AMENDMENT AND RESPONSE UNDER 37 CFR §1.116

Commissioner for Patents
Mail Stop AF
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

In response to the Office Action mailed March 12, 2009, please amend the above-identified application as follows:

Amendments to the Claims are reflected in the listing of claims which begins on the page entitled "Amendments to the Claims."

Remarks begin on the page entitled "Remarks."
Amendments to the Claims

This listing of claims replaces all prior versions, and listings, of claims in the above-identified application:

1. (Previously Presented) A method for detecting endometrial pathology in a patient comprising:
   obtaining a patient's biological test sample;
   detecting a plurality of polypeptides in the biological test sample to yield a test protein profile;
   comparing the test protein profile with a reference protein profile; and
   determining that said patient is at risk of endometrial pathology when there is a difference between the test protein profile and the reference protein profile,
   wherein the difference between the test protein profile and the reference protein profile comprises a difference in the amount of at least one biomarker polypeptide represented by a M/Z peak value in Tables 3, 4, 5, 6 or 7; and
   wherein at least one of the following is true:
   the test protein profile and the reference protein profile are provided to a user in a user-readable format, or
   the difference between the test protein profile and the reference protein profile is provided to a user in a user-readable format.

2. (Original) The method of claim 1 wherein the reference protein profile represents at least one biomarker polypeptide.

3. (Original) The method of claim 1 wherein the reference protein profile represents a plurality of biomarker polypeptides.
4. (Canceled)

5. (Original) The method of claim 1 wherein the comparing step comprises discriminating between different disease states or between a disease state and normal state.

6. (Original) The method of claim 1 wherein the difference between the test protein profile and the reference protein profile is indicative of the progression or regression of endometrial pathology in the patient.

7. (Original) The method of claim 6 wherein the reference protein profile is derived from a sample previously obtained from the patient.

8. (Original) The method of claim 1 wherein the comparing step comprises evaluating or monitoring the efficacy of treatment of the patient.

9. (Original) The method of claim 1 further comprising designing a classification model or algorithm based on at least one difference between the test protein profile and the reference protein profile.

10. (Canceled)

11. (Original) The method of claim 10 wherein the test protein profile is generated using mass spectrometry, and the amount of the biomarker polypeptide is indicated as a spectral peak intensity.

12. (Canceled)
13. (Currently Amended) A method for detecting endometrial pathology in a patient comprising:

obtaining a patient's biological test sample;
detecting at least one biomarker polypeptide in the biological test sample;
detecting at least one reference polypeptide in the test sample;
comparing the amount of the biomarker polypeptide to the amount of the reference polypeptide in the test sample to yield a test value;
comparing the test value to a predetermined reference value; and
determining that said patient is at risk of endometrial pathology when there is a difference between the test value and the predetermined reference value,

wherein the biomarker polypeptide is represented by a M/Z peak value in Tables 3, 4, 5, 6 or 7; and

wherein at least one of the following is true:

the test value protein profile and the reference value protein profile are provided to a user in a user-readable format, or

the difference between the test value protein profile and the reference value protein profile is provided to a user in a user-readable format.

14-19. (Canceled)

20. (Previously presented) The method of claims 1, 10, or 13 further comprising immobilizing the plurality of polypeptides on a microarray prior to detecting the polypeptides.

21. (Original) The method of claim 20 wherein the plurality of polypeptides is detected using surface-enhanced laser desorption/ionization time of flight (SELDI-TOF) mass spectrometry.
22. (Previously presented) The method of claims 1, 10, or 13 wherein the endometrial pathology comprises endometrial cancer, hyperplasia or endometriosis.

23. (Previously presented) The method of claims 1, 10, or 13 wherein the biological sample comprises blood, serum or vaginal secretions.

24-40. (Canceled)

41. (Previously Presented) A method for detecting endometrial pathology in a patient comprising:
   obtaining a patient's biological test sample;
   detecting a plurality of polypeptides in the biological test sample to yield a test protein profile;
   comparing the test protein profile with a reference protein profile; and
   determining that said patient is at risk of endometrial pathology when there is a difference between the test protein profile and the reference protein profile in the amount of at least one biomarker polypeptide; and
   wherein the at least one biomarker polypeptide is selected from:
   a polypeptide that remains captured on a reversed phase hydrophobic microarray and has a surface enhanced laser desorption and ionization with time of flight detection (SELDI-TOF) mass spectrometry M/Z peak value of M9331 +/- 10%, M7790 +/- 10%, M10301 +/- 10%, M8722 +/- 10%, M6873 +/- 10%, M8593 +/- 10%, M7041 +/- 10%, M3444 +/- 10%, M8642 +/- 10%, M8961 +/- 10%, M5145 +/- 10%, M5921 +/- 10%, M3561 +/- 10%, M4890 +/- 10%, M3167 +/- 10%, M3773 +/- 10%, M6913 +/- 10%, M22511 +/- 10%, M1539 +/- 10%, M2218 +/- 10%, M2986 +/- 10%, M17358 +/- 10%, M3325 +/- 10%, M3896 +/- 10%, M3499 +/- 10%, or M6452 +/- 10%;
a polypeptide that remains captured on a copper metal affinity microarray, pH <5 fraction, and has a SELDI-TOF mass spectrometry M/Z peak value of M3158 +/- 10%, M4035 +/- 10%, M3274 +/- 10%, M4344 +/- 10%, M4300 +/- 10%, M3974 +/- 10%, M4281 +/- 10%, M3681 +/- 10%, M4313 +/- 10%, M3067 +/- 10%, M4329 +/- 10%, M3082 +/- 10%, M2325 +/- 10%, M4469 +/- 10%, M8596 +/- 10%, M3881 +/- 10%, M2312 +/- 10%, M2026 +/- 10%, M2727 +/- 10%, M8924 +/- 10%, M3324 +/- 10%, M3317 +/- 10%, or M8656 +/- 10%;

a polypeptide that remains captured on a copper metal affinity microarray, pH 5-7 fraction, and has a SELDI-TOF mass spectrometry M/Z peak value of M1867 +/- 10%, M1027 +/- 10%, M4018 +/- 10%, M1930 +/- 10%, M2025 +/- 10%, M9005 +/- 10%, M1887 +/- 10%, M3159 +/- 10%, M3973 +/- 10%, M3990 +/- 10%, M4282 +/- 10%, M4035 +/- 10%, M4006 +/- 10%, M3292 +/- 10%, M1076 +/- 10%, M2789 +/- 10%, M2311 +/- 10%, M2726 +/- 10%, M5012 +/- 10%, M3068 +/- 10%, M4241 +/- 10%, M4006 +/- 10%, M2053 +/- 10%, M5395 +/- 10%, M4648 +/- 10%, M1156 +/- 10%, M1531 +/- 10%, M3957 +/- 10%, or M3275 +/- 10%;

a polypeptide that remains captured on a copper metal affinity microarray, pH > 7 fraction, and has a SELDI-TOF mass spectrometry M/Z peak value of M2726 +/- 10%, M2030 +/- 10%, M2093 +/- 10%, M3337 +/- 10%, M3355 +/- 10%, M3273 +/- 10%, M5068 +/- 10%, M3030 +/- 10%, M2882 +/- 10%, M9280 +/- 10%, M4110 +/- 10%, M2273 +/- 10%, M2213 +/- 10%, M4094 +/- 10%, M3510 +/- 10%, M2250 +/- 10%, M6621 +/- 10%, M4078 +/- 10%, M3810 +/- 10%, M7561 +/- 10%, M5857 +/- 10%, M8907 +/- 10%, M9030 +/- 10%, M8945 +/- 10%, M1451 +/- 10%, M5132 +/- 10%, M3971 +/- 10%, M9342 +/- 10%, M2368 +/- 10%, M1841 +/- 10%, M1780 +/- 10%, M4644 +/- 10%, M1946 +/- 10%, M4034 +/- 10%, M3955 +/- 10%, M4666 +/- 10%, or M4054 +/- 10%;

or a polypeptide that remains captured on a copper metal affinity microarray, pH nonfractionated, and has a SELDI-TOF mass spectrometry M/Z peak value of M9288 +/- 10%, M3955 +/- 10%, M7768 +/- 10%, M1533 +/- 10%, M3029 +/- 10%, M3974 +/- 10%, M1595 +/- 10%, M4300 +/- 10%, M4503 +/- 10%, M4656 +/- 10%, M2953 +/- 10%, M7885 +/- 10%, M7816 +/- 10%, M2187 +/- 10%, M4131 +/- 10%, M4281 +/- 10%, M4017 +/- 10%, M7751 +/-
10%, M3995 +/- 10%, M9341 +/- 10%, M4018 +/- 10%, M3275 +/- 10%, M5341 +/- 10%,
M5912 +/- 10%, M2087 +/- 10%, M2273 +/- 10%, M2862 +/- 10%, M5970 +/- 10%, M2726 +/-
10%, M4433 +/- 10%, M3356 +/- 10%, M2026 +/- 10%, M3315 +/- 10%, M5330 +/- 10%,
M8958 +/- 10%, M4038 +/- 10%, M4643 +/- 10%, M2012 +/- 10%, M9419 +/- 10%, M5931 +/-
10%, M2397 +/- 10%, M2985 +/- 10%, M2211 +/- 10%, or M1657 +/- 10%;

wherein at least one of the following is true:

the test protein profile and the reference protein profile are provided to a user in a
user-readable format, or

the difference between the test protein profile and the reference protein profile is
provided to a user in a user-readable format.

42. (Previously Presented) A method for detecting endometrial pathology in a patient
comprising:

obtaining a patient's biological test sample;

detecting a plurality of polypeptides in the biological test sample to yield a test protein
profile showing the amount of at least one biomarker polypeptide in the sample;

comparing the amount of the biomarker polypeptide in the sample with at least one
predetermined reference value; and

determining that said patient is at risk of endometrial pathology when there is a difference
between the amount of the biomarker polypeptide in the sample and the predetermined reference
value; and

wherein the at least one biomarker polypeptide is selected from:

a polypeptide that remains captured on a reversed phase hydrophobic microarray and has a
surface enhanced laser desorption and ionization with time of flight detection (SELDI-TOF) mass
spectrometry M/Z peak value of M9331 +/- 10%, M7790 +/- 10%, M10301 +/- 10%, M8722 +/-
10%, M6873 +/- 10%, M8593 +/- 10%, M7041 +/- 10%, M3444 +/- 10%, M8642 +/- 10%,
M8961 +/- 10%, M5145 +/- 10%, M5921 +/- 10%, M3561 +/- 10%, M4890 +/- 10%, M3167 +/-
10%, M3773 +/- 10%, M6913 +/- 10%, M22511 +/- 10%, M1539 +/- 10%, M2218 +/- 10%, M2986 +/- 10%, M17358 +/- 10%, M3325 +/- 10%, M3896 +/- 10%, M3499 +/- 10%, or M6452 +/- 10%;

a polypeptide that remains captured on a copper metal affinity microarray, pH <5 fraction, and has a SELDI-TOF mass spectrometry M/Z peak value of M3158 +/- 10%, M4035 +/- 10%, M3274 +/- 10%, M4344 +/- 10%, M4300 +/- 10%, M3974 +/- 10%, M4281 +/- 10%, M3681 +/- 10%, M4313 +/- 10%, M3067 +/- 10%, M4329 +/- 10%, M3082 +/- 10%, M2325 +/- 10%, M4469 +/- 10%, M8596 +/- 10%, M3881 +/- 10%, M2312 +/- 10%, M2026 +/- 10%, M2727 +/- 10%, M8924 +/- 10%, M3324 +/- 10%, M3317 +/- 10%, or M8656 +/- 10%;

a polypeptide that remains captured on a copper metal affinity microarray, pH 5-7 fraction, and has a SELDI-TOF mass spectrometry M/Z peak value of M3158 +/- 10%, M4035 +/- 10%, M4018 +/- 10%, M1930 +/- 10%, M2025 +/- 10%, M9005 +/- 10%, M1887 +/- 10%, M3159 +/- 10%, M3973 +/- 10%, M3990 +/- 10%, M4282 +/- 10%, M4035 +/- 10%, M4006 +/- 10%, M3292 +/- 10%, M1076 +/- 10%, M2789 +/- 10%, M2311 +/- 10%, M2726 +/- 10%, M5012 +/- 10%, M3608 +/- 10%, M4241 +/- 10%, M4006 +/- 10%, M2053 +/- 10%, M5395 +/- 10%, M4648 +/- 10%, M1156 +/- 10%, M1531 +/- 10%, M957 +/- 10%, or M3275 +/- 10%;

a polypeptide that remains captured on a copper metal affinity microarray, pH > 7 fraction, and has a SELDI-TOF mass spectrometry M/Z peak value of M2726 +/- 10%, M2030 +/- 10%, M2093 +/- 10%, M3337 +/- 10%, M3355 +/- 10%, M3273 +/- 10%, M5068 +/- 10%, M3030 +/- 10%, M2882 +/- 10%, M9280 +/- 10%, M4110 +/- 10%, M2273 +/- 10%, M2213 +/- 10%, M4094 +/- 10%, M3510 +/- 10%, M2250 +/- 10%, M6621 +/- 10%, M4078 +/- 10%, M3810 +/- 10%, M7561 +/- 10%, M5857 +/- 10%, M8907 +/- 10%, M9030 +/- 10%, M8945 +/- 10%, M1451 +/- 10%, M5132 +/- 10%, M3971 +/- 10%, M9342 +/- 10%, M2368 +/- 10%, M1841 +/- 10%, M1780 +/- 10%, M4644 +/- 10%, M1946 +/- 10%, M4034 +/- 10%, M3955 +/- 10%, M4666 +/- 10%, or M4054 +/- 10%;

or a polypeptide that remains captured on a copper metal affinity microarray, pH nonfractionated, and has a SELDI-TOF mass spectrometry M/Z peak value of M9288 +/- 10%,
For: DETECTION OF ENDOMETRIAL PATHOLOGY

M3955 +/- 10%, M7768 +/- 10%, M1533 +/- 10%, M3029 +/- 10%, M3974 +/- 10%, M1595 +/- 10%, M4300 +/- 10%, M4503 +/- 10%, M4656 +/- 10%, M2953 +/- 10%, M7885 +/- 10%, M7816 +/- 10%, M2187 +/- 10%, M4131 +/- 10%, M4281 +/- 10%, M4017 +/- 10%, M7751 +/- 10%, M3995 +/- 10%, M9341 +/- 10%, M4018 +/- 10%, M3275 +/- 10%, M5341 +/- 10%, M5912 +/- 10%, M2087 +/- 10%, M2273 +/- 10%, M2862 +/- 10%, M5970 +/- 10%, M2726 +/- 10%, M4433 +/- 10%, M3356 +/- 10%, M2026 +/- 10%, M3315 +/- 10%, M5330 +/- 10%, M8958 +/- 10%, M4038 +/- 10%, M4643 +/- 10%, M2012 +/- 10%, M9419 +/- 10%, M5931 +/- 10%, M2397 +/- 10%, M2985 +/- 10%, M2211 +/- 10%, or M1657 +/- 10%

wherein at least one of the following is true:

- the test protein profile and the reference value are provided to a user in a user-readable format, or
- the difference between the test protein profile and the reference value is provided to a user in a user-readable format.

43. (Previously Presented) A method for detecting endometrial pathology in a patient comprising:

- obtaining a patient's biological test sample;
- detecting at least one biomarker polypeptide in the biological test sample;
- detecting at least one reference polypeptide in the test sample;
- comparing the amount of the biomarker polypeptide to the amount of the reference polypeptide in the test sample to yield a test value;
- comparing the test value to a predetermined reference value; and
- determining that said patient is at risk of endometrial pathology when there is a difference between the test value and the predetermined reference value;

and wherein the at least one biomarker polypeptide is selected from:

- a polypeptide that remains captured on a reversed phase hydrophobic microarray and has a surface enhanced laser desorption and ionization with time of flight detection (SELDI-TOF) mass
spectrometry M/Z peak value of M9331 +/- 10%, M7790 +/- 10%, M10301 +/- 10%, M8722 +/- 10%, M6873 +/- 10%, M8593 +/- 10%, M7041 +/- 10%, M3444 +/- 10%, M8642 +/- 10%,
M8961 +/- 10%, M5145 +/- 10%, M5921 +/- 10%, M3561 +/- 10%, M4890 +/- 10%, M3167 +/- 10%, M3773 +/- 10%, M6913 +/- 10%, M22511 +/- 10%, M1539 +/- 10%, M2218 +/- 10%,
M2986 +/- 10%, M17358 +/- 10%, M3325 +/- 10%, M3896 +/- 10%, M3499 +/- 10%, or M6452 +/- 10%;

a polypeptide that remains captured on a copper metal affinity microarray, pH <5 fraction,
and has a SELDI-TOF mass spectrometry M/Z peak value of M3158 +/- 10%, M4035 +/- 10%,
M3274 +/- 10%, M4344 +/- 10%, M4300 +/- 10%, M3974 +/- 10%, M4281 +/- 10%, M3681 +/- 10%,
M4313 +/- 10%, M3067 +/- 10%, M4329 +/- 10%, M3082 +/- 10%, M2325 +/- 10%,
M4469 +/- 10%, M8596 +/- 10%, M3881 +/- 10%, M2312 +/- 10%, M2026 +/- 10%, M2727 +/- 10%,
M8924 +/- 10%, M3324 +/- 10%, M3317 +/- 10%, or M8656 +/- 10%;

a polypeptide that remains captured on a copper metal affinity microarray, pH 5-7 fraction,
and has a SELDI-TOF mass spectrometry M/Z peak value of M1867 +/- 10%, M1027 +/- 10%,
M4018 +/- 10%, M1930 +/- 10%, M2025 +/- 10%, M9005 +/- 10%, M1887 +/- 10%, M3159 +/- 10%,
M3973 +/- 10%, M3990 +/- 10%, M4282 +/- 10%, M4035 +/- 10%, M4006 +/- 10%,
M3292 +/- 10%, M1076 +/- 10%, M2789 +/- 10%, M2311 +/- 10%, M2726 +/- 10%, M5012 +/- 10%,
M3068 +/- 10%, M4241 +/- 10%, M4006 +/- 10%, M2053 +/- 10%, M5395 +/- 10%,
M4648 +/- 10%, M1156 +/- 10%, M1531 +/- 10%, M3957 +/- 10%, or M3275 +/- 10%;

a polypeptide that remains captured on a copper metal affinity microarray, pH > 7 fraction,
and has a SELDI-TOF mass spectrometry M/Z peak value of M2726 +/- 10%, M2030 +/- 10%,
M2093 +/- 10%, M3337 +/- 10%, M3355 +/- 10%, M3273 +/- 10%, M5068 +/- 10%, M3030 +/- 10%,
M2882 +/- 10%, M9280 +/- 10%, M4110 +/- 10%, M2273 +/- 10%, M2213 +/- 10%,
M4094 +/- 10%, M3510 +/- 10%, M2250 +/- 10%, M6621 +/- 10%, M4078 +/- 10%, M3810 +/- 10%,
M7561 +/- 10%, M5857 +/- 10%, M8907 +/- 10%, M9030 +/- 10%, M8945 +/- 10%,
M1451 +/- 10%, M5132 +/- 10%, M3971 +/- 10%, M9342 +/- 10%, M2368 +/- 10%, M1841 +/- 10%,
M1780 +/- 10%, M4644 +/- 10%, M1946 +/- 10%, M4034 +/- 10%, M3955 +/- 10%,
M4666 +/- 10%, or M4054 +/- 10%;

or a polypeptide that remains captured on a copper metal affinity microarray, pH
nonfractionated, and has a SELDI-TOF mass spectrometry M/Z peak value of M9288 +/- 10%,
M3955 +/- 10%, M7768 +/- 10%, M1533 +/- 10%, M3029 +/- 10%, M3974 +/- 10%, M1595 +/-
10%, M4300 +/- 10%, M4503 +/- 10%, M4656 +/- 10%, M2953 +/- 10%, M7885 +/- 10%,
M7816 +/- 10%, M2187 +/- 10%, M4131 +/- 10%, M4281 +/- 10%, M4017 +/- 10%, M7751 +/-
10%, M3995 +/- 10%, M9341 +/- 10%, M4018 +/- 10%, M3275 +/- 10%, M5341 +/- 10%,
M5912 +/- 10%, M2087 +/- 10%, M2273 +/- 10%, M2862 +/- 10%, M5970 +/- 10%, M2726 +/-
10%, M4433 +/- 10%, M3356 +/- 10%, M2026 +/- 10%, M3315 +/- 10%, M5330 +/- 10%,
M8958 +/- 10%, M4038 +/- 10%, M4643 +/- 10%, M2012 +/- 10%, M9419 +/- 10%, M5931 +/-
10%, M2397 +/- 10%, M2985 +/- 10%, M2211 +/- 10%, or M1657 +/- 10%;

wherein at least one of the following is true:

the test value and the reference value are provided to a user in a user-readable
format, or

the difference between the test value and the reference value is provided to a user
in a user-readable format.

44. (Previously Presented) The method of claim 1 further comprising fractionating the
biological test sample,

wherein detecting a plurality of polypeptides in the biological test sample comprises
detecting a plurality of polypeptides in a fraction of the biological test sample.

45 (Previously Presented) The method of claim 10 further comprising fractionating the
biological test sample, wherein detecting a plurality of polypeptides in the biological test sample
comprises detecting a plurality of polypeptides in a fraction of the biological test sample.
46. (Previously Presented) The method of claim 13 further comprising fractionating the biological test sample, wherein detecting at least one biomarker polypeptide in the biological test sample comprises detecting at least one biomarker polypeptide in a fraction of the biological test sample.

47. (Previously Presented) The method of claim 32 further comprising fractionating the biological test sample, wherein producing a protein profile from the test sample comprises producing a protein profile from a fraction of the test sample.

48. (Previously Presented) The method of claim 41 further comprising fractionating the biological test sample, wherein detecting a plurality of polypeptides in the biological test sample comprises detecting a plurality of polypeptides in a fraction of the biological test sample.

49. (Previously Presented) The method of claim 42 further comprising fractionating the biological test sample, wherein detecting a plurality of polypeptides in the biological test sample comprises detecting a plurality of polypeptides in a fraction of the biological test sample.

50. (Previously Presented) The method of claim 43 further comprising fractionating the biological test sample, wherein detecting at least one biomarker polypeptide in the biological test sample comprises detecting at least one biomarker polypeptide in a fraction of the biological test sample.
Remarks

The Office Action mailed March 12, 2009, has been received and reviewed. Claims 1-3, 5-11, 13, 20-23, 32, 33, and 41-50 are pending. Claims 10, 32, and 33 are canceled without prejudice. Thus, after entry of the amendment, claims 1-3, 5-9, 11, 13, 20-23, and 41-50 will be pending and under consideration. Reconsideration and withdrawal of the rejections are respectfully requested.

Claim Amendments

Claim 13 is amended to correct informalities. The amendments do not introduce new matter, do not necessitate further search, and place the claim in better condition for allowance.

Claim Objections

Claims 10 and 13 are objected to as being substantial duplicates of claim 1.

Applicants respectfully disagree that claims 10 and 13 are substantial duplicates of claim 1. Nevertheless, and solely to expedite prosecution, claim 10 is canceled, obviating the objection with respect to claim 10.

With respect to claim 13, M.P.E.P. §706.03(k) states, “[C]ourt decisions have confirmed applicant’s right to restate (i.e., by plural claiming) the invention in a reasonable number of ways. Indeed, a mere difference in scope between claims has been held to be enough.” (emphasis added).

Applicants submit that differences in scope exist between claim 1 and claim 13. In particular, claim 1 recites detecting a plurality of polypeptides, yielding a test protein profile and then comparing the test protein profile to a reference protein profile. In contrast, claim 13 recites detecting at least one biomarker polypeptide and at least one reference polypeptide from within the sample, making an internal comparison of the amount of the biomarker polypeptide and the amount of the reference polypeptide in the sample to yield a test value, and comparing the test value to a reference value. Thus, while the practice of certain embodiments of Applicants’ methods may be encompassed by both claim 1 and claim 13, certain embodiments are
encompassed by either claim 1 or claim 13, but not both. Thus, claim 1 and claim 13 are of different scope.

Because claim 1 and claim 13 are of different scope, Applicants respectfully submit that claim 13 is not a substantial duplicate of claim 1 and request that the objection to claim 13 be withdrawn.

The 35 U.S.C. §103 Rejection


Applicants respectfully disagree that the cited documents render claims 32 and 33 unpatentable for at least all of the reasons of record. Nevertheless, and solely to expedite prosecution, claims 32 and 33 are canceled herein without prejudice, obviating the rejection.
Summary

It is respectfully submitted that the pending claims are in condition for allowance and notification to that effect is respectfully requested. The Examiner is invited to contact Applicants’ Representatives at the telephone number listed below if it is believed that prosecution of this application may be assisted thereby.

Respectfully submitted
By
Mueting, Raasch & Gebhardt, P.A.
P.O. Box 581336
Minneapolis, MN 55458-1336
Phone: (612) 305-1220
Facsimile: (612) 305-1228
Customer Number 26813

By: __________________________
Christopher D. Gram
Reg. No. 43,643
Direct Dial (612) 305-0412

April 7, 2009

CERTIFICATE UNDER 37 CFR §1.8:
The undersigned hereby certifies that this paper is being transmitted via the U.S. Patent and Trademark Office electronic filing system in accordance with 37 CFR §1.6(a)(4) to the Patent and Trademark Office addressed to the Commissioner for Patents, Mail Stop AF, P.O. Box 1450, Alexandria, VA 22313-1450, on this 7 day of April, 2009.

By: _______________________________________
Name: Sandy Truehart