reference method. The co-oximetry method on the ABL gives results more quickly and is less expensive and less labor-intensive than the manual hemiglobincyanide method.

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Detection of SARS Coronavirus RNA in the Cerebrospinal Fluid of a Patient with Severe Acute Respiratory Syndrome

To the Editor:

Severe acute respiratory syndrome (SARS) is a recently emerged disease caused by a novel coronavirus, the SARS coronavirus (SARS-CoV) *(1, 2)*. Although the respiratory manifestations of SARS are well recognized, the neurologic manifestations have been much less studied *(1)*. Here we report a SARS patient with clinical and laboratory evidence of neurologic involvement.

A 59-year-old woman with IgA nephropathy was admitted to the Prince of Wales Hospital in Hong Kong in early May 2003 because of swinging fever, chills, productive cough, and diarrhea. She was previously admitted in April with fungal peritonitis related to her peritoneal dialysis. Despite antifungal and antibiotic therapy, her respiratory function deteriorated. She became increasingly dyspneic and required supplemental oxygen. High-resolution computer tomography of the thorax revealed progressive bilateral consolidation. On day 5 of admission, she began to vomit, and episodes of four-limb twitching were documented. Within a few hours, she became confused and disorientated. Laboratory investigation showed electrolyte and blood pH values within the appropriate reference intervals and a static urea of 20 mmol/L. Seizures recurred despite phenytoin administration and became prolonged, lasting >30 min. Oxygen saturation decreased to 40%, requiring immediate resuscitation and intensive care support. She was ventilated and sedated with propofol, and valporate therapy was commenced.

In view of the progressive respiratory failure despite conventional antibiotic therapy, SARS was suspected. The Prince of Wales Hospital was the site of a major SARS outbreak in Hong Kong *(1)*. Confirmed SARS exposure was traceable to her last admission. SARS-CoV was isolated from the tracheal aspirate, and seroconversion was subsequently demonstrable. Ribavirin and pulse steroids were initiated, but her seizures persisted.

A computer tomography of her brain showed no intracranial lesions, cerebral edema, or stroke. Lumbar puncture was performed within 24 h of her first seizure, and the opening pressure was normal. The cerebrospinal fluid (CSF) was clear with no cells detected microscopically. The CSF protein and glucose were 0.28 g/L (reference interval, 0.15–0.45 g/L) and 5.9 mmol/L (reference interval, 2.8–4.2 mmol/L), respectively. Bacteriologic and fungal cultures of the CSF were negative. After additional doses of propofol and phenytoin, she remained seizure free from day 7 of admission onward and was discharged on day 19.

Further virologic investigations were performed in view of the seizures. We analyzed the extracted RNA from the CSF and serum samples of the patient by real-time quantitative RT-PCR assay targeting the polymerase region (orf1ab polyprotein) of the SARS-CoV genome *(3)*. Our data showed that SARS-CoV RNA was present in both the CSF and serum, with viral loads of 6884 and 6750 copies/mL, respectively. These positive results were confirmed by another real-time RT-PCR system targeting the nucleocapsid region of the SARS-CoV genome *(3)*.

These results represent the first demonstration of the entry of SARS-CoV into the CSF. This is also the first case report of status epilepticus associated with SARS. In this regard, it is interesting to note that coronaviruses have been implicated in demyelinating brain pathology *(4)*. Arbour et al. *(4)* documented the presence of the seemingly harmless human respiratory coronavirus OC43 in the brain parenchyma of patients with multiple sclerosis. Murine hepatitis virus, another coronavirus, has been linked to chronic inflammation and demyelination of the central nervous system *(5)*. Therefore, SARS-CoV infection of the brain is a distinct possibility. Our data thus suggest that a severe acute neurologic syndrome might occasionally accompany

SARS. Further studies will be needed to demonstrate conclusively that SARS-CoV is indeed causative of neurologic manifestations such as those described here and to address the potential neuropathologic sequelae of SARS-CoV infection of the central nervous system.

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Protein Microarrays: A Literature Survey

To the Editor:

We have previously published literature surveys on microchips, microarrays, and nanotechnology that were compiled by the IFCC Working Group on Nanotechnology *(1–3)*. The Working Group has now completed a survey on the protein microarray literature. The current survey covers the protein, peptide, and antibody microarray literature up to the middle of 2003.

A protein microarray is a collection of proteins arranged on a planar solid surface (membrane, glass slide, or silicon chip) or immobilized on individual microbeads trapped in the ends of the fibers in a fiber optic bundle, or a collection of coded microbeads in solution (known as a liquid or 3D array). The scope of arrayed protein includes peptides, antigens, antibodies, and allergens. In common with the cDNA and oligonucleotide microarrays, a protein microarray facilitates simultaneous multianalyte assays. These analytical devices are now an important tool in studies to characterize the human and other proteomes and for characterizing protein interactions (e.g., protein–protein and protein–DNA). The literature survey has been divided into four sections: (1) General (books, reviews, editorials); (2) Fabrication (array construction and detection methodologies); (3) Applications (protein identification and quantification, array-based proteomics, protein interactions); and (4) Patents (only US patents listed currently). The database can be accessed at *Clinical Chemistry Online* at http://www.clinchem.org/content/vol49/issue12/ Other useful resources for general information on protein microarrays and chips are the DNA Microarray (Genome Chip; at www.gene-chips.com) and BioChipNet (www.biochipnet.de) web sites.

This compilation is based in part on a survey undertaken by the IFCC Working Group on Nanotechnology, chaired by Dr. Larry J. Kricka. Members of the Working Group are listed in the data supplement that accompanies this letter at *Clinical Chemistry Online* (http://www.clinchem.org/content/vol49/issue12/).

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Improved Real-Time PCR Assay for Homogeneous Multiplex Genotyping of Four *CYP2C9* Alleles with Hybridization Probes

To the Editor:

The human cytochrome P450 2C (CYP2C) subfamily consists of four members (CYP2C8, -9, -18, and -19), which share >82% amino acid identity *(1)*. The enzyme CYP2C9 metabolizes ~10% of therapeutically important drugs (e.g., phenytoin and warfarin). The gene *CYP2C9* is very polymorphic, with >10 alleles result-