WHAT IS CLAIMED IS:

1. A method for diagnosing multiple sclerosis or another demyelinating disorder or the risk of multiple sclerosis or another demyelinating disorder in a patient, the method comprising the steps of:

a) analyzing a sample obtained from a patient to obtain quantifying data for one or more than one metabolite marker;

b) comparing the quantifying data for said one or more than one metabolite marker to corresponding data obtained from one or more than one reference sample; and

c) using said comparison to diagnose multiple sclerosis or another demyelinating disorder or the risk of multiple sclerosis or another demyelinating disorder,

wherein the one or more than one metabolite marker is represented by one or more than one accurate mass feature listed in Table 1, 2, 3, 4, 5, 6 or any combination thereof.

2. The method of claim 1 wherein the sample is whole blood, plasma, serum, or a subfraction of whole blood.

3. The method of claim 1 wherein step a) comprises the extraction of said metabolites into an organic solvent.

4. The method of claim 1 wherein step a) comprises the extraction of said metabolites into an aqueous solvent.

5. The method of claim 1 wherein step a) comprises analyzing the sample by mass spectrometry.

6. The method of claim 5 wherein the mass spectrometer is a Fourier Transform Ion Cyclotron Resonance Mass Spectrometer (FTMS).

7. The method of claim 6 wherein step c) comprises analyzing the sample by positive electrospray ionization, negative electrospray ionization, positive atmospheric pressure chemical ionization, or negative atmospheric pressure chemical ionization.

8. The method of claim 1 wherein said one or more than one reference sample is a plurality of samples obtained from control individuals; one or more than one baseline sample obtained from the patient at an earlier date; or a combination thereof.

9. The method of claim 1 wherein the multiple sclerosis metabolite markers are selected from the group consisting of: relapsing-remitting as compared to a normal reference sample and the metabolites are listed in Table 1, primary-progressive as compared to a normal reference sample and the metabolites are listed in Table 2, secondary-progressive as compared to a normal reference sample and the metabolites are listed in Table 3, relapsing-remitting as compared to secondary-progressive and the metabolites are listed in Table 4, relapsing-remitting transiting to secondary-progressive as compared to relapsing-remitting and the metabolites are listed in Table 5, and relapsing-remitting transiting to secondary-progressive as compared to secondary-progressive and the metabolites are listed in Table 6.

10. A method for diagnosing multiple sclerosis or another demyelinating disorder or the risk of multiple sclerosis or another demyelinating disorder in a patient, the method comprising the steps of:

a) analyzing a sample obtained from a patient to obtain quantifying data for one or more than one metabolite marker;

b) comparing the quantifying data for said one or more than one metabolite marker to corresponding data obtained from one or more than one reference sample; and

c) using said comparison to diagnose multiple sclerosis or another demyelinating disorder or the risk of multiple sclerosis or another demyelinating disorder,

wherein the one or more than one metabolite marker is selected from the metabolites listed in Table 22.

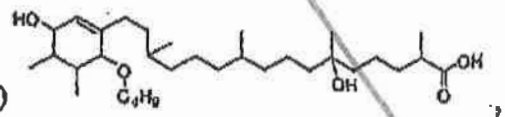
11. The method of claim 10 wherein the multiple sclerosis metabolite markers are relapsing-remitting as compared to a normal reference sample and the metabolite markers comprise metabolites with accurate masses in Daltons of, or substantially equivalent to, a) 496.4157, b) 524.4448, c) 540.4387, d) 580.5089, e) 594.4848, f) 596.5012 or g) 578.4923.

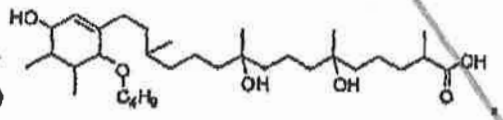
12. The method of claim 11 wherein the one or more than one metabolite is further characterized by molecular formula a) $C_{30}H_{56}O_5$, b) $C_{32}H_{60}O_5$, c) $C_{32}H_{60}O_6$, d) $C_{36}H_{68}O_5$, e) $C_{36}H_{66}O_6$, f) $C_{36}H_{68}O_6$ or g) $C_{36}H_{66}O_5$, respectively.

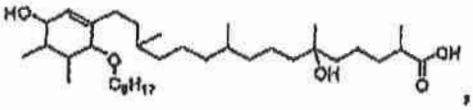
13. The method of claim 12 wherein the one or more than one metabolite is further characterized by the MS/MS fragmentation data as shown in Tables 24, 25, 26, 29, 30, 31 or 28, respectively.

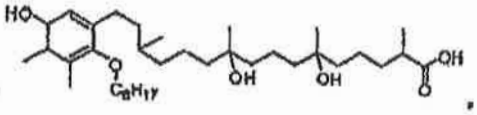
14. The method of claim 12 wherein the one or more than one metabolite is further characterized by the molecular structures:

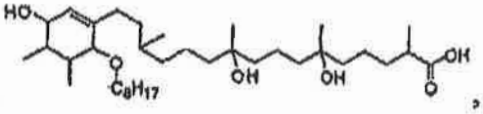
a) ,

b) ,

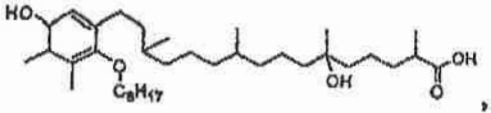
c) ,

d) ,

e) ,

f) ,

or

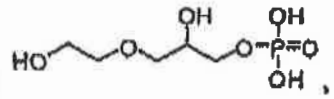
g) , respectively.

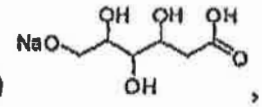
15. The method of claim 10 wherein the multiple sclerosis metabolite markers are primary-progressive as compared to a normal reference sample and the metabolite markers comprise metabolites with accurate masses in Daltons of, or substantially equivalent to a) 216.04, b) 202.0453, c) 244.0559 or d) 857.7516.

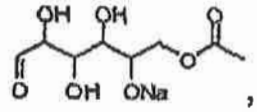
16. The method of claim 15 wherein the one or more than one metabolite is further characterized by molecular formula a) $C_5H_{13}O_7P$, b) $C_6H_{11}O_6Na$, c) $C_8H_{13}O_7Na$ or d) $C_{54}H_{99}NO_6$, respectively.

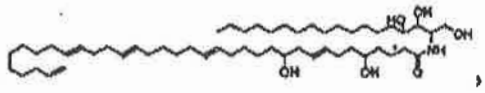
17. The method of claim 16 wherein the one or more than one metabolite is further characterized by the MS/MS fragmentation data as shown in Tables 33, 36, 37 or 41, respectively.

18. The method of claim 16 wherein the one or more than one metabolite is further characterized by the structure

a) ,

b) ,

c) , or

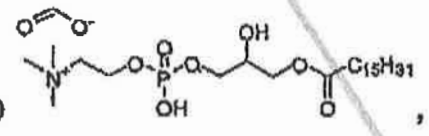
d) , respectively.

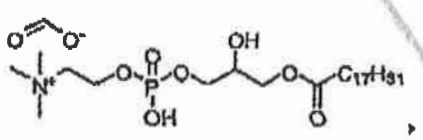
19. The method of claim 10 wherein the multiple sclerosis metabolite markers are secondary-progressive as compared to a normal reference sample and the metabolite markers comprise metabolites with accurate masses in Daltons of, or substantially equivalent to a) 541.3415, b) 565.3391, c) 428.3653, d) 805.5609, e) 194.0803 or f) 578.423.

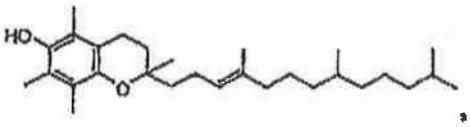
20. The method of claim 19 wherein the one or more than one metabolite is further characterized by molecular formula a) $C_{25}H_{52}NO_9P$, b) $C_{27}H_{52}NO_9P$, c) $C_{29}H_{48}O_2$, d) $C_{48}H_{80}NO_8P$, e) $C_7H_{14}O_6$ or f) $C_{36}H_{66}O_5$, respectively.

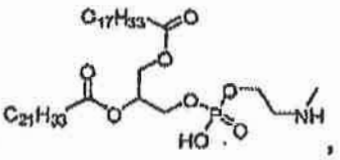
21. The method of claim 20 wherein the one or more than one metabolite is further characterized by the MS/MS fragmentation data as shown in Tables 34, 35, 38, 39, 40 or 28, respectively.

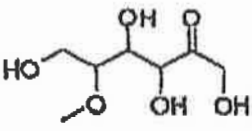
22. The method of claim 20 wherein the one or more than one metabolite is further characterized by the structure:

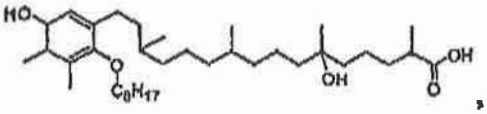
a) ,

b) ,

c) ,

d) ,

e) , or

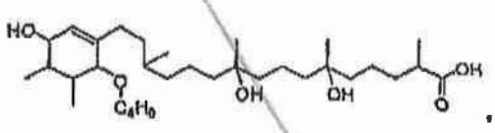
f) , respectively.

23. The method of claim 10 wherein the multiple sclerosis metabolite markers are relapsing-remitting as compared to a secondary-progressive reference sample and the metabolite markers comprise metabolites with accurate masses in Daltons of, or substantially equivalent to a) 540.4387 or b) 576.4757.

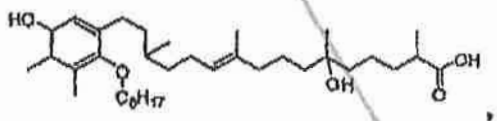
24. The method of claim 23 wherein the one or more than one metabolite is further characterized by molecular formula a) $C_{32}H_{60}O_6$ or b) $C_{36}H_{64}O_5$.

25. The method of claim 24 wherein the one or more than one metabolite is further characterized by the MS/MS fragmentation data as shown in Tables 26 or 27, respectively.

26. The method of claim 24 wherein the one or more than one metabolite is further characterized by the structure:

a) 

, or

b) 

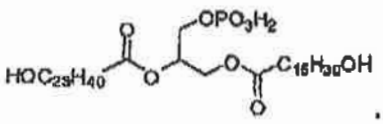
, respectively.

27. The method of claim 10, wherein the multiple sclerosis metabolite markers are relapsing-remitting transitioning to secondary-progressive as compared to a secondary-progressive reference sample and the metabolite markers comprise metabolites with accurate masses in Daltons of, or substantially equivalent to a) 786.5408.

28. The method of claim 27 wherein the one or more than one metabolite is further characterized by molecular formula a) $C_{43}H_{79}O_{10}P$.

29. The method of claim 28 wherein the one or more than one metabolite is further characterized by the MS/MS fragmentation data as shown in Table 32.

30. The method of claim 28 wherein the one or more than one metabolite is further characterized by the structure:

a) 

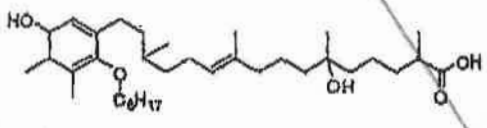
.

31. The method of claim 10 wherein the multiple sclerosis metabolite markers are relapsing-remitting transitioning to secondary-progressive as compared to a relapsing-remitting reference sample and the metabolite markers comprise metabolites with accurate masses in Daltons of, or substantially equivalent to a) 576.4757 or b) 578.4923.

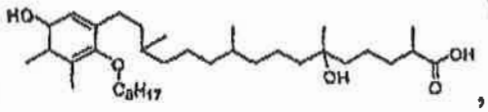
32. The method of claim 31 wherein the one or more than one metabolite is further characterized by molecular formula a) $C_{36}H_{64}O_5$ or b) $C_{36}H_{66}O_5$, respectively.

33. The method of claim 32 wherein the one or more than one metabolite is further characterized by the MS/MS fragmentation data as shown in Tables 27 or 28, respectively.

34. The method of claim 32 wherein the one or more than one metabolite is further characterized by the structure:

a) 

, or

b) 

, respectively.

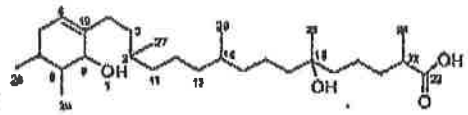
35. A compound selected from the group consisting of the metabolites with accurate masses measured in Daltons of, or substantially equivalent to, a) 452.3868, b) 496.4157, c) 524.4448, d) 540.4387, e) 576.4757, f) 578.4923, g) 580.5089, h) 594.4848, i) 596.5012, j) 786.5408 k) 216.04, l) 541.3415, m) 565.3391, n) 202.0453, o) 244.0559 p) 428.3653, and s) 857.7516.

36. The compound of claim 35 further characterized by molecular formula a) $C_{28}H_{52}O_4$, b) $C_{30}H_{56}O_5$, c) $C_{32}H_{60}O_5$, d) $C_{32}H_{60}O_6$, e) $C_{36}H_{64}O_5$, f) $C_{36}H_{66}O_5$, g) $C_{36}H_{68}O_5$, h) $C_{36}H_{66}O_6$, i) $C_{36}H_{68}O_6$, j) $C_{43}H_{79}O_{10}P$, k) $C_5H_{13}O_7P$, l) $C_{28}H_{52}NO_9P$, m) $C_{27}H_{52}NO_9P$ n) $C_6H_{11}O_6Na$, o) $C_8H_{13}O_7Na$, p) $C_{29}H_{48}O_2$, , s) $C_{54}H_{99}NO_6$, respectively.

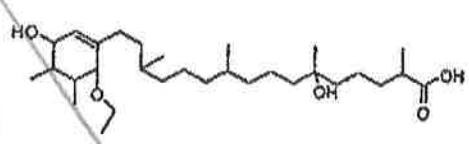
37. The compound of claim 36, further characterized by the MS/MS fragmentation data as shown in Tables 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, or 41, respectively.

38. The compound of claim 36, further characterized by the structure:

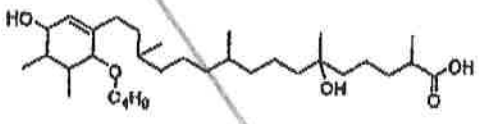
a)



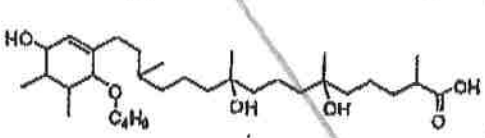
b)



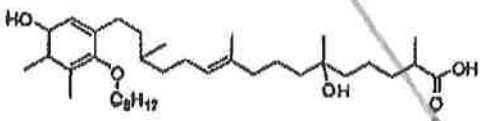
c)



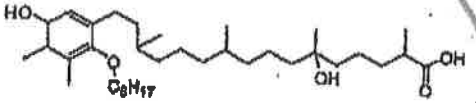
d)



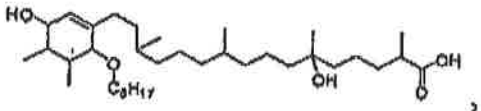
e)



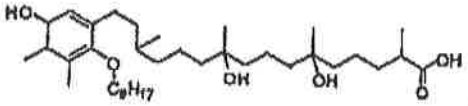
f)



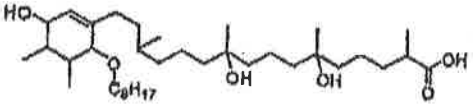
g)



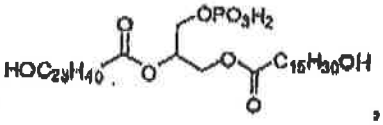
h)



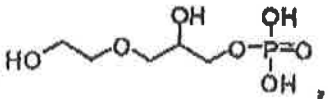
i)

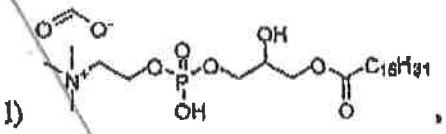


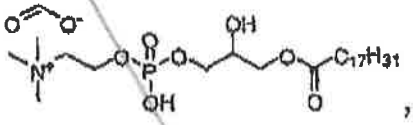
j)

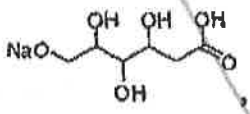


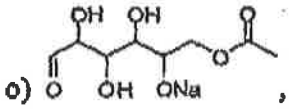
k)

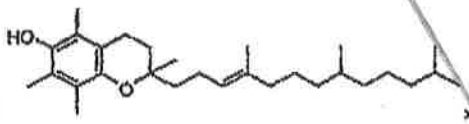


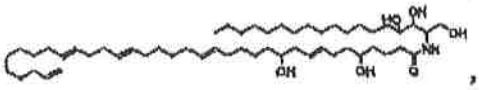
l) ,

m) ,

n) ,

o) ,

p) , or

s) , respectively.

39. A use of one or more than one compound as defined in any one of claims 35 to 38 for the diagnosis of multiple sclerosis or another demyelinating disorder.

WHAT IS CLAIMED:

1. A method for diagnosing a patient's multiple sclerosis health state, or change in multiple sclerosis health state, or for diagnosing another demyelinating disorder, or for diagnosing the risk of multiple sclerosis or another demyelinating disorder in a patient, the method comprising the steps of:

a) analyzing a blood sample from said patient to obtain quantifying data for one or more than one metabolite marker;

b) comparing the quantifying data for said one or more than one metabolite marker to corresponding data obtained from one or more than one reference sample to identify an increase or decrease in the level of said one or more than one metabolite marker in said sample; and

c) using said increase or decrease in the level of said one or more than one metabolite marker in said sample to diagnose said patient's multiple sclerosis health state, or change in multiple sclerosis health state, or for diagnosing another demyelinating disorder, or for diagnosing the risk of multiple sclerosis or another demyelinating disorder,

wherein the one or more than one metabolite marker comprises one or more molecule selected from the molecular formulae consisting of $C_{28}H_{52}O_4$, $C_{30}H_{56}O_5$, $C_{32}H_{60}O_5$, $C_{32}H_{60}O_6$, $C_{36}H_{64}O_5$, $C_{36}H_{66}O_5$, $C_{36}H_{68}O_5$, $C_{36}H_{66}O_6$, $C_{36}H_{68}O_6$, $C_{43}H_{79}O_{10}P$, $C_5H_{13}O_7P$, $C_{25}H_{52}NO_9P$, $C_{27}H_{52}NO_9P$, $C_6H_{11}O_6Na$, $C_8H_{13}O_7Na$, $C_{29}H_{48}O_2$, $C_{46}H_{80}NO_8P$, $C_7H_{14}O_6$ and $C_{54}H_{99}NO_6$,

the metabolite having the molecular formula of $C_{28}H_{52}O_4$ being characterized by a collision induced dissociation (CID) MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 451, 433, 407, 389, 281, 279, 183, 169, 153, 139, 125, 111 and 97,

the metabolite having the molecular formula of $C_{30}H_{56}O_5$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 495, 477, 451, 433, 415, 307, 297, 279, 235, 223, 215, 197, 179, 181, 169, 157, 155, 153, 141, 139, 127, 125 and 113,

the metabolite having the molecular formula of $C_{32}H_{60}O_5$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 523, 505, 487, 479, 463, 461, 443, 365, 337, 299, 297,

281, 279, 271, 269, 253, 251, 243, 225, 197, 171, 169, 157, 155, 143, 141, 139, 127, 125, 123, 115, 113, 111 and 83,

the metabolite having the molecular formula of $C_{32}H_{60}O_6$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 539, 521, 503, 495, 477, 461, 459, 419, 335, 315, 313, 297, 279, 259, 255, 253, 243, 241, 225, 223, 213, 179, 171, 155, 141 and 127,

the metabolite having the molecular formula of $C_{36}H_{64}O_5$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 575, 557, 539, 531, 513, 495, 417, 403, 371, 297, 279, 251 and 183,

the metabolite having the molecular formula of $C_{36}H_{66}O_5$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 577, 559, 541, 533, 515, 497, 419, 405, 387, 373, 297, 281 and 279,

the metabolite having the molecular formula of $C_{36}H_{68}O_5$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 579, 561, 543, 535, 517, 499, 421, 407, 389, 375, 299, 297, 281, 279, 263, 253, 185 and 171,

the metabolite having the molecular formula of $C_{36}H_{66}O_6$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 593, 575, 557, 549, 531, 513, 495, 421, 371, 315, 297, 279, 201, 171, 141 and 127,

the metabolite having the molecular formula of $C_{36}H_{68}O_6$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 595, 577, 559, 551, 515, 497, 423, 373, 315, 297, 281, 279, 269, 251, 171, 155, 153, 141, 139 and 127,

the metabolite having the molecular formula of $C_{43}H_{79}O_{10}P$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 785, 529, 425, 169 and 97,

the metabolite having the molecular formula of $C_5H_{13}O_7P$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 215, 197, 171, 153 and 135,

the metabolite having the molecular formula of $C_{25}H_{52}NO_9P$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 540, 480, 255, 242, 224, 168, 153 and 79,

the metabolite having the molecular formula of $C_{27}H_{52}NO_9P$ being characterized by a CID MS/MS fragmentation pattern under negative ionization comprising the following daughter ions: 564, 504, 279, 242, 224, 168, 153 and 79,

the metabolite having the molecular formula of $C_6H_{11}O_6Na$ being characterized by a CID MS/MS fragmentation pattern under positive ionization comprising the following daughter ions: 203, 159, 115, 89 and 97,

the metabolite having the molecular formula of $C_8H_{13}O_7Na$ being characterized by a CID MS/MS fragmentation pattern under positive ionization comprising the following daughter ions: 245, 227, 209, 191, 155, 125 and 83,

the metabolite having the molecular formula of $C_{29}H_{48}O_2$ being characterized by a CID MS/MS fragmentation pattern under positive ionization comprising the following daughter ions: 429, 205 and 165,

the metabolite having the molecular formula of $C_{46}H_{80}NO_8P$ being characterized by a CID MS/MS fragmentation pattern under positive ionization comprising the following daughter ions: 806, 478, 237 and 184,

the metabolite having the molecular formula of $C_7H_{14}O_6$ being characterized by a CID MS/MS fragmentation pattern under positive ionization comprising the following daughter ions: 195, 177, 165, 163, 138 and 123, and

the metabolite having the molecular formula of $C_{54}H_{99}NO_6$ being characterized by a CID MS/MS fragmentation pattern under positive ionization comprising the following daughter ions: 858, 602, 576, 314, 165, 151 and 95.

2. The method of claim 1, wherein the multiple sclerosis metabolite markers are relapsing-remitting as compared to a normal reference sample and are selected from the molecular formulae consisting of a) $C_{30}H_{56}0_5$, b) $C_{32}H_{60}O_5$, c) $C_{32}H_{60}O_6$, d) $C_{36}H_{68}O_5$, e) $C_{36}H_{66}O_6$, f) $C_{36}H_{68}O_6$, and g) $C_{36}H_{66}O_5$, including combinations thereof.

3. The method of claim 2, wherein the samples are analyzed by MS/MS transition and one or more daughter ions are selected for:

a) $C_{30}H_{56}O_5$ selected from 495, 477, 451, 433, 415, 307, 297, 279, 235, 223, 215, 197, 179, 181, 169, 157, 155, 153, 141, 139, 127, 125 and 113;

b) $C_{32}H_{60}O_5$ selected from 523, 505, 487, 479, 463, 461, 443, 365, 337, 299, 297, 281, 279, 271, 269, 253, 251, 243, 225, 197, 171, 169, 157, 155, 143, 141, 139, 127, 125, 123, 115, 113, 111 and 83;

c) $C_{32}H_{60}O_6$ selected from 539, 521, 503, 495, 477, 461, 459, 419, 335, 315, 313, 297, 279, 259, 255, 253, 243, 241, 225, 223, 213, 179, 171, 155, 141 and 127;

d) $C_{36}H_{68}O_5$ selected from: 579, 561, 543, 535, 517, 499, 421, 407, 389, 375, 299, 297, 281, 279, 263, 253, 185 and 171;

e) $C_{36}H_{66}O_6$ selected from 593, 575, 557, 549, 531, 513, 495, 421, 371, 315, 297, 279, 201, 171, 141 and 127;

f) $C_{36}H_{68}O_6$ selected from 595, 577, 559, 551, 515, 497, 423, 373, 315, 297, 281, 279, 269, 251, 171, 155, 153, 141, 139 and 127; or

g) $C_{36}H_{66}O_5$ selected from 577, 559, 541, 533, 515, 497, 419, 405, 387, 373, 297, 281 and 279.

4. The method of claim 1, wherein the multiple sclerosis metabolite markers are primary-progressive as compared to a normal reference sample and are selected from the molecular formulae consisting of a) $C_5H_{13}O_7P$, b) $C_6H_{11}O_6Na$, c) $C_8H_{13}O_7Na$, and d) $C_{54}H_{99}NO_6$, including combinations thereof.

5. The method of claim 4, wherein the samples are analyzed by MS/MS transition and one or more daughter ions are selected for:

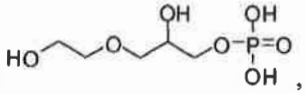
a) $C_5H_{13}O_7P$ selected from 215, 197, 171, 153 and 135;

b) $C_6H_{11}O_6Na$ selected from 203, 159, 115, 89 and 97;

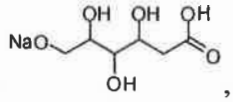
c) $C_8H_{13}O_7Na$ selected from 245, 227, 209, 191, 155, 125 and 83; or

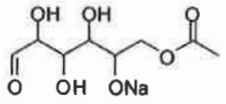
d) $C_{54}H_{99}NO_6$ selected from 858, 602, 576, 314, 165, 151 and 95.

6. The method of claim 4 or 5, wherein the one or more than one metabolite is further characterized by the structure

a) 

,

b)  , or a non sodium adduct thereof, or

c)  a non sodium adduct thereof.

7. The method of claim 1, wherein the multiple sclerosis metabolite markers are secondary-progressive as compared to a normal reference sample and are selected from the molecular formulae consisting of a) $C_{25}H_{52}NO_9P$, b) $C_{27}H_{52}NO_9P$, c) $C_{29}H_{48}O_2$, d) $C_{48}H_{80}NO_8P$, e) $C_7H_{14}O_6$, and f) $C_{36}H_{66}O_5$.

8. The method of claim 7, wherein the samples are analyzed by MS/MS transition and one or more daughter ions are selected for:

a) $C_{25}H_{52}NO_9P$ selected from 540, 480, 255, 242, 224, 168, 153 and 79;

b) $C_{27}H_{52}NO_9P$ selected from 564, 504, 279, 242, 224, 168, 153 and 79;

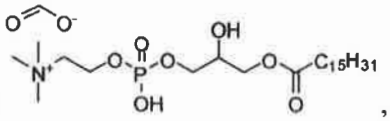
c) $C_{29}H_{48}O_2$ selected from 429, 205 and 165;

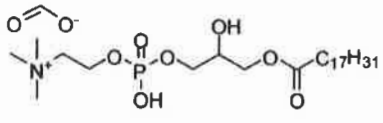
d) $C_{46}H_{80}NO_8P$ selected from 806, 478, 237 and 184;

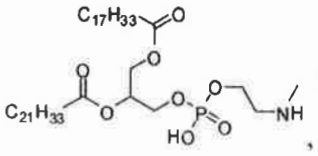
e) $C_7H_{14}O_6$ selected from 195, 177, 165, 163, 138 and 123; or

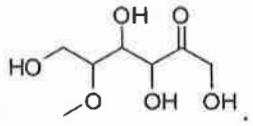
f) $C_{36}H_{66}O_5$ selected from 577, 559, 541, 533, 515, 497, 419, 405, 387, 373, 297, 281 and 279.

9. The method of claim 7 or 8, wherein the one or more than one metabolite is further characterized by the structure:

a)  , or a non formate adduct thereof,

b)  , or a non formate adduct thereof,

d)  , or

e) 

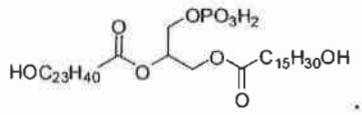
10. The method of claim 1, wherein the multiple sclerosis metabolite markers are relapsing-remitting as compared to a secondary-progressive reference sample and are selected from the molecular formulae consisting of a) $C_{32}H_{60}O_6$, and b) $C_{36}H_{64}O_5$, including combinations thereof.

11. The method of claim 2, wherein the samples are analyzed by MS/MS transition and one or more daughter ions are selected for:
a) $C_{32}H_{60}O_6$ selected from 539, 521, 503, 495, 477, 461, 459, 419, 335, 315, 313, 297, 279, 259, 255, 253, 243, 241, 225, 223, 213, 179, 171, 155, 141 and 127; or
b) $C_{36}H_{64}O_5$ selected from 575, 557, 539, 531, 513, 495, 417, 403, 371, 297, 279, 251 and 183.

12. The method of claim 1, wherein the multiple sclerosis metabolite markers are relapsing-remitting transitioning to secondary-progressive as compared to a secondary-progressive reference sample and comprise the molecular formula of a) $C_{43}H_{79}O_{10}P$.

13. The method of claim 12, wherein the samples are analyzed by MS/MS transition and one or more daughter ions are selected for the metabolite having the molecular formula of a) $C_{43}H_{79}O_{10}P$ selected from 785, 529, 425, 169 and 97.

14. The method of claim 12 or 13, wherein the metabolite is further characterized by the structure

a) 

15. The method of claim 1, wherein the multiple sclerosis metabolite markers are relapsing-remitting transitioning to secondary-progressive as compared to a relapsing-remitting reference sample and are selected from the molecular formulae consisting of a) $C_{36}H_{64}O_5$, and b) $C_{36}H_{66}O_5$, including combinations thereof.

16. The method of claim 15, wherein the samples are analyzed by MS/MS transition and one or more daughter ions are selected for:

a) $C_{36}H_{64}O_5$ selected from 575, 557, 539, 531, 513, 495, 417, 403, 371, 297, 279, 251 and 183; or

b) $C_{36}H_{66}O_5$ selected from 577, 559, 541, 533, 515, 497, 419, 405, 387, 373, 297, 281 and 279.

17. The method of claim 1, wherein the increase or decrease in the level of said one or more than one metabolite marker in said sample is identified in the comparing step (b) using a colorimetric chemical assay, an antibody-based enzyme-linked immunosorbant assay (ELISA), a dipstick chemical assay, or a mass spectrometry-based system.

18. The method of any one of claims 1 to 17, wherein the sample is whole blood, plasma, serum, or a subfraction of whole blood.

19. The method of any one of claims 1 to 18, wherein said one or more than one reference sample is a plurality of samples obtained from control individuals; one or more than one baseline sample obtained from the patient at an earlier date; or a combination thereof.

20. A method for diagnosing a patient's multiple sclerosis health state, or change in multiple sclerosis health state, or for diagnosing another demyelinating disorder, or for diagnosing the risk of multiple sclerosis or another demyelinating disorder in a patient, the method comprising the steps of:

a) analyzing a blood sample from said patient by high resolution mass spectrometry to obtain accurate mass intensity data;

b) comparing the accurate mass intensity data to corresponding data obtained from one or more than one reference sample to identify an increase or decrease in accurate mass intensity; and

c) using said increase or decrease in accurate mass intensity to diagnose said patient's multiple sclerosis health state, or change in multiple sclerosis health state, or for diagnosing another demyelinating disorder or for diagnosing the risk of multiple sclerosis or another demyelinating disorder,

wherein the accurate mass intensity is measured at or ± 5 ppm of a hydrogen and electron adjusted accurate mass or neutral accurate mass in Daltons selected from the group consisting of: 161.1051, 174.1411, 181.9806, 188.0143, 188.1567, 194.0803, 200.1566, 202.0453, 202.1721, 203.1157, 205.8867, 207.8836, 209.8525, 211.8495, 214.1721, 216.04, 216.1877, 217.9124, 218.0192, 218.0371, 226.0688, 239.939, 243.0719, 244.0559, 244.2189, 246.1467, 246.1468, 246.1472, 246.2345, 249.9677, 253.8165, 255.8135, 256.24, 257.8106, 260.004, 260.2137, 263.8453, 264.9759, 265.8424, 267.811, 268.1287, 269.132, 269.8081, 271.8051, 273.8743, 273.9985, 274.1777, 274.1778, 275.1811, 275.8713, 277.8861, 278.1494, 280.2413, 281.2447, 282.1444, 282.2572, 283.2602, 290.1737, 296.1601, 296.2357, 297.1634, 303.108, 303.1081, 304.2398, 305.8792, 306.2568, 310.1758, 311.7754, 312.231, 314.2461, 318.1421, 326.1708, 327.0307, 328.2393, 328.2415, 331.957, 333.8302, 333.9539, 340.2407, 345.8738, 364.3123, 366.3284, 367.3325, 368.1656, 374.2613, 376.2759, 377.2801, 378.2921, 378.9906, 379.2536, 379.2957, 380.3079, 381.311, 382.1084, 384.3399, 385.3428, 392.294, 428.3653, 432.2365, 432.3252, 438.3354, 440.3526, 446.2525, 446.341, 447.3433, 448.3194, 448.3562, 450.3729, 452.3868, 460.2681, 462.3346, 462.3716, 464.3524, 466.3656, 467.3711, 468.3577, 468.384, 469.3863, 474.2846, 474.3731, 476.3869, 477.3218, 478.4044, 480.3473, 482.3604, 484.3788, 488.2996, 490.3676, 492.3832, 493.385, 494.3968, 495.3321, 495.3322, 495.4018, 496.4157, 501.3217, 502.3165, 502.4054, 503.3194, 504.4188, 506.2853, 506.4338, 508.3782, 510.3937, 512.4079, 513.4116, 517.3141, 518.3969, 519.3322, 519.3998, 520.4131, 521.3478, 521.4188, 522.4313, 523.3637, 523.4337, 524.296, 524.4448, 530.4379, 532.1851, 532.4503, 534.3912, 534.4645, 536.41, 537.4142, 538.4257, 539.4274, 539.4286, 540.4387, 541.3141, 541.3415, 541.4422, 542.3447, 544.3636, 546.3413, 546.4298, 548.4438, 550.4602, 550.4954, 551.4646, 551.4976, 551.4991, 552.3273, 552.4784, 552.5008, 555.3102, 556.4497, 557.4527, 558.3761, 558.4649, 558.4663, 559.4688, 560.478, 560.4821, 561.4863, 562.4989, 563.5013, 564.4396, 564.513, 565.3391, 566.3431, 566.454, 567.3547, 568.4723, 569.3687, 569.4769, 570.4903, 572.4455, 574.4594, 574.4635, 574.4958, 575.4628, 576.4757, 576.4765, 577.4795, 578.4923, 579.4958, 580.5089, 581.5126, 584.2641, 590.4585, 590.4964, 591.4614, 592.4717, 593.4736, 594.4848, 594.4875, 595.4883, 595.4928, 596.5012, 596.5053, 597.5062, 597.5068, 598.5107, 606.4872, 610.3691, 610.482, 610.5204, 611.3724, 612.4994, 613.3404, 616.4675, 617.0921, 618.4834, 622.4973, 623.5003,

632.5038, 633.3232, 634.3951, 646.5702, 648.5861, 649.5895, 662.4267, 684.6037, 686.4879, 687.4916, 688.5048, 689.5083, 693.631, 694.6323, 702.4175, 708.4632, 712.5074, 713.5097, 715.5228, 716.4323, 716.4987, 718.4736, 720.4696, 722.479, 723.6395, 726.5438, 729.5727, 730.4535, 731.5464, 733.501, 734.488, 734.508, 736.5031, 737.5045, 739.5146, 741.5302, 742.4745, 742.5366, 743.5461, 743.5475, 744.55, 744.5516, 745.5643, 746.5118, 746.5701, 747.5121, 747.5761, 757.5008, 758.4785, 760.5231, 761.529, 763.5153, 764.5196, 765.5316, 766.5051, 766.5372, 767.5473, 768.5468, 768.5525, 769.5638, 770.5108, 770.569, 772.5265, 775.5514, 779.5828, 780.5303, 780.5872, 781.5619, 781.6001, 783.6174, 784.5238, 784.6228, 785.5287, 786.51, 786.5408, 787.5452, 788.5549, 789.5658, 791.5488, 792.555, 793.4936, 793.5663, 794.5718, 804.5476, 805.5609, 806.5643, 808.5225, 809.5264, 813.5871, 816.5159, 819.5831, 820.589, 821.5288, 823.5427, 827.5445, 827.5446, 828.5477, 828.5479, 828.7213, 830.5634, 831.5758, 831.5992, 832.5211, 832.6022, 833.5931, 833.7541, 834.5372, 834.5963, 835.5417, 835.6094, 839.6019, 851.5686, 852.5724, 854.737, 855.6009, 855.6798, 856.6045, 856.7527, 872.6715, 886.5582, 886.7896, 899.5871, 1016.9279, 1017.9316, 1018.9399, 1228.1101, 1251.1042, 1253.1236 and 1254.1311, or any combination thereof.

21. The method of claim 20, wherein the blood sample is whole blood, plasma, serum, or a subfraction of whole blood.

22. The method claim 20 or 21, wherein a decrease in accurate mass intensity is identified in the comparing step (b).

23. The method claim 20 or 21, wherein an increase in accurate mass intensity is identified in the comparing step (b).

24. The method of any one of claims 20 to 23, wherein a liquid/liquid extraction is performed on the blood sample whereby non-polar metabolites are dissolved into an organic solvent and polar metabolites are dissolved into an aqueous solvent.

25. The method of claim 24, wherein the accurate mass intensity data is obtained using a Fourier Transform Ion Cyclotron Resonance, time of flight, magnetic sector, quadrupole or triple quadrupole mass spectrometer.

26. The method of claim 24, wherein accurate mass intensity data is obtained from the ionization of the extracted samples using an ionization method selected from the group consisting of: positive electrospray ionization, negative electrospray ionization, positive atmospheric pressure chemical ionization, and negative atmospheric pressure chemical ionization, or a combination thereof.

27. The method of any one of claims 20 to 26, wherein said one or more than one reference sample is a plurality of samples obtained from control individuals; one or more than one baseline sample obtained from the patient at an earlier date; or a combination thereof.

28. The method of any one of claims 20 to 27, wherein the increase or decrease in accurate mass intensity is used to diagnose:

relapsing-remitting as compared to a normal reference sample wherein the accurate mass intensity is measured at or ± 5 ppm of a hydrogen and electron adjusted accurate mass or neutral accurate mass in Daltons selected from the group consisting of: 188.0143, 202.0453, 205.8867, 207.8836, 209.8525, 211.8495, 218.0192, 243.0719, 244.0559, 246.1467, 249.9677, 253.8165, 255.8135, 256.24, 257.8106, 260.004, 263.8453, 265.8424, 267.811, 268.1287, 269.8081, 271.8051, 273.8743, 274.1778, 275.1811, 277.8861, 280.2413, 281.2447, 282.2572, 283.2602, 290.1737, 296.1601, 296.2357, 304.2398, 306.2568, 311.7754, 312.231, 314.2461, 318.1421, 327.0307, 328.2393, 333.8302, 333.9539, 345.8738, 364.3123, 366.3284, 367.3325, 374.2613, 376.2759, 377.2801, 378.2921, 378.9906, 379.2957, 380.3079, 381.311, 382.1084, 384.3399, 385.3428, 392.294, 428.3653, 432.3252, 438.3354, 440.3526, 446.2525, 446.341, 447.3433, 448.3194, 448.3562, 450.3729, 452.3868, 460.2681, 462.3346, 462.3716, 464.3524, 466.3656, 467.3711, 468.3577, 468.384, 469.3863, 474.2846, 474.3731, 476.3869, 478.4044, 480.3473, 482.3604, 484.3788, 488.2996, 490.3676, 492.3832, 493.385, 494.3968, 495.3322, 495.4018, 496.4157, 502.3165, 502.4054, 503.3194, 504.4188, 506.2853, 508.3782, 510.3937, 512.4079, 513.4116, 518.3969, 519.3998, 520.4131, 521.4188, 522.4313, 523.4337, 524.296, 524.4448, 530.4379, 532.4503, 534.3912, 534.4645, 536.41, 537.4142, 538.4257, 539.4274, 540.4387, 541.4422, 542.3447, 544.3636, 546.3413, 546.4298, 548.4438, 550.4602, 550.4954, 551.4646, 551.4976, 552.3273, 552.4784, 552.5008, 556.4497, 557.4527, 558.3761, 558.4649, 558.4663, 559.4688, 560.478, 562.4989, 563.5013, 564.4396,

564.513, 566.454, 568.4723, 569.4769, 570.4903, 572.4455, 574.4594, 574.4635, 575.4628, 576.4757, 576.4765, 577.4795, 578.4923, 579.4958, 580.5089, 581.5126, 590.4585, 591.4614, 592.4717, 593.4736, 594.4848, 594.4875, 595.4883, 595.4928, 596.5012, 596.5053, 597.5062, 597.5068, 598.5107, 610.3691, 610.482, 611.3724, 612.4994, 616.4675, 618.4834, 632.5038, 634.3951, 646.5702, 648.5861, 649.5895, 686.4879, 687.4916, 688.5048, 689.5083, 693.631, 694.6323, 702.4175, 708.4632, 712.5074, 713.5097, 715.5228, 716.4323, 722.479, 730.4535, 734.488, 736.5031, 737.5045, 739.5146, 741.5302, 742.5366, 743.5461, 743.5475, 744.55, 744.5516, 745.5643, 746.5701, 747.5761, 758.4785, 763.5153, 765.5316, 766.5051, 766.5372, 767.5473, 768.5525, 769.5638, 770.569, 775.5514, 781.5619, 781.6001, 789.5658, 791.5488, 792.555, 793.5663, 794.5718, 831.5992, 832.6022, 833.7541, 855.6009, 855.6798, 856.6045, 886.5582, 1016.9279, 1017.9316, 1018.9399, 1251.1042, 1253.1236 and 1254.1311 or a combination thereof,

primary-progressive as compared to a normal reference sample wherein the accurate mass intensity is measured at or ± 5 ppm of a hydrogen and electron adjusted accurate mass or neutral accurate mass in Daltons selected from the group consisting of: 161.1051, 188.0143, 202.0453, 203.1157, 216.04, 217.9124, 218.0192, 218.0371, 226.0688, 243.0719, 244.0559, 246.1467, 246.1472, 253.8165, 257.8106, 260.004, 263.8453, 268.1287, 269.132, 273.8743, 273.9985, 274.1778, 275.8713, 278.1494, 282.1444, 290.1737, 296.1601, 297.1634, 310.1758, 318.1421, 326.1708, 328.2393, 328.2415, 333.9539, 432.2365, 446.2525, 460.2681, 474.2846, 488.2996, 503.3194, 506.2853, 506.4338, 517.3141, 546.3413, 610.3691, 611.3724, 613.3404, 622.4973, 623.5003, 634.3951, 791.5488, 792.555, 793.4936, 819.5831, 827.5445, 828.5479, 831.5992, 832.6022, 899.5871, 1228.1101 or a combination thereof,

secondary-progressive as compared to a normal reference sample wherein the accurate mass intensity is measured at or ± 5 ppm of a hydrogen and electron adjusted accurate mass or neutral accurate mass in Daltons selected from the group consisting of: 194.0803, 202.0453, 243.0719, 244.0559, 246.1468, 249.9677, 253.8165, 255.8135, 311.7754, 312.231, 328.2393, 328.2415, 382.1084, 384.3399, 385.3428, 428.3653, 438.3354, 440.3526, 446.341, 448.3194, 448.3562, 464.3524, 466.3656, 467.3711, 468.3577, 468.384, 469.3863, 474.3731, 480.3473, 482.3604, 484.3788, 490.3676, 492.3832, 493.385, 494.3968, 495.3321, 495.4018, 508.3782, 510.3937, 512.4079, 513.4116, 518.3969, 519.3322, 519.3998, 520.4131, 521.3478, 521.4188,

522.4313, 523.3637, 523.4337, 534.3912, 536.41, 537.4142, 538.4257, 539.4274, 540.4387, 541.3141, 541.3415, 541.4422, 542.3447, 546.4298, 548.4438, 550.4602, 551.4646, 552.4784, 558.4663, 560.4821, 564.4396, 565.3391, 566.3431, 566.454, 568.4723, 569.3687, 569.4769, 574.4594, 574.4635, 575.4628, 576.4757, 576.4765, 577.4795, 578.4923, 579.4958, 580.5089, 590.4585, 590.4964, 592.4717, 593.4736, 594.4848, 594.4875, 595.4883, 595.4928, 596.5012, 596.5053, 597.5062, 597.5068, 598.5107, 606.4872, 610.482, 610.5204, 613.3404, 616.4675, 618.4834, 622.4973, 684.6037, 694.6323, 720.4696, 723.6395, 763.5153, 764.5196, 765.5316, 766.5372, 768.5468, 791.5488, 792.555, 793.4936, 805.5609, 806.5643, 819.5831, 820.589, 821.5288, 827.5446, 828.5477, 851.5686, 852.5724, 855.6798, 872.6715, 886.5582 and 1228.1101, or a combination thereof,

relapsing-remitting as compared to secondary-progressive wherein the accurate mass intensity is measured at or ± 5 ppm of a hydrogen and electron adjusted accurate mass or neutral accurate mass in Daltons selected from the group consisting of: 194.0803, 264.9759, 274.1777, 327.0307, 340.2407, 366.3284, 368.1656, 378.9906, 428.3653, 438.3354, 440.3526, 446.341, 447.3433, 448.3562, 450.3729, 452.3868, 462.3346, 462.3716, 464.3524, 466.3656, 467.3711, 468.384, 469.3863, 474.3731, 476.3869, 477.3218, 478.4044, 480.3473, 482.3604, 484.3788, 490.3676, 492.3832, 493.385, 494.3968, 495.4018, 496.4157, 501.3217, 502.4054, 504.4188, 506.4338, 508.3782, 510.3937, 512.4079, 513.4116, 518.3969, 519.3998, 520.4131, 521.4188, 522.4313, 523.4337, 524.4448, 530.4379, 532.1851, 532.4503, 534.3912, 534.4645, 536.41, 537.4142, 538.4257, 539.4274, 539.4286, 540.4387, 541.3141, 541.4422, 546.4298, 548.4438, 550.4602, 551.4646, 551.4991, 552.4784, 556.4497, 557.4527, 558.4649, 558.4663, 559.4688, 560.4821, 561.4863, 562.4989, 563.5013, 564.4396, 564.513, 566.454, 568.4723, 569.4769, 570.4903, 572.4455, 574.4594, 574.4635, 575.4628, 576.4757, 576.4765, 577.4795, 578.4923, 579.4958, 580.5089, 581.5126, 590.4585, 590.4964, 591.4614, 592.4717, 593.4736, 594.4848, 594.4875, 595.4883, 595.4928, 596.5012, 596.5053, 597.5062, 597.5068, 598.5107, 606.4872, 610.482, 610.5204, 612.4994, 616.4675, 618.4834, 632.5038, 634.3951, 646.5702, 662.4267, 729.5727, 780.5303, 786.51, 793.4936, 805.5609, 806.5643, 821.5288, 833.5931, 834.5963, 835.6094, 851.5686, 852.5724, 856.6045, 872.6715 and 886.7896, or a combination thereof,

relapsing-remitting transiting to secondary-progressive as compared to relapsing-remitting wherein the accurate mass intensity is measured at or ± 5 ppm of a hydrogen and electron adjusted accurate mass or neutral accurate mass in Daltons selected from the group consisting of: 174.1411, 181.9806, 188.1567, 200.1566, 202.1721, 214.1721, 216.1877, 239.939, 244.2189, 246.2345, 260.2137, 277.8861, 303.108, 327.0307, 331.957, 333.9539, 345.8738, 378.9906, 384.3399, 438.3354, 440.3526, 446.341, 447.3433, 448.3562, 450.3729, 452.3868, 462.3346, 462.3716, 464.3524, 466.3656, 467.3711, 468.384, 469.3863, 474.3731, 476.3869, 478.4044, 480.3473, 482.3604, 484.3788, 490.3676, 492.3832, 493.385, 494.3968, 495.4018, 496.4157, 502.4054, 504.4188, 506.4338, 508.3782, 510.3937, 512.4079, 513.4116, 518.3969, 519.3998, 520.4131, 521.4188, 522.4313, 523.4337, 524.4448, 530.4379, 532.4503, 534.3912, 534.4645, 536.41, 537.4142, 538.4257, 539.4274, 540.4387, 541.3141, 541.4422, 546.3413, 546.4298, 548.4438, 550.4602, 551.4646, 552.4784, 556.4497, 557.4527, 558.4649, 558.4663, 559.4688, 560.478, 560.4821, 561.4863, 562.4989, 563.5013, 564.4396, 564.513, 566.454, 568.4723, 569.4769, 570.4903, 572.4455, 574.4594, 574.4635, 575.4628, 576.4757, 576.4765, 577.4795, 578.4923, 579.4958, 580.5089, 581.5126, 584.2641, 590.4585, 590.4964, 591.4614, 592.4717, 593.4736, 594.4848, 594.4875, 595.4883, 595.4928, 596.5012, 596.5053, 597.5062, 597.5068, 598.5107, 610.482, 610.5204, 612.4994, 616.4675, 618.4834, 718.4736, 726.5438, 731.5464, 743.5475, 744.55, 747.5121, 779.5828, 780.5872, 781.6001, 783.6174, 784.6228, 793.4936, 804.5476, 813.5871, 816.5159, 821.5288, 823.5427, 828.5477, 830.5634, 831.5758, 832.5211, 834.5372, 834.5963, 835.5417 and 839.6019, or a combination thereof, and

relapsing-remitting transiting to secondary-progressive as compared to secondary-progressive wherein the accurate mass intensity is measured at or ± 5 ppm of a hydrogen and electron adjusted accurate mass or neutral accurate mass in Daltons selected from the group consisting of: 239.939, 246.1468, 249.9677, 303.1081, 305.8792, 331.957, 333.9539, 379.2536, 541.3141, 555.3102, 565.3391, 566.3431, 567.3547, 574.4958, 617.0921, 633.3232, 684.6037, 716.4987, 718.4736, 733.501, 734.508, 742.4745, 746.5118, 747.5121, 757.5008, 760.5231, 761.529, 770.5108, 772.5265, 783.6174, 784.5238, 784.6228, 785.5287, 786.5408, 787.5452, 788.5549, 808.5225, 809.5264, 828.7213, 854.737, 856.7527 and 872.6715, or a combination thereof.