[005] As an alternative, mass spectroscopy (MS) offers sensitive and precise measurement of cancer-specific biomarkers including glycopeptides. *See*, for example, Ruhaak, L.R., *et al.*, Protein-Specific Differential Glycosylation of Immunoglobulins in Serum of Ovarian Cancer Patients DOI: 10.1021/acs.jproteome.5b01071; *J. Proteome Res.*, 2016, 15, 1002−1010 (2016); also Miyamoto, S., *et al.*, Multiple Reaction Monitoring for the Quantitation of Serum Protein Glycosylation Profiles: Application to Ovarian Cancer, DOI: 10.1021/acs.jproteome.7b00541, J. Proteome Res. 2018, 17, 222−233 (2017), the entire contents of which are herein incorporated by reference in its entirety for all purposes. However, using MS to diagnose cancer, generally, or ovarian cancer specifically, has not been demonstrated to date in a clinically relevant manner.

[006] What is needed are new biomarkers and new methods of using MS to diagnose disease states such as cancer using these biomarkers. Set forth herein in the disclosure below are such biomarkers comprising glycans, peptides, and glycopeptides, as well as fragments thereof, and methods of using the biomarkers with MS to diagnose ovarian cancer.

SUMMARY

[007] In one example, set forth herein is a glycopeptide or peptide consisting of an amino acid sequence selected from SEQ ID NOs:1-262, and combinations thereof.

[008] In another example, set forth herein is a glycopeptide or peptide consisting essentially of an amino acid sequence selected from SEQ ID NOs:1-262, and combinations thereof.

[009] In one aspect, set forth herein is a method for detecting one or more MRM transitions, comprising: obtaining a biological sample from a patient; digesting and/or fragmenting a glycopeptide in the sample; and detecting a multiple-reaction-monitoring (MRM) transition selected from the group consisting of transitions 1 – 150, described herein.

[0010] In one aspect, set forth herein a method for identifying a classification for a sample, the method comprising: quantifying by mass spectroscopy (MS) one or more glycopeptides in a sample wherein the glycopeptides each, individually in each instance, comprises a glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262, and combinations thereof; and inputting the quantification into a trained model to generate a output probability; determining if the output probability is above or below a threshold for a classification; and identifying a classification

for the sample based on whether the output probability is above or below a threshold for a classification.

[0011] In yet another example, set forth herein is a method for classifying a biological sample, comprising: obtaining a biological sample from a patient; digesting and/or fragmenting a glycopeptide in the sample; detecting a MRM transition selected from the group consisting of transitions 1 – 150; and quantifying the glycopeptides; inputting the quantification into a trained model to generate a output probability; determining if the output probability is above or below a threshold for a classification; and classifying the biological sample based on whether the output probability is above or below a threshold for a classification.

[0012] In another example, set forth herein is a method for treating a patient having ovarian cancer; the method comprising: obtaining a biological sample from the patient; digesting and/or fragmenting one or more glycopeptides in the sample; and detecting and quantifying one or more multiple-reaction-monitoring (MRM) transitions selected from the group consisting of transitions 1 – 150; inputting the quantification into a trained model to generate an output probability; determining if the output probability is above or below a threshold for a classification; and classifying the patient based on whether the output probability is above or below a threshold for a classification, wherein the classification is selected from the group consisting of: (A) a patient in need of a chemotherapeutic agent; (B) a patient in need of a immunotherapeutic agent; (C) a patient in need of hormone therapy; (D) a patient in need of a targeted therapeutic agent; (E) a patient in need of surgery; (F) a patient in need of neoadjuvant therapy; (G) a patient in need of chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic agent, neoadjuvant therapy, or a combination thereof, before surgery; (H) a patient in need of chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic agent, neoadjuvant therapy, or a combination thereof, after surgery; (I) or a combination thereof; administering a therapeutically effective amount of a therapeutic agent to the patient: wherein the therapeutic agent is selected from chemotherapy if classification A or I is determined; wherein the therapeutic agent is selected from immunotherapy if classification B or I is determined; or wherein the therapeutic agent is selected from hormone therapy if classification C or I is determined; or wherein the therapeutic agent is selected from targeted therapy if classification D or I is determined wherein the therapeutic agent is selected from neoadjuvant therapy if classification F or I is determined; wherein the therapeutic agent is selected from chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic

agent, neoadjuvant therapy, or a combination thereof if classification G or I is determined; and wherein the therapeutic agent is selected from chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic agent, neoadjuvant therapy, or a combination thereof if classification H or I is determined.

[0013] In another aspect, set forth herein is a method for training a machine learning algorithm, comprising: providing a first data set of MRM transition signals indicative of a sample comprising a glycopeptide consisting of, or consisting essentially of, an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-262; providing a second data set of MRM transition signals indicative of a control sample; and comparing the first data set with the second data set using a machine learning algorithm.

[0014] In another aspect, set forth herein is a method for diagnosing a patient having ovarian cancer; the method comprising: obtaining a biological sample from the patient; performing mass spectroscopy of the biological sample using MRM-MS with a QQQ and/or qTOF spectrometer to detect and quantify one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 - 262; or to detect and quantify one or more MRM transitions selected from transitions 1-150; inputting the quantification of the detected glycopeptides or the MRM transitions into a trained model to generate an output probability, determining if the output probability is above or below a threshold for a classification; and identifying a diagnostic classification for the patient based on whether the output probability is above or below a threshold for a classification; and diagnosing the patient as having ovarian cancer based on the diagnostic classification. In some examples, the method includes performing mass spectroscopy of the biological sample using MRM-MS with a QQQ.

[0015] In another aspect, set forth herein is a kit comprising a glycopeptide standard, a buffer, and one or more glycopeptides consisting of, or consisting essentially of, an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262.

[0016] In another aspect, set forth herein is a glycopeptide consisting of, or consisting essentially of, an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262.

[0016a] In another aspect, set forth herein is a method for classifying a biological sample, comprising: obtaining a biological sample from a patient, wherein the biological sample

comprises one or more glycopeptides; digesting and/or fragmenting one or more glycopeptides in the sample; detecting and quantifying at least one or more multiple-reaction-monitoring (MRM) transition selected from the group consisting of transitions 1 - 150; and inputting the quantification into a trained model to generate an output probability; determining if the output probability is above or below a threshold for a classification; and classifying the biological sample based on whether the output probability is above or below a threshold for a classification.

[0016b] In another aspect, set forth herein is a method for classifying a biological sample, comprising: obtaining a biological sample from a patient, wherein the biological sample comprises one or more glycopeptides; digesting and/or fragmenting one or more glycopeptides in the sample; detecting and quantifying at least one or more multiple-reaction-monitoring (MRM) transition associated with at least one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 262, and combinations thereof; and inputting the quantification into a trained model to generate an output probability; determining if the output probability is above or below a threshold for a classification; and classifying the biological sample based on whether the output probability is above or below a threshold for a classification.

[0016c] In another aspect, set forth herein is a use of a therapeutic agent in the manufacture of a medicament for treating a patient having ovarian cancer, wherein the patient is classified based on whether an output probability is above or below a threshold for a classification, wherein the output probability is determined from a biological sample obtained from the patient, wherein one or more glycopeptides in the sample are digested and/or fragmented, one or more multiple-reaction-monitoring (MRM) transitions selected from the group consisting of transitions 1–150 are detected and quantified, and the quantification is input into a trained model to generate an output probability, wherein the classification is selected from the group consisting of: (A) a patient in need of a chemotherapeutic agent; (B) a patient in need of a immunotherapeutic agent; (C) a patient in need of hormone therapy; (D) a patient in need of a targeted therapeutic agent; (E) a patient in need of surgery; (F) a patient in need of neoadjuvant therapy; (G) a patient in need of a chemotherapeutic agent, an immunotherapeutic agent, hormone therapy, a targeted therapeutic agent, neoadjuvant therapy, or a combination thereof, before surgery; (H) a patient in need of a chemotherapeutic agent, an immunotherapeutic agent, hormone therapy, a targeted therapeutic agent, neoadjuvant therapy, or a combination thereof, after surgery; (I) or a combination thereof; wherein the therapeutic agent is selected from chemotherapy if classification A or I is determined; wherein the therapeutic agent is selected from immunotherapy if classification B or I is determined; or wherein the therapeutic agent is selected from hormone therapy if classification C or I is determined; or wherein the therapeutic

agent is selected from targeted therapy if classification D or I is determined wherein the therapeutic agent is selected from neoadjuvant therapy if classification F or I is determined; wherein the therapeutic agent is selected from chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic agent, neoadjuvant therapy, or a combination thereof if classification G or I is determined; and wherein the therapeutic agent is selected from the chemotherapeutic agent, the immunotherapeutic agent, hormone therapy, the targeted therapeutic agent, neoadjuvant therapy, or a combination thereof if classification H or I is determined.

[0016d] In another aspect, set forth herein is a glycopeptide consisting essentially of an amino acid sequence selected from the group consisting essentially of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194, and combinations thereof.

[0016e] In another aspect, set forth herein is a kit comprising a glycopeptide standard, a buffer, and one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194.

[0016f] In another aspect, set forth herein is a computer-implemented method of training a neural network for detecting an MRM transition, comprising: collecting a set of mass spectroscopy spectra of one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262; annotating the spectra including identifying at least one of a start, stop, maximum, or combination thereof, of a peak in a spectra to create an annotated set of mass spectroscopy spectra; creating a first training set comprising the collected set of mass spectroscopy spectra, the annotated set of mass spectroscopy spectra, and a second set of mass spectroscopy spectra of one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262; training the neural network in a first stage using the first training set; creating a second training set for a second stage of training comprising the first training set and mass spectroscopy spectra that are incorrectly detected as comprising one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262 after the first stage of training; and training the neural network in a second stage using the second training set.

What is claimed is:

1. A method for classifying a biological sample, comprising:

obtaining a biological sample from a patient, wherein the biological sample comprises one or more glycopeptides;

digesting and/or fragmenting one or more glycopeptides in the sample;

detecting and quantifying at least one or more multiple-reaction-monitoring (MRM) transition selected from the group consisting of transitions 1 – 150; and

inputting the quantification into a trained model to generate an output probability;

determining if the output probability is above or below a threshold for a classification; and

classifying the biological sample based on whether the output probability is above or below a threshold for a classification.

2. The method of claim 1, further comprising using a machine learning algorithm to train a model using the MRM transitions as inputs.

3. A method for classifying a biological sample, comprising:

obtaining a biological sample from a patient, wherein the biological sample comprises one or more glycopeptides;

digesting and/or fragmenting one or more glycopeptides in the sample;

detecting and quantifying at least one or more multiple-reaction-monitoring (MRM) transition associated with at least one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262, and combinations thereof; and

inputting the quantification into a trained model to generate an output probability;

determining if the output probability is above or below a threshold for a classification; and

classifying the biological sample based on whether the output probability is above or below a threshold for a classification.

4. The method of claim 3, comprising detecting and quantifying at least one or more multiple-reaction-monitoring (MRM) transition associated with at least one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69,

82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194, and combinations thereof.

5. The method of claims 1 or 3, comprising training a machine learning algorithm using the MRM transitions as inputs.

6. Use of a therapeutic agent in the manufacture of a medicament for treating a patient having ovarian cancer,

wherein the patient is classified based on whether an output probability is above or below a threshold for a classification,

wherein the output probability is determined from a biological sample obtained from the patient, wherein one or more glycopeptides in the sample are digested and/or fragmented, one or more multiple-reaction-monitoring (MRM) transitions selected from the group consisting of transitions 1–150 are detected and quantified, and the quantification is input into a trained model to generate an output probability,

wherein the classification is selected from the group consisting of:

(A) a patient in need of a chemotherapeutic agent;

(B) a patient in need of a immunotherapeutic agent;

(C) a patient in need of hormone therapy;

(D) a patient in need of a targeted therapeutic agent;

(E) a patient in need of surgery;

(F) a patient in need of neoadjuvant therapy;

(G) a patient in need of a chemotherapeutic agent, an immunotherapeutic agent, hormone therapy, a targeted therapeutic agent, neoadjuvant therapy, or a combination thereof, before surgery;

(H) a patient in need of a chemotherapeutic agent, an immunotherapeutic agent, hormone therapy, a targeted therapeutic agent, neoadjuvant therapy, or a combination thereof, after surgery;

(I) or a combination thereof;

wherein the therapeutic agent is selected from chemotherapy if classification A or I is determined;

wherein the therapeutic agent is selected from immunotherapy if classification B or I is determined; or

wherein the therapeutic agent is selected from hormone therapy if classification C or I is determined; or

wherein the therapeutic agent is selected from targeted therapy if classification D or I is determined

wherein the therapeutic agent is selected from neoadjuvant therapy if classification F or I is determined;

wherein the therapeutic agent is selected from chemotherapeutic agent, immunotherapeutic agent, hormone therapy, targeted therapeutic agent, neoadjuvant therapy, or a combination thereof if classification G or I is determined; and

wherein the therapeutic agent is selected from the chemotherapeutic agent, the immunotherapeutic agent, hormone therapy, the targeted therapeutic agent, neoadjuvant therapy, or a combination thereof if classification H or I is determined.

7. The use of claim 6, comprising conducting multiple-reaction-monitoring mass spectroscopy (MRM-MS) on the biological sample.
8. The use of claim 6 or 7, comprising quantifying one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262 and combinations thereof.
9. The use of claim 6 or 7, comprising quantifying one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194 and combinations thereof.
10. The use of any one of claims 6-9, comprising inputting the quantification of the amount of a glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-262 into a machine learning algorithm to train a model.
11. The use of any one of claims 6-10, comprising inputting the quantification of the amount of a glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194 into a machine learning algorithm to train a model.

12. The use of claim 11, wherein the machine learning algorithm is selected from the group consisting of a deep learning algorithm, a neural network algorithm, an artificial neural network algorithm, a supervised machine learning algorithm, a linear discriminant analysis algorithm, a quadratic discriminant analysis algorithm, a support vector machine algorithm, a linear basis function kernel support vector algorithm, a radial basis function kernel support vector algorithm, a random forest algorithm, a genetic algorithm, a nearest neighbor algorithm, k-nearest neighbors, a naive Bayes classifier algorithm, a logistic regression algorithm, or a combination thereof.
13. The use of any one of claims 6-12, wherein the analyzing the transitions comprises selecting peaks and/or quantifying detected glycopeptide fragments with a machine learning algorithm.
14. A method of detecting one or more multiple-reaction-monitoring (MRM) transitions, comprising:
obtaining, or having obtained, a biological sample from a patient, wherein the biological sample comprises one or more glycans or glycopeptides;
digesting and/or fragmenting a glycopeptide in the sample; and
detecting a MRM transition selected from the group consisting of transitions 1 - 150.

15. The method of claim 14, wherein the fragmenting a glycopeptide in the sample occurs after introducing the sample, or a portion thereof, into the mass spectrometer.

16. The method of any one of claims 14-15, wherein the fragmenting a glycopeptide in the sample produces a peptide or glycopeptide consisting essentially of an ammo acid sequence selected from the group consisting of SEQ ID NOs: 1 - 262, and combinations thereof.

17. The method of any one of claims 14-16, wherein the fragmenting a glycopeptide in the sample produces a peptide or glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194, and combinations thereof.

18. The method of any one of claims 14-17, wherein the MRM transition is selected from the transitions, or any combinations thereof, in any one of Tables 1-5.

19. The method of any one of claims 14-18, wherein detecting a MRM transition selected from the group consisting of transitions 1 - 150 comprises detecting a MRM transition using a triple quadrupole (QQQ) mass spectrometer or a quadrupole time-of-flight (qTOF) mass spectrometer.

20. The method of any one of claims 14-19, wherein the one or more glycopeptides comprises a peptide or glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 262, and combinations thereof.

21. The method of any one of claims 14-20, wherein the one or more glycopeptides comprises a peptide or glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194, and combinations thereof.

22. The method of any one of claims 14-21, comprising detecting one or more MRM transitions indicative of one or more glycans selected from the group consisting of glycan 3200, 3210, 3300, 3310, 3320, 3400, 3410, 3420, 3500, 3510, 3520, 3600, 3610, 3620, 3630, 3700, 3710, 3720, 3730, 3740, 4200, 4210, 4300, 4301, 4310, 4311, 4320, 4400, 4401, 4410, 4411, 4420, 4421, 4430, 4431, 4500, 4501, 4510, 4511, 4520, 4521, 4530, 4531, 4540, 4541, 4600, 4601, 4610, 4611, 4620, 4621, 4630, 4631, 4641, 4650,4700, 4701, 4710, 4711, 4720, 4730, 5200, 5210, 5300, 5301, 5310, 5311, 5320, 5400, 5401, 5402, 5410, 5411, 5412, 5420, 5421, 5430, 5431, 5432, 5500, 5501, 5502, 5510, 5511, 5512, 5520, 5521, 5522, 5530, 5531, 5541, 5600, 5601, 5602, 5610, 5611, 5612, 5620, 5621, 5631, 5650, 5700, 5701, 5702, 5710, 5711, 5712, 5720, 5721, 5730, 5731, 6200, 6210, 6300, 6301, 6310, 6311, 6320, 6400, 6401, 6402, 6410, 6411, 6412, 6420, 6421, 6432, 6500, 6501, 6502, 6503, 6510, 6511, 6512, 6513, 6520, 6521, 6522, 6530, 6531, 6532, 6540, 6541, 6600, 6601, 6602, 6603, 6610, 6611, 6612, 6613, 6620, 6621, 6622, 6623, 6630, 6631, 6632, 6640, 6641, 6642, 6652, 6700, 6701, 6711, 6721, 6703, 6713, 6710, 6711, 6712, 6713, 6720, 6721, 6730, 6731, 6740, 7200, 7210, 7400, 7401, 7410, 7411, 7412, 7420, 7421, 7430, 7431, 7432, 7500, 7501, 7510, 7511, 7512, 7600,

7601, 7602, 7603, 7604, 7610, 7611, 7612, 7613, 7614, 7620, 7621, 7622, 7623, 7632, 7640, 7700, 7701, 7702, 7703, 7710, 7711, 7712, 7713, 7714, 7720, 7721, 7722, 7730, 7731, 7732, 7740, 7741, 7751, 8200, 9200, 9210, 10200, 11200, 12200, and combinations thereof.

23. The method of claim 22, further comprising quantifying a first glycan and quantifying a second glycan; and further comprising comparing the quantification of the first glycan with the quantification of the second glycan.

24. The method of claim 22 or 23, further comprising associating the detected glycan with a peptide residue site, whence the glycan was bonded.

25. The method of any one of claims 14-24, comprising normalizing the amount of glycopeptide based on the amount of a peptide or glycopeptide consisting essentially of an amino acid having a SEQ ID. No: 1-262.

26. A method for identifying a classification for a sample, the method comprising quantifying by mass spectroscopy (MS) one or more glycopeptides in a sample wherein the glycopeptides each, individually in each instance, comprises a glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 262, and combinations thereof; and inputting the quantification into a trained model to generate an output probability; determining if the output probability is above or below a threshold for a classification; and identifying a classification for the sample based on whether the output probability is above or below a threshold for a classification.

27. The method of any one of claims 1-5 and 26, wherein the sample is a biological sample from a patient or individual having a disease or condition.

28. The method of claim 27, wherein the patient has ovarian cancer.

29. The method of claim 27, wherein the individual has cancer, an autoimmune disease, fibrosis, or an aging condition.

30. The method of any one of claims 26-29, wherein the MS is MRM-MS with a QQQ and/or qTOF mass spectrometer.

31. The method of any one of claims 1-5 and 26-30, wherein the trained model was trained using a machine learning algorithm selected from the group consisting of a deep learning algorithm, a neural network algorithm, an artificial neural network algorithm, a supervised machine learning algorithm, a linear discriminant analysis algorithm, a quadratic discriminant analysis algorithm, a support vector machine algorithm, a linear basis function kernel support vector algorithm, a radial basis function kernel support vector algorithm, a random forest algorithm, a genetic algorithm, a nearest neighbor algorithm, k-nearest neighbors, a naive Bayes classifier algorithm, a logistic regression algorithm, or a combination thereof.

32. The method of any one of claims 1-5 and 26-31, wherein the classification is a disease classification or a disease severity classification.

33. The method of any one of claims 1-5 and 26-32, wherein the classification is having ovarian cancer or not having ovarian cancer.

34. The method of claim 32 or 33, wherein the classification is identified with greater than 80 % confidence, greater than 85 % confidence, greater than 90 % confidence, greater than 95 % confidence, greater than 99 % confidence, or greater than 99.9999 % confidence.

35. The method of any one of claims 26-34, further comprising:
quantifying by MS a first glycopeptide in a sample at a first time point; quantifying by MS a second glycopeptide in a sample at a second time point; and comparing the quantification at the first time point with the quantification at the second time point.

36. The method of claim 35, further comprising:
quantifying by MS a third glycopeptide in a sample at a third time point;
quantifying by MS a fourth glycopeptide in a sample at a fourth time point; and
comparing the quantification at the fourth time point with the quantification at the third time point.

37. The method of any one of claims 26-36, further comprising monitoring the health status of a patient.

38. The method of claim 37, wherein monitoring the health status of a patient comprises monitoring the onset and progression of disease in a patient with risk factors such as genetic mutations, as well as detecting cancer recurrence.

39. The method of any one of claims 26-38, further comprising quantifying by MS an amino acid sequence selected from the group consisting of SEQ ID NOs: 1 - 262.

40. The method of any one of claims 26-39, further comprising quantifying by MS an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, and 194.

41. The method of any one of claims 26-38, further comprising quantifying by MS one or more glycans selected from the group consisting of glycans 3200, 3210, 3300, 3310, 3320, 3400, 3410, 3420, 3500, 3510, 3520, 3600, 3610, 3620, 3630, 3700, 3710, 3720, 3730, 3740, 4200, 4210, 4300, 4301, 4310, 4311, 4320, 4400, 4401, 4410, 4411, 4420, 4421, 4430, 4431, 4500, 4501, 4510, 4511, 4520, 4521, 4530, 4531, 4540, 4541, 4600, 4601, 4610, 4611, 4620, 4621, 4630, 4631, 4641, 4650,4700, 4701, 4710, 4711, 4720, 4730, 5200, 5210, 5300, 5301, 5310, 5311, 5320, 5400, 5401, 5402, 5410, 5411, 5412, 5420, 5421, 5430, 5431, 5432, 5500, 5501, 5502, 5510, 5511, 5512, 5520, 5521, 5522, 5530, 5531, 5541, 5600, 5601, 5602, 5610, 5611, 5612, 5620, 5621, 5631, 5650, 5700, 5701, 5702, 5710, 5711, 5712, 5720, 5721, 5730, 5731, 6200, 6210, 6300, 6301, 6310, 6311, 6320, 6400, 6401, 6402, 6410, 6411, 6412, 6420, 6421, 6432, 6500, 6501, 6502, 6503, 6510, 6511, 6512, 6513, 6520, 6521, 6522, 6530, 6531, 6532, 6540, 6541, 6600, 6601, 6602, 6603, 6610, 6611, 6612, 6613, 6620, 6621, 6622, 6623, 6630, 6631, 6632, 6640, 6641, 6642, 6652, 6700, 6701, 6711, 6721, 6703, 6713, 6710, 6711, 6712, 6713, 6720, 6721, 6730, 6731, 6740, 7200, 7210, 7400, 7401, 7410, 7411, 7412, 7420, 7421, 7430, 7431, 7432, 7500, 7501, 7510, 7511, 7512, 7600, 7601, 7602, 7603, 7604, 7610, 7611, 7612, 7613, 7614, 7620, 7621, 7622, 7623, 7632, 7640, 7700, 7701, 7702,

7703, 7710, 7711, 7712, 7713, 7714, 7720, 7721, 7722, 7730, 7731, 7732, 7740, 7741, 7751, 8200, 9200, 9210, 10200, 11200, 12200, and combinations thereof.

42. The method of any one of claims 26-41, further comprising diagnosing a patient with a disease or condition based on the classification.

43. The method of claim 42, further comprising diagnosing the patient as having ovarian cancer based on the classification.

44. The method of any one of claims 26-43, further comprising treating the patient with a therapeutically effective amount of a therapeutic agent selected from the group consisting of a chemotherapeutic agent, an immunotherapy, a hormone therapy, a targeted therapy, and combinations thereof.

45. A method for training a machine learning algorithm, comprising:

providing a first data set of MRM transition signals indicative of a sample comprising one or more glycopeptides, each glycopeptide, individually, consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-262;

providing a second data set of MRM transition signals indicative of a control sample; and

comparing the first data set with the second data set using a machine learning algorithm.

46. The method of claim 45, wherein the sample comprising a glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-262 wherein the sample is from a patient having ovarian cancer or wherein the sample is a pooled sample from one or more patients having ovarian cancer.

47. The method of claim 45, wherein the sample comprising a glycopeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194 wherein the sample is from a patient having ovarian cancer or wherein the sample is a pooled sample from one or more patients having ovarian cancer.

48. The method of claim 45, 46 or 47, wherein the control sample is a sample from a patient not having ovarian cancer or wherein the control sample is a pooled sample from one or more patients not having ovarian cancer.

49. A method for diagnosing a patient having ovarian cancer; the method comprising:

obtaining, or having obtained, a biological sample from the patient;

performing mass spectroscopy of the biological sample using MRM-MS with a QQQ and/or qTOF spectrometer to detect and quantify one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 - 262; or to detect one or more MRM transitions selected from transitions 1-150;

inputting the quantification of the detected glycopeptides or the MRM transitions into a trained model to generate an output probability,

determining if the output probability is above or below a threshold for a classification; and

identifying a diagnostic classification for the patient based on whether the output probability is above or below a threshold for a classification; and

diagnosing the patient as having ovarian cancer based on the diagnostic classification.

50. The method of claim 49, wherein the analyzing the detected glycopeptides comprises using a machine learning algorithm.

51. The method of claim 50, comprising performing mass spectroscopy of the biological sample using MRM-MS with a QQQ and/or qTOF spectrometer to detect and quantify one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, and 194.

52. A glycopeptide consisting essentially of an amino acid sequence selected from the group consisting essentially of SEQ ID NOs:1 – 262, and combinations thereof.

53. A glycopeptide consisting essentially of an amino acid sequence selected from the group consisting essentially of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194, and combinations thereof.

54. A kit comprising a glycopeptide standard, a buffer, and one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262.

55. A kit comprising a glycopeptide standard, a buffer, and one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, 194.

56. A computer-implemented method of training a neural network for detecting an MRM transition, comprising:

collecting a set of mass spectroscopy spectra of one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262;

annotating the spectra including identifying at least one of a start, stop, maximum, or combination thereof, of a peak in a spectra to create an annotated set of mass spectroscopy spectra;

creating a first training set comprising the collected set of mass spectroscopy spectra, the annotated set of mass spectroscopy spectra, and a second set of mass spectroscopy spectra of one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262;

training the neural network in a first stage using the first training set;

creating a second training set for a second stage of training comprising the first training set and mass spectroscopy spectra that are incorrectly detected as comprising one or more glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs:1 – 262 after the first stage of training; and

training the neural network in a second stage using the second training set.

57. The method of claim 55, wherein the one or more glycopeptides are in each instance glycopeptides consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 5, 9, 12, 22, 24, 28, 32, 34, 35, 36, 37, 38, 53, 61, 65, 69, 82, 99, 104, 114, 115, 126, 128, 136, 146, 147, 150, 154, 177, 184, 190, and 194.