What is claimed is:

1. An assay comprising:

(1) contacting a biological sample with at least one proteolytic enzyme to produce at least one peptide fragment of the protein C1q present in the biological sample wherein the at least one peptide fragment has an amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26); and

(2) performing selected reaction monitoring mass spectrometry (SRM-MS) to measure the abundance of the at least one C1q peptide fragment having the amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26), wherein the abundance of the at least C1q peptide fragment having the amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26) determines the concentration of C1q in the biological sample.

2. The assay of claim 1, further comprising between step (1) and step (2), adding to the biological sample at least one labeled, synthetic C1q peptide fragment comprising an amino acid sequence identical to the amino acid sequence of the at least one C1q peptide fragment having the amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26).

3. The assay of claim 1 or claim 2, wherein measuring the abundance of the at least one C1q peptide fragment having the amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26) comprises comparing a signal corresponding to the at least one C1q peptide having the amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26) generated by SRM-MS to a standard curve.

4. The assay of claim 1, wherein the biological sample is a blood sample.

5. The assay of claim 1, wherein the biological sample is a human sample.

6. The assay of claim 1, wherein the biological sample is a non-human primate sample.

7. The assay of claims 1, wherein the selected reaction monitoring mass spectrometry is LC-SRM-MS/MS.

8. The assay of claim 1, wherein the at least one proteolytic enzyme is trypsin.

9. The assay of claim 3, wherein the standard curve is produced using a method comprising:

(a) preparing at least two C1q concentration standards by mixing known quantities of purified C1q protein and C1q-depleted serum;

(b) adding to the at least two C1q concentration standards at least one labeled, synthetic peptide fragment with an amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26);

(c) contacting the at least two labeled C1q concentration standards with a proteolytic enzyme to produce at least one peptide fragment of C1q having the amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26);

(d) performing selected reaction monitoring mass spectrometry to determine the strength of the signal that corresponds to the at least one peptide fragment of C1q having the amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26) and the strength of the signal that corresponds to the at least one labeled, synthetic peptide fragment having the amino acid sequence of SLGFCDTTNK (SEQ ID NO: 26) in each of the at least two labeled C1q concentration standards; and

(e) determining a standard curve using the signals and the known quantities of C1q protein.

10. An assay comprising:

(1) contacting a biological sample with at least one proteolytic enzyme to produce at least one peptide fragment of the protein C1q present in the biological sample, wherein the at least one peptide fragment has an amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36); and

(2) performing selected reaction monitoring mass spectrometry (SRM-MS) to measure the abundance of the at least one C1q peptide fragment having the amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36), wherein the abundance of the at least C1q peptide fragment having the amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36) determines the concentration of C1q in the biological sample.

11. The assay of claim 10, further comprising between step (1) and step (2), adding to the biological sample at least one labeled, synthetic C1q peptide fragment comprising an amino acid sequence identical to the amino acid sequence of the at least one C1q peptide fragment having the amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36).

12. The assay of claim 10, wherein measuring the abundance of the at least one C1q peptide fragment having the amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36) comprises comparing a signal corresponding to the at least one C1q peptide fragment having the amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36) generated by SRM-MS to a standard curve.

13. The assay of claim 10, wherein the biological sample is a blood sample.

14. The assay of claim 10, wherein the biological sample is a human sample.

15. The assay of claim 10, wherein the biological sample is a non-human primate sample.

16. The assay of claim 10, wherein the selected reaction monitoring mass spectrometry is LC-SRM-MS/MS.

17. The assay of claim 10, wherein the at least one proteolytic enzyme is trypsin.

18. The assay of claim 12, wherein the standard curve is produced using a method comprising:

(a) preparing at least two C1q concentration standards by mixing known quantities of purified C1q protein and C1q-depleted serum;

(b) adding to the at least two C1q concentration standards at least one labeled, synthetic peptide fragment with an amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36);

(c) contacting the at least two labeled C1q concentration standards with a proteolytic enzyme to produce at least one peptide fragment of C1q having the amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36);

(d) performing selected reaction monitoring mass spectrometry to determine the strength of the signal that corresponds to the at least one peptide fragment of C1q having the amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36) and the strength of the signal that corresponds to the at least one labeled, synthetic peptide fragment having the amino acid sequence of QTHQPPAPNSLIR (SEQ ID NO: 36) in each of the at least two labeled C1q concentration standards; and

(e) determining a standard curve using the signals and the known quantities of C1q protein.