Supplemental Fig S5: Annotated spectra for peptide spectrum matches identified based on MVH score in the colorectal cancer study.
sample: TCGA−A6−3807−01A, spectrum: 60863
AAAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=39.2847
p−value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 40146
AAPSVTLFPPSSEELQANK, T2A
MVH=49.8487
p−value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 143487
ACNVLQSSHLEDYPFDAEY, N16D
MVH=29.2490
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 11442
AGVETTTPSK, K7T
MVH=59.1995
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 49174
APSQHLSSFDPCFYR, R5H
MVH=51.8049
p-value=0.0001
sample: TCGA−A6−3807−01A, spectrum: 151516
AQQNLSWEELTK, A11T
MVH=48.0058
p−value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 152200
ASSSLLLNESEPTTNLQLR, D8N
MVH=63.7950
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 38687
ATAECLQHPWLNS, R8Q
MVH=22.4037
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 94924
ATSNLTQENLPTLFVESVLEVHGK, M10I
MVH=38.9029
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 115171
AVDVVLDCFLVK, A11V
MVH=58.8872
p–value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 16366
AWLSSQAAELER, V7A
MVH=51.1678
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 115508
CDPGALVLPFSGALELKL, Y1C
MVH=59.7595
p−value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 144864
DCGEAAQWLTSFLK, T6A
MVH=60.5922
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 18775
DFYVVEPLAFEGTPEQK, I4V
MVH=40.9231
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 140432
DGYGFLNR, N1D
MVH=39.4116
p-value=0.0006
sample: TCGA-A6-3807-01A, spectrum: 56238
DLTTGYDSSQPNKK, V2I
MVH=19.6183
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 60353
DVPGLQSQSGGPQPAVWHR, N11S
MVH=27.3292
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 121982
DVTVLQNTDGNNNDWA9K, E14D
MVH=61.9126
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 78159
ECPCVHNNDLYSSSAK, G14S
MVH=25.1665
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 90221
EHTLHLEAELEK, S4L
MVH=36.8478
p-value=0.0002
sample: TCGA–A6–3807–01A, spectrum: 69289
ELVDDSLNNVR, V7I
MVH=54.9703
p–value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 142006
EQPGSPEWLQLDK, Q13K
MVH=21.2340
p-value=0.0001
sample: TCGA−A6−3807−01A, spectrum: 51701
ESALEPGPVPEAPAGGPVHAVTVVTLEK, R6P
MVH=36.6716
p−value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 6751
FFGSLPDSWAR, S11R
MVH=37.1168
p-value=0.0001
sample: TCGA−A6−3807−01A, spectrum: 68998
FLDKLPQQTGDR, H12R
MVH=43.6212
p−value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 19362
FNKPFVFLMLDQNTK, E11D
MVH=59.4932
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 82652
FNLSQESSYLATQYSLRPR, S2N
MVH=27.3716
p−value=0.0002
sample: TCGA–A6–3807–01A, spectrum: 152047
FNSVTELCAELPEQK, V11I
MVH=39.5203
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 88135
FQTATVTEK, I3T
MVH=27.9440
p-value=0.0012
sample: TCGA-A6-3807-01A, spectrum: 118551
FTVGDHSR, I3V
MVH=40.3168
p-value=0.0003
sample: TCGA−A6−3807−01A, spectrum: 72389
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK,A9G
MVH=57.7321
p−value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 58948
GALQFVTHYQQSSTQR, H11Q
MVH=51.0320
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 6839
GFGTDEQALLDCLGSCSNK, R16C
MVH=58.8265
p–value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 5644
GLCVSENELVGGSQWK, P2L
MVH=77.3499
p-value=0.0001
sample: TCGA−A6−3807−01A, spectrum: 50509
GQTGALLQNTVESLSK, D9N
MVH=68.1979
p−value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 27004
GVAGSSVAVLCPYNR, G5S
MVH=57.6998
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 102851
KKPSEEEAAAAAGPPGPGPQVNPLPVTDEVV, V10A
MVH=40.2504
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 62100
LATGSDDNCVAFFEGPPFK, A10V
MVH=47.7349
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 92195
LCLDAMHGVVGPYVK, R2C
MVH=35.7304
p-value=0.0001
sample: TCGA−A6−3807−01A, spectrum: 40330
LFEEDPAVGALVLTGGDK, T1I
MVH=75.0482
p−value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 3033
LHGHLYTPGQELTNDCK, E17K
MVH=86.6852
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 19856
LLNLLADLVER, R4L
MVH=56.1915
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 133754
LLSDLPPPSTGFQEAQSR, S5L
MVH=38.1729
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 88811
LQELTPSSGDGEHPASTHK, P4L
MVH=65.1847
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 125445
LSDLQEQALDQALNHVR, Y14H
MVH=51.6341
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 6065
LSTEVDLTNVDLSTVSDKQSLAPK, G6D
MVH=33.2229
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 132006
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=34.2640
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 16091
MQYAPNTQVELLPQGR, H16R
MVH=47.1073
p–value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 25628
MVAVGLCR, H8R
MVH=37.0630
p-value=0.0006
sample: TCGA–A6–3807–01A, spectrum: 93714
NEGATYAAALLFR, V11I
MVH=67.8278
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 125017
NEVLWHPTLNPLSPQGTyr, A3V
MVH=35.7508
p-value=0.0001
sample: TCGA−A6−3807−01A, spectrum: 40269
NPLLDLAAYDQEGR, R3L
MVH=48.1908
p−value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 79307
NTNSVPETAPAALPETR, K17R
MVH=38.9131
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 23496
QMPSGPTKPSEGPAK, T2M
MVH=22.5570
p–value=0.0003
sample: TCGA–A6–3807–01A, spectrum: 68955
QQHEGAQGALDSGEPPPLCR, Q17L
MVH=34.9326
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 130921
QTVQVDEHARPQTTLEQLQK, M3V
MVH=50.7018
p-value=0.0001
sample: TCGA−A6−3807−01A, spectrum: 92174
QVTASTFVKPLFSR, A2V
MVH=28.0711
p−value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 153322
SAVGELSEDSSNVVHLK, Q15H
MVH=44.4566
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 41751
SELPLDPLPLPTEEGNPLLK, V10L
MVH=50.1007
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 59674
SFDMYSGDVMHLVK, A1S
MVH=26.1091
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 51858
SFQGPVLLGSSHGGVNLEDVAAETPEALLK, S24T
MVH=36.8281
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 19781
SGGTLVLVGLGSEMTTVPLLHAALR, N4T
MVH=34.9729
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 68061
SPADPTDLGGQTSPR, I6T
MVH=58.7409
p-value=0.0009
sample: TCGA-A6-3807-01A, spectrum: 23254
SSSYSGEYGSGGGK, G10S
MVH=63.0392
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 23180
SSSYSGEYGSGGGKR, G10S
MVH=52.7313
p-value=0.0002
sample: TCGA-A6-3807-01A, spectrum: 99268
TTPLEAASSGAR, T11A
$MVH=35.5995$
$p$-value=$0.0001$
sample: TCGA–A6–3807–01A, spectrum: 83947
TVEDLDGLLQQL YR, H10Q
MVH=61.9215
p−value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 39507
TVVQLEGDNKLVTAFK, T14A
MVH=64.7184
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 98225
VLGTAGTEEGQK, I1V
MVH=50.1946
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 6980
VPGFADDPTELACQVVDK, R14Q
MVH=47.6179
p–value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 66226
VPVTQATR, L3V
MVH=39.3747
p–value=0.0012
sample: TCGA–A6–3807–01A, spectrum: 5541
VQFCPFEENVEST, K8E
MVH=46.8152
p–value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 115439
VQLPTESLQELLDLHR, T7S
MVH=37.7016
p-value=0.0001
sample: TCGA–A6–3807–01A, spectrum: 135006
VQVLAAGLLSEMKA, D11E
MVH=49.4804
p−value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 154624
VVLQPEALFSLYSK, F8L
MVH=56.9589
p-value=0.0001
sample: TCGA-A6-3807-01A, spectrum: 71246
YVSLLYTNYEAGKDDYVK, I2V
MVH=30.5202
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 52337
AAPSVTLFPPSSEELQANK, T2A
MVH=53.5284
p-value=0.0001
sample: TCGA−A6−3808−01A, spectrum: 10907
AGVETTTPSK, K7T
MVH=53.4093
p−value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 10660
AGVETTTPSKQSNNK, K7T
MVH=33.0763
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 61764
ALFMDGCLHAR, T4M
MVH=43.2606
p−value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 163627
ASSSLLLNESEPTTNLQLR, D8N
MVH=49.9051
p–value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 75990
AVEVATVVLQPTVLR, S12T
MVH=41.7771
p−value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 121668
CDPGALVLPFSGAELK, Y1C
MVH=49.8501
p-value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 18483
DFYVVEPLAFEGTPEQK, I4V
MVH = 61.9913
p-value = 0.0001
sample: TCGA-A6-3808-01A, spectrum: 150330
DGYGFLNR, N1D
MVH=39.5191
p-value=0.0006
sample: TCGA–A6–3808–01A, spectrum: 37950
DTEEEDFHVDQATTVK, V12A
MVH=57.3931
p−value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 107065
ECTSLCCEALTCK, N4S
MVH=41.5554
p-value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 16028
EPSAPSLPTPAYQSLPAGGHAPTPPTPAPR, S15L
MVH=30.2254
p-value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 54024
ESALEPGPVPEAPAGGPVHAVTVVTLEK, R6P
MVH=26.1909
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 72539
FLDKLPQQTGDR, H12R
MVH=50.0488
p-value=0.0001
sample: TCGA−A6−3808−01A, spectrum: 76328
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=61.4728
p−value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 96998
FYLGPGTTSVR, I9V
MVH=51.5907
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 35926
GEAGAAGPAGPAGPQGSPGER, R15Q
MVH=55.6296
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 164692
GGTLSTPQTGSENDALYEYL, G5S
MVH=48.6420
p–value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 140361
GKWERPFEVKDTEEEDFHVDQATTVK, V22A
MVH=65.1258
p–value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 27155
GVAGSSVAVLCPYNR, G5S
MVH=41.7771
p-value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 38155
KALFMDGCLHAR, T5M
MVH=40.0666
p-value=0.0002
sample: TCGA–A6–3808–01A, spectrum: 73425
KENVATTDTLESTTVGSSV, T17S
MVH=48.8750
p−value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 109399
KKPSEEEAAAGGPPGQPQVNPLPVTDEVV: V10A
MVH=50.9780
p−value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 137459
KSVEEYANCHLAR, P2S
MVH=77.4779
p−value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 64412
LADGGAGGTFQPYPYLTLR, V1L
MVH=58.9472
p-value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 41583
LFEEDPAVGALVLTGGDK, T1I
MVH=68.9613
p-value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 19157
LLNLLADLVER, R4L
MVH=54.4926
p-value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 131229
LLSDLLPPSTGTFQEAQSR, S5L
MVH=43.7105
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 132240
LSDLQEALDQALNHVR, Y14H
MVH=60.1478
p–value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 111754
LTGSSVEMLQDVLDMK, R2T
MVH=50.5460
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 15888
MQYAPNTQVELLPQGR, H16R
MVH=53.0540
p-value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 25701
MVAVGLCR, H8R
MVH=41.6761
p-value=0.0006
sample: TCGA–A6–3808–01A, spectrum: 140180
NDYATMLPDSTELNQDTLNR, D14N
MVH=51.2363
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 84156
NTNSVPETAPAALPETR, K17R
MVH=30.5266
p-value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 31238
SALSGHLETLLLGLLK, V10L
MVH=45.1387
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 164886
SAVGELEDSSNVVHLLK, Q15H
MVH=62.4835
p–value=0.0001
sample: TCGA-A6-3808-01A, spectrum: 126800
SVEEYANCHLAR, P1S
MVH=62.2009
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 71139
TYGQVSGEALK, D2Y
MVH=45.0342
p–value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 103878
VLSTTNAER, D6N
MVH=33.5326
p−value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 132372
VPLASQGLGPGSTVLLVVDKCDEPLNLLVR, S26N
MVH=62.4399
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 69212
VPVTQATR, L3V
MVH=39.0125
p-value=0.0012
sample: TCGA–A6–3808–01A, spectrum: 121603
VQLPTESLQELLDLHR, T7S
MVH=62.4723
p-value=0.0001
sample: TCGA–A6–3808–01A, spectrum: 49688
VWQTVSPVESR, G10S
MVH=36.0998
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 52415
AAAAAAAAAAAAAAATATTAATTAATAAQA, P17A
MVH=45.9949
p–value=0.0001
sample: TCGA−A6−3810−01A, spectrum: 67338
AAAPAPVSEAVSR, C12S
MVH=50.8813
p−value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 43394
AAPSVTLFPPSEELQANK, T2A
MVH=54.3045
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 10080
AGVETTTPSK, K7T
MVH=61.0953
p−value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 36173
ALEDVFDALEGK, M5V
MVH=55.5759
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 80463
APPRPGPVPEAAQPFLFTTR, P19T
MVH=56.2981
p–value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 136452
ASSSLLNSEEPTTNLQLR, D8N
MVH=34.1284
p−value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 100442
CDPGALVLPFSGLK, Y1C
MVH=36.5994
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 16634
DFYVVEPLAFEGTPEQK, I4V
MVH=44.8720
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 124647
DGYFLRN, N1D
MVH=40.5540
p-value=0.0006
sample: TCGA–A6–3810–01A, spectrum: 31984
DTEEEDFHVDQATTVK, V12A
MVH=42.4141
p–value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 61230
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=30.1600
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 45359
EALDVLDAVLK, G7D
MVH=45.0342
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 89352
EELGHQLNDLTSLENDK, M10L
MVH=33.8606
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 126287
EQPGSPEWLQLDK, Q13K
MVH=23.1680
p–value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 53863
ESALEPGPVPEAPAGGPVHAVTVTLEK, R6P
MVH=34.5912
p-value=0.0001
sample: TCGA−A6−3810−01A, spectrum: 59888
FADVFAK, E7K
MVH=35.6397
p−value=0.0084
sample: TCGA−A6−3810−01A, spectrum: 6044
FFGSLPDSWAR, S11R
MVH=31.9733
p−value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 17138
FNKPFVFLMLDQNTK, E11D
MVH=51.7311
p-value=0.0001
sample: TCGA−A6−3810−01A, spectrum: 75709
FQTATVTEK, I3T
MVH=29.9433
p−value=0.0024
sample: TCGA–A6–3810–01A, spectrum: 102549
FTVGDHSR, I3V
MVH=36.7271
p−value=0.0003
sample: TCGA–A6–3810–01A, spectrum: 71442
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=54.4838
p–value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 78573
FYLGAGPTSVR, I9V
MVH=48.2574
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 6158
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-A6-3810-01A, spectrum: 23886
GVAGSSVAVLCPYNR, G5S
MVH=24.5710
p-value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 113368
KSVEEYANCHLAR, P2S
MVH=56.2646
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 52712
LADGGAGGTFQPYLDTLR, V1L
MVH=36.8666
p-value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 2698
LALQPGTVGPQGR, V3I
MVH=56.6159
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 35015
LFEEDPAVGALVLTGGDK, T1I
MVH=87.4640
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 138897
LLDTAFDLDLFK, V10I
MVH=76.2131
p−value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 17561
LLNLLADLVER, R4L
MVH=50.2256
p-value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 16014
LQPEDMFVYDLNEK, C9Y
MVH=27.9439
p-value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 109541
LSDLQEALDQALNHVR, Y14H
MVH=50.6346
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 51270
LTLQALTEK, A2T
MVH=49.4017
p−value=0.0005
sample: TCGA–A6–3810–01A, spectrum: 12821
MAQWGNKPLC, V9I
MVH=38.6963
p-value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 14458
MQYAPNTQVELLPQGR, H16R
MVH=70.4520
p-value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 50649
MVDFAGMK, V7M
MVH=29.7478
p-value=0.0006
sample: TCGA–A6–3810–01A, spectrum: 118403
NEVLWHPTLNLPSPQGTVR, A3V
MVH=39.7079
p–value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 34971
NPLLDLAAYDQEGR, R3L
MVH=53.2529
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 68206
NTNSVPETAPAALPETR, K17R
MVH=33.8932
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 62143
QGTLTEYCTSLMSLPTK, G9S
MVH=43.2359
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 137440
SAVGELSEDSSNVVHLLK, Q15H
MVH=46.3390
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 36340
SELPLDPLPLPTEEGNPLLK, V10L
MVH=38.2215
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 45337
SFQGPVLLGSSHGGVNLEDVAAETPEALLK, S24T
MVH=28.4060
p–value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 85684
SLNDLTAR, K8R
MVH=40.0313
p-value=0.0006
sample: TCGA–A6–3810–01A, spectrum: 72199
SNPNWLLPDSVDWR, R5W
MVH=19.3496
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 58112
SPADPTDLGGQTSPR, I6T
MVH=58.7409
p-value=0.0009
sample: TCGA-A6-3810-01A, spectrum: 104413
SVEEYANCHLAR, P1S
MVH=52.0724
p-value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 52187
SVMDDTQLAGLNCLR, A5T
MVH=48.6627
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 85592
TTPLEAASSGAR, T11A
MVH=49.9422
p-value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 54411
TVASPGVSVEEAVEQLDLLGGVTLLR, T8S
MVH=32.1781
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 72708
TVEDLDGLLQQL YR, H10Q
MVH=62.7789
p–value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 17509
VLFPGCTPPAYLLDGLVR, C11Y
MVH=27.7670
p−value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 60667
VLLDG\text{VQNL}R, P9L
MVH=65.5417
p-value=0.0001
sample: TCGA-A6-3810-01A, spectrum: 65619
VPVTQATR, L3V
MVH=37.6992
p-value=0.0012
sample: TCGA-A6-3810-01A, spectrum: 100376
VQLPTESLQELDLHR, T7S
MVH=45.4061
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 7258
VVLQPEALFSLYSK, F8L
MVH=61.5789
p-value=0.0001
sample: TCGA–A6–3810–01A, spectrum: 41282
VWQTVSPVESR, G10S
MVH=35.3294
p−value=0.0001
sample: TCGA−AA−3518−01A, spectrum: 55672
AAAAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=51.1795
p−value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 71260
AAAPAPVSEAVSR, C12S
MVH=58.3994
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 46012
AAPSVTLPSSSEELQANK, T2A
MVH=60.5202
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 133672
ACNVLQSSHLEDYPFDAQY, N16D
MVH=45.4144
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 10520
AGVETTTPSK, K7T
MVH=48.7461
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 69660
ALDRPYTSK, E3D
MVH=31.4084
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 62995
ALFMDCLHAR, T4M
MVH=30.8075
p-value=0.0004
sample: TCGA-AA-3518-01A, spectrum: 14125
ANPQLGAYAPPHPVSLGR, I14V
MVH=28.6067
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 142072
ASSSLLLNESEPTTNLQLR, D8N
MVH=49.7273
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 118953
AVLTLDDK, E7K
MVH=37.9092
p-value=0.0006
sample: TCGA–AA–3518–01A, spectrum: 17661
AVPPNNSNAEDDLPTVELQGLVPR, V22L
MVH=30.1962
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 105236
AVMTPVPLFSEQ, K12E
MVH=31.7541
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 106539
CDPGALVLPFSGAELK, Y1C
MVH=58.7606
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 135403
CSGLQVLFSPLEEEVK, A3G
MVH=43.3929
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 17573
DFYVVEPLAFEGTPEQK, I4V
MVH=71.6133
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 120986
DGYGFLNR, N1D
MVH=41.3881
p–value=0.0006
sample: TCGA–AA–3518–01A, spectrum: 32959
DTEEEDFHVDQATTVK, V12A
MVH=39.2997
p–value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 46654
DVGLPLCQALVEAK, E14K
MVH=39.9972
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 54992
DVPGFLQSQSSGPGQPAVWHR, N11S
MVH=35.4765
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 112258
DVTVLQNTDGNNNDAWAK, E14D
MVH=71.1584
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 47690
EALDVLDAVLK, G7D
MVH=52.6904
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 120910
ELGSLDVQQR, Q10R
MVH=28.7178
p-value=0.0004
sample: TCGA-AA-3518-01A, spectrum: 62571
ELVDDSLNNVR, V7I
MVH=49.1254
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 132218
EQPGSPEWLQLDK, Q13K
MVH=38.2081
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 47417
ESALEPGPVEAPAGGPVHAVTVVLLEK, R6P
MVH=38.3825
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 131896
EVAQQAVDADVHAVGVSTLAAGHK, I16V
MVH=49.0154
p-value=0.0002
sample: TCGA–AA–3518–01A, spectrum: 7003
FFGSLPDSWAR, S11R
MVH=36.7688
p–value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 8055
FGQDLLSPLLSVR, K13R
MVH=52.5457
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 62287
FLDKLPQQTGDR, H12R
MVH=51.7176
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 114207
FLQENVFVAANHNASPLSLK, G14A
MVH=38.2285
p-value=0.0001
Sample: TCGA-AA-3518-01A, spectrum: 72944
FLSGHTSELGNFR, D11N
MVH=46.4580
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 75803
FNLSQESSYLATQYSLRPR, S2N
MVH=30.2303
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 18882
FSLDALLTNVLFEK, I10V
MVH=45.9608
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 108661
FTVGDHSR, I3V
MVH=41.2423
p-value=0.0003
sample: TCGA-AA-3518-01A, spectrum: 83246
FYLGPTSVR, I9V
MVH=51.5907
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 7006
GFGTDEQALLDCLGSCSNK, R16C
MVH=77.5366
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 7149
GLLDDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-3518-01A, spectrum: 46170
GQTGALLQNTVESLSK, D9N
MVH=61.1319
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 24534
GVAGSSVAVLCPYNR, G5S
MVH=51.8261
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 103963
KKPSEEEAAAAAGGPPGPGQVNPLPVTDEVV→V10A
MVH=57.3401
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 8017
LEGLLEGLGLR, G6E
MVH=59.8084
p-value=0.0006
sample: TCGA-AA-3518-01A, spectrum: 36585
LFEEDPAVGALVLTGGDK, T1I
MVH=82.3445
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 28495
LLNLLADLVER, R4L
MVH=58.2884
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 124062
LLSDLLPPSTGTFQEAQSR, S5L
MVH=51.4589
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 100898
LQQQHSEQPPLQPSPVTTR, M17T
MVH=57.1689
p-value=0.0001
Sample: TCGA-AA-3518-01A, spectrum: 87001
LSVTWPEGDELLPNELRPAGTPLGALR, V16I
MVH=43.1484
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 144396
LTLVPVYTSPQLDMSCLLQQNK, A4V
MVH=70.5428
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 86486
LTQAQLFDYSELPNFPR, G10S
MVH=52.0074
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 15020
MQYAPNTQVELLPQGR, H16R
MVH=77.1163
p-value=0.0001
Sample: TCGA-AA-3518-01A, spectrum: 22975
MVAVGLCR, H8R
MVH=44.3044
p-value=0.0006
sample: TCGA-AA-3518-01A, spectrum: 36498
NPLLIDLAAYDQEGR, R3L
MVH=65.1266
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 72269
NTNSVPETAPAALPETR, K17R
MVH=46.3159
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 32700
PVAEYWNSQK, D2V
MVH=45.6743
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 17337
RAVPPNNSNAEDDLPTVELQGLVPR, V23L
MVH=41.9363
p−value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 143079
SAVGELEDSSNVVHLLK, Q15H
MVH=44.9181
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 38112
SELPLDPLPLPTEEGNPLLK, V10L
MVH=58.0563
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 85210
SGTPQLSLPFAAR, R7S
MVH=27.3843
p-value=0.0004
sample: TCGA–AA–3518–01A, spectrum: 18479
SLSAFLVPMPTPGTLTGK, G1S
MVH=34.8040
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 100808
SPPGAAAPAAAKPPPLSAK, S8P
MVH=40.0083
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 52775
SQNKEDYDGLKEEFR, A8D
MVH=68.6983
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 62000
SQNKEDYDGLKEEFRK, A8D
MVH=86.5181
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 20572
SSSYSGEYGSGGGKR, G10S
MVH=39.0132
p−value=0.0002
sample: TCGA-AA-3518-01A, spectrum: 38167  
SVVSDVPEELDFLVPK, A3V  
MVH=55.3268  
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 56642
TLDPFETMLK, S2L
MVH=30.9765
p-value=0.0002
sample: TCGA-AA-3518-01A, spectrum: 57861
TVASPGVSVEAEVEQLDLGGVTLLR, T8S
MVH=52.9199
p−value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 77333
TVEDLDGLLQQL YR, H10Q
MVH=65.3603
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 35708
TVVQLEGDNKLVTAFK, T14A
MVH=51.6345
p-value=0.0001
sample: TCGA−AA−3518−01A, spectrum: 59473
VPVTQATR, L3V
MVH=45.4462
p−value=0.0012
sample: TCGA-AA-3518-01A, spectrum: 106457
VQLPTESLQELLDLHR, T7S
MVH=42.1514
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 125310
VQVLAAQLLEMK, D11E
MVH=55.2739
p–value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 144407
VVLQPEALFSLYSK, F8L
MVH=77.1405
p-value=0.0001
sample: TCGA–AA–3518–01A, spectrum: 133666
WWVADSNVFTK, E11K
MVH=52.9082
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 139202
YFHNQEEFVR, L9V
MVH=43.0225
p-value=0.0001
sample: TCGA-AA-3518-01A, spectrum: 64633
YVSLLYTNYEAGKDDYVK, I2V
MVH=28.9063
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 5881
AAAAAAAAAPAAAATAATTAATAATAAQ, P17A
MVH=42.5994
p-value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 135895
AAPSVTLFPPSSEELQANK, T2A
MVH=48.0235
p–value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 42870
AGVETTTPSK, K7T
MVH=45.8469
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 127603
ALEDVFDALEGK, M5V
MVH=58.8872
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 56273
ALSSVSSPQSPGDALR, A5V
MVH=44.2677
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 58594
APWLEQERPEYWDQETR, G8R
MVH=77.6273
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 60266
ASLEAALADAEQHGLALK, R13H
MVH=69.9222
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 87351
ASSSLLLNESEPTTNLQLR, D8N
MVH=53.3880
p-value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 96415
AWLSSQAAELER, V7A
MVH=50.5872
p−value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 147216
DFNHLDEVLSSLLGK, N6D
MVH=48.8596
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 107643
DFYVVEPLAFEGTPEQK, I4V
MVH=47.2989
p-value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 56738
DGYGFLNR, N1D
MVH=43.8062
p-value=0.0006
sample: TCGA-AA-3525-01A, spectrum: 97215
DSKEPFSSVELQAALSK, E3K
MVH=47.0731
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 74680
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=89.3795
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 85207
eq DTEEEDFHVDQATTVK, V12A
MVH=27.4013
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 32423
EASQGSSASSAPQSVK, H13Q
MVH=32.5277
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 116773
ELAPYDDNWFYTR, E7D
MVH=41.5554
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 113406
ELVDDSLNNVR, V7I
MVH=49.1254
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 58427
EQPGSPEWLQLDK, Q13K
MVH=26.2924
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 7300
ESALEEPGPVPEAPAGGPVHAVTVTLEK, R6P
MVH=26.3868
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 57177
ETLNNSALSAQLR, K4N
MVH=45.3892
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 12520
FLDKLPQQTGDR, H12R
MVH=38.4148
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 98899
FLGQLLTAFPALR, A3G
MVH=45.1846
p-value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 86064
FTQNEFNLESK, R3Q
MVH=52.6518
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 16372
FVSSSSSGGGYYGGVLTASDGLLAGNEK, A9G, MVH=71.3799
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 97708
GFGTDEQALLDCLGSCSNK, R16C
MVH=63.5642
p-value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 57963
GKWERPFEVKDTEEDFHVDQATTVK, V22A
MVH=69.5907
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 88533
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-3525-01A, spectrum: 146345
GQTGALLQNTVESLSK, D9N
MVH=53.8603
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 14876
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=67.9848
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 120831
KADLLNR, V5I
MVH=41.4826
p-value=0.0044
sample: TCGA-AA-3525-01A, spectrum: 15181
KKPSEEEAAAAAGGPPGGPQVNPLPVTDEVV11V10A
MVH=35.7027
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 6351
LADGGGAGGTFQPYLDTLR, V1L
MVH=43.5624
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 76811
LDSTDFTSTLK, G8S
MVH=45.0323
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 136245
LFEEDPAVGALVLTGGDK, T1I
MVH=63.6788
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 98858
LFSLLSTALLR, V8A
MVH=48.3676
p-value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 60968
LLNLLADLVER, R4L
MVH=56.2209
p–value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 103268
LLNNTDNLVR, E6D
MVH=49.7672
p-value=0.0002
sample: TCGA–AA–3525–01A, spectrum: 38750
LLSDLPPSTGTFQEAQSR, S5L
MVH=36.3920
p−value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 38490
LPDQLVLLYMK, D9Y
MVH=38.4866
p-value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 141927
LQELTPSSGDPEHDPASTHK, P4L
MVH=41.8274
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 34716
LQQQHSEQPPLQPSPVTTR, M17T
MVH=42.3006
p-value=0.0001
sample: TCGA−AA−3525−01A, spectrum: 57406
NLPSLAEGASDPPTVASR, K7E
MVH=77.0161
p−value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 132745
NTNSVPETAPAALPETR, K17R
MVH=41.9507
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 14690
NTVLATWQPYSTSK, T11S
MVH=39.3106
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 67865
QLAQAYEVLSDAK, S3A
MVH=39.4032
p-value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 46302
QTVQVDEHARPQTTLEQLQKM3V
MVH=25.9423
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 79088
SAVGELSEDSSNVVHLKK, Q15H
MVH=52.1481
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 58924
SEALPTDLPTPSAPDLTEPK, A10T
MVH=48.1714
p-value=0.0001
sample: TCGA–AA–3525–01A, spectrum: 6314
SLSLLDSPGLLSGEK, V4I
MVH=44.3163
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 112168
SPADPTDLGGQTSPR, I6T
MVH=58.7409
p-value=0.0009
sample: TCGA-AA-3525-01A, spectrum: 53686
SSSYSGEYGSGGGK, G10S
MVH=46.4733
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 101882
STESLQTNVQR, A7T
MVH=53.6827
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 111714
TSLSAPPNTSSTENPK, S9T
MVH=35.2278
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 140255
VLSTTNAER, D6N
MVH=38.2967
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 78593
VPSFETAEGLGAELK, T12A
MVH=41.7771
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 110479
VPVTQATR, L3V
MVH=39.7386
p-value=0.0012
Sample: TCGA-AA-3525-01A, spectrum: 40159
VSADLGAEAGLQQLLGALR, P2S
MVH=87.5162
p-value=0.0001
sample: TCGA-AA-3525-01A, spectrum: 9982
VVGACGVGK, R5C
MVH=31.4911
p-value=0.0014
sample: TCGA-AA-3525-01A, spectrum: 34979
YPVDTLPTSK, I3V
MVH=38.9130
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 51789
AAPSVTLPSSSEELQANK, T2A
MVH=49.3604
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 14619
AFSEYLGTDQSK, G4E
MVH=54.7958
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 11287
AGVETTTPSK, K7T
MVH=51.7009
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 51050
APSQHLSSFDPCFYR, R5H
MVH=49.8981
p–value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 159712
ASSSLLLNESEPTTTNLQLR, D8N
MVH=55.1674
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 85945
AVEVATVVLQPTVLR, S12T
MVH=45.3610
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 7000
AVGEPMRPLAECCQLGLGLCDQVDDADLRR, P27A
MVH=51.8858
p−value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 18882
AVPPNNSNAEDDLPTVELQGLVPR, V22L
MVH=32.8798
p–value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 16444
AWLSSQAAELER, V7A
MVH=62.8426
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 151612
CSGLLQVLFSPLEEEVK, A3G
MVH=43.4511
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 82545
DAGNEQDLGLQYK, N1D
MVH=42.7213
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 18853
DFYVVEPLAFEGTPEQK, I4V
MVH=59.6361
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 146892
DGYGFLNR, N1D
MVH=43.2774
p-value=0.0006
sample: TCGA–AA–3529–01A, spectrum: 36180
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=79.3124
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 37390
DTEEEDFHVDQATTVK, V12A
MVH=63.9162
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 73774
DVPGFLQSQSSGPGQPAVWHRN11S
MVH=35.3594
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 53529
EALDVLDIVALK, G7D
MVH=57.1244
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 107080
EELGHLQNDLTSLENDK, M10L
MVH=32.8251
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 83001
EHTLHLEAELEK, S4L
MVH=35.8189
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 71393
ELVDDSLNNVR, V7I
MVH=49.1254
p−value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 148763
EQPGSPEWLQLDK, Q13K
MVH=24.6418
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 64336
ESALEPGPVPEAPAGGPVHAVTVTLEK, R6P
MVH=34.9716
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 72226
FADVFAK, E7K
MVH=35.6403
p-value=0.0084
sample: TCGA-AA-3529-01A, spectrum: 6956
FFGSLPDSWAR, S11R
MVH=41.1282
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 71177
FLDKLPQQTGDR, H12R
MVH=45.1069
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 53822
FLGQLLTAFPALR, A3G
MVH=35.7507
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 72074
FLSLESDR, G6S
MVH=27.7231
p-value=0.0012
sample: TCGA-AA-3529-01A, spectrum: 16135
FPGPCDYNFASDCR, L4P
MVH=50.1006
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 19731
FSLDALLTNVLPFEK, I10V
MVH=30.9741
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 123465
FTVGDHSR, l3V
MVH=38.1607
p−value=0.0003
sample: TCGA-AA-3529-01A, spectrum: 94807
FYLGGPTSVR, I9V
MVH=48.2574
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 6785
GFGTDEQALLDCLGSCSNK, R16C
MVH=57.6097
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 52361
GQTGALLQNTVESLSK, D9N
MVH=53.4113
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 27196
GVAGSSVAVLCPYNR, G5S
MVH=44.5977
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 129837
HLAVLNGAMVSTPHYPGGLLEK, V9M
MVH=70.4586
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 130457
HVGSSETNLLQHLLEACGR, K8N
MVH=51.8892
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 3088
KAFSEYLGTDQSK, G5E
MVH=70.9323
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 19562
KFSLDALLTNVLPFEK, I11V
MVH=40.1263
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 117990
KKPSEEEAAAAGGPQGVNPLPVTDEVV V10A
MVH=42.6529
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 29796
LALLLMASQEPQR, T2A
MVH=53.1326
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 145571
LCNNPAPQFGGK, T6A
MVH=54.3813
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 158272
LDSTDFTSTLK, G8S
MVH=45.0323
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 41198
LFEEDPAVGLVLVTGGDK, T1I
MVH=83.3876
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 53774
LFSLLSTALLR, V8A
MVH=67.0168
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 134296
LGGLQPSQDR, G7S
MVH=34.3336
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 49603
LHVLVEPDHFK, Q2H
MVH=67.7586
p-value=0.0002
sample: TCGA-AA-3529-01A, spectrum: 31100
LLNLLADLVER, R4L
MVH=53.1193
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 38599
LLTQDEGPALVPGSR, G14S
MVH=40.7966
p–value=0.0001
sample: TCGA−AA−3529−01A, spectrum: 92285
LQELTPSSGDPGEHDPASTHK, P4L
MVH=41.3805
p−value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 125389
LQQQHSEQPPLQPSPVTTR, M17T
MVH=49.3823
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 130750
LSDLQEALDQALNHVR, Y14H
MVH=53.0023
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 16267
LTPVSAQFDLEGK, L8F
MVH=33.7107
p–value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 84760
MKDVPGLQSQSSGPGQPAVWHR, N13S
MVH=72.1946
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 16219
MQYAPNTQVELLPQGR, H16R
MVH=60.5486
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 37217
MVAVGLCR, H8R
MVH=39.8859
p-value=0.0006
sample: TCGA–AA–3529–01A, spectrum: 52813
NPGAVNACHLSCSALLQDNLADAVACAK, T1N
MVH=61.9849
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 41086
NPLLDLAAYDQEGR, R3L
MVH=61.9215
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 82505
NTNSVPETAPAALPETR, K17R
MVH=36.8621
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 146744
NVSPVALPR, N3S
MVH=33.7419
p-value=0.0002
sample: TCGA–AA–3529–01A, spectrum: 37223
PVAEYWNSQK, D2V
MVH=42.1554
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 107135
QVTSTASTFVKPLFSR, A2V
MVH=28.9710
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 7729
RLELLEGLGLR, G7E
MVH=48.1416
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 31270  
SALSGHLETLLLGLLK, V10L  
MVH=81.9512  
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 160783
SAVGELSEDSSNVVHLLK, Q15H
MVH=59.1530
p−value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 63972
SDPVTLNVL YGPDVPTLSPSK, G14V
MVH=46.5426
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 149285
SEALPTDLPTPSAPDLTEPK, A10T
MVH=50.6658
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 19499
SGGTLVLVGLGSEMTTVPLLHAALR-N4T
MVH=33.5375
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 103121
SLNDLTAR, K8R
MVH=37.4255
p-value=0.0006
sample: TCGA-AA-3529-01A, spectrum: 69915
SPADPTDLGGQTSPR, I6T
MVH=56.9878
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 114665
SPPGAAAPAAAKPPPLSAK, S8P
MVH=33.3954
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 159480
SPVGSGAPQAAAPAAHVAGNPGGDAAPAATGTAAASLAAAAGSEDAAEKK, T42A
MVH=65.6252
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 22941
SSSYGSEYGGGGK, G10S
MVH=59.1285
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 22781
SSSYSGEYGSGGGKR, G10S
MVH=53.2129
p-value=0.0002
sample: TCGA–AA–3529–01A, spectrum: 87312
TVEDLDGLQQL YR, H10Q
MVH=59.6703
p−value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 51768
TVVQLEGDNKLVTAFK, T14A
MVH=46.7772
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 69827
TYGQVSGEALK, D2Y
MVH=46.5440
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 160214
VPSFETAEGLGAELK, T12A
MVH=60.9367
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 67849
VPVTQATR, L3V
MVH=41.3881
p-value=0.0012
sample: TCGA–AA–3529–01A, spectrum: 120194
VQLPTESLQELDLHR, T7S
MVH=66.1329
p–value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 112533
VVGACGVGK, R5C
MVH=31.5316
p-value=0.0042

m/z

Intensity(%)
sample: TCGA-AA-3529-01A, spectrum: 7942
VVLQPEALFSLYSK, F8L
MVH=56.5665
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 38527
VYGDLLEYTPAK, H7Y
MVH=26.2121
p-value=0.0001
sample: TCGA-AA-3529-01A, spectrum: 95725
YVSLLYTYEAGK, I2V
MVH=45.3578
p-value=0.0001
sample: TCGA–AA–3529–01A, spectrum: 73785
YVSLLYTNYEAGKDDYVK, l2V
MVH=66.4643
p−value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 77301
AAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=61.1643
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 57134
AAPSVTLPSPSSEELQANK, T2A
MVH=54.4562
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 7412
AEEEQAGSAPGAGGTATK, S14G
MVH=28.4218
p−value=0.0005
sample: TCGA-AA-3531-01A, spectrum: 6462
AETSLGLPSPSELSTEVK, G9S
MVH=25.2604
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 10429
AGVETTTPSK, K7T
MVH=54.4897
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 126949
ALSFNFGYAK, N3S
MVH=31.0278
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 18204
APFAAPLPFAELVLPPQQ, S7L
MVH=29.5968
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 62448
ASGVQLEAK, A4V
MVH=41.8945
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 128549
AVDVVLDCFLVK, A11V
MVH=52.7174
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 25141
AWLSSQALEL, V7A
MVH=56.3703
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 128745
CDPGALVLPFSGALELK, Y1C
MVH=39.8523
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 62116
CPAAPPPPAGGAANNHGAGSGAGGR, G1C
MVH=37.0959
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 84104
DAGNEQDLGLQYK, N1D
MVH=44.6038
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 27337
DFYVVEPLAFEGTPEQK, I4V
MVH=56.2359
p–value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 144061
DGYGFLNR, N1D
MVH=44.2130
p-value=0.0006
sample: TCGA-AA-3531-01A, spectrum: 14997
DTCVQSPFLSSFPR, C13R
MVH=48.9165
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 43571
DTEEEDFHVDQATTVK, V12A
MVH=55.6542
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 114278
DVDGLTSLNAGR, K12R
MVH=50.5858
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 134125
DVQEFLNNPK, D7N
MVH=38.4267
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 125028
DVTVLQNTDGNNNDWAK, E14D
MVH=42.2454
p–value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 10457
EASQGSSASSAPQSVK, H13Q
MVH=36.9418
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 74553
ELVDDSLNNVR, V7I
MVH=50.7540
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 25081
EPSAPSLPTPAYQSLPAGGHAPTPPTPAPR, S15L
MVH=26.7637
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 146095
EQPGSPEWLQLDK, Q13K
MVH=41.1892
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 85130
FADVFAK, E7K
MVH=36.3336
p-value=0.0084
sample: TCGA-AA-3531-01A, spectrum: 107518
FGLQAQLVTTDFQK, M7L
MVH=58.5724
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 5740
FNSVTELCAELPEQK, V11I
MVH=34.2662
p-value=0.0001
sample: TCGA−AA−3531−01A, spectrum: 66598
FPASVPTGAQDLLSK, M7T
MVH=56.0821
p−value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 121112
FTVGDHSR, I3V
MVH=27.1628
p-value=0.0006
sample: TCGA-AA-3531-01A, spectrum: 87912
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=35.5433
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 105571
FYLGPTSVR, I9V
MVH=47.0405
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 52031
GAQEKPQLSAAQSTQPQK, R3Q
MVH=49.5073
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 16783
GFGTDEQALLDCLGSCSNK, R16C
MVH=62.1648
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 67713
GQTGALLQNTVESLSK, D9N
MVH=64.2610
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 44955
GVAGSSVAVLCPYNR, G5S
MVH = 33.5777
p-value = 0.0001
sample: TCGA-AA-3531-01A, spectrum: 116729
KKPSEEEAAAAGGPPGGPQVNLPVTDEVV-V10A
MVH=51.1151
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 20297
KTGSPGSPGASGVQSTAK, G11S
MVH=46.8340
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 142781
LCNNPAPQFGGK, T6A
MVH=53.7890
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 4425
LDSTDFSTSLK, G8S
MVH=55.5252
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 47323
LFEEDPAVGALVLTGGDK, T1I
MVH=77.5599
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 87529
LGLTPEGQSYLDQFR, V3I
MVH=50.3630
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 147550
LLSDLLPPSTGFQEAQSR, S5L
MVH=53.1353
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 102956
LPAEPLTR, E3A
MVH=31.5660
p-value=0.0025
sample: TCGA-AA-3531-01A, spectrum: 92845
LQELTPSSGDPGEHDPASTHK, P4L
MVH=35.0519
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 123212
LQQQHSEQPPLQPSPVTTR, M17T
MVH=55.0881
p–value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 97459
LSVFSTLDAPVAPSDK, V7I
MVH=46.7226
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 24976
LTPVSAQFQDLEGK, L8F
MVH=51.2588
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 95585
LVDGLVLTK, I2V
MVH=39.0635
p-value=0.0005
sample: TCGA-AA-3531-01A, spectrum: 16220
LVTDYTLEADAALQK, E11D
MVH=66.7074
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 35131
MQYAPNTQVELLPQGR, H16R
MVH=46.1031
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 136202
NDYATMLPDSTELNQDTLNR, D14N
MVH=63.5890
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 57803
NPLLDLAAYDQEGR, R3L
MVH=55.1354
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 52096
NSLSETVR, M3L
MVH=38.4978
p-value=0.0006
sample: TCGA-AA-3531-01A, spectrum: 20588
NSTLSEPGRSGR, P4L
MVH=46.0209
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 84050
NTNSVPETAPAALPETR, K17R
MVH=45.4375
p–value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 95612
SAGLAPDCEASATAETTVSSVGCEAAK, G28A
MVH=42.2219
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 146696
SEALPTDLPTPSAPDLTEPK, A10T
MVH=57.1417
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 48437
SELPPLDPLPLPTEEGNPLLK, V10L
MVH=54.5545
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 67705
SLSLLDSPGLLSGEK, V4I
MVH=55.2863
p-value=0.0001
sample: TCGA--AA--3531--01A, spectrum: 73149
SPADPTDLGGQTSPR, I6T
MVH=57.2048
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 113223
SPPGAAAPAAAKPPPLSAK, S8P
MVH=44.6179
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 47111
SSTTSTWELLDPR, Q12P
MVH=35.4211
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 62562
STESLQTNVQR, A7T
MVH=57.4316
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 58959
SVVSDVPEELDFLVPK, A3V
MVH=26.9817
p–value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 30548
TGSPGSPGASGVQSTAK, G10S
MVH=50.5338
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 105956
TLEGLQVEEEPVYK, E14K
MVH=53.2529
p–value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 148567
TPFAAPSPFAELVLPPQQ, A1T
MVH=38.3920
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 102512
TTPLEAASSGAR, T11A
MVH=48.4902
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 57081
TVVQLEGDNKLVTAFAK, T14A

MVH=46.3855
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 126720
VLDALQVLK, A7V
MVH=64.4272
p-value=0.0005
sample: TCGA–AA–3531–01A, spectrum: 101355
VLGTAGTEEGQK, I1V
MVH=38.4816
p-value=0.0001
sample: TCGA–AA–3531–01A, spectrum: 86045
VLLDGQVQLNR, P9L
MVH=62.9161
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 75917
VLTGTGNVNVLQPNYPAAAR, I10V
MVH=53.0826
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 6404
VPSFETAEEGLAELK, T12A
MVH=58.7409
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 71263
VPVTQATR, L3V
MVH=42.8744
p-value=0.0012
sample: TCGA-AA-3531-01A, spectrum: 132768
VSDLAATAYK, N2S
MVH=55.3536
p-value=0.0001
sample: TCGA-AA-3531-01A, spectrum: 44746
VSTLAGLGLQGTDK, V4I
MVH=52.9928
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 53757
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=49.8174
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 59492
AAAPAPVSEAVSR, C12S
MVH=34.1705
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 37220
AAPSVTLFPPSEELQANK, T2A
MVH=56.1078
p–value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 15387
AGVETTTPSK, K7T
MVH=45.1099
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 13304
APFAAPLPFAELVLPPQQ, S7L
MVH=34.5196
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 64405
APSPLYSVEFSEEPFGVLVHR, R20H
MVH=39.8533
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 64284
AQLNVGNVPVGTMEGLVCCLEEKPGDR, I5V
MVH=30.9704
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 63309
AVEVATVVLQPTVLR, S12T
MVH=40.5039
p–value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 52498
AYVVLLR, E1A
MVH=40.6613
p-value=0.0084
sample: TCGA-AA-3534-01A, spectrum: 81351
CLFASGSPFEPVK, G10E
MVH=48.3744
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 12593
DFYVVEPLAFEGTPEQK, I4V
MVH=58.6440
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 26942
DTEEEDFHVDQATTVK, V12A
MVH=38.0524
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 53423
DVPGFLQQSQSSGPQPAVWHR, N11S
MVH=25.3313
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 38716
EALDVLDAVLK, G7D
MVH=52.9082
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 64198
EATSVPHLYALGDVVEGRPELTPTALMAGR, I24T
MVH=78.5949
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 51353
ELVDDSLNNVR, V7I
MVH=51.6576
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 46453
ESALEPGPVPEAPAGGPGVHAVTVVTLLEK, R6P
MVH=23.2908
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 5120
FFGSLPDSWAR, S11R
MVH=43.1517
p–value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 5789
FGQDLLSSPLSVR, K13R
MVH=44.8887
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 106721
FLQENVFVAANHNASPLSLK, G14A
MVH=36.2035
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 13429
FSLDALLTNVLPFEK, I10V
MVH=40.4824
p-value=0.0001
sample: TCGA−AA−3534−01A, spectrum: 119859
GCAGVLTLPK, T3A
MVH=36.4721
p−value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 4992
GFGTDEQALLDCLGSCSNK, R16C
MVH=56.9119
p−value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 105145
GKWERPFEVKDTEEDFHVDQATTVK, V22A
MVH=60.8996
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 37724
GQTGALLQNTVESLSK, D9N
MVH=62.1997
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 19049
GVAGSSVAVLCPYNR, G5S
MVH=32.2497
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 99839
GVNECDLESLVLGWGR, F10L
MVH=33.9386
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 98279
KFFGSLPDSWAR, S12R
MVH=52.7455
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 13290
KFSLDALLTNVPFEK, I11V
MVH=46.2693
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 89109
KKPSEEEAADGPPGPGQVNPVTDENVV, V10A
MVH=46.7203
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 73240
KPAAGLSAAPVPTTPAAGAPLMDFGNDFVPPAPR, A14T
MVH=52.5125
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 20968
LALLLMASQEPQR, T2A
MVH=50.9334
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 29853
LFEEDPAVGALVLTGGDK, T1I
MVH=72.8371
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 45688
LFQAEAQDLFR, E3Q
MVH=26.2509
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 22230
LLNLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 99570
LSDLQEALDQALNHVR, Y14H
MVH=52.5339
p-value=0.0001
Sample: TCGA-AA-3534-01A, spectrum: 105063
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=38.3685
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 10426
MQYAPNTQVELLPQGR, H16R
MVH=39.8520
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 26776
MVAVGLCR, H8R
MVH=37.1016
p-value=0.0006
sample: TCGA-AA-3534-01A, spectrum: 43808
MVDFAGMK, V7M
MVH=23.0905
p-value=0.0092
sample: TCGA-AA-3534-01A, spectrum: 105780
NDYATMLPDSLNLNQDTLNR, D14N
MVH=61.1904
p-value=0.0001
sample: TCGA–AA–3534–01A, spectrum: 107615
NEVLWHPTLNPLPSPQGTVR, A3V
MVH=47.9696
p−value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 53039
NTVLATWQPYSTSK, T11S
MVH=49.6123
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 6439
NTVLCNVVEKFLQADLAR, Q10K
MVH=36.2879
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 30837
SELPLDPLPLPTEEGNPLLK, V10L
MVH=66.4633
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 21962
SLSAFLVPMPTPGLTLGK, G1S
MVH=32.0166
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 50280
SPADPTDLGGQTSPR, I6T
MVH=26.5882
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 93830
TPQEWAPHTAR, Q8H
MVH=46.3293
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 37275
TVVQLEGDNKLVTAFK, T14A
MVH=55.1429
p-value=0.0001
sample: TCGA-AA-3534-01A, spectrum: 1372
VSEVLLSR, G8R
MVH=40.9453
p-value=0.0025
sample: TCGA-AA-3534-01A, spectrum: 60121
YQAVTDTLEEK, A6D
MVH=40.8602
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 60699
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=51.0535
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 65201
AAAPAPVSEAVSR, C12S
MVH=56.3104
p−value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 44700
AAPSVTLFPPSSEELQANK, T2A
MVH=57.3900
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 8153
AGVETTTPSK, K7T
MVH=23.8639
p-value=0.0002
sample: TCGA–AA–3552–01A, spectrum: 43173
AQALCAVLRP, P8L
MVH=35.8586
p-value=0.0005
sample: TCGA-AA-3552-01A, spectrum: 27633
CDEPLNLLVR, S6N
MVH=41.4868
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 101776
CDPGALVLPFSGAELEK, Y1C
MVH=45.4375
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 81594
DFENSLNQVK, M6I
MVH=41.4868
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 21002
DFVYVVEPLAEFGTPEQK, I4V
MVH=54.7355
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 104901
DGYGFLNR, N1D
MVH=46.2273
p-value=0.0006
sample: TCGA–AA–3552–01A, spectrum: 33165
DTEEEDFHVDQATTVK, V12A
MVH=45.1068
p−value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 60364
DVPGLQSQSSQPGQPAVWHR, N11S
MVH=37.9878
p–value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 108933
EAGFPPGVVNLLTGYGPTAGAALAQHMDVDK, V27M
MVH=35.3133
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 45821
EALDVLDAVLK, G7D
MVH=60.3518
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 28188
EAPETDTSPSLWNVEFAK, D13N
MVH=30.9540
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 75983
EELGHLQNDLTSLENDK, M10L
MVH=26.8794
p–value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 106657
EQPGSPEWLQLDK, Q13K
MVH=32.4524
p–value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 53959
ESAEPGPVPEAPAGGPVHATVTVTLLEK, R6P
MVH=41.9440
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 59086
FADVFAK, E7K
MVH=40.0526
p-value=0.0084
sample: TCGA-AA-3552-01A, spectrum: 12466
FFGSLPDSWAR, S11R
MVH=43.8173
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 66026
FLDKLPQQTGDR, H12R
MVH=57.8762
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 3686
FNSVTELCAELPEQK, V11I
MVH=39.3048
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 71989
FQTATVTEK, I3T
MVH=36.3010
p-value=0.0005
sample: TCGA-AA-3552-01A, spectrum: 21777
FSLDALLTNVLPEK, I10V
MVH=42.6791
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 69163
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=62.1271
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 12591
GLLDLLEER, V3I
MVH=44.7386
p-value=0.0038
sample: TCGA−AA−3552−01A, spectrum: 44782
GQTGALLQNTVESLSK, D9N
MVH=72.6838
p−value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 64457
HNYEVAYR, F7Y
MVH=37.1728
p-value=0.0006
sample: TCGA-AA-3552-01A, spectrum: 100341
KFFGSLPDSWAR, S12R
MVH=58.8393
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 13749
KFSLDALLTNVLPFEK, I11V
MVH=40.1404
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 83759
KKPSEEEEAAAAAGGPPGPGPNLPVTDEVV.V10A
MVH=46.1117
p–value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 96665
KSVEEYANCHLAR, P2S
MVH=60.9745
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 34245
KVLLDGVQNLRR, P10L
MVH=52.7339
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 53028
LADGGAGGTFQPYLTLR, V1L
MVH=58.1021
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 75595
LAFASLGYEK, L3F
MVH=55.3536
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 20388
LALLLMASQEPQR, T2A
MVH=27.4874
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 83790
LCLDAMHGVVGPYVK, R2C
MVH=44.8081
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 2569
LDSTDFTSTLK, G8S
MVH=55.4896
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 36352
LFEEDPAVGALVLTGGDK, T11
MVH=76.6299
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 101151
LLDAETTAGAWPNVAAVSLTGR, A9G
MVH=48.6284
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 21641
LLNLLADLVER, R4L
MVH=54.2038
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 107888
LLSDLLPSPSTGTFQEAQSR, S5L
MVH=36.8174
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 34092
LLTQDEGPALVPGSR, G14S
MVH=48.7387
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 80419
LPAEPLTR, E3A
MVH=33.2970
p-value=0.0012
sample: TCGA–AA–3552–01A, spectrum: 108166
LPPSLAPTVLSVPAGTTLVK, S5L
MVH=37.1672
p–value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 88783
LQQQHSEQPPLQPSPVTTR, M17T
MVH=53.3625
p−value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 101717
LSDLQEALDQALNHVR, Y14H
MVH=37.8988
p–value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 11618  
LSTEVDLTNVDLSTVDKQSLAPK, G6D  
MVH=27.1761  
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 68709
LSVFSTLDAPVAPSDK, V7I
MVH=37.0457
p–value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 5770
LTAEFEEAQTSACLLQEELEK, R14L
MVH=48.1099
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 11813
LVTDYTLAEADAALQK, E11D
MVH=59.4000
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 60384
LYEPVVLPVGR, K11R
MVH=40.9100
p-value=0.0002
sample: TCGA–AA–3552–01A, spectrum: 17320
MAQWGNKPLC, V9I
MVH=41.9625
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 2135
MGAQELLR, T1M
MVH=44.0097
p-value=0.0006
sample: TCGA-AA-3552-01A, spectrum: 18758
MQYAPNTQVELLPQGR, H16R
MVH=64.7569
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 21742
NSTLVFPLPLDLQGLLGAK, M12T
MVH=52.2905
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 65961
NTNSVPETAPAALPETR, K17R
MVH=46.7217
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 108670
QKLTAEFEEAQTSACLLQEELEK, R16L
MVH=42.0531
p–value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 34076
QVGDFHQVLLR, A2V
MVH=38.9352
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 89751
RDDDGTLHAACQVQPSATLDAQPR, A6T
MVH=76.1187
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 69674
RLPTLLADNAGYDSADLVAQLR, M1R
MVH=76.7565
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 56992
SLQEEQSRPTTAVSSPGGPAR, P10T
MVH=49.7503
p−value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 52936
SLSLLDSPGLLSGEK, V4I
MVH=60.5922
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 88641
SPPGAAAPAAAKPPPLSAK, S8P
MVH=28.2199
p-value=0.0003
sample: TCGA-AA-3552-01A, spectrum: 41858
SQNKEDYDGLKEEFR, A8D5
MVH=67.1576
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 49614
SQNKEDYDGLKEEFRK, A8D
MVH=94.0558
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 69679
SSGGPGAGLCLFPLDEVHAK, K16E
MVH=45.6609
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 48129
STESLQTNVQR, A7T
MVH=57.4309
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 96923
SVEEYANCHLAR, P1S
MVH=36.0664
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 61933
TLDPFETMLK, S2L
MVH=33.8527
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 75226
TLEGLQVEEEPVYK, E14K
MVH=55.1354
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 56585
TSLSAPPNTSSTENPK, S9T
MVH=35.5475
p−value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 72368
TTPLEAASSGAR, T11A
MVH=52.3273
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 54447
TVASPGVSVEEAQVELDLGGVTLLR, T8S
MVH=61.1365
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 44154
TVVQLEGDNKLVTAFK, T14A
MVH=49.9903
p-value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 67595
VLLDGVQNL, P9L
MVH=65.9168
p–value=0.0001
sample: TCGA–AA–3552–01A, spectrum: 108991
VPLASQGLGPGSTVLLVVDKCDEPLNLLVR, S26N
MVH=77.2616
p–value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 4314
VPSFETAEGLGAELK, T12A
MVH=43.4057
p-value=0.0001
sample: TCGA-AA-3552-01A, spectrum: 1544
YFHNQEEFVR, L9V
MVH=31.8203
p-value=0.0004
sample: TCGA–AA–3552–01A, spectrum: 97263
YPVDTLPTSK, I3V
MVH=45.9288
p-value=0.0001
sample: TCGA–AA–3554–01A, spectrum: 44594
AAPSVTLFPPSSEELQANK, T2A
MVH=56.0047
p–value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 10680
AGVETTTPSK, K7T
MVH=50.3071
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 99432
AGVLTHLEEER, A5T
MVH=47.6383
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 138175
ATLEQDGYAQLLR, R5Q
MVH=56.0378
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 72766
AVEVATVVLQPTVLR, S12T
MVH=48.7280
p-value=0.0001
sample: TCGA-AH-3554-01A, spectrum: 26520
CDEPLNLLVR, S6N
MVH=36.5110
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 112563
CDPGALVLPFSGAELK, Y1C
MVH=46.4424
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 49060
CPAAPPPAGGAANNHGAGSGAGGR, G1C
MVH=26.3761
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 69764
DAGNEQDLGLQYK, N1D
MVH=37.8642
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 17776
DFYVVEPLAFEQGTEQK, I4V
MVH=54.7355
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 18633
DGTVLCELLNAL YPK, E15K
MVH=64.9297
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 127246
DGYGFLNR, N1D
MVH=43.2774
p-value=0.0006
sample: TCGA-AA-3554-01A, spectrum: 31911
DSRPSQAAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=101.7277
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 33032
DTEEEDFHVDQATTVK, V12A
MVH=43.1723
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 62565
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=26.9671
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 79846
EHTLHLEAELEK, S4L
MVH=31.9780
p-value=0.0001
sample: TCGA–AA–3554–01A, spectrum: 60584
ELVDDSLNNVR, V7I
MVH=43.8173
p–value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 128985
EQPGSPEWLQLDK, Q13K
MVH=26.3225
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 55401
ESALEPGPVPEAPAGGPVHAVTVVTLEK, R6P
MVH=36.5053
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 6988
FFGSLPDSWAR, S11R
MVH=33.5055
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 7791
FGQDLLSPLLSVR, K13R
MVH=44.7002
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 60360
FLDKLPQQTGDR, H12R
MVH=43.5131
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 18575
FSLDALLTNVLPFEK, I10V
MVH=43.5822
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 105547
FTVGDHSR, I3V
MVH=44.9986
p-value=0.0003
sample: TCGA–AA–3554–01A, spectrum: 63724
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=77.3854
p−value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 80610
FYLGGPTSVR, I9V
MVH=48.2574
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 45151
GQTGALLQNTVESLSK, D9N
MVH=60.9985
p-value=0.0001
sample: TCGA–AA–3554–01A, spectrum: 24870
GVAGSSVAVLCPYNR, G5S
MVH=50.0433
p−value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 100960
GYQQDAYDGKDYLALNEDLR: R3Q
MVH=49.4657
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 86580
HMTAVVK, Y1H
MVH=33.0005
p-value=0.0044
sample: TCGA-AA-3554-01A, spectrum: 136672
HNYGAVESFTVQR, V5A
MVH=55.5837
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 3445
KAFSEYLGTDQSK, G5E
MVH=57.4332
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 18419
KFSLDALLTNVLPFEK, I11V
MVH=37.5472
p-value=0.0001
sample: TCGA–AA–3554–01A, spectrum: 101197
KKPSEEEAAAAAGGPPGQVNPLPVTDEVV V10A
MVH=62.8362
p–value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 54415
LADGGGAGGTFQPYLDTLR, V1L
MVH=59.6817
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 91820
LCLDAMHGTVGYPYVK, R2C
MVH=41.2012
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 128876
LEGSDVQLLEYK, E12K
MVH=42.6204
p-value=0.001
sample: TCGA-AA-3554-01A, spectrum: 36341
LFEEDPAVGA/LVTGGDK, T1I
MVH=62.9828
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 46477
LFSLLSTALLR, V8A
MVH=54.8445
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 115520
LGGLQPSQDR, G7S
MVH=42.3707
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 42639
LHVLVEPDHFK, Q2H
MVH=77.1697
p-value=0.0001
Sample: TCGA-AA-3554-01A, spectrum: 111894
LLDAETTAGAWPNVAAVSLTGR, A9G
MVH=52.8654
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 28262
LLNLLADLVER, R4L
MVH=54.7605
p-value=0.0001
sample: TCGA–AA–3554–01A, spectrum: 126216
LPAPTHTPATAPVPAR, R6H
MVH=35.7449
p–value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 78290
LQELTPSSGDPGEHDPASTHK, P4L
MVH=58.7259
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 107338
LQQQHSEQPPLQPSPVTTR, M17T
MVH=51.8871
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 112486
LSDLQEALDQALNHVR, Y14H
MVH=43.2459
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 24199
LSVATGALEAAQGSKPQCQTR, S16P
MVH=37.8190
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 6271
LVTLDYLAEADAALQK, E11D
MVH=61.9302
p-value=0.0001
Sample: TCGA-AA-3554-01A, spectrum: 15344
MQYAPNTQVELLPQGR, H16R
MVH=57.9690
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 28342
NSTLVFPLPLDTLQGLLGAK, M12T
MVH=56.8268
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 69681
NTNSVPETAPAALPETR, K17R
MVH=34.0961
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 27055
NYQQLVDTTVELANK, R3Q
MVH=53.9142
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 90349
QDLQSDGFSLETCK, K4Q
MVH=57.7764
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 63553
QGTLTEYCSTLMSLPTK, G9S
MVH=56.5177
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 106407
QLTVGVPR, K8R
MVH=25.7984
p-value=0.0018
sample: TCGA-AA-3554-01A, spectrum: 102222
QPFCDGSHFFQCTGLSPLK, R12C
MVH=26.5799
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 116374
RGDLFYTSK, E2G
MVH=35.8432
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 28403
SALSGHLETLLLGLLK, V10L
MVH=76.4895
p-value=0.0001
sample: TCGA–AA–3554–01A, spectrum: 139564
SAVGELSEDSSNVVHLLK, Q15H
MVH=58.2286
p−value=0.0001
sample: TCGA–AA–3554–01A, spectrum: 55021
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=44.1028
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 37375
SELPLDPLPLPTEEGNPLLK, V10L
MVH=54.1478
p-value=0.0008
sample: TCGA-AA-3554-01A, spectrum: 18373
SGGTLVLVGLGSEMTTVPLLHAALRN4T
MVH=38.9582
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 59280
SPADPTDLGGQTSPR, I6T
MVH=57.2048
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 98104
SPPGAAAPAAAKPPPLSAK, S8P
MVH=35.5213
p-value=0.0003
sample: TCGA-AA-3554-01A, spectrum: 73733
SSGGPGAGLCLFPLDEVHAK, K16E
MVH=37.9542
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 20858
SSSYSGEYGSGGGKR, G10S
MVH=24.4044
p-value=0.0002
sample: TCGA-AA-3554-01A, spectrum: 128403
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=66.6135
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 17137
TCSFDGAVEDLSK, G3S
MVH=57.4399
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 83341
TTGLVVDSDGVTHVPLYEYALPHALLR, M6V
MVH=26.1158
p-value=0.0001

m/z
0 500 1000 1500 2000
Intesity(%)
0 20 40 60 80 100 120

b4−H2O b5 b5−H2O b10−H2O b10−NH3 b11−H2O b15 b15−NH3 b15++−NH3 b16−H2O b16−NH3 b17++−NH3 b19++−H2O b20++−H2O b20++−NH3 b22++−H2O b22++−NH3 b23++−H2O b23++−NH3 b24++−H2O b25++−H2O b25++−NH3 b26++−NH3

y6 y6++−NH3 y7 y8 y9−H2O y10 y10++ y11 y11++ y12 y12++ y14 y14++ y15++ y17++ y18++ y18++−H2O y18++−NH3 y20++ y20++−H2O y21++ y22++ y23++−H2O y24++ y24++−NH3 y26++−H2O y28++−NH3
sample: TCGA-AA-3554-01A, spectrum: 88120
TTPLEAASSGAR, T11A
MVH=50.1651
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 55833
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=49.9670
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 74147
TVEDLDGLLQQL YR, H10Q
MVH=61.7247
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 71421
VFSVAELQAR, S9A
MVH=58.7158
p-value=0.0002
sample: TCGA-AA-3554-01A, spectrum: 66861
VPVTQATR, L3V
MVH=36.9778
p-value=0.0012
sample: TCGA-AA-3554-01A, spectrum: 103269
VQLPTESLQELLDLHR, T7S
MVH=30.3543
p-value=0.0001
sample: TCGA–AA–3554–01A, spectrum: 7896
VVLQPEALFSLYSK, F8L
MVH=61.5789
p−value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 42237
VWQTVSPVESR, G10S
MVH=33.1598
p-value=0.0001
sample: TCGA-AA-3554-01A, spectrum: 27966
WLLLLCNPGLANTLVEK, D11N
MVH=76.7847
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 6261
AAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=46.7557
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 30660
AAAPAPVSEAVSR, C12S
MVH=53.7687
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 132152
AAPSVTLFPSSSLELQANK, T2A
MVH=59.5442
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 108913
AGVETTTPSK, K7T
MVH=58.7320
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 29041
ALDRPYTSK, E3D
MVH=35.7968
p-value=0.0003
sample: TCGA-AA-3561-01A, spectrum: 131200
APSQHLSSFDPCFYR, R5H
MVH=67.9752
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 67603
ASSAAAPHTVSYPDNLNYR, T17N
MVH=39.4365
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 53961
CDPGALVLPFSGALELK, Y1C
MVH=68.5506
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 10612
CPAAPPPPPAGGAANNHGAGSGAGGR, G1C
MVH=30.2846
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 66945
DAALATALGEKK, D10E
MVH=61.6720
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 60201
DEPLHALYDNVEK, V2E
MVH=37.3408
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 76403
DGYGFLNR, N1D
MVH=47.1393
p-value=0.0006
sample: TCGA-AA-3561-01A, spectrum: 124752
DLGDLLEATGFDR, E10G
MVH=63.8506
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 15127
DVPGFLQSQSSGPGQPAVWHR, N11S
MVH=43.6190
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 133500
EALDVLDAVLK, G7D
MVH=54.9703
p-value=0.0001
sample: TCGA–AA–3561–01A, spectrum: 114549
ELTVSNNDLNEAGVHLQGLK, R15H
MVH=28.2713
p–value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 22380
ELVDDSLNNVR, V7I
MVH=54.9703
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 78233
EQPGSPEWLQLDK, Q13K
MVH=42.5296
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 7944
ESALEPGPVPEAPAGGPVHAVTVVTLLEK, R6P
MVH=35.7161
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 86929
EVAQQAVDADVHAVGVSTLAAGHK, I16V
MVH=54.1073
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 97344
FFGSLPDSWAR, S11R
MVH=46.1748
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 12720
FLDKLPQQTGDR, H12R
MVH=61.0345
p-value=0.0001
sample: TCGA–AA–3561–01A, spectrum: 116055
FNKPFVFLMLDQNTK, E11D
MVH=57.1781
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 38748
FQTATVTEK, I3T
MVH=27.8208
p-value=0.0026
sample: TCGA-AA-3561-01A, spectrum: 25707
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=56.1101
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 106174
GFGTDEQALLDCLGSCSNK, R16C
MVH=62.6537
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 106412
GLLDLLEER, V3I
MVH=55.6905
p-value=0.0038
sample: TCGA-AA-3561-01A, spectrum: 113388
GPLPAAPLVAPER, P8L
MVH=56.3419
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 52319
KFFGSLPDSWAR, S12R
MVH=59.3526
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 51858
KKPSEEAAAAAGGPGGPNPLPVITDEVV V10A
MVH=59.2765
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 121709
KVLLDVQNLRL, P10L
MVH=36.9809
p-value=0.0001
sample: TCGA–AA–3561–01A, spectrum: 75128
LCNNPAPQFGGK, T6A
MVH=52.2221
p–value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 94862
LDSTDFTSTLK, G8S
MVH=59.2753
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 123930
LFEEDPAVGALVLTGGDK, T1I
MVH=83.6844
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 43464
LGRPGLGGSSGLAGAWLK, K3R
MVH=61.2436
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 125235
LLNLLADLVER, R4L
MVH=58.8683
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 57825
LQQQHSEQPPLQPSPVTTR, M17T
MVH=56.2294
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 62611
LSDLQEALDQALNHVR, Y14H
MVH=52.8004
p-value=0.0001
sample: TCGA–AA–3561–01A, spectrum: 30213
LTGHGAEDSLADQAANK, R4H
MVH=57.9101
p–value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 104710
LTPVSAQFQDLEGK, L8F
MVH=57.0889
p-value=0.0001
sample: TCGA–AA–3561–01A, spectrum: 132465
NPLLDLAAYDQEGR, R3L
MVH=67.5131
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 31506
NTNSVPETAPAALPETR, K17R
MVH=51.0467
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 98793
NTVLCNVVEKFLQADLAR, Q10K
MVH=77.0483
p-value=0.0001
sample: TCGA–AA–3561–01A, spectrum: 75118
RGDLFYTSK, E2G
MVH=41.9625
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 41929
SAGLAPDCEASATAETTVSSVGTCCEAAK, G28A
MVH=31.2964
p-value=0.0001
sample: TCGA–AA–3561–01A, spectrum: 7475
SDPVTLNVL YGPDVPTLSPSK, G14V
MVH=42.0180
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 133398
SLDPGLKEDTLEFLLK, Q12E
MVH=35.9168
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 21201
SPADPTDLGGQTSPR, I6T
MVH=71.2206
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 12847
SQNKEDYDGLKEEFR, A8D
MVH=54.6266
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 21940
SQNKEDYDGLKEEFRK, A8D
MVH=91.6342
p-value=0.0001
sample: TCGA–AA–3561–01A, spectrum: 86734
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=81.2156
p−value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 48087
TTPLEAASSGAR, T11A
MVH=37.9655
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 8372
TVASPGRSVEEAEQLDGGVTLRL, T8S
MVH=50.4625
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 77873
VLFSCAAGFGQR, T2I
MVH=57.6542
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 14472
VLLDGVQNL, P9L
MVH=59.4441
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 34445
VLLDGVQNLRAEDLVGK, P9L
MVH=32.6843
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 46612
VLSTTNAER, D6N
MVH=37.9585
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 96757
VPSFETAEGLGAELK, T12A
MVH=54.9384
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 19403
VPVTQATR, L3V
MVH=50.8009
p-value=0.0012
sample: TCGA-AA-3561-01A, spectrum: 53900
VQLPTESLQELLDLHR, T7S
MVH=25.0969
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 66054
VSDLAAATAYK, N2S
MVH=59.1603
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 89431
VVLQPEALFSLYSK, F8L
MVH=70.1364
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 107045
VYPYLCWALK, R7W
MVH=39.5567
p-value=0.0001
sample: TCGA-AA-3561-01A, spectrum: 24558
YVSLLYTNYEAGKDDYVK, I2V
MVH=36.0560
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 40358
AAAAAAAAPAAAATAATTAATTAATAAAQ, P17A
MVH=44.5459
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 34443
AAPSVTLFPPSSEELQANK, T2A
MVH=52.5844
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 13407
AGVETTTPSK, K7T
MVH=26.5855
p-value=0.0002
sample: TCGA-AA-3664-01A, spectrum: 34012
APSQHLSSFDPCFYR, R5H
MVH=41.8344
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 53087
AQLNVGNVLPVGTMPEGTLVCCLEEKPGDR, I5V
MVH=35.5382
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 75946
CDPGALVLPFSGALELK, Y1C
MVH=73.3762
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 17320
DFYVVEPLAFEGTPEQK, I4V
MVH=57.3944
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 78140
DGYGFLNR, N1D
MVH=48.8163
p-value=0.0006
sample: TCGA-AA-3664-01A, spectrum: 29993
DMAGAQAAAVALEEFLK, R18K
MVH = 79.9513
p-value = 0.0001
sample: TCGA-AA-3664-01A, spectrum: 34502
DSMFGGLTVK, A7T
MVH=43.1189
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 71875
DVDGLTSLNAGR, K12R
MVH=64.3030
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 72654
DVTVLQNTDGNNNDAWAK, E14D
MVH=69.6713
p-value=0.0001
sample: TCGA–AA–3664–01A, spectrum: 36066
EALDVLDVAVLK, G7D
MVH=57.1244
p–value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 55958
EALELDSLR, V2A
MVH=39.0927
p-value=0.0009
sample: TCGA-AA-3664-01A, spectrum: 43844
ELVDDSLNNVR, V7I
MVH=57.6516
p-value=0.0001
sample: TCGA–AA–3664–01A, spectrum: 85828
EQPGSPEWLQLDK, Q13K
MVH=37.2253
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 50092
FADVFAK, E7K
MVH=36.3324
p-value=0.0084
sample: TCGA-AA-3664-01A, spectrum: 11108
FFGSLPDSWAR, S11R
MVH=41.7680
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 11987
FGQDLLSPLLSVR, K13R
MVH=51.5420
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 20970
FQLGNSGPNSTLK, S4G
MVH=44.5364
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 40782
FQPQSADFLDLTNPK, P6A
MVH=70.8152
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 52260
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=61.6256
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 11257
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-3664-01A, spectrum: 84027
GLSFDAATSGGSASSEK, T2I
MVH=81.2590
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 34960
GQTGALLQNTVESLSK, D9N
MVH=76.0424
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 862
GVALSNVVK, I8V
MVH=48.7687
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 67568
KKPSEEEAAAAAGPPGQPQVNPLPVTDEVV V10A
MVH=48.8884
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 67659
LAGALGPCLSLNVK, V9I
MVH=59.8805
p-value=0.0001
sample: TCGA–AA–3664–01A, spectrum: 2104
LDSTDFTSTLK, G8S
MVH=57.2310
p−value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 60809
LDVDKDGFVTEGELK, A3V
MVH=30.0944
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 29249
LFEEDPAVGALVLTGGDK, T1I
MVH=94.0835
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 18028
LLNLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 27112
LLTQDEGPALVPGSR, G14S
MVH=49.9163,
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 71131
LQQQHSEQPQLQPSPVTTR, M17T
MVH=49.1186
p-value=0.0001
sample: TCGA–AA–3664–01A, spectrum: 58322
LTQQLFDYSELPLNPFR, G10S
MVH=41.8226
p–value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 21632
LTVAPPLAEPGAGK, P1L
MVH=53.5678
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 65278
NLVACESLGR, V2L
MVH=41.4868
p-value=0.0001
sample: TCGA–AA–3664–01A, spectrum: 49058
NTNSVPETAPAALPETR, K17R
MVH=39.4740
p–value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 31916
PVAEYWNSQK, D2V
MVH=40.4678
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 40941
QALTLLNELK, V2A
MVH=37.3733
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 19180
QQHEGAQGTLDSGEPPQCR, A9T
MVH=30.0349
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 78225
QTVQVDEHARPQTTLEQLQK, M3V
MVH=44.8435
p-value=0.0001
sample: TCGA–AA–3664–01A, spectrum: 46964
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=40.1848
p–value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 70952
SPPGAAAPAAAKPPPLSAK, S8P
MVH=27.3648
p-value=0.0010
sample: TCGA-AA-3664-01A, spectrum: 6329
STESLQTNVQR, A7T
MVH=30.6144
p-value=0.0001
sample: TCGA–AA–3664–01A, spectrum: 44893
VLTGTGNVNVLPNYPAAAR, I10V
MVH=31.5047
p−value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 3685
VPSFETAEGLGAELK, T12A
MVH=68.5668
p-value=0.0001
sample: TCGA–AA–3664–01A, spectrum: 17838
VSLAEIAQASNSLLTWGR, A15T
MVH=52.5502
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 11307
VSLVLAPALVACGCK, A10V
MVH=68.9307
p-value=0.0001
sample: TCGA-AA-3664-01A, spectrum: 27061
VSTLAGLGLQGTDK, V4I
MVH=63.0392
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 60015
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=48.3198
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 38607
AAGNWTENLLR, D4N
MVH=37.5907
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 49310
AAPSVTLPSSSEELQANK, T2A
MVH=52.9275
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 11160
AGVETTTPSK, K7T
MVH=53.9793
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 91956
APPRPGPVPEAAQPFLF+TR, P19T
MVH=60.4226
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 150651
ASSSLLLNESEPTTNLQLR, D8N
MVH=61.7127
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 81622
AVEVATVVLQPTVLR, S12T
MVH=39.5157
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 58267
AYVVLLR, E1A
MVH=45.4507
p-value=0.0084
sample: TCGA-AA-3666-01A, spectrum: 55103
CPAAPPPPPAGGAANNHGAGSGAGGR, G1C
MVH=28.2248
p-value=0.0002
sample: TCGA-AA-3666-01A, spectrum: 153428
DCGEAAQWLTSFLK, T6A
MVH=66.2771
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 109540
DEPLHALYDNVEK, V2E
MVH=44.5364
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 18058
DFYVVEPLAFEGTPEQK, I4V
MVH=67.0310
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 137931
DGYGFLNR, N1D
MVH=43.8062
p-value=0.0006
sample: TCGA-AA-3666-01A, spectrum: 40596
DMAGAQAAVALNEEFLK, R18K
MVH=71.1443
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 35353
DSRPSQAAGDNQGDEVKEQTFSGGTSDTK, A16V
MVH=93.9158
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 36424
DTEEEDFHVDQATTVK, V12A
MVH=59.2218
p–value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 726
EASQGSSASSAPQSVK, H13Q
MVH=33.2034
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 146241
EEPVSSGPEEAAGK, V12A
MVH=33.7107
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 89280
EHTLHLEAELEK, S4L
MVH=34.7532
p-value=0.0002
sample: TCGA-AA-3666-01A, spectrum: 15789
EPSAPSLPTPAYQSLPAGGHAPTPPTPAPR, S15L
MVH=34.9939
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 139576
EQPGSPEWLQLDK, Q13K
MVH=29.5119
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 61420
ESALEPGPVPEAPAGGPVHAVTVTLLEK, R6P
MVH=35.5908
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 6944
FFGSLPDSWAR, S11R
MVH=30.8186
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 67977
FLDKLPQQTGDR, H12R
MVH=49.2906
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 51500
FLGQLLTAFPALR, A3G
MVH=55.1914
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 82173
FNLSQEYSLATQYSLRPR, S2N
MVH=32.6974
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 91024
FSVPVQHFCGPNSTPLQVR, Q20R
MVH=64.7965
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 115046
FTVGDHSR, I3V
MVH=47.8450
p-value=0.0003
sample: TCGA-AA-3666-01A, spectrum: 71629
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=61.5493
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 90005
FYLGPGVPSVR, I9V
MVH=36.4257
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 57973
GALQFVTHYQQSSTQR, H11Q
MVH=51.2937
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 7056
GFGTDEQALLDCLGCSNK, R16C
MVH=54.3776
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 7012
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA–AA–3666–01A, spectrum: 49791
GQTAGALLQNTVESLSK, D9N
MVH=71.2235
p−value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 139136
GVNCLDYCSGDKPYLLSGADDR, Y8C
MVH=53.4533
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 76822
HNYEVAYR, F7Y
MVH=35.5666
p-value=0.0006
sample: TCGA-AA-3666-01A, spectrum: 91480
KAPPRPGPVPEAAQPFLFTTR+P20T
MVH=67.8094
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 109966
KKPSEEEAAAAGGPPGGPQVNPLPVTDEVV V10A
MVH=48.6645
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 83243
KPAAGLSAAPVPTTPAAPGAPLMDFGNDFVPPAPR, A14T
MVH=28.7470
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 60295
LADGGGAGGTFQPYLDTLR, V1L
MVH=42.4404
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 91218
LCLDAMHGVVGPYVK, R2C
MVH=34.9056
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 149254
LDSTDFTSTLK, G8S
MVH=59.2753
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 7931
LEGLLEGLGLR, G6E
MVH=54.8445
p-value=0.0006
sample: TCGA-AA-3666-01A, spectrum: 39654
LFEEDPAVGLVLTGGDK, T1I
MVH=86.7937
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 71272
LGLTPEGQSYLDQFR, V3I
MVH=39.4047
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 142459
LKQEYFVASTLQDLLR, A10S
MVH=51.2812
p−value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 18563
LLNLEGFLSGSQSR, P8L
MVH=67.5131
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 29851
LLNLLADLVER, R4L
MVH=56.6730
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 37384
LLTQDEGPALVPGSR, G14S
MVH=39.0262
p−value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 87890
LQELTPSSGDPEHDPASTHK, P4L
MVH=61.7568
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 131286
LQQELDDLATMDLEQQQQLVSTLEK, R16Q
MVH=57.8252
p−value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 116847
LQQQHSEQPPLQSPVTTR, M17T
MVH=63.1136
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 122014
LSDLQEALDQALNHVR, Y14H
MVH=53.3828
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 93123
LTQAQLFDYSELPNFPR, G10S
MVH=41.8770
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 6356
LVTDYTLAEADAALQK, E11D
MVH=60.4230
p–value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 15582
MQYAPNTQVELLPQGR, H16R
MVH=50.9680
p–value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 128117
NLPSLAEGASAQPPTVASR, K7E
MVH=57.6197
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 78608
NTNSVPETAPAALPETR, K17R
MVH=46.1025
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 37235
QVGDFHQVLLR, A2V
MVH=34.7766
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 7671
RLEGLLEGLGLR, G7E
MVH=46.3183
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 152569
RWLLLCLNPGLANTLVEK,D12N
MVH=60.4909
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 151768
SAVGELSEDSSNVHLLK, Q15H
MVH=59.4096
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 122432
SDPLCLLLQDVGGGSWAELGR, V6I
MVH=80.4537
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 60936
SDPVTLNVLYGPDVPTLSK, G14V
MVH=44.7560
p–value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 51094
SFQGPVLLGSSHGGVNLEDVAAETPEALLK, S24T
MVH=47.0150
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 18961
SGGTLVLVGLGSEMTTVPLLHAALR, N4T
MVH=42.7762
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 97110
SLNDLTAR, K8R
MVH=36.3745
p-value=0.0012
sample: TCGA-AA-3666-01A, spectrum: 66978
SLQEEQSRPTTAVSSPGGPAR, P10T
MVH=50.2839
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 82944
SNPNWLLPDSVDWR, R5W
MVH=27.9619
p−value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 107086
SPPGAAAPAAAKPPPLSAK, S8P
MVH=29.2106
p-value=0.0003
sample: TCGA-AA-3666-01A, spectrum: 67770
SQNKEDYDGLKEEFRK, A8D
MVH=76.3372
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 55508
STESLQTNVQR, A7T
MVH=55.0229
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 62306
SVSFEQAVQLLQDDVACDLLK, R9Q
MVH=55.1201
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 96896
TTPLEAASSGAR, T11A
MVH=44.3385
p-value=0.0001
sample: TCGA–AA–3666–01A, spectrum: 62163
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=71.7159
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 83505
TVEDLDGLLQQL YR, H10Q
MVH=60.7245
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 140921
TVEHGFPHQPSALGYSPSLHLLALGTR, R20H
MVH=76.6829
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 66963
TYGQVSGEALK, D2Y
MVH=45.0342
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 69706
VLLDGVQNLK, P9L
MVH=51.9117
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 75722
VPVTQATR, L3V
MVH=33.5360
p-value=0.0012
sample: TCGA-AA-3666-01A, spectrum: 112404
VQLPTESLQELLDLHR, T7S
MVH=69.7218
p-value=0.0001
sample: TCGA-AA-3666-01A, spectrum: 34254
VSRPESEQLR, N6S
MVH=61.7121
p-value=0.0002
sample: TCGA-AA-3666-01A, spectrum: 29506
WLLLCNPGLANTLVEK, D11N
MVH=55.2296
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 6210
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=38.7609
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 124158
AAAPAPVSEAVSR, C12S
MVH=31.5877
p-value=0.0001

m/z

Intensity(%)
sample: TCGA−AA−3672−01A, spectrum: 137159
AAPSVTLFPPSSEELQANK, T2A
MVH=51.4692
p−value=0.0001
sample: TCGA–AA–3672–01A, spectrum: 44717
AGVETTTPSK, K7T
MVH=58.0016
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 106704
ANPQLGAYAPPVHLGR, I14V
MVH=28.4068
p-value=0.0002
sample: TCGA-AA-3672-01A, spectrum: 79399
ASSSLLLNESEPTTNLQLR, D8N
MVH=68.9247
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 109835
DFYVVEPLAFEGTPEQK, I4V
MVH=55.9158
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 47858
DGYGFLNR, N1D
MVH=39.4116
p-value=0.0006
sample: TCGA–AA–3672–01A, spectrum: 98907
DSKEPFSSVELQAALSK, E3K
MVH=53.3176
p−value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 77188
DTEEEDFHVDQATTVK, V12A
MVH=62.4723
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 25491
DVDGLTSLNAGR, K12R
MVH=43.9800
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 5762
DVPGFLQSQSSGPGQPAVWHR, N11S
MVH=24.5103
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 33746
EASQGSSASSAPQSVK, H13Q
MVH=22.8919
p-value=0.0001
sample: TCGA−AA−3672−01A, spectrum: 123946
ELTDVVQK, A4D
MVH=33.4898
p−value=0.0006
sample: TCGA-AA-3672-01A, spectrum: 60033
EQPGSPEWLQLDK, Q13K
MVH=26.2924
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 51826
FGQDLLSPLLSVR, K13R
MVH=49.6405
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 91247
FLGQLLTAFPALR, A3G
MVH=39.1657
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 18024
FNLSQESSYLATQYSRLPR, S2N
MVH=28.0381
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 79294
FNSVTELCAELPEQK, V11I
MVH=33.9255
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 22893
FTVGDHSR, l3V
MVH=33.3645
p-value=0.0003
sample: TCGA-AA-3672-01A, spectrum: 17987
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=71.4805
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 89882
GFGTDEQALLDCLGSCSNK, R16C
MVH=59.1502
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 49007
GKWERPFEVKDTEEDFHVDQATTVK, V22A
MVH=71.1949
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 90155
GLLDDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-3672-01A, spectrum: 146936
GQTMALLQNTVESLSK, D9N
MVH=49.0782
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 116534
GVAGSSVAVLCPYNR, G5S
MVH=56.1263
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 2005
HQSVQLPR, N3S
MVH=43.5952
p-value=0.0006
sample: TCGA-AA-3672-01A, spectrum: 122675
KADLLNR, V5I
MVH=41.8436
p-value=0.0044
sample: TCGA-AA-3672-01A, spectrum: 78909
KLDSVFEEPLSK, R9P
MVH=40.4748
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 68949
LDSTDFTSTLK, G8S
MVH=59.2753
p-value=0.0001
sample: TCGA–AA–3672–01A, spectrum: 128413
LFEEDPAVGALVTGGDK, T1I
MVH=75.9895
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 62679
LLNLLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 40042
LLSDLPPSTGFQEAQSR, S5L
MVH=37.6866
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 116383
LLTQDEGPALVPGSR, G14S
MVH=38.5510
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 24601
LQQQHSEQPPLQPSPVTTR, M17T
MVH=48.9453
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 115858
LSVATGALEAAQGSKPQCQTR, S16P
MVH=34.9262
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 97912
LTPVSAQFQDLEGK, L8F
MVH=45.4411
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 89367
LVTDYTLAEADAALQK, E11D
MVH=59.1820
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 97903
MQYAPNTQVELLPQGR, H16R
MVH=39.8520
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 48864
NDYATMLPDSTELNQDTLNR, D14N
MVH=40.7401
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 55687
NSTLSEPGSGR, P4L
MVH=28.4011
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 124999
NTNSVPETAPAALPETR, K17R
MVH=41.9507
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 147435
QATFEYSFLPAEPMGR, G16R
MVH=25.7382
p-value=0.0001
sample: TCGA–AA–3672–01A, spectrum: 80378
SAVGELSEDSSNVVHLLK, Q15H
MVH=60.6718
p–value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 7295
SDPVTLNVL YGPDVPTLSPSK, G14V
MVH=45.4473
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 129515
SELPLDPLPLPTEEGNPLLK, V10L
MVH=59.7521
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 51993
SGGTLVVLGSGGEMTTVPLLHAALRN4T
MVH=29.9007
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 8218
SLDLDDWPLELLK, V9I
MVH=38.9939
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 138826
SLDPGLKEDTLEFLK, Q12E
MVH=35.9726
p-value=0.0001
sample: TCGA–AA–3672–01A, spectrum: 146916
SLSLLDSPGLLSGEK, V4I
MVH=42.6791
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 114231
SPADPTDLGGQTSPR, I6T
MVH=57.3957
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 96309
SQNKEDYDGLKEEFR, A8D
MVH=77.3423
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 105336
SQNKEDYDGLKEEFRK, A8D
MVH=73.3324
p-value=0.0001
sample: TCGA–AA–3672–01A, spectrum: 113751
TSLSAPPNTSSTENPK, S9T
MVH=38.4816
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 142625
TTPLEAASSGAR, T11A
MVH=41.5137
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 103711
VADNTQQQYVR, A5T
MVH=47.1074
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 1042
VLGTAGTEEGQK, I1V
MVH=33.1002
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 146368
VLTNQHNNPAGLYSSENLSNFNNALESK, Y6H
MVH=36.0138
p−value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 79855
VPSFETAEGLGAELK, T12A
MVH=54.0757
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 112581
VPVTQATR, L3V
MVH=43.6164
p-value=0.0012
sample: TCGA-AA-3672-01A, spectrum: 30444
VQLPTESLQELLDLHR, T7S
MVH=32.6515
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 86384
VSEVLLSR, G8R
MVH=39.3777
p-value=0.0025
sample: TCGA-AA-3672-01A, spectrum: 69283
VVFPSEEVVEQK, G6E
MVH=43.8982
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 38395
WERPFEVKDTEEDFHVDQATTVK, V20A
MVH=59.1739
p-value=0.0001
sample: TCGA-AA-3672-01A, spectrum: 62344
WLLLCNPGLANTLVEK, D11N
MVH=59.2218
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 59873
AAAAAAAPAAATAATTAATTAATAAQ, P17A
MVH=42.9896
p-value=0.0001
sample: TCGA–AA–3684–01A, spectrum: 38268
AAPSVTLPSSSEELQANK, T2A
MVH=50.1534
p–value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 8287
AEELGLPLLGLLR, V11I
MVH=56.1569
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 10855
AGVETTTPSK, K7T
MVH=60.5853
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 149822
AQQNLSWEELTK, A11T
MVH=41.7680
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 150411
ASSSLNLNESEPPTNLQLR, D8N
MVH=52.3211
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 58239
AYVVLLR, E1A
MVH=40.4767
p-value=0.0084
sample: TCGA-AA-3684-01A, spectrum: 142691
DCGEEAAAQWLTSFLK, T6A
MVH=52.2620
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 98510
DFENSLNQVK, M6I
MVH=41.4868
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 17854
DFYVVEPLAFEGTPEQK, I4V
MVH=63.8627
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 138203
DGYGFLNR, N1D
MVH=42.7768
p-value=0.0006
sample: TCGA-AA-3684-01A, spectrum: 50881
EALDVLDAVLK, G7D
MVH=43.5738
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 808
EASQGSSASSAPQSVK, H13Q
MVH=31.0264
p-value=0.0001
sample: TCGA–AA–3684–01A, spectrum: 76411
ECPCVHNNDLYSSSAK, G14S
MVH=41.3258
p–value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 50747
ESALEPGPVPEAPAGGPVHAVTVTLEK, R6P MVH=35.1090
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 6619
FFGSLPDSWAR, S11R
MVH=28.6491
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 67840
FLDKLPQQTGDR, H12R
MVH=48.0255
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 18343
FNKPVFVLMLDQNTK, E11D
MVH=65.4408
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 132292
FSLDALLTNVLPFEK, I10V
MVH=18.0345
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 115256
FTVGDHSR, I3V
MVH=39.1089
p-value=0.0003
sample: TCGA–AA–3684–01A, spectrum: 71270
FVSSSSSSGYYGGYGGVLTASDGLLAGNEK, A9G
MVH=52.7659
p–value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 89148
FYLGPTSVR, I9V
MVH=41.1613
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 6675
GFGTDEQALLDCLGSCSNK, R16C
MVH=55.8970
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 151262
GGTLSTPQTGSENDALYEYLR, G5S
MVH=38.6522
p-value=0.0001
sample: TCGA–AA–3684–01A, spectrum: 49444
GQTGALLQNTVESLSK, D9N
MVH=66.0021
p-value=0.0001
GAGSSVAVLCPYNR, G5S
MVH=36.1491
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 110269
KKPSEEEAAAAGGPPGPQVNPLPVTDEVV, V10A
MVH=45.1630
p-value=0.0001
sample: TCGA–AA–3684–01A, spectrum: 116662
KSVEEYANCHLAR, P2S
MVH=64.2509
p–value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 60176
LADGAGGAGGTQPYLDTLR, V1L
MVH=47.7226
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 90329
LCLDAMHGVVGPYVK, R2C
MVH=40.0176
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 33696
LEGANVQEAQK, T4A
MVH=52.6904
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 39207
LFEEDPAVGALVLGGDK, T1I
MVH=84.4088
p-value=0.0001
sample: TCGA–AA–3684–01A, spectrum: 3162
LHGHL YTPGQELTNDCK, E17K
MVH=66.9398
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 46809
LHVLVEPDHFK, Q2H
MVH=70.6713
p-value=0.0001
sample: TCGA–AA–3684–01A, spectrum: 130759
LLSDLPPSTGTFQEAQSR, S5L
MVH=36.8276
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 121607
LNEAVVAVQALLADPK, I5V
MVH=63.6178
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 152624
LTAEFEEAQTSACLLQEELEK, R14L
MVH=72.5699
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 137417
MELQETQLK, M6T
MVH=24.8876
p-value=0.0016
sample: TCGA–AA–3684–01A, spectrum: 129776
NDYATMLPDSTELNQDTLNR, D14N
MVH=54.1196
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 128538
NLPSLAEGASDPPTVASR, K7E
MVH=68.5950
p-value=0.0001
sample: TCGA–AA–3684–01A, spectrum: 71275
NLSLSGHVGFDLPDKLVNK, Q16K
MVH=31.5324
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 39131
NPLLDLAAYDQEGR, R3L
MVH=51.9933
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 54701
QLTVGVPRLR, K8R
MVH=27.8791
p-value=0.0006
sample: TCGA-AA-3684-01A, spectrum: 151457
SAVGELSEDSSNVVHLK, Q15H
MVH=41.4607
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 60923
SDPVTLNVLYGPDVPTLPSK, G14V,
MVH=53.1972
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 40572
SELPLDPLPLPTEEGNPLLK, V10L
MVH=44.3363
p-value=0.0001
sample: TCGA–AA–3684–01A, spectrum: 18488
SGGTLVLVGLGSEMTTVPLLHAALR, N4T
MVH=27.6068
p–value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 18622
SLSAFLVPMPTPGLTGK, G1S
MVH=27.9399
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 66839
SPADPTDLGGQTSPR, I6T
MVH=60.5276
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 117040
SVEEYANCHLAR, P1S
MVH=53.0607
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 87954
TDDLLASPPR, A1T
MVH=41.9237
p-value=0.0002
sample: TCGA-AA-3684-01A, spectrum: 96925
TTPLEAASSGAR, T11A
MVH=28.3714
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 38378
TVVQLEGDNKLVTAFK, T14A
MVH=45.4559
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 95892
VLGTAGTEEGQK, I1V
MVH=52.3017
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 64898
VPVTQATR, L3V
MVH=43.9760
p-value=0.0012
sample: TCGA-AA-3684-01A, spectrum: 112539
VQLPTESSQELLDLHR, T7S
MVH=35.0078
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 131921
VQVLAAQLLSEMK, D11E
MVH=59.9073
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 66770
VSYGLGEEEHDQEGGR, D7E
MVH=29.7732
p-value=0.0001
sample: TCGA-AA-3684-01A, spectrum: 7876
VVLQPEALFSLYSK, F8L
MVH=61.5789
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 62066
AAAAAAPAPAATAATTAATTAATAAQQ, P17A
MVH=49.3411
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 45709
AAPSVTLFPPSSEELQANK, T2A
MVH=56.7605
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 7854
AGVETTTPSK, K7T
MVH=35.3446
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 73898
APPRPGPVPEAAQPFLLTR, P19T
MVH=34.4678
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 44800
APSQHLSSFDPCFYR, R5H
MVH=70.4762
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 88805
AVDVLDCFLVK, A11V
MVH=69.0752
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 20188
AWLSSQAAELER, V7A
MVH=57.0542
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 60997
AYVLLR, E1A
MVH=39.7562
p-value=0.0084
sample: TCGA-AA-3695-01A, spectrum: 88972
CDPGALVLPFSGALELK, Y1C
MVH=51.9816
p-value=0.0001
sample: TCGA–AA–3695–01A, spectrum: 5792
CSGLLQVLFSPLEEVEVK, A3G
MVH=36.4264
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 22283
DFYVVEPLAFEGTPEQK, I4V
MVH=43.9679
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 101652
DGYGFLNR, N1D
MVH=40.5540
p-value=0.0006
sample: TCGA-AA-3695-01A, spectrum: 45379
DSMFGLTVK, A7T
MVH=44.8252
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 77559
DVDGLTSLNAGR, K12R
MVH=50.5872
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 61760
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=30.6745
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 46961
EALDVLDAVLK, G7D
MVH=58.7558
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 111357
EELGHLQNDLTSLENDK, M10L
MVH=40.5737
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 95217
EQPGSPEWLQLDK, Q13K
MVH=34.3981
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 55758
ESALEPGPVEAPAGGPPVHAVTVVTLEK, R6P
MVH=25.7804
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 12797
FFGSLPDSWAR, S11R
MVH=33.2448
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 96214
FLQENVFVAANHNASPLSLK, G14A
MVH=37.2592
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 22536
FNKPFVFLMLDQNTK, E11D
MVH=58.9314
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 112337
FNLSQESSYLATQYSLRPR, S2N
MVH=28.5561
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 82696
FTVGDHSR, I3V
MVH=22.8577
p-value=0.0003
sample: TCGA–AA–3695–01A, spectrum: 68710
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=64.8085
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 110161
FYLGAPTSVR, I9V
MVH=43.2106
p-value=0.0001
sample: TCGA-AA3695-01A, spectrum: 66621
GEAVLRPGLDSEPELSPEEQR, A11S
MVH=57.2219
p-value=0.0001
sample: TCGA–AA–3695–01A, spectrum: 12672
GFGTDEQALLDCLGSCSNK, R16C
MVH=51.4606
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 12957
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA–AA–3695–01A, spectrum: 45925
GQTGALLQNTVESLSK, D9N
MVH=51.6907
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 79358
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=37.9542
p-value=0.0001
sample: TCGA–AA–3695–01A, spectrum: 111828
KAPPRPGPVPEAAQPFLLFTTR, P20T
MVH=67.8333
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 83796
KSVEEYANCHLAR, P2S
MVH=58.9916
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 37724
LFEEDPAVGALVLTGGDK, T1I
MVH=72.1141
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 22960
LLNLLADLVER, R4L
MVH=49.1714
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 21723
LQPEDMFVYDLNEK, C9Y
MVH=27.9536
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 97397
LSDLQEALDQALNHVR, Y14H
MVH=29.8042
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 94647
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=49.9048
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 112860
LTQ AQL FDY Selpnfpr, G10S
MVH=44.4184
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 19900
MQYAPNTQVELLPQGR, H16R
MVH=60.3675
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 52757
MVDFAGMK, V7M
MVH=27.9099
p-value=0.0018
sample: TCGA-AA-3695-01A, spectrum: 105304
NEVLWHPTNLPLSPQGTVR, A3V
MVH=44.5354
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 37695
NPLLDLAAYDQEGR, R3L
MVH=49.9323
p-value=0.0001
sample: TCGA–AA–3695–01A, spectrum: 101525
NVSPVALPR, N3S
MVH=40.6664
p-value=0.0002
sample: TCGA-AA-3695-01A, spectrum: 63141
SDPVTLNLYGPDVPTLSPSK, G14V
MVH=42.4313
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 38713
SELPLDPLPLPTEEGNPLLK, V10L
MVH=52.7370
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 14083
SGGTLLVLGLGSEMTTVPLLHAALR-N4T
MVH=31.5615
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 63745
SLDLDDWPLELLK, V9I
MVH=41.1892
p-value=0.0001
sample: TCGA–AA–3695–01A, spectrum: 58494
SLQEEQSRPTTAVSSPGGPAR, P10T
MVH=39.2580
p–value=0.0001
sample: TCGA–AA–3695–01A, spectrum: 58512
SPADPTDLGGQTSPR, I6T
MVH=69.3729
p−value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 69200
SSGPGAGLCLFPLDEVHAK, K16E
MVH=42.0511
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 84116
SVEEYANCHLAR, P1S
MVH=54.3523
p-value=0.0001
sample: TCGA–AA–3695–01A, spectrum: 102790
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=65.1329
p−value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 21640
TCSFDFTGAVEDLSK, G3S
MVH=70.5122
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 58057
TSLSAPPNTSSTENPK, S9T
MVH=25.9194
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 88917
VQLPTESLQELLDLHR, T7S
MVH=33.9848
p-value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 92054
VSDLAATAYK, N2S
MVH=49.8843
p-value=0.0001
sample: TCGA–AA–3695–01A, spectrum: 22753
VSLAEELAQLSNSLLTWGR, A15T
MVH=57.4597
p–value=0.0001
sample: TCGA-AA-3695-01A, spectrum: 52013
VWQTVSPVESR, G10S
MVH=37.5518
p-value=0.0001
sample: TCGA–AA–3695–01A, spectrum: 35391
VYGDLLYTPAK, H7Y
MVH=42.6972
p–value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 42812
AAAAAAAAAPAAATAATTAATTAATAAQ, P17A
MVH=40.8481
p−value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 57724
AAAPAPVSEAVSR, C12S
MVH=64.1148
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 24488
AAPSVLTPPSESSEELQANK, T2A
MVH=53.6205
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 114262
ACNVLQSSHLEDYPFDAEY, N16D
MVH=38.5317
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 95061
AGDKDDLTEPALCALR, V12I
MVH=49.7612
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 9664
AGVETTPSK, K7T
MVH=55.6825
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 9451
AGVETTTPSKQSNNK, K7T
MVH=49.4143
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 16896
ALEDVFDALEGK, M5V
MVH=64.9728
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 61874
APPRPGPVPEAAQPFLFTTR, P19T
MVH=61.4747
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 29291
AQACNLĐQSGTNVAK, R4C
MVH=61.7247
p–value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 121769
ASSSLLLNESEPTTNLQLR, D8N
MVH=63.7950
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 28812
CALTGDEVKK, Y1C
MVH=50.4332
p−value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 106910
CSGLLQVLFSPLEEEVK, A3G
MVH=59.6568
p–value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 7443
DFYVVEPLAFEGTPEQK, I4V
MVH=48.2502
p−value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 110987
DGYGFLNR, N1D
MVH=46.1226
p-value=0.0006
sample: TCGA-AA-3710-01A, spectrum: 20539
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=94.0863
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 42398
DVPGFLQSQSSGPGQPAVWHR, N11S
MVH=31.3000
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 94676
DVTVLQNTDGNNNDWA, E14D
MVH=63.4942
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 26199
EALDVLDAVLK, G7D
MVH=57.1536
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 59087
EHLPEFLKDEQNK, S3L
MVH=26.0447
p-value=0.0002
sample: TCGA–AA–3710–01A, spectrum: 49557
ELVDDSLNNVR, V7I
MVH=57.2310
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 130306
EPSAPSLPTPAYQSLPAGGHAPTPPTPAPR, S15L
MVH=27.0118
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 112860
EQPGSPEWLQLDK, Q13K
MVH=39.6793
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 35454
ESALEPGPVPEAPAGGPVHAVTVTLEK, R6P
MVH=41.0248
p−value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 29255
EVDTTSPAPSTSSTVK, A4T
MVH=56.7911
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 122886
FFGSLPDSWAR, S11R
MVH=46.9156
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 49432
FLDKLPQQTGDR, H12R
MVH=52.9009
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 52766
FNLSQESSYLATQYSRLPR, S2N
MVH=23.4131
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 5012
FPGPCDYNFASDCR, L4P
MVH=59.6703
p−value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 99568
FTVGDHSR, I3V
MVH=44.9644
p-value=0.0003
sample: TCGA-AA-3710-01A, spectrum: 52815
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK-A9G
MVH=66.7540
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 59744
FYLGGPTSVR, I9V
MVH=51.3866
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 41031
GALQFVTHYQQSSTQR, H11Q
MVH=59.5024
p–value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 131702
GFGTDEQALLDCLGSCSNK, R16C
MVH=61.6639
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 131912
GLLDLLEER, V3I
MVH=45.4290
p-value=0.0038
sample: TCGA–AA–3710–01A, spectrum: 109964
GLLVDSR, I4V
MVH=38.5419
p−value=0.0012
sample: TCGA-AA-3710-01A, spectrum: 47148
GLVEGACQK, K4E
MVH=42.6362
p−value=0.0003
sample: TCGA−AA−3710−01A, spectrum: 24804
GQTGALLQNTVESLSK, D9N
MVH=74.8679
p−value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 13433
GVAGSSVAVLCPYNR, G5S
MVH=47.7610
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 4021
GVAGSSVAVLCPYNRK, G5S
MVH=33.5711
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 87330
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=66.0295
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 73681
HMTAVVK, Y1H
MVH=31.8535
p-value=0.0044
sample: TCGA-AA-3710-01A, spectrum: 121778
HTDFEEREYVVLLR, E3D
MVH=30.3781
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 56103
KADLLNR, V5I
MVH=45.4507
p-value=0.0044
sample: TCGA-AA-3710-01A, spectrum: 52310
KAPPRPGPVPEAAQPFLFTTR, P20T
MVH=42.0479
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 19515
KKEVDTTSPAPSTSSTVK, A6T
MVH=49.1699
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 87735
KKPSEEEAAAAAGGPPGGPQVNPLPVTDEVV10A
MVH=50.2701
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 121229
KLDSVFEELSK, R9P
MVH=54.7683
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 70086
LAGALGPCLSLNVK, V9I
MVH=63.0392
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 132864
LALSPNAQLLALASGSSLHL YNTR, V9I
MVH=55.2066
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 60967
LCLDAMHGTVGPYVK, R2C
MVH=37.9772
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 25022
LFEEDPAVGLVLGDK, T1I
MVH=83.2222
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 31609
LHVLVEPDHFK, Q2H
MVH=64.0628
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 89016
LLDAETTAGAWPNVAAVSLTGR, A9G
MVH=30.0545
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 75472
LQELTPSSGDPEHDPASTHK, P4L
MVH=50.1939
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 131985
LRDALCSLLTLSR, R6C
MVH=51.5758
p-value=0.0002
sample: TCGA-AA-3710-01A, spectrum: 61011
LTFGCLGGSDNFK, S4G
MVH=65.5785
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 51488
MKDVPGFLQQSQSSGPGQPAVWHR, N13S
MVH=56.7154
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 5009
MQYAPNTQVELLPQGR, H16R
MVH=65.3670
p−value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 29054
NKSTESLQTNVQR, A9T
MVH=56.5196
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 24938
NPLLDAAYDQEGR, R3L
MVH=61.7247
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 58602
NTNSVPETAPAALPETR, K17R
MVH=42.1487
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 42001
NTVLATWQPYSTSK, T11S
MVH=63.4727
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 133371
NTVLCNVVEKFLQADLAR, Q10K
MVH=52.3598
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 131529
QSGGSSQAGAVTVSDVQELMR, V10A
MVH=38.4877
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 102427
QTVQVDEHARPQTTLEQQLQK, M3V
MVH=25.3883
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 45024
QVEEEDGSRDPLFDFLESCLR, L2V
MVH=25.8616
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 13262
QVGDFHQVLLR, A2V
MVH=32.2839
p-value=0.0002
sample: TCGA-AA-3710-01A, spectrum: 17628
SALSGHLETLLLGLLK, V10L
MVH=81.5570
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 122819
SAVGELSEDSSNVVHLK, Q15H
MVH=65.1459
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 113417
SEALPTDLPTPSAPDLTEPK, A10T
MVH=41.2065
p–value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 133186
SGGTLVLVGLGSEMTTVPLLHAALR-N4T
MVH=35.8507
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 129156
SGGVERPFVLAR, M4V
MVH=57.2779
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 32863
SKLTFGCLGGSDNFK, S6G
MVH=55.4179
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 26053
SLDPGLKEDTLEFLKL, Q12E
MVH=48.0210
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 40318
SQNKEDYDGLKEEFR, A8D5
MVH=63.6151
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 49169
SQNKEDYDGLKEEFRK, A8D
MVH=84.2252
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 30011
SSSSVTSETQPCTPSSSDCSDLQR\*Y20C
MVH=44.8819
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 19069
SSSYSGEYGSGGGK, G10S
MVH=64.9144
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 9753
SSSYSGEYGS>GGR, G10S
MVH=47.7688
p-value=0.0002
sample: TCGA-AA-3710-01A, spectrum: 47647
STESLQTNVQR, A7T
MVH=61.1628
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 112372
TAASGVEASSRPLDHAQPPSSLVLDKESERVYK, N9S
MVH=76.0932
p-value=0.0001
sample: TCGA–AA–3710–01A, spectrum: 62254
TLAQLNPESSLFLTASK, I14T
MVH=82.9845
p-value=0.0001
sample: TCGA- AA-3710-01A, spectrum: 44143
TLDPFETMLK, S2L
MVH=43.9885
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 75104
TTPLEAASSGAR, T11A
MVH=59.5418
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 35910
TVASPGVSVEEAQEQLDLGGVTLR, T8S
MVH=37.8031
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 24262
TVVQLEGDNKLVTAFK, T14A
MVH=45.1844
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 41794
VEHWGLDKPLLK, Q8K
MVH=64.4311
p-value=0.0001
Sample: TCGA-AA-3710-01A, spectrum: 82703
VLGTAGTEEGQK, I1V
MVH = 46.1178
p-value = 0.0001
sample: TCGA-AA-3710-01A, spectrum: 73672
VLSTTNAER, D6N
MVH=48.0722
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 122276
VPSFETAEGLGAELK, T12A
MVH=61.3114
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 55706
VPVTQATR, L3V
MVH=44.9486
p-value=0.0012
sample: TCGA-AA-3710-01A, spectrum: 81035
VQLPTESLQELLDLHR, T7S
MVH=38.6046
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 28795
VSRPESQELR, N6S
MVH=46.8055
p-value=0.0001
sample: TCGA-AA-3710-01A, spectrum: 69470
YFHPYLAYCSNEVYQQR, H1Y
MVH=54.8770
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 52574
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=30.9239
p-value=0.0010
sample: TCGA-AA-3715-01A, spectrum: 9146
AGVETTTPSK, K7T
MVH=60.9511
p-value=0.0001
sample: TCGA−AA−3715−01A, spectrum: 100060
AVDVVLDCFLVK, A11V
MVH=54.3035
p−value=0.0001
sample: TCGA–AA–3715–01A, spectrum: 115739
CSGLLQVLFSPLEEVEVK, A3G
MVH=27.8985
p−value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 111747
DGYGFLNR, N1D
MVH=42.7733
p-value=0.0006
sample: TCGA-AA-3715-01A, spectrum: 34276
DLEAHVDSANK, I6V
MVH=26.6749
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 69697
DYCVLLEGSLALR, G3C
MVH=84.9984
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 46606
EALDVLDKVK, G7D
MVH=41.6461
p-value=0.0001
sample: TCGA–AA–3715–01A, spectrum: 57999
ELVDDSLNNVR, V7I
MVH=52.6904
p−value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 113268
EQPGSPEWLQLDK, Q13K
MVH=32.3628
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 54018
ESALEPGPVPVEAPAGGPVHAVTVTLEK, R6P
MVH=28.2763
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 77448
FGLQAQLVTTDFQK, M7L
MVH=64.9011
p-value=0.0001
sample: TCGA–AA–3715–01A, spectrum: 52302
FGNEVLPVTVAVK, T11A
MVH=46.2037
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 15854
FGQDLLSPLLSVR, K13R
MVH=49.4889
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 57845
FLDKLPQQTGDR, H12R
MVH=43.1535
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 80714
FTVGDHSR, I3V
MVH=46.3250
p-value=0.0003
sample: TCGA-AA-3715-01A, spectrum: 69272
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=49.6899
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 111133
GVALSNVVKH, I8V
MVH=50.3998
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 31455
LALLLMASQEPQR, T2A
MVH=44.4953
p−value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 99181
LFEEDPAVGALVLTGGDK, T1I
MVH=67.4657
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 106790
LLSDLLPPSTGTFQEAQSR, S5L
MVH=32.4367
p-value=0.0001
sample: TCGA–AA–3715–01A, spectrum: 109943
STESLQTNVQR, A7T
MVH=55.5643
p−value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 81511
TTPLEAASSGAR, T11A
MVH=32.3809
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 31162
VLGTLLGTVVK, D10V
MVH=49.3897
p-value=0.0001
sample: TCGA−AA−3715−01A, spectrum: 55325
VPVTQATR, L3V
MVH=45.3803
p-value=0.0012
sample: TCGA-AA-3715-01A, spectrum: 70364
VQLPTESLQELLDLHR, T7S
MVH=31.4203
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 107625
VQVLAAQLLSEMK, D11E
MVH=74.6985
p-value=0.0001
sample: TCGA-AA-3715-01A, spectrum: 43121
VWQTVSPVESR, G10S
MVH=30.9327
p-value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 53970
AAAAA###APAAAATAATTTAATTAATAAAQ, P17A
MVH=44.6011
p−value=0.0002
sample: TCGA-AA-3818-01A, spectrum: 45330
AAPSVTTLFPPSSEELQANK, T2A
MVH=49.3199
p-value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 125144
ACNVLQSSHLEDYPDAEY, N16D
MVH=32.0337
p–value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 10595
AGVETTPSK, K7T
MVH=53.2156
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 108766
CDPGALVLPFSGAELK, Y1C
MVH=55.3359
p-value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 17368
DFYVVEPLAFEGTPEQK, I4V
MVH=52.9330
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 121948
DGYGFLNR, N1D
MVH=46.2273
p-value=0.0006
sample: TCGA-AA-3818-01A, spectrum: 31999
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=73.5889
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 46280
EALDVLDAVLK, G7D
MVH=44.8565
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 60727
ELVDDSLNNVR, V7I
MVH=46.9072
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 123786
EQPGSPEWLQLDK, Q13K
MVH=40.3777
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 55471
ESALEPGPVPEAPAGGPVHAVTVTLLEK, R6P
MVH=37.0534
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 6887
FFGSLPDSWAR, S11R
MVH=36.7688
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 68605
FLDKLPQQTGDR, H12R
MVH=47.1287
p-value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 23634
FQLGNSGPNSTLK, S4G
MVH=44.9621
p–value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 78533
FYLGGPTSVR, I9V
MVH=44.2923
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 6753
GFGTDEQALLDCLGSCSNK, R16C
MVH=59.0984
p-value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 45339
GQTGALLQNTVESLSK, D9N
MVH=53.4752
p−value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 24667
GVAGSSVAVLCPYNR, G5S
MVH=37.8578
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 107406
KFFGSLPDSWAR, S12R
MVH=48.3066
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 97616
KKPSEEEAAAAAGGPPGGPQVNPLPVTD RVA V10A
MVH=43.9043
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 81543
KPAAGLSAAPVPTTPAAGAPLMDFGNDVFPPAPR, A14T
MVH=57.1841
p-value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 34289
KVLLDVQNL, P10L
MVH=60.4025
p–value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 54552
LADGGAGGTFQPYLDTLR, V1L
MVH=58.1021
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 135360
LASDLLEWLQR, R10Q
MVH=72.3513
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 36449
LFEEDPAVGLVLTGGDK, T1I
MVH=73.0826
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 46549
LFSLLSTALLR, V8A
MVH=51.6590
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 135571
LLDTAFDLDFLK, V10I
MVH=82.5130
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 28322
LLNLLADLVER, R4L
MVH=54.9723
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 108725
LSDLQEALDQALNHVR, Y14H
MVH=58.6488
p-value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 23190
LVVVGADGVGK, G7D
MVH=43.1517
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 13291
MAQWGNKPLC, V9I
MVH=44.1134
p-value=0.0002
sample: TCGA-AA-3818-01A, spectrum: 70756
MKDVPGFLQQSQSSGPGQPAVWHB, N13S
MVH=81.4689
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 14919
MQYAPNTQVELLPQGR, H16R
MVH=58.9518
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 32867
MVAVGLCR, H8R
MVH=44.4169
p-value=0.0006
sample: TCGA-AA-3818-01A, spectrum: 126041
NPSLLPLEAR, Q2P
MVH=44.3385
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 68544
NTNSVPETAPAALPETR, K17R
MVH=33.1631
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 131128
NVSPVALPR, N3S
MVH=38.5716
p-value=0.0003
sample: TCGA–AA–3818–01A, spectrum: 34127
QVGDFHQVLLR, A2V
MVH=36.5579
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 86911
RQDLQSDGFSLETCK, K5Q
MVH=48.7372
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 7477
RWLLLCNPGLANTLVEK, D12N
MVH=70.5575
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 55169
SDPVTLNVLYGPDVPTLS, G14V
MVH=52.8130
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 18001
SGGTLVLVLGSEMPLLHAALRN4T
MVH=45.2734
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 59393
SPADPTDLGGQTSPR, I6T
MVH=61.3114
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 103550
SPPGAAAPAAAKPPPLSAK, S8P
MVH=30.5961
p-value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 133037
SPVGSGAPQAAAPAPAAHVAGNPGGDAAPAATGTAASLAAAAGSEDDEKK, T42A
MVH=75.8147
p–value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 60375
SQNKEDYDGLKEEFRK, A8D
MVH=75.5523
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 49355
STESLQTNVQR, A7T
MVH=53.0252
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 132096
TAASGVEASSRPLDHAQPPSSLVLDK, N9S
MVH=50.3414
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 123229
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=62.9345
p-value=0.0001
Sample: TCGA-AA-3818-01A, spectrum: 70510
TMMNTWTLQR, K10R
MVH=46.8638
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 84921
TTPLEAASSGAR, T11A
MVH=49.4009
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 55895
TVASPGVSVEEAQVEQLDLGGVTLLR, T8S
MVH=41.0358
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 72861
TVEDLDGLLQQL YR, H10Q
MVH=57.8836
p-value=0.0001
sample: TCGA–AA–3818–01A, spectrum: 125224
TVEHGFPHQPSALGYSPSLHLLALGTR, R20H
MVH=107.1276
p–value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 59306
TYGQVSGEALK, D2Y
MVH=55.1322
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 70255
VLLDGVQNL, P9L
MVH=59.9100
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 126131
VPADLGAEAGLQQLLGLR, A17T
MVH=100.7055
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 99604
VQLPTESLQELDLHR, T7S
MVH=36.9861
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 51513
VWQTVSPVESR, G10S
MVH=36.7859
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 27950
WLLLCPGPLANTLVEK, D11N
MVH=71.9213
p-value=0.0001
sample: TCGA-AA-3818-01A, spectrum: 7938
YLTLDSFDAMFR, G6S
MVH=56.7570
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 82586
AAAPAPVSEAVSR, C12S
MVH=47.5845
p–value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 52099
AAPSVTTLFPPSSEELQANK, T2A
MVH=60.0328
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 11476
AGVETTTPSK, K7T
MVH=58.9374
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 11237
AGVETTTPSKQSNNK, K7T
MVH=36.2632
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 50732
APSQHLSSFDPCFYR, R5H
MVH=59.9831
p–value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 16741
AWLSSQAAELER, V7A
MVH=55.8333
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 57542
CPAAPPPAGGAANNNHGAGSGAGGR, G1C
MVH=24.9437
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 83750
DAGNEQDLGLQYK, N1D
MVH=44.6038
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 85703
DDANNDPQWCEEQLLA, S10C
MVH=38.5347
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 19222
DFYVVEPLAFEGTPEQK, I4V
MVH=50.0498
p–value=0.0001
sample: TCGA-00-0000-01A, spectrum: 153421
DGYGLNR, N1D
MVH=41.6414
p-value=0.0006
sample: TCGA-AA-3848-01A, spectrum: 36164
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=100.8986
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 37406
DTEEEDFHVDQATTVK, V12A
MVH=66.7074
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 118704
DVDGLTSLNAGR, K12R
MVH=54.7958
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 74477
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=44.9356
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 134903
EAGFPPGVVNLTLTGYGPTAGAALAQHMDVDK, V27M
MVH=25.4864
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 29954
EAPETDTSPSLWNVEFAK, D13N
MVH=41.7109
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 110146
EELGHLQNDLTSLENDK, M10L
MVH=47.8957
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 96016
EHTLHLEAELEK, S4L
MVH=36.2908
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 155532
EQPGSPEWLQLDK, Q13K
MVH=29.2242
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 64868
ESALEPGPVEAPAGGPVHAVTVTLLEK, R6P
MVH=30.8141
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 7064
FFGSLPDSWAR, S11R
MVH=35.0065
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 7976
FGQDLLSPLLSDVR, K13R
MVH=44.7002
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 71748
FLDKLPQQTGDR, H12R
MVH=45.9368
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 87729
FNLSQESSYLATQYSLRPR, S2N
MVH=25.4793
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 20085
FSLDALLTNVLPFEK, I10V
MVH=39.3048
p–value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 54035
FSPLLTNLNLLAENGR, T5I
MVH=46.4325
p–value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 127087
FTVGDHSR, I3V
MVH=42.0941
p-value=0.0003
sample: TCGA-AA-3848-01A, spectrum: 75787
FVSSSSSGGYGGGYGGVTASDGLLAGNEK_A9G
MVH=63.9491
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 96857
FYLGPGTTSVR, I9V
MVH=45.6760
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 142897
GKWERPFEVKDTEEDFHVDQATTVK, V22A
MVH=97.8768
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 7211
GLLDDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA–AA–3848–01A, spectrum: 19926
KFSLDALLTNVLPFEK, I11V
MVH=37.6882
p–value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 121134
KKPSEEEAAAAGGPPGQPQVNLPVTDEVV10A
MVH=50.6547
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 88804
KPAAGLSAAPVPPTTPAAAPLMDFGNDVFPPAPR, A14T
MVH=47.2453
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 63693
LADGGGAGGTFQPYLDTLR, V1L
MVH=56.4295
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 165898
LDSTDFTSTLK, G8S
MVH=54.0278
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 41353
LFEEDPAVGALVLTGGDK, T1I
MVH=80.0011
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 8195
LLDLFYPGDQSQVTGFLK, T17I
MVH=34.6264
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 7649
LLFTQSEPLVPSAAALAR, A4T
MVH=40.4505
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 145051
LLSDLLPPSTGFQEAQSR, S5L
MVH=40.9317
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 152246
LPAPTHTPATAPVPAR, R6H
MVH=54.7000
p–value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 94257
LQELTPSSGDPEHDPASTHK, P4L
MVH=61.3848
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 129105
LQQQHSEQPPLQPSPVTTR, M17T
MVH=41.5696
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 134887
LSDLQEALDQALNHVR, Y14H
MVH=59.9752
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 49727
LSQELDFVSHHVR, R3Q
MVH=32.0897
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 87156
LSVFSTLDAPVAPSDK, V7I
MVH=42.2657
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 100608
LSVTWPEGDELLPNELRPAGTPLGALR, V16I
MVH=22.8311
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 6273
LVTDYTLEADAAKLQK, E11D
MVH=55.2451
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 86143
MKDVPGLQSQSSGPGPQAVWHR, N13S
MVH=71.0897
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 16456
MQYAPNTQVELLPQGR, H16R
MVH=48.8799
p–value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 142292
NLPSLAEQGASDPPTVASR, K7E
MVH=54.5902
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 41274
NPLLDLAAAYDQEGR, R3L
MVH=56.4215
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 83654
NTNSVPETAPAALPETR, K17R
MVH=36.8621
p-value=0.0001
sample: TCGA-AE-3848-01A, spectrum: 28198
QATVGNLINTERPGMLDFTGK, D6N
MVH=18.3822
p-value=0.0002
sample: TCGA–AA–3848–01A, spectrum: 83158
QQPNPGSELCYK, N7S
MVH=30.5671
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 12554
RTDKDTELTSEQVR, R13Q
MVH=44.1767
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 31599
SALSGHLETLLLGLLK, V10L
MVH=65.9942
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 168819
SAVGELSEDSSNVVHLK, Q15H
MVH=64.7327
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 64503
SDPVTNLNLGYGPDLVTLLSPSK, G14V
MVH=51.1349
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 156083
SEALPTDLPTPSAPDLTEPK, A10T
MVH=47.8952
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 42505
SELPLDPLPLPTEEGNPLLK, V10L
MVH=60.0678
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 105967
SLNDLTAR, K8R
MVH=38.1920
p-value=0.0006
sample: TCGA-AA-3848-01A, spectrum: 70499
SPADPTDLGGQTSPR, I6T
MVH=66.6237
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 23056
SSSYSGEYGSGGGK, G10S
MVH=57.5207
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 22869
SSYSGEYGSGGGKR, G10S
MVH=42.9260
p-value=0.0002
sample: TCGA-AA-3848-01A, spectrum: 109299
TLEGLQVEEPEPVYK, E14K
MVH=56.3475
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 105828
TTPLEAASSGAR, T11A
MVH=41.7680
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 65355
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=76.7452
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 88967
TVEDLDGLQQL YR, H10Q
MVH=60.7245
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 30425
VELFFKDDANNDPQWCSEQLLAAK, S16C
MVH=33.9691
p-value=0.0001
sample: TCGA–AA–3848–01A, spectrum: 85716
VFSVAELQAR, S9A
MVH=47.2857
p-value=0.0002
sample: TCGA-AA-3848-01A, spectrum: 146312
VPLASQGLGPGSTVLLVVDKCDEPLNLLVR, S26N
MVH=76.0465
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 80323
VPVTQATR, L3V
MVH=44.2980
p-value=0.0012
sample: TCGA–AA–3848–01A, spectrum: 123520
VQLPTESLQELDLHR, T7S
MVH=63.7789
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 2638
VSEVLLSR, G8R
MVH=39.6737
p-value=0.0025
sample: TCGA-AA-3848-01A, spectrum: 166325
VVFPSEEVVEQK, G6E
MVH=22.0225
p-value=0.0001
sample: TCGA-AA-3848-01A, spectrum: 31057
WLLLLCNPGLANTLVEK, D11N
MVH=78.2122
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 85782
AAAAAAAAAPAAAATAATTAATTAATTAATAAQ, P17A
MVH=21.8284
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 88741
AAAPAPVSEAVSR, C12S
MVH=47.5845
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 60994
AAPSVTTLFFPSSEELQANK, T2A
MVH=49.3897
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 11805
AGVETTTPSK, K7T
MVH=56.9341
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 87074
ALDRPYTSK, E3D
MVH=34.3021
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 60215
APSQHLSSFDPCFYR, R5H
MVH=61.7039
p-value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 17247
ASSSSLLLNESEPTTNLQLR, D8N
MVH=48.8006
p−value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 15779
ATQFTGATGTLMTTETTK, A10T
MVH=39.6073
p–value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 28198
AWLSSQAAELER, V7A
MVH=58.2173
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 66015
CPAAPPPPPAGGAANNNHGAGSGAGGR, G1C
MVH=32.7654
p-value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 30654
DFYVVEPLAFEGTPEQK, I4V
MVH=39.1165
p–value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 154164
DGYGFLNR, N1D
MVH=44.3623
p-value=0.0006
sample: TCGA-AA-3864-01A, spectrum: 35645
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=50.5837
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 47421

DTEEEDFHVDQATTVK, V12A
MVH=60.7312
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 62762
EALDVLDAVLK, G7D
MVH=54.8445
p-value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 11829
EASQGSSASSAPQSVK, H13Q
MVH=21.2510
p–value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 60679
EGAAHTFAQYNMDQFTPVK, A6T
MVH=39.4976
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 80231
ENVATTDTLESTTVGSSV, T16S
MVH=62.6694
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 156122
EQPGSPEWLQLDK, Q13K
MVH=34.5324
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 73232
ESALEPGPVEAPAGGPVHAVTVVTLLEK, R6P
MVH=29.5286
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 18564
FFGSLPDSWAR, S11R
MVH=35.0065
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 113698
FGLQAQLVTTDFQK, M7L
MVH=57.0889
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 19641
FGQDLLSPLLSVR, K13R
MVH=46.1650
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 112887
FGVLFCDK, R6C
MVH=55.0048
p-value=0.0002
sample: TCGA-AA-3864-01A, spectrum: 89691
FLDKLPQQTGDR, H12R
MVH=40.9921
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 63090
FLGQLLTAFPALR, A3G
MVH=49.3003
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 31004
FNKPFVFLMLDQNTK, E11D
MVH=68.9195
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 103620
FNLSQESSYLATQYSLRPR, S2N
MVH=26.1612
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 128989
FTVGDHSR, I3V
MVH=37.1016
p-value=0.0003
sample: TCGA-AA-3864-01A, spectrum: 93863
FVSSSSSGGYYGGYGGVLTASDGLLAGNEK, A9G
MVH=60.9328
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 111567
FYLGPGPTSVR, I9V
MVH=43.2106
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 18263
GGTLSTPQTGSENDALYEYLR, G5S
MVH=41.5284
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 144257
GKWERPFEVKDTEEEEDFHVDQAPTVK, V22A
MVH=91.6106
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 71989
GQTGALLQNTVESLSK, D9N
MVH=59.3453
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 123360
GYQQDAYDGKDYLANEDLR, R3Q
MVH=56.6212
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 26173
HASSGSFLSSANEHLK, P9S
MVH=46.8698
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 108049
HLSQTYQQQYGR, R1H
MVH=68.8205
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 76361
KADLLNR, V5I
MVH=39.2553
p-value=0.0044
sample: TCGA-AA-3864-01A, spectrum: 79817
KENVATTDTLESTTVGSSV, T17S
MVH=42.9082
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 88770
KNPDSHYGELLEK, Q6H
MVH=42.9581
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 50672
LAKVDATEVSDLQQYGVRE9V
MVH=40.2518
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 136026
LCGVYN Active MDVVK, D3G
MVH=45.5170
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 157430
LCGVYNAVMDVVKK, D3G
MVH=44.7986
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 113035
LCLDAMHGVVGPYVK, R2C
MVH=36.5882
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 13139
LDDLLSGHKK, V5I
MVH=37.8692
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 4579
LDSTDFTSTLKL, G8S
MVH=59.2753
p-value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 147858
LDSVLEFNLPDSLLLLR, S8N
MVH=34.3190
p−value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 155934
LEGSDVQLLEYK, E12K
MVH=58.6864
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 51245
LFEEDPAVGALVLTGGDK, T1I
MVH=79.0900
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 63034
LFSLLSTALLR, V8A
MVH=60.8567
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 131243
LGETYKDHENLVLTK, A14T
MVH=65.8532
p-value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 140563
LGGLQPSQDR, G7S
MVH=32.2470
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 67831
LGLQSLHNR, R7H
MVH=43.0792
p-value=0.0002
sample: TCGA-AA-3864-01A, spectrum: 26968
LKDLNTLEPLK, S5N
MVH=47.6774
p-value=0.0002
sample: TCGA-AA-3864-01A, spectrum: 29589
LLENELEGFDLR, G10D
MVH=62.5224
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 33846
LNHEGEVNCAR, R9C
MVH=25.9784
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 130933
LQQQHSEQPPLQPSPVTTR, M17T
MVH=45.6573
p−value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 147629
LSDLQEALDQALNHVR, Y14H
MVH=54.6108
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 111918
LTLTFNCTR, R7C
MVH=40.1483
p-value=0.0005
sample: TCGA-AA-3864-01A, spectrum: 61682
NPLLDLAAYDQEGR, R3L
MVH=53.5678
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 56041
NSLSEETVR, M3L
MVH=39.5114
p-value=0.0006
sample: TCGA–AA–3864–01A, spectrum: 23587
NSTLSEPGSGR, P4L
MVH=41.0849
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 89702
NTNSVPETAPAALPETR, K17R
MVH=47.2989
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 83630
SALVHLLNYQDDAELATHALPELTK, R18H
MVH=69.1762
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 7403
SAVGELSEDSSNVVHLLK, Q15H
MVH=26.4805
p-value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 156646
SEALPTDLPTPSAPDLTEPK, A10T
MVH=47.5660
p–value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 52406
SELPLDPLPLPTEEGNPLLK, V10L
MVH=48.6127
p−value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 82669
SFDMYSGDVMHLVK, A1S
MVH=35.9903
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 20137
SGGTLVLVGLGSEMTTVPLLHAALR, N4T
MVH=50.6708
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 62626
SLDPGLKEDTLEFLKLK, Q12E
MVH=32.8158
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 116
SPAADAKPAPK, T3A
MVH=48.0577
p-value=0.0004
sample: TCGA−AA−3864−01A, spectrum: 77852
SPADPTDLGGQTSPR, I6T
MVH=54.8417
p−value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 120273
SPPGAAAPAAAKPPPLSAK, S8P
MVH=34.5257
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 109782
SQLCDNATLYAQK, A8T
MVH=68.2527
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 58080
SQNKEDYDGLKEEFR, A8D
MVH=57.9442
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 7654
TVEHGFPHPQPSALGYSPLHALLALGTR, R20H
MVH=81.8415
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 17657
VDATEVSDLQQGVR, E6V
MVH=95.5346
p-value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 28573
VGGTKPAGGDFGEVLNSTANASATTTEPLPEK, A18T
MVH=52.1283
p–value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 107346
VLSTTNAER, D6N
MVH=32.0039
p-value=0.0003
sample: TCGA–AA–3864–01A, spectrum: 147795
VPLASQGLGPGSTVLLVDKCDEPLNLLVR, S26N
MVH=57.2389
p-value=0.0001
sample: TCGA–AA–3864–01A, spectrum: 75999
VPVTQATR, L3V
MVH=49.1024
p-value=0.0012
sample: TCGA-AA-3864-01A, spectrum: 14304
VSEVLLSR, G8R
MVH=38.3776
p-value=0.0025
sample: TCGA-AA-3864-01A, spectrum: 133703
WERPFEVKDTEEEDFHVDQATTVK, V20A
MVH=68.8045
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 92246
YVPSGFYLASGDVSGK, A2V
MVH=37.0457
p-value=0.0001
sample: TCGA-AA-3864-01A, spectrum: 92530
YVSLLYTNYEAGKDDYVK, I2V
MVH=38.7946
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 56118
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=55.0234
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 42117
AAPSVTTLFPSSSEELQANK, T2A
MVH=57.6849
p-value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 7628
AGVETTTPSK, K7T
MVH=49.4887
p–value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 101040
APWLEQERPEYWDQETR, G8R
MVH=71.8758
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 21475
ASLLNNAFQLLSLGK, V11I
MVH=60.8289
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 11252
ASSSLLLNESEPTTNLQLR, D8N
MVH=47.1466
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 28212
AVPPNNSNAAEDDLPTVELQGLVPR, V22L
MVH=38.7975
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 55086
AYVLLR, E1A
MVH=39.3505
p-value=0.0084
sample: TCGA–AA–3986–01A, spectrum: 102789
CPSPPMTNLLLSVGGQHQGVFLPR, I7T
MVH=72.5454
p−value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 99295
DGYGFLNR, N1D
MVH=45.5688
p-value=0.0006
sample: TCGA-AA-3986-01A, spectrum: 41535
DSMFGGLTVK, A7T
MVH=50.5739
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 31725
DTEEEDFHVDQATTVK, V12A
MVH=66.7074
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 96222
EAGFPPGVVNLTLTGYGPTAGAALADVHMDD, V27M
MVH=46.2947
p-value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 43272
EALDVLDVLKV, G7D
MVH=54.9703
p-value=0.0003
sample: TCGA-AA-3986-01A, spectrum: 67964
EALELDSLR, V2A
MVH=44.1134
p-value=0.0005
sample: TCGA–AA–3986–01A, spectrum: 75261
EELGHNLQNDLTSLENDK, M10L
MVH=31.6407
p-value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 46546
ELVDDSLNNVR, V7I
MVH=54.9703
p–value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 100903
EQPGSPEWLQLDK, Q13K
MVH=44.5364
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 50516
ESALEPGPVEAPAGPVHAVTVTRLLEK, R6P
MVH=41.6924
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 9892
EVTNVNLSPR, K1E
MVH=39.6834
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 3160
FEEGENSLLHLK, A4G
MVH=49.4475
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 21248
FNKPFVFLMLDQNTK, E11D
MVH=57.2004
p-value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 63280
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=72.0464
p−value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 67893
FYLGPGTSEVR, I9V
MVH=35.7099
p-value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 12279
GFGTDEQALLDCLGSCSNK, R16C
MVH=59.3348
p–value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 99066
GLSFDAATSGGSASSEK, T2I
MVH=83.8295
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 49406
GQTGALLQNTVESLSK, D9N
MVH=74.2790
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 32855
GVAGSSVAVLCPYNR, G5S
MVH=53.2559
p-value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 81415
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=64.1875
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 1822
HNYGAVESFTVQR, V5A
MVH=58.8231
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 31966
KALFMDCLHAR, T5M
MVH=54.6179
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 75752
KAPPRPGPVPEAAQPFLFTTR, P20T
MVH=73.5623
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 75268
KKPSEEEAAAAAAGGPPGGPQVNPLPVTDEVV EV10A
MVH=68.0131
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 32884
KVLLDGVQNLR, P10L
MVH=46.9072
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 75295
LCLDAMHGVVGPYVK, R2C
MVH=48.0084
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 2361
LDSTDFSTLKLK, G8S
MVH=57.1244
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 74345
LDVDKDGFVTEGELK, A3V
MVH=46.0864
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 34882
LFEEDPAVGALVLTGGDK, T11
MVH=77.7881
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 89393
LLDAETTAGAWPNVAAVSLTGR, A9G
MVH=40.9841
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 21648
LLNLLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 102144
LLSDLLPPSTGTFQEAQSR, S5E
MVH=45.2539
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 85321
LQQQHSEQPPLQPSPVTTR, M17T
MVH=48.3674
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 96199
LSDLQEALDQALNHVR, Y14H
MVH=61.1499
p-value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 34053
LTDETVLGCSGFHGDCCLTLTK, K4E
MVH=58.3071
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 31618
MVAVGLCR, H8R
MVH=40.5301
p-value=0.0012
sample: TCGA-AA-3986-01A, spectrum: 47415
MVDFAGMK, V7M
MVH=48.2524
p-value=0.0006
sample: TCGA-AA-3986-01A, spectrum: 42207
NPLLDLAAYDQEGR, R3L
MVH=65.3603
p-value=0.0001
sample: TCGA–AA–3986–01A, spectrum: 61978
NTVLATWQPYSTSK, T11S
MVH=58.9378
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 14182
NTVLCNVVEKFLQADLAR, Q10K
MVH=91.0772
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 1740
NVSPVALPR, N3S
MVH=53.3963
p-value=0.0002
sample: TCGA-AA-3986-01A, spectrum: 81773
QVTASTFVKPLFSR, A2V
MVH=26.1663
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 79925
RDDGTLHAAACQVQPSATLDAQPR, A6T
MVH=78.2482
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 13911
SGGTLVVLGSEGEMTVPLLHAALR, N4T
MVH=43.5078
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 50935
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=38.4205
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 52608
TYGQVSGEALK, D2Y
MVH=43.5738
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 61729
VLLDGVQNL, P9L
MVH=56.3425
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 90020
VQLPTESLQELLDLHR, T7S
MVH=41.3160
p-value=0.0001
sample: TCGA-AA-3986-01A, spectrum: 1194
YFHNQEEFVR, L9V
MVH=52.0821
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 53961
AAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=37.9040
p-value=0.0002
sample: TCGA-AA-3989-01A, spectrum: 45198
AAPSVTLPSSSEELQANK, T2A
MVH=52.7541
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 10393
AGVETTTPSK, K7T
MVH=47.2535
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 101921
ALSFNFGYAK, N3S
MVH=39.4290
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 44074
APSQHLSSFDPCFYR, R5H
MVH=50.4663
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 49083
CPAAPPPPGAGGAANNHGAGSGAGGR, G1C
MVH=24.2672
p-value=0.0003
sample: TCGA-AA-3989-01A, spectrum: 70231
DAGNEQDLGLQYK, N1D
MVH=39.7467
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 140226
DCGEAAQWLTSLK, T6A
MVH=68.9511
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 17453
DFYVVEPLAFEGTPEQK, I4V
MVH=59.5472
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 126222
DGYGFLNR, N1D
MVH=42.0068
p-value=0.0006
sample: TCGA-AA-3989-01A, spectrum: 36776
DMAGAQAAAVALEELNF, R18K
MVH=75.1467
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 31551
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=90.8591
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 32642
DTEEEDFHVDQATTVK, V12A
MVH=60.7312
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 62805
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=45.7791
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 26789
EAPETDTSPSLWNVEFAK, D13N
MVH=48.0108
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 92386
EELGHLQNDLTSLENDK, M10L
MVH=46.7713
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 80808
EHTLHLEAELEK, S4L
MVH=41.1629
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 27603
ELSELVYMDVLDR, T8M
MVH=59.9073
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 60692
ELVDDSLNNVR, V7I
MVH=47.7825
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 127930
EQPGSPEWLQLDK, Q13K
MVH=37.2253
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 55412
ESALEPGPVEAPAGGPVHAVTVVTLEK, R6P
MVH = 34.1933
p-value = 0.0001
sample: TCGA-AA-3989-01A, spectrum: 6830
FFGSLPDSWAR, S11R
MVH=38.7958
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 60429
FLDKLPQQTGDR, H12R
MVH=46.4019
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 46714
FLGQLLTAFPALR, A3G
MVH=44.1415
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 73768
FNLSQESSYLATQYSLRPR, S2N
MVH=31.6051
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 54333
FQPQSADFLDLTNPK, P6A
MVH=45.2061
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 40668
FSKEEPVSSGPEEAAGK, V15A
MVH=62.0901
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 73798
FVSSSSSGGYGGYGGVLTASDGLLAGNEK:A9G
MVH=69.2994
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 81599
FYLGPGTTSVR, I9V
MVH=44.2923
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 135024
GCAGVLTLNRPK, T3A
MVH=37.9655
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 118026
GKWERPFEVKEEEDFHVDQATTVK, V22A
MVH=110.5881
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 6964
GLLDDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA–AA–3989–01A, spectrum: 45282
GQGTGALLQNTVESLSK, D9N
MVH=55.2598
p−value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 101275
GYQQDAYDGKDYLANEDLR, R3Q
MVH=77.0085
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 13374
HASSGSFLSSANEHLK, P9S
MVH=50.1584
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 67669
KADLLNR, V5I
MVH=40.2984
p-value=0.0044
sample: TCGA-AA-3989-01A, spectrum: 31044
KFSKEEKPVSSGPEEAAGK, V16A
MVH=50.5720
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 101485
KKPSEEEAAAAGGPPGGPQVNPLPVTDEVV V10A
MVH=61.5924
p−value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 74791
KPAAGLSAAPVPTTPAAGAPLMDFGNDFVPPAPR, A14T
MVH=45.2116
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 17736
LALSPNAQLLALASGSSLHL YNTR, V9I
MVH=45.1078
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 36032
LFEEDPAVGALVLTGGDK, T1I
MVH=77.6525
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 46661
LFSLLSTALLR, V8A
MVH=37.7263
p–value=0.0003
sample: TCGA-AA-3989-01A, spectrum: 111664
LLDAETTAGAWPNVAAVSLTGR, A9G
MVH=40.5061
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 27990
LLNLLADLVER, R4L
MVH=57.1911
p-value=0.0001
sample: TCGA−AA−3989−01A, spectrum: 125218
LPAPTHTPATAPVPAR, R6H
MVH=36.1234
p−value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 138827
LPNVVEAEVPKPLPPASKDEDEDLQSLR, S3N
MVH=71.7381
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 79328
LQELTPSSGDPGEHDPASTHK, P4L
MVH=68.2681
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 112317
LSDLQEALDQALNHVR, Y14H
MVH=57.4308
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 73301
LSVFSTLDAPVAPSDK, V7I
MVH=43.0065
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 6149
LVTDYTLAEADAALQK, E11D
MVH=79.7463
p−value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 72365
MKDVPQFLQQSQSSGQPAVWHR, N13S
MVH=85.3216
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 14984
MQYAPNTQVELLPQGR, H16R
MVH=50.9680
p–value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 138851
SAVGELSEDSSNVVHLLK, Q15H
MVH=58.0551
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 55017
SDPVTLNLYGPDVPTLSPSK, G14V
MVH=52.8090
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 18070
SGGTLVLVGLGSEMTTVPLLHAALRN4T
MVH=35.7506
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 14049
SGGVERPFVLAR, M4V
MVH=59.7650
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 59380
SPADPTDLGGQTSPR, I6T
MVH=65.1525
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 98477
SPPGAAAPAAAKPPPLSAK, S8P
MVH=34.1899
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 127342
TAASGVEASSRPLDHAQPPSSLVLDKESEVYKIN9S
MVH=84.5094
p–value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 91614
TLEGLQVEEEPVYK, E14K
MVH=48.5136
p−value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 106776
TPQEWAPHTAR, Q8H
MVH=32.6952
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 88671
TTPLEAASSGAR, T11A
MVH=39.3493
p-value=0.0001
sample: TCGA–AA–3989–01A, spectrum: 55857
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=73.5170
p–value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 74936
TVEDLDGLLQQL YR, H10Q
MVH=65.1266
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 129442

TVEHGFPHQPSALGYSPSLHLLALGTR, R20H
MVH=89.7425
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 44686
TVVQLEGDNKLVTAFK, T14A
MVH=49.0956
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 67311
VPVTQATR, L3V
MVH=39.3087
p-value=0.0012
sample: TCGA-AA-3989-01A, spectrum: 103759
VQLPTESLQELLDLHR, T7S
MVH=34.1827
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 59408
VSYGLGEEEHDQEGR, D7E
MVH=26.2917
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 42314
VWQTVSPVESR, G10S
MVH=35.3294
p-value=0.0001
sample: TCGA-AA-3989-01A, spectrum: 91842
YFHPYLAYCSNEVYQQR, H1Y
MVH=43.2121
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 57418
AAAAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=37.8229
p-value=0.0003
sample: TCGA-AA-A00E-01A, spectrum: 75117
AAAPAPVSEAVSR, C12S
MVH=52.7613
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 37300
AAPSVTLFPPSEELQANK, T2A
MVH=50.3764
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 117644
AFDQGADALYDHVNEGK, I13V
MVH=45.7973
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 11140
AGVETTTTPSK, K7T
MVH=57.1978
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 38642
ALEDVFDLEGK, M5V
MVH=58.7783
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 149557
ASSSLLLNESEPTTNLQLR, D8N
MVH=49.5469
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 36024
ATAECLQHPWLNS, R8Q
MVH=30.1043
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 110939
AVDVVLDCFLVK, A11V
MVH=58.8872
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 34930
AVQGLCGWR, D4G
MVH=35.3735
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 108478
DEPLHALYDNVEK, V2E
MVH=39.3581
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 18088
DFYVVEPLAFEGTPEQK, I4V
MVH=48.3533
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 137228
DGYGFLNR, N1D
MVH=44.9486
p-value=0.0006
sample: TCGA-AA-A00E-01A, spectrum: 42617
DLEAHVDSANK, l6V
MVH=54.9703
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 38365
DMAGAQAALNEEFLK, R18K
MVH=72.4206
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 33242
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=79.4272
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 34365
DTEEEDFHVDQATTVK, V12A
MVH=63.9371
p−value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 106908
DVDGLTSLNAGR, K12R
MVH=56.3703
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 56909
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=38.5657
p-value=0.0001
sample: TCGA–AA–A00E–01A, spectrum: 117661
DVTVLQNTDGNNDKAW, E14D
MVH=48.0235
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 48816
EALDVLDVAVLK, G7D
MVH=43.8173
p-value=0.0001
sample: TCGA–AA–A00E–01A, spectrum: 700
EASQGSSASSAPQSVK, H13Q
MVH=39.9233
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 99025
EELGHLQNDLTSLENDK, M10L
MVH=34.1735
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 101365
ELELMQLLTR, D1E
MVH=39.6750
p-value=0.0002
sample: TCGA-AA-A00E-01A, spectrum: 27310
ELTVSNNDLNEAGVHVLCQGLK, R15H
MVH=30.6956
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 65583
ELVDDLNNVR, V7I
MVH=52.6904
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 138972
EQPGSPEWLQLDK, Q13K
MVH=30.5209
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 6735
FFGSLPDSWAR, S11R
MVH=33.2448
p-value=0.0001
sample: TCGA–AA–A00E–01A, spectrum: 65314
FLDKLPQQTGDR, H12R
MVH=55.8265
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 149445
FNSVTELCAELPEQK, V11I
MVH=42.2452
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 19243
FSLDALLTNVLPFEK, I10V
MVH=22.7551
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 114187
FTVGDHSR, I3V
MVH=44.6942
p-value=0.0003
sample: TCGA-AA-A00E-01A, spectrum: 68938
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=63.4350
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 42630
GAQEKPQLSAAQSTQPQK, R3Q
MVH=45.4769
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 5675
GLCVSENELEVGGSQWK, P2L
MVH=77.2345
p-value=0.0001
sample: TCGA–AA–A00E–01A, spectrum: 126547
GLSFDAAATSGGSASSEK, T2I
MVH=51.5299
p–value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 47528
GQTGALLQNTVESLSK, D9N
MVH=66.0021
p−value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 25743
GVAGSSVAVLCPYNR, G5S
MVH=50.0756
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 37454
LFEEDPAVGLVLTGGDK, T1I
MVH=79.3482
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 25898
LLESGDLSMSSVK, I12V
MVH=51.8332
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 129880
LLSDLLPPSTGTFQEAQSR, S5L
MVH=43.4642
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 85430
LQELTPSSGDPGEHDPASTHK, P4L
MVH=67.4064
p-value=0.0002
sample: TCGA-AA-A00E-01A, spectrum: 116681
LQEQHLSSPQGVQLDR, I16R
MVH=73.8639
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 100332
LQSGTHCLWMDQLLQGSEK, T10M
MVH=63.9839
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 78065
MKDVPGFLQQSQSSGPGQPAVWHR, N13S
MVH=81.7478
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 15721
MQYAPNTQVELLPQGR, H16R
MVH=70.2171
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 33684
NKPGPNLESGNEDDDTSFK, A16T
MVH=48.0708
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 127715
NLPSLAEQGASDPPTVAVSR, K7E
MVH=69.6530
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 37403
NPLLDLAAYDQEGR, R3L
MVH=61.0914
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 52737
NSLSETVR, M3L
MVH=40.3242
p-value=0.0006
sample: TCGA-AA-A00E-01A, spectrum: 76080
NTNSVPETAPAALPETR, K17R
MVH=43.1752
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 150549
SAVGELSEDSSNVVHLLK, Q15H
MVH=46.5953
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 58412
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=51.0678
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 38830
SELPLDPLPLPTEEGNPLLK, V10L
MVH=52.6610
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 64351
SPADPTDLGGQTSPR, I6T
MVH=60.5276
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 22086
SSSYSGEYGSGGGK, G10S
MVH=61.1568
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 22014
SSSYSGEYGSGGGKR, G10S
MVH=37.0291
p-value=0.0001
sample: TCGA–AA–A00E–01A, spectrum: 57189
SVMDTTQLAGLNCLR, A5T
MVH=57.1028
p−value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 138082
TAASGVEASSRPLDHAQPPSSLVLDK, N9S
MVH=49.5175
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 98217
TLEGLQVEEEPVYK, E14K
MVH=56.4215
p-value=0.0001
sample: TCGA–AA–A00E–01A, spectrum: 79922
TTGLVVDSDGVTHTVPLYEGYALRHALLR, M6V
MVH=79.4348
p−value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 95240
TTPLEAASSGAR, T11A
MVH=43.1594
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 80752
TVEDLDGLQQLYR, H10Q
MVH=64.0724
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 14544
VLLNDGGYYDPK, E12K
MVH=52.1014
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 95047
VMQVDEK, I1V
MVH=48.5828
p-value=0.0019
sample: TCGA-AA-A00E-01A, spectrum: 6871
VPGFADDPTELACQVVDTK, R14Q
MVH=52.8599
p-value=0.0001
sample: TCGA-AA-A00E-01A, spectrum: 62415
VPVTQATR, L3V
MVH=43.5664
p-value=0.0012
sample: TCGA-AA-A00E-01A, spectrum: 131073
VQVLAQQQLSEM, D11E
MVH=59.9073
p-value=0.0001
sample: TCGA–AA–A00F–01A, spectrum: 78745
AAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=44.0057
p–value=0.0002
sample: TCGA-AA-A00F-01A, spectrum: 58665
AAPSVTLPSSSEELQANK, T2A
MVH=52.6380
p-value=0.0001
sample: TCGA–AA–A00F–01A, spectrum: 148028
ACNVLQSSHLEDYPFDAEY, N16D
MVH=34.8487
p–value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 11632
AGVETTTPSK, K7T
MVH=59.3379
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 57686
APSQHLSSFDPCFYR, R5H
MVH=54.7000
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 100321
AVEVATVVLQPTVLR, S12T
MVH=42.7742
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 29631
DFYVVEPLAFEGTPEQK, I4V
MVH=50.0498
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 144631
DGYGFLNR, N1D
MVH=42.7733
p-value=0.0006
sample: TCGA–AA–A00F–01A, spectrum: 125051
DVTVLQNTDGNNNDAAWAK, E14D
MVH=56.9569
p–value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 75881
ELVDDSLNNVR, V7I
MVH=50.7540
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 76943
ENVATTDITLESTTVGSSV, T16S
MVH=66.6063
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 146517
EQPGSPEWLQLDK, Q13K
MVH=31.2747
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 70138
ESALEPGPVEAPAGGVPHAVTVVTLEK, R6P
MVH=39.1254
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 43451
EVDTTSPAPSTSSTVK, A4T
MVH=41.4531
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 18499
FFGSLPDSWAR, S11R
MVH=31.5658
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 85943
FLDKLPQQTGDR, H12R
MVH=50.1426
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 29978
FNKPFVFLMLDQNTK, E11D
MVH=60.7352
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 100805
FNLSQESSYLATQYSLRPR, S2N
MVH=36.2465
p-value=0.0001
sample: TCGA–AA–A00F–01A, spectrum: 89837
FVSSSSSSGGYYGGYGGVLTASDGLLAGNEK, A9G
MVH=73.0275
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 107482
FYLGPTSVR, I9V
MVH=41.0544
p-value=0.0001
sample: TCGA–AA–A00F–01A, spectrum: 18437
GFGTDEQALLDCLGSCSNK, R16C
MVH=60.4647
p–value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 68932
GQTGALLQNTVESLSK, D9N
MVH=70.3572
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 46543
GVAGSSVAVLCPYNR, G5S
MVH=46.5291
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 73049
KADLLNR, V5I
MVH=31.1300
p-value=0.0044
sample: TCGA-AA-A00F-01A, spectrum: 109342
KAPPRPGPVPEAAQPFLFTTR, P20T
MVH=67.4884
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 127251
KFFGSLPDSWAR, S12R
MVH=56.8462
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 117612
KKPSEEEAAAAAGGPPGQPQVNPLPVTDEVVE V10A
MVH=54.9778
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 101889
KPAAGLSAAPVPTTPAAGAPLMDFGNDFVPPAPR, A14T
MVH=45.6351
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 133154
KSVEEYANCHLAR, P2S
MVH=46.4548
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 49001
LFEEDPAVGALVLTGGDK, T1I
MVH=85.7362
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 95571
LQELTPSSGDPGEHDPASTHK, P4L
MVH=33.7600
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 139405
LSDLQEALDQALNHVR, Y14H
MVH=56.4195
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 135944
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=41.8280
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 36397
MQYAPNTQVELLPQGR, H16R
MVH=48.7932
p-value=0.0001
sample: TCGA−AA−A00F−01A, spectrum: 59166
NPLLDLAAYDQEGR, R3L
MVH=40.0915
p−value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 22911
NSTLSEPGSGR, P4L
MVH=25.9642
p-value=0.0002
sample: TCGA-AA-A00F-01A, spectrum: 85858
NTNSVPETAPAALPETR, K17R
MVH=46.0189
p-value=0.0001
sample: TCGA−AA−A00F−01A, spectrum: 3779
NVSPVALPR, N3S
MVH=36.5501
p−value=0.0003
sample: TCGA-AA-A00F-01A, spectrum: 80872
QVEEEDGSRDSPFLDFLESCLR, L2V
MVH=48.7778
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 80403
SALVHLLNYQDDAE/LATHALPELTK, R18H
MVH=83.3806
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 80001
SDPVTNLNYGPDVPTLPSK, G14V
MVH=49.2362
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 147012
SEALPTDLPTPSAPDLTEPK, A10T
MVH=52.5908
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 50190
SELPLDPLPLPTEEGNPLLK, V10L
MVH=53.0991
p-value=0.0001
sample: TCGA–AA–A00F–01A, spectrum: 60224
SFQGPVLLGSSHGGVNLEDVAAETPEALLK, S24T
MVH=52.0785
p−value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 20034
SGGTLVLVGLGSEMTTVPLLHAALR, N4T
MVH=47.1128
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 126
SPAADAKPAPK, T3A
MVH=45.8475
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 74519
SPADPTDLGGQTSPR, I6T
MVH=60.5276
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 22651
SSSYSGEYGSGGGKR, G10S
MVH=24.9711
p-value=0.0002
sample: TCGA-AA-A00F-01A, spectrum: 48775
SSTTSTWELLDPR, Q12P
MVH=32.7632
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 63899
STESLQTNVQR, A7T
MVH=46.7800
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 123806
SVEEYANCHLAR, P1S
MVH=48.4338
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 145865
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=94.4495
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 28812
TCSFDFTGAVEDLSK, G3S
MVH=73.0936
p-value=0.0001
sample: TCGA–AA–A00F–01A, spectrum: 102056
TVEDLDGLLQQL YR, H10Q
MVH=59.3382
p–value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 87807
VLLDGVQNL, P9L
MVH=59.4441
p-value=0.0001
sample: TCGA-AA-A00F-01A, spectrum: 72586
VPVTQATR, L3V
MVH=42.2916
p-value=0.0012
sample: TCGA-AA-A00F-01A, spectrum: 30253
VSLAEQAQSNSLLTWGR, A15T
MVH=54.1883
p-value=0.0001
sample: TCGA–AA–A00F–01A, spectrum: 97655
YGLLVGGAVSHR, A9V
MVH=60.9158
p–value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 37678
AAAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=30.3838
p-value=0.0001
sample: TCGA–AA–A00J–01A, spectrum: 22158
AAPSVTTLFPPSSEELQANK, T2A
MVH=66.2550
p–value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 70889
AEELGLPVGLVLG, I8V
MVH=69.0814
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 8549
AGVETTTPSK, K7T
MVH=57.5665
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 47147
APSPLYSYSVEFSEEPFGVLVHR, R20H
MVH=51.3029
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 28611
AYVVLLE, E1A
MVH=41.6585
p-value=0.0084
sample: TCGA-AA-A00J-01A, spectrum: 30956
DFNHLDEVLSSLGK, N6D
MVH=43.3530
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 6847
DFYVVEPLAFEGTPEQK, I4V
MVH=45.6354
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 96811
DGYYGLNR, N1D
MVH=40.5540
p-value=0.0006
sample: TCGA–AA–A00J–01A, spectrum: 25594
DLEAHVDSANK, I6V
MVH=47.2282
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 18160
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=57.2346
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 37324
DVPGFLQSQSSGPGQPAVWH, N11S
MVH=53.2335
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 529
EASQGSSASSAPQSVK, H13Q
MVH=30.3172
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 68974
EELGHLQNDLTSLENDK, M10L
MVH=37.2237
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 43318
ELVDDSLNNVR, V7I
MVH=55.4896
p-value=0.0001
sample: TCGA–AA–A00J–01A, spectrum: 98459
EQPGSPEWLQLDK, Q13K
MVH=38.2081
p−value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 105659
FEEGENSLHLK, A4G
MVH=38.6103
p-value=0.0003
sample: TCGA-AA-A00J-01A, spectrum: 107206
FFGSLPDSWAR, S11R
MVH=22.9546
p-value=0.0002
sample: TCGA-XX-A00J-01A, spectrum: 108006
FGQDLLSPLLSVR, K13R
MVH=52.6745
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 43155
FLDKLPQQTGDR, H12R
MVH=58.5193
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 4594
FPGPCDYNFASDCR, L4P
MVH=66.5440
p-value=0.0001
sample: TCGA–AA–A00J–01A, spectrum: 12491
FPGPCDYNFASDCRGSYK, L4P
MVH=38.9089
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 79573
FTVGDHSR, I3V
MVH=46.6812
p-value=0.0003
sample: TCGA-AA-A00J-01A, spectrum: 46262
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=61.5615
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 52224
FYLGPGPTSVR, I9V
MVH=50.7821
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 114896
GFGTDEQALLDCLGSCSNK, R16C
MVH=59.1502
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 113976
GLCVSENELGVGTSQWK, P2L
MVH=59.7255
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 30173
GQTGALLQNTVESLSK, D9N
MVH=50.2498
p-value=0.0001
sample: TCGA–AA–A00J–01A, spectrum: 91529
GTDECALESVAVAATPLPK, I10V
MVH=40.1717
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 14203
LAALAESGVEQQVLLGDQLPK, R11Q
MVH=61.8711
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 104940
LDSTDFTSTLK, G8S
MVH=59.2753
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 108014
LEGLLEGGLGR, G6E
MVH=62.7048
p-value=0.0006
sample: TCGA-AA-A00J-01A, spectrum: 22321
LFEEDPAVGLVLTGGDK, T1I
MVH=87.7545
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 99970
LFEGNALLWR, R9W
MVH=56.3425
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 36586
LGSALATGNVVMK, P3S
MVH=67.4414
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 45867
LSVFSTLDAPVAPSDK, V7I
MVH=46.7522
p−value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 50040
LTGHGAEDSLADQAANK, R4H
MVH=51.8923
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 3527
LTLDKLDVEGKR, K9E
MVH=54.4246
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 23610
MVLPLACLLTPLK, V3I
MVH=52.6436
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 10873
PVAEYWNSQK, D2V
MVH=47.2989
p−value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 74660
RYEVPLETPR, H10R
MVH=42.7303
p−value=0.0003
sample: TCGA-AA-A00J-01A, spectrum: 60285
SAGLAPDCEASATAETTVSSVGTCEAAK, G28A
MVH=26.3468
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 107178
SAVGELSEDSNVHLLK, Q15H
MVH=49.0739
p-value=0.0001
sample: TCGA–AA–A00J–01A, spectrum: 30805
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=51.3220
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 70748
SKAEELGLPVLGVLR, I10V
MVH=58.2066
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 30191
SLSLLDSPGLLSGEK, V4I
MVH=58.1810
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 73918
SPPGAAAPAAAKPPPLSAK, S8P
MVH=31.0660
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 33666
STESLQTNVQR, A7T
MVH=49.9630
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 54506
TLAQLNPESSLFLTAS, I14T
MVH=73.5701
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 65574
TTPLEAASSGAR, T11A
MVH=48.4902
p-value=0.0001
sample: TCGA–AA–A00J–01A, spectrum: 15497
TVLLMELLNNVTK, A12T
MVH=73.8486
p–value=0.0001
sample: TCGA–AA–A00J–01A, spectrum: 72203
VLGTAGTEEGQK, I1V
MVH=45.1451
p-value=0.0001
sample: TCGA–AA–A00J–01A, spectrum: 106633
VPSFETAEGGLGAELK, T12A
MVH=65.4716
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 48551
VPVTQATR, L3V
MVH=41.8305
p-value=0.0012
sample: TCGA-AA-A00J-01A, spectrum: 70825
VQLPTESLQELLDLHR, T7S
MVH=51.5888
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 27561
VWQTVSPVESR, G10S
MVH=45.8685
p-value=0.0001
sample: TCGA-AA-A00J-01A, spectrum: 45256
YVSLLYTNYEAGKDDYVK, I2V
MVH=43.8420
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 38120
AAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=28.2814
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 28084
AAPSVTLPFPSSSEELQANK, T2A
MVH=47.2704
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 106159
AFDQGADALYDHVNEGK, I13V
MVH=53.1040
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 4046
AFSEYLGTDQSK, G4E
MVH=52.0475
p-value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 11175
AGVETTTPSK, K7T
MVH=56.2168
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 19091
ALEDVFDALEGK, M5V
MVH=64.9728
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 60769
APSPLYSVEFSEEPFGVLVHR, R20H
MVH=45.9098
p-value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 64477
ATGGGLSSAGGSSTLK, V9A
MVH=61.9553
p−value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 59421
AVEVATVVLQPTVLR, S12T
MVH=47.7500
p-value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 84654
AVSTTLSSPQPGK, M2V
MVH=58.1698
p−value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 17383
CDEPLNLLVR, S6N
MVH=36.5110
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 90776
CDPGALVLPFSGALELK, Y1C
MVH=54.4027
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 8467
DFYVVEPLAFEGTPEQK, I4V
MVH=66.2286
p-value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 123853
DGYGFLNR, N1D
MVH=46.2273
p-value=0.0006
sample: TCGA-AA-A00O-01A, spectrum: 37940
DSMFGLTVK, A7T
MVH=43.4999
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 23384
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=64.8895
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 35086
DTEEEDFHVDQATTVK, V12A
MVH=57.3193
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 48082
DVPGFLQSQSSGPGQPAVWHR, N11S
MVH=23.5520
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 87638
EALELDSLRL, V2A
MVH=34.6912
p-value=0.0009
sample: TCGA-AA-A00O-01A, spectrum: 727
EASQGSSASSAPQSVK, H13Q
MVH=43.9241
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 60563
EATSVPHLYALGDVVEGRPELTPTALMAGR, I24T
MVH=46.1112
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 131084
EEPVSSGPEEAAGK, V12A
MVH=29.6613
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 56125
ELVDDSLNNVR, V7I
MVH=52.6904
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 125947
EQPGSPEWLQLDK, Q13K
MVH=43.0716
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 125619
EVAQQAVDADVHAVGVSTLAAGHK, I16V
MVH=56.8250
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 56971
FADVFAK, E7K
MVH=48.3703
p-value=0.0084
sample: TCGA-AA-A00O-01A, spectrum: 137181
FFGSLPDSWAR, S11R
MVH=46.5440
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 55971
FLDKLPQQTGDR, H12R
MVH=53.8294
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 38616
FQPQSDFLDLTNPK, P6A
MVH=63.0027
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 68750
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=56.5504
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 111396
FTVGDHSR, I3V
MVH=41.4004
p-value=0.0003
sample: TCGA-AA-A00O-01A, spectrum: 59719
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=56.1668
p-value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 67727
FYLGGPTSVR, I9V
MVH=54.7993
p−value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 147077
GFGTDEQALLDCLGSCSNK, R16C
MVH=66.6593
p-value=0.0003
sample: TCGA-AA-A00O-01A, spectrum: 136872
GGTLSTPQTGSENDALYEYLR, G5S
MVH=59.0984
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 147332
GLLDLLEER, V3I
MVH=44.7346
p-value=0.0038
sample: TCGA-AA-A00O-01A, spectrum: 54901
GPSYGEDLSNTTTAQK, V8I
MVH=74.2790
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 25791
HTLSFVDVGTGK, Y5F
MVH=50.5858
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 33399
KFSKEEPVSSGPEEAAGK, V16A
MVH=39.0803
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 117209
KPPEADMNLFEDTGDYVPSTTK, I13T
MVH=33.8045
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 103747
KSVEEYANCHLAR, P2S
MVH=40.6825
p−value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 15247
LAALALASSENSSSTPEECEETSEKPK, M22T
MVH=64.7107
p–value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 134329
LDSTDFTSTLK, G8S
MVH=47.8873
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 87758
LDVDKDGFVTEGELK, A3V
MVH=47.1050
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 32808
LEGANVQEAQK, T4A
MVH=60.2974
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 138041
LEGLLEGLGLR, G6E
MVH=57.2310
p-value=0.0006
sample: TCGA-AA-A00O-01A, spectrum: 28475
LFEEDPAVGALVLTGGDK, T1I
MVH=81.0179
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 138010
LKEVFPMAALMPGAEK, T7M
MVH=40.4208
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 90116
LLDAETTAGAWPNVAAVSLTGR, A9G
MVH=40.0685
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 85062
LQELTPSSGDPGEHDPASTHK, P4L
MVH=49.1057
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 7693
LQPEDMFVYDLNEK, C9Y
MVH=46.8152
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 94993
LQQQHSEQPPLQPSPVTTR, M17T
MVH=48.3986
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 115665
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=51.4875
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 145401
LTPVSAQFQDLEGK, L8F
MVH=54.3695
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 90618
LTVLPPELANLDLTGQK, G9A
MVH=52.4614
p-value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 58327
MKDVPGFLQQSQSSGPGQPAVWHR, N13S
MVH=64.0586
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 5759
MQYAPNTQVELLPQGR, H16R
MVH=56.3650
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 115614
NPEQEPLPTVLR, I9T
MVH=44.5651
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 28448
NPLLDLAAYDQEGR, R3L
MVH=66.6542
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 43499
NSLSETVR, M3L
MVH=37.5311
p-value=0.0006
sample: TCGA-AA-A00O-01A, spectrum: 38778
QALTLLNELK, V2A
MVH=39.6750
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 15312
QVGDFHQVLLR, A2V
MVH=31.4256
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 137102
SAVGELSEDSSNVVHLLLK, Q15H
MVH=30.4567
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 49815
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=46.0153
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 29804
SELPLDPLPLPTEEGNPLLK, V10L
MVH=55.4940
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 65147
SPADPTDLGGQTSPR, I6T
MVH=81.5771
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 94874
SPPGAAAPAAAKPPPLSAK, S8P
MVH=25.0887
p-value=0.0002
sample: TCGA-AA-A00O-01A, spectrum: 43595
STESLQTNVQR, A7T
MVH=59.5386
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 104163
SVEEYANCHLAR, P1S
MVH=63.2924
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 125409
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=80.6453
p-value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 7595
TCSFDFTGAVEDLSK, G3S
MVH=71.9970
p−value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 6127
TGGAVDWLTDTSR, R7W
MVH=46.7167
p-value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 106083
TLNEADCATLPPALR, V10I
MVH=50.7830
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 84668
TTPLEAASSGAR, T11A
MVH=54.3730
p-value=0.0001
sample: TCGA–AA–A00O–01A, spectrum: 23321
VFHELTQTDK, I1V
MVH=53.2058
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 83083
VLSTTNAER, D6N
MVH=33.3106
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 93834
VMQVVEDK, I1V
MVH=49.0148
p-value=0.0019
sample: TCGA–AA–A00O–01A, spectrum: 136468
VPSFETAEGLGAELK, T12A
MVH=61.6907
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 63077
VPVTQATR, L3V
MVH=46.9290
p-value=0.0012
sample: TCGA-AA-AA0O-01A, spectrum: 109442
VQVLAQQLLSEM, D11E
MVH=61.7363
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 112870
VSDLAATAYK, N2S
MVH=49.8843
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 35370
VWQTVSPVESR, G10S
MVH=39.9701
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 68598
YVSLLYTNYEAGK, I2V
MVH=49.8006
p-value=0.0001
sample: TCGA-AA-A00O-01A, spectrum: 58528
YVSLLYTNYEAGKDDYVK, I2V
MVH=57.6775
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 56466
AAAAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=59.3905
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 49090
AAPSVTTLPPSSEELQANK, T2A
MVH=60.3294
p-value=0.0001
sample: TCGA–AA–A00U–01A, spectrum: 8537
AGVETTTPSK, K7T
MVH=28.1024
p−value=0.0002
sample: TCGA-AA-A00U-01A, spectrum: 29575
ANPQLGAYAPPHELGR, I14V
MVH=31.8098
p-value=0.0002
sample: TCGA-AA-A00U-01A, spectrum: 35490
ASSEGTLPQAR, V10A
MVH=31.6945
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 106750
AVDVVLDCFLVK, A11V
MVH=58.8872
p-value=0.0001
sample: TCGA−AA−A00U−01A, spectrum: 21720
AWLSSQAAELER, V7A
MVH=62.8426
p−value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 63187
AYVVLLR, E1A
MVH=43.3878
p-value=0.0084
sample: TCGA-AA-A00U-01A, spectrum: 106932
CDPGALVLPFSGAELEK, Y1C
MVH=69.7363
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 6613
CSGLLQVLFSPLEEEVK, A3G
MVH=45.1538
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 111483
DGYGFLNR, N1D
MVH=49.1228
p-value=0.0006
sample: TCGA-AA-A00U-01A, spectrum: 48563
DSMFGGLTVK, A7T
MVH=44.2028
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 27611
DSRPSQAAGDNQGDEVKEQTFSGGTSDK, A16V
MVH=108.8771
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 11920
DTCVQSPSSDFPR, C13R
MVH=54.2172
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 94416
DVDGLTSLNAGR, K12R
MVH=50.5872
p-value=0.0001
sample: TCGA–AA–A00U–01A, spectrum: 57367
EADLLFLSVNTPTK, V5I
MVH=58.5724
p–value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 50004
EALDVLDAVLK, G7D
MVH=44.8565
p−value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 113320
EQPGSPEWLQLDK, Q13K
MVH=34.5629
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 13960
FFGSLPDSWAR, S11R
MVH=39.0482
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 69536
FLDKLPQQTGDR, H12R
MVH=48.7944
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 21425
FPGPCDYNFASDCR, L4P
MVH=49.0598
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 60136
FQLGNSGPNSTLK, S4G
MVH=34.1950
p-value=0.0005
sample: TCGA-AA-A00U-01A, spectrum: 88063
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=53.6869
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 72899
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=51.9933
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 78814
FYLGPGTTSVR, I9V
MVH=39.5567
p-value=0.0001
sample: TCGA–AA–A00U–01A, spectrum: 62775
GALQFVTHYQQSSTQR, H11Q
MVH=45.1822
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 43966
GAQEKPLSAAQSTQPQK, R3Q
MVH=43.2886
p-value=0.0001
sample: TCGA–AA–A00U–01A, spectrum: 13856
GFGTDEQALLDCLGSCSNK, R16C
MVH=54.8127
p–value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 49065
GQTGALLQNTVESLSK, D9N
MVH=64.2610
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 38795
GVAGSSVAVLCPYNR, G5S
MVH=53.2559
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 105606
KFFGSLPDSWAR, S12R
MVH=44.6951
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 803
KGCAGVLTLLNPK, T4A
MVH=34.9673
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 88235
FKPSEEEAAAAAGGPPGGPQVNPLPVTDEVV V10A
MVH=59.9100
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 38854
KVLLDGVQNL, P10L
MVH=47.0573
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 96627
LAGALGPCLSLNVK, V9I
MVH=66.0558
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 10003
LALQPGTVGPQGR, V3I
MVH=44.3662
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 2559
LDSTDFTSTLK, G8S
MVH=48.1208
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 41026
LFEEDPAVGALVLTGGDK, T1I
MVH=86.6435
p-value=0.0001
sample: TCGA–AA–A00U–01A, spectrum: 14912
LLDLFYPGDQSQVTFGLK, T17I
MVH=39.3045
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 24419
LLNLLADLVER, R4L
MVH=54.9821
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 101824
LQQQHSEQPPLQPSVTTR, M175
MVH=48.2358
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 112751
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=54.1164
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 13190
LVTDYTLAEADAALQK, E11D
MVH=56.8973
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 19614
MAQWGNKPLC, V9I
MVH=38.6963
p-value=0.0002
sample: TCGA-AA-A00U-01A, spectrum: 21337
MQYAPNTQVELLPQGR, H16R
MVH=57.6529
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 43916
NKSTESLQTNVQR, A9T
MVH=45.8813
p-value=0.0001
sample: TCGA–AA–A00U–01A, spectrum: 112220
NLPSLAEQGASDPPTVASR, K7E
MVH=70.2757
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 41056
NPLLQLAAYDQEGR, R3L
MVH=43.2150
p−value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 123703
NPSLLPLLLEAR, Q2P
MVH=55.6347
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 69381
NTNSVPETAPAALPETR, K17R
MVH=47.1790
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 38670
QVGDFHQVLLR, A2V
MVH=32.8120
p−value=0.0002
sample: TCGA-AA-A00U-01A, spectrum: 24587
SALSGHLETLLLGLLK, V10L
MVH=76.3612
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 65272
SDPVTLNVL YGPDVPTLSPSK, G14V
MVH=43.8558
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 41946
SELPLDPLPLPTEEGNPLLK, V10L
MVH=45.3695
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 15144
SGGTLVLVGLGSEMTTVPLLHAALR, N4T
MVH=41.9290
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 60645
SLQEEQSRPTTAVSSPGGPAR, P10T
MVH=30.4971
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 88504
SSRPTSLFAVTVAPPGAR, G3R
MVH=45.4164
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 51963
STESLQTNVQR, A7T
MVH=61.1044
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 121088
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=77.5431
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 23081
TCSFDFTGAVEDLSK, G3S
MVH=70.5122
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 71455
TMMNTWTLQR, K10R
MVH=47.2857
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 60255
TSLSAPPNTSSTENPK, S9T
MVH=30.3400
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 76188
TTPLEAASSGAR, T11A
MVH=49.9422
p-value=0.0001
sample: TCGA–AA–A00U–01A, spectrum: 73656
TVEDLDGLLQQL YR, H10Q
MVH=63.6746
p−value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 71153
VLLDGQQLR, P9L
MVH=62.4730
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 63032
VLTGTGNVNVLQPNYPAAAR, I10V
MVH=53.2770
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 84305
VMQVVDEK, I1V
MVH=43.9792
p-value=0.0019
sample: TCGA-AA-A00U-01A, spectrum: 52736
VSYGGLGEEHDEQGGR, D7E
MVH=37.4770
p-value=0.0001
sample: TCGA-AA-A00U-01A, spectrum: 24037
WLLLCPGLANTLVEK, D11N
MVH=68.1722
p-value=0.0001
sample: TCGA–AA–A00U–01A, spectrum: 71940
YVSLLYTNYEAGKDDYVK, I2V
MVH=34.7935
p–value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 59229
AAAGAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=36.1509
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 48788
AAPSVTLPSSSEELQANK, T2A
MVH=57.3548
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 11420
AGVETTTPSK, K7T
MVH=54.7554
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 74520
ALDRPYTSK, E3D
MVH=34.6341
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 90757
APPRPGPVPEAAQPFLFTTR, P19T
MVH=40.2711
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 148581
ASSSLLLNESEPTTNLQLR, D8N
MVH=63.2270
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 18434
DFYVVEPLAFEGTPEQK, I4V
MVH=51.5018
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 136636
DGYGFLNR, N1D
MVH=42.0068
p-value=0.0006
sample: TCGA-AA-A010-01A, spectrum: 34347
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=75.5756
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 58692
DVPGFLQSQSSGPQPQAVWHR, N11S
MVH=32.8094
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 88041
EHTLHLEAELEK, S4L
MVH=36.1445
p-value=0.0002
sample: TCGA-AA-A010-01A, spectrum: 102781
ELELMQLLTR, D1E
MVH=43.9744
p-value=0.0002
sample: TCGA–AA–A010–01A, spectrum: 66805
ELVDDSLNNVR, V7I
MVH=46.9156
p–value=0.0001
sample: TCGA–AA–A010–01A, spectrum: 16213
EPSAPSLPTPAYQSLPAGGHA{PTPAPR, S15L
MVH=31.0124
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 138279
EQPGSPEWLQLDK, Q13K
MVH=33.4494
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 6682
FFGSLPDSWAR, S11R
MVH=43.6043
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 7746
FGQDLLSPLLSVR, K13R
MVH=43.0127
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 66592
FLDKLPQQTGDR, H12R
MVH=41.1022
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 77658
FLSGHTSELGNFR, D11N
MVH=39.5268
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 18903
FNKPFVFLMLDQNTK, E11D
MVH=63.1175
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 148447
FNSVTELCAELPEQK, V11I
MVH=36.710
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 115107
FTVGDHSR, I3V
MVH=45.6282
p-value=0.0003
sample: TCGA-AA-A010-01A, spectrum: 69915
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=63.1795
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 88794
FYLLGPTSVR, I9V
MVH=43.2106
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 6705
GFGTDEQALLDCLGSCSNK, R16C
MVH=50.1337
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 49092
GQTGALLQNTVESLSK, D9N
MVH=70.3572
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 25281
KALFMDCLGAR, T5M
MVH=42.8379
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 79561
KAPPRPGPVPEAAQPFLFTTR, P20T
MVH=38.2425
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 145333
KGCAGVLTNLNRPK, T4A
MVH=44.4785
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 110183
KKPSEEAAAAAGGPPGGPQVNPLPVTDEVV V10A
MVH=34.7193
p-value=0.0001
sample: TCGA–AA–A010–01A, spectrum: 25075
KLVFVTEK, D7E
MVH=46.0722
p–value=0.0006
sample: TCGA-AA-A010-01A, spectrum: 76108
KNPDSHYGELLEK, Q6H
MVH=54.8194
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 36490
KVLLDGVQNLR, P10L
MVH=37.7263
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 28596
LALLLMASQEPQR, T2A
MVH=53.1326
p-value=0.0001
sample: TCGA−AA−A010−01A, spectrum: 38661
LFEEDPAVGLVLTGSDK, T1I
MVH=76.6299
p−value=0.0001
sample: TCGA–AA–A010–01A, spectrum: 30153
LLNLLADLVER, R4L
MVH=53.0317
p–value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 26316
LLTQDEGPALVPGSR, G14S
MVH=43.3002
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 117565
LQEQLSPLQGVQQLDR, I16R
MVH=65.7987
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 150733
LTAEFEAQTSACLLQEELEK, R14L
MVH=48.4262
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 75802
LTGHGAEDSLADQAANK, R4H
MVH=48.1438
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 77389
LVFVTEK, D6E
MVH=45.3177
p-value=0.0044
sample: TCGA–AA–A010–01A, spectrum: 58748
LYEPVVLPVGR, K11R
MVH=32.7976
p-value=0.0002
sample: TCGA-AA-A010-01A, spectrum: 16022
MQYAPNTQVELLPQGR, H16R
MVH=58.1182
p-value=0.0001
sample: TCGA–AA–A010–01A, spectrum: 24978
MVAVGLCR, H8R
MVH=46.8373
p−value=0.0006
sample: TCGA–AA–A010–01A, spectrum: 66516
QQHEGAQGALDSGEPPLCR, Q17L
MVH=41.7718
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 23620
QQHEGAQGTLDGEPPQCR, A9T
MVH=38.0601
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 26209
QVGDFHQVLLR, A2V
MVH=37.2612
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 108397
RDDDGTLHAACQVQPSATLDAAQPR, A6T
MVH=69.7794
p-value=0.0001
sample: TCGA–AA–A010–01A, spectrum: 60673
SALVHLLNYQDDAELATHALPELTK, R18H
MVH=52.9144
p–value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 8000
SGGTLVVLGLGSEMTTVPLLHAALR, N4T
MVH=27.0042
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 96983
SLNDLTAR, K8R
MVH=38.6096
p-value=0.0006
sample: TCGA–AA–A010–01A, spectrum: 81094
SNPNWLLPDSVDWR, R5W
MVH=30.4885
p–value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 56673
SQNKEDYDGLKEEFR, A8D
MVH=43.5177
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 66302
SQNKEDYDGKKEEFRK, A8D
MVH=68.3489
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 80830
SSGGPGAGLCLFPLDEVHAK, K16E
MVH=45.4214
p-value=0.0001
sample: TCGA–AA–A010–01A, spectrum: 22635
SSYSGEYGSGGGK, G10S
MVH=64.3558
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 22306
SSSYSGEYGSGGGKR, G10S
MVH=44.5843
p-value=0.0002
sample: TCGA-AA-A010-01A, spectrum: 80548
TLAQLNPESSLFLTASK, I14T
MVH=70.4489
p-value=0.0001
sample: TCGA–AA–A010–01A, spectrum: 99748
TLEGLQVEEEPVYK, E14K
MVH=51.2436
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 61234
TVASPGVSVEEAVEQLDLGGVTLRR, T8S
MVH=25.5760
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 15845
VELFFKDDANNDPQWCEEQLLAOK, S16C
MVH=50.9663
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 68210
VLLDGVQNLR, P9L
MVH=59.4441
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 95538
VLSTTNAER, D6N
MVH=32.9451
p-value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 63694
VPVTQATR, L3V
MVH=36.5093
p-value=0.0012
sample: TCGA-AA-A010-01A, spectrum: 112376
VQLPTESLQELLDLHR, T7S
MVH=28.6462
p-value=0.0001
sample: TCGA–AA–A010–01A, spectrum: 151054
YLTLDSFDAMFR, G6S
MVH=49.9422
p–value=0.0001
sample: TCGA-AA-A010-01A, spectrum: 117168
YPVDTLPTSK, I3V
MVH=43.9885
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 46788
AAAAAABAPAAATAATTAATTAATAAQ, P17A
MVH=50.6819
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 62921
AAAPAPVSEAVSR, C12S
MVH=64.5969
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 26977
AAPSVTLPSSSEELQANK, T2A
MVH=52.5098
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 711
AGVETTTPSK, K7T
MVH=58.9181
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 506
AGVETTTPSKQSNNK, K7T
MVH=33.4398
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 25932
APSQHLSSFDPCFYR, R5H
MVH=40.9414
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 133316
ASSSLLLNESEPTTNLQLR, D8N
MVH=50.6809
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 57274
AVEVATVVLQPTVLR, S12T
MVH=47.6220
p−value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 27841
AVPTWANVQVVDDPGSLASVESPGTPK, SZN
MVH=35.5404
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 113088
AVTDFTEVTYDPGR, A14P
MVH=38.4764
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 8165
DFYVVEPLAFEGTPEQK, I4V
MVH=55.7857
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 121226
DGYGFLNR, N1D
MVH=47.6805
p-value=0.0006
sample: TCGA-AA-A017-01A, spectrum: 143924
DSKEPFSSVELQAALSK, E3K
MVH=43.4552
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 22404
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=80.6020
p−value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 102406
DVDGLTSLNAGR, K12R
MVH=56.3703
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 46372
DVPGFLQSQSSGPGQPAVWHR, N11S
MVH=39.2803
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 103303
DVTVLQNTDGNNNDAWAK, E14D
MVH=46.7798
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 704
EASQGSSASSAPQSVK, H13Q
MVH=56.4329
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 85967
EELGHLQNDLTSLENDK, M10L
MVH=36.9718
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 123286
EQPGSPEWLQLDK, Q13K
MVH=43.7544
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 38630
ESALEPGPVPEAPAGGPVHAVTVTLEK, R6P
MVH=46.3549
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 54823
FADVFAK, E7K
MVH=44.7857
p-value=0.0084
sample: TCGA-AA-A017-01A, spectrum: 134544
FFGSLPDSWAR, S11R
MVH=50.5395
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 135488
FGQDLLSPLLSVR, K13R
MVH=62.0988
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 6279
FGQGSGPVLDEVR, D12E
MVH=58.1019
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 53830
FLDKLPQQTGDR, H12R
MVH=51.5519
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 5584
FPGPCDYNFASDCR, L4P
MVH=64.2263
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 57646
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=58.8239
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 65065
FYLGPGTSVR, I9V
MVH=53.8943
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 27264
GQTGALLQNTVESLSK, D9N
MVH=72.1967
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 4970
GVAGSSVAVLCPYNR, G5S
MVH=44.2677
p–value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 6219
GVGGAVPGAVLEPVAPAPSVR, R16P
MVH=62.9181
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 95339
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=59.0359
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 140902
HASSGSFLSSANEHLK, P9S
MVH=45.2804
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 129758
KGCAGVLTLNRPK, T4A
MVH=47.6202
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 95569
KKPSEEEAAAAAGGPPGGPQVNPLPVTDEVV10A
MVH=53.5127
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 47326
LADGGAGGTQFQPYLDTLR, V1L
MVH=54.7509
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 140387
LALQPGTVGPQGR, V3I
MVH=58.1881
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 131686
LDSTDFTSTLK, G8S
MVH=53.1193
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 27462
LFEEDPAVGALVTGGDK, T1I
MVH=83.9346
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 57200
LGLTPEGQSYLDQFR, V3I
MVH=48.5008
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 23451
LGCHLYTPQELTNDC, E17K
MVH=54.6391
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 145671
LLDLFYPGDQSVTFGLK, T17I
MVH=47.2982
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 26782
LLDVDNVDLAMGK, I4V
MVH=84.8595
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 18889
LLNLADLVER, R4L
MVH=50.7351
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 105730
LLSDLPPSTGTFQEAQSR, S5L
MVH=40.2726
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 132534
LPQGLPTEENMSNTCLK, A7T
MVH=38.8517
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 7491
LQPEDMFVYDLNEK, C9Y
MVH=50.0916
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 143871
LVTDYTLAEADAALQK, E11D
MVH=77.2273
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 57752
NLSLSGHVGFDSPDKLVNK, Q16K
MVH=31.4436
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 27416
NPLLDLAAAYDQEGR, R3L
MVH=57.0889
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 45894
NTVLATWQPYSTSK, T11S
MVH=67.5131
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 47435
QGTLTEYCYSTLMSLPTK, G9S
MVH=57.3632
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 21925
QQHEGAQGTLDSGEPPQCR, A9T
MVH=36.2833
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 125536
RWLLLCNPGPLLRTVEK, D12N
MVH=52.3834
p–value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 134526
SAVGELSEDSSNVVHLLK, Q15H
MVH=49.8988
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 28757
SELPLDPLPLPTEEGNPLLK, V10L
MVH=52.7240
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 29292
SSMSPTTNVLLSPSLVATALSALSLGAEQR, T3M
MVH=25.1876
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 20840
SSSYSGEYGGGGK, G10S
MVH=67.3413
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 10601
SSSYSGEYGSGGGKR, G10S
MVH=47.7522
p-value=0.0002
sample: TCGA-AA-A017-01A, spectrum: 425

TAASGVEASSR, N9S

MVH=54.4793

p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 122702
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=63.3902
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 48209
TLDPFETMLK, S2L
MVH=27.9090
p-value=0.0001
sample: TCGA−AA−A017−01A, spectrum: 26671
TVVQLEGDNKLVTAFK, T14A
MVH=41.0093
p−value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 3418
VGVVSLGAR, I3V
MVH=42.2516
p-value=0.0005
sample: TCGA-AA-A017-01A, spectrum: 55598
VLLDGVQNL, P9L
MVH=59.4441
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 133885
VPSFETAEGLGAELK, T12A
MVH=71.2206
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 60721
VPVTQATR, L3V
MVH=47.6805
p−value=0.0012
sample: TCGA-AA-A017-01A, spectrum: 106685
VQVLAAQLLSEMK, D11E
MVH=69.3307
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 110223
VSDLAATAYK, N2S
MVH=55.3536
p-value=0.0001
sample: TCGA–AA–A017–01A, spectrum: 135596
VVLQPEALFSLYSK, F8L
MVH=63.8301
p-value=0.0001
sample: TCGA-AA-A017-01A, spectrum: 18526
WLCLCNPLAINTLVEK, D11N
MVH=81.0536
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 63092
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=49.1895
p−value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 51973
AAPSVTLFPPSEELQANK, T2A
MVH=61.2768
p-value=0.0001
Sample: TCGA-AA-A01C-01A, spectrum: 15141
AFSEYLGTDQSK, G4E
MVH=50.5858
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 11995
AGVETTTPSK, K7T
MVH=60.5959
p-value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 20198
APFAAPLPFAELVLPPQQ, S7L
MVH=22.3351
p-value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 87525
APSPLYSFSEEPFGVLVHR, R20H
MVH=65.9594
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 50921
APSQHLSSFDPCFYR, R5H
MVH=56.7578
p-value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 158873
ASSSLLLNESEPTTNLQLR, D8N
MVH=49.4845
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 19249
AVPPNNSNAEDDLPTVELQGLVPR, V22L
MVH=25.4972
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 61416
AYVVLLR, E1A
MVH=44.7547
p-value=0.0084
sample: TCGA-AA-A01C-01A, spectrum: 115642
DDDGTLHAACQVQPSATLDAQPR, A5T
MVH=49.1436
p-value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 19122
DFYVVEPLAFEGTPEQK, I4V
MVH=51.0831
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 145813
DGYGFLNR, N1D
MVH=44.9810
p-value=0.0006
sample: TCGA-AA-A01C-01A, spectrum: 46970
DLEAHVDSANK, I6V
MVH=49.0791
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 31049
DLGDLLEATGFDR, E10G
MVH=61.2692
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 42250
DMAGAQAAAVALNEEFLK, R18K
MVH=76.2262
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 36745
DSRPSQAAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=86.2825
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 53600
EALDVLDVLK, G7D
MVH=54.9216
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 837
EASQGSSASSAPQSVK, H13Q
MVH=36.6172
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 106898
EELGHLQNDLTSLENDK, M10L
MVH=31.3038
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 16892
EPSAPSLPTPAYQSLPAGGHAHPTPPTAPR, S15L
MVH=31.1344
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 147588
EQPGSPEWLQLDK, Q13K
MVH=28.5292
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 53468
ESALEPGPVPEAPAGGPVHAVTVVTLEK, R6P
MVH=22.9703
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 7131
FFGSLPDSWAR, S11R
MVH=29.2864
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 96795
FGLQAQLVTTDFQK, M7L
MVH=66.6542
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 8169
FGQDLLSPLLSVR, K13R
MVH=49.7889
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 71474
FLDKLPQQTGDR, H12R
MVH=46.6054
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 83387
FLSGHTSELGNFR, D11N
MVH=46.1271
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 19630
FNKPVFVLMLDQNTK, E11D
MVH=59.8900
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 86294
FNLSQESSYLATQYSLRPR, S2N
MVH=32.5609
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 20256
FSLDALLTNVLPFEK, I10V
MVH=48.7387
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 75074
FVSSSSSGGYGGGYGGLTASDGLLAGNEK, A9G
MVH=59.5106
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 94916
FYLGGPTSVR, I9V
MVH=44.7252
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 127573
GDPTVDPEELFR, G2D
MVH=29.5833
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 7307
GLDLLEER, V3I
MVH=33.1773
p-value=0.0038
sample: TCGA–AA–A01C–01A, spectrum: 52278
GQTGALLQNTVESLSK, D9N
MVH=70.3572
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 148220
GTDECALESVAATPLPK, I10V
MVH=31.9077
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 27673
GVAGSSVAVLCPYNR, G5S
MVH=51.6041
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 106741
KKPSEEEAAAAAGGPPGPGPQVNPLPVTDEVVTV10A
MVH=48.8855
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 63415
LADGGAGGTFQPYLDTLR, V1L
MVH=63.5724
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 157429
LDSTDFTSTLK, G8S
MVH=47.8873
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 35698
LEGANVQEAQK, T4A
MVH=68.2879
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 41382
LFEEDPAVGALVLTGGDK, T1I
MVH=86.8184
p-value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 38880
LGLHSTLLDEK, A6T
MVH=56.6484
p−value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 31608
LLNLADLVER, R4L
MVH=58.8016
p−value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 38928
LLTQDEGPALVPGSR, G14S
MVH=34.2555
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 103354
LPAEPLTR, E3A
MVH=31.8754
p-value=0.0012
sample: TCGA-AA-A01C-01A, spectrum: 158130
LPQGLPTEENMSNTCLK, A7T
MVH=47.9394
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 92672
LQELTPSSGDPEHDPASTEHK, P4L
MVH=51.3313
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 18478
LQPEDMFVYDLNEK, C9Y
MVH=38.0907
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 136212
LTGSSAQAESGVALGEAPDHSYESLR, E9A
MVH=49.3331
p−value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 61777
LTLQALTEK, A2T
MVH=47.2006
p-value=0.0005
sample: TCGA-AA-A01C-01A, spectrum: 14854
MAQWGNKPLC, V9I
MVH=34.6912
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 53351
MGTPVLEALGDGEFVK, V9L
MVH=28.4004
p−value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 84786
MKDVPGFLQQSQSSGPGQPAVWHR, N13S
MVH=82.4782
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 138595
MQLLQLLTTEK, E5Q
MVH=59.2753
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 16693
MQYAPNTQVELLPQGR, H16R
MVH=67.9365
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 138831
NEVLWHPTLNLPLSPQGTVR, A3V
MVH=38.2788
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 135710
NLPSLAEGQASDPPTVSR, K7E
MVH=51.4746
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 41313
NPLLDLAAYDQEGR, R3L
MVH=49.8289
p-value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 82646
NTNSVPETAPAALPETR, K17R
MVH=46.4424
p-value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 73442
NTVLATWQPYSTSK, T11S
MVH=43.9072
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 28574
QATVGNLINTERPGMLDFTGK, D6N
MVH=20.6149
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 74829
QGTLTEYCTLMSLPTK, G9S
MVH=44.6021
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 115287
RDDDGTLHAACQVQPSATLDAQQRR, A6T
MVH=78.3727
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 64622
SALVHLLNYQDDAELATHALPELTK; R18H
MVH=71.4389
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 64074
SDPVTLNVLYGP DVPTLSPSK, G14V
MVH=64.3358
p-value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 139042
SKLEDLANAALAAASAVTQLAK, V19I
MVH=49.5207
p-value=0.0001
sample: TCGA-MA-A01C-01A, spectrum: 65093
SLDDLDDWPLELLK, V9I
MVH=43.9436
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 70405
SPADPTDLGGQTSPR, I6T
MVH=61.5227
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 23641
SSSYSGEYGSGGGK, G10S
MVH=62.4008
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 23492
SSSYSGEYGSGGGKR, G10S
MVH=27.9619
p-value=0.0002
sample: TCGA-AA-A01C-01A, spectrum: 37282
TGSPGSPGASGVQSTAK, G10S
MVH=28.6166
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 64140
TLDPFETMLK, S2L
MVH=25.9480
p-value=0.0003
sample: TCGA-AA-A01C-01A, spectrum: 87636
TVEDLDGLLQQL YR, H10Q
MVH=64.0724
p-value=0.0001
sample: TCGA–AA–A01C–01A, spectrum: 101659
VLSTTNAER, D6N
MVH=34.4257
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 68391
VPVTQATR, L3V
MVH=38.8950
p-value=0.0012
sample: TCGA-AA-A01C-01A, spectrum: 5966
VQFCPFEENVESTR, K8E
MVH=45.1277
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 119351
VQLPTESLQELLDLHR, T7S
MVH=29.7779
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 70358
VSYGLGEEEHQGEGR, D7E
MVH=28.2693
p-value=0.0001
sample: TCGA-AA-A01C-01A, spectrum: 73820
YVSLLYNYEAGKDDYVK, I2V
MVH=37.9658
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 54580
AAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=37.8229
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 69490
AAAPAPVSEAVSR, C12S
MVH=43.1391
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 44626
AAPSVTLPSPSEELQANK, T2A
MVH=62.2254
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 126347
ACNLQSSHLDEYPFDAEY, N16D
MVH=29.3333
p-value=0.0003
sample: TCGA-AA-A01D-01A, spectrum: 9930
AGVETTTPSK, K7T
MVH=57.5665
p-value=0.0001
sample: TCGA–AA–A01D–01A, spectrum: 34745
AHDGGGLYALSWSPDSTR, H17R
MVH=47.1716
p–value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 37000
ALEDFDALEGK, M5V
MVH=61.6720
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 53080
AYVVLLR, E1A
MVH=40.4767
p-value=0.0084
sample: TCGA-AA-A01D-01A, spectrum: 101728
CDPGALVLPFSGALELK, Y1C
MVH=55.9646
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 16386
DFYVVEPLAFEGTPEQK, I4V
MVH=38.6432
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 123492
DGYGFLNR, N1D
MVH=38.7115
p-value=0.0006
sample: TCGA-AA-A01D-01A, spectrum: 32845
DTEEEDFHVDQATTVK, V12A
MVH=62.4723
p-value=0.0001
sample: TCGA–AA–A01D–01A, spectrum: 106788
DVTVLQNTDGNNDWAK, E14D
MVH=61.7127
p−value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 46498
EALDVLDVAVLK, G7D
MVH=50.7540
p-value=0.0001
sample: TCGA–AA–A01D–01A, spectrum: 14298
EPSAPSLPTPAYQLSPAGHAPTPPTAPPR, S15L
MVH=30.3098
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 56016
ESALEPGPVPEAPAGGPVHAVTVTLEK, R6P
MVH=34.0940
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 82264
FGLQAOQLVTDFQK, M7L
MVH=59.3047
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 7170
FGQDLLSPLLSVR, K13R
MVH=47.3466
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 61205
FLDKLPQQTGDR, H12R
MVH=44.3718
p-value=0.0001
sample: TCGA–AA–A01D–01A, spectrum: 46863
FLGQLLTAFPALR, A3G
MVH=47.0606
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 81576
FSVPVQHFCGNNPSTPLQVR, Q20R
MVH=38.2324
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 103662
FTVGDHSR, I3V
MVH=40.0195
p-value=0.0003
sample: TCGA-AA-A01D-01A, spectrum: 107684
GECVPGGQEPEPPLLPR, E7G
MVH=52.9364
p-value=0.0001
sample: TCGA–AA–A01D–01A, spectrum: 115322
GKWERPFEVKDTEEEDFHVDQATTVK, V22A
MVH=82.8064
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 99463
KKPSEEEEEAAAAAGGPPGGPQVNPLPVTDEVV V10A
MVH=51.3039
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 54858
LADGGAGGTFQPYLDTLR, V1L
MVH=31.1767
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 133326
LDSTDFTSTLK, G8S
MVH=48.1208
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 89852
LDVDKDG芙FTEGELK, A3V
MVH=36.3769
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 35842
LFEEDPAVGALVLTGGDK, T1I
MVH=84.7268
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 77691
LGLHEDSTNCR, R10C
MVH=37.2612
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 127502
LKQEYFVASTLQDLLR, A10S
MVH=46.2405
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 27642
LLNLLADLVER, R4L
MVH=59.9977
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 110020
LSDLQEALDQALNHVR, Y14H
MVH=56.6415
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 46928
LVLDEMVVELLEK, S3I
MVH=62.7905
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 114819
NLPSLAEGASDPTVASR, K7E
MVH=58.1158
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 52069
PLAVALDTK, V2I
MVH=44.1072
p-value=0.0002
sample: TCGA-AA-A01D-01A, spectrum: 6935
RLEGLLEGLGLR, G7E
MVH=40.0133
p-value=0.0001
sample: TCGA–AA–A01D–01A, spectrum: 135526
SAVGELSEDSSNVVHLLK, Q15H
MVH=25.6202
p–value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 110410
SDPLCLLLQDVGGGSWAELGR, V6I
MVH=68.1149
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 37183
SELPLDPLPLPTEEGNPLLK, V10L
MVH=51.4746
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 46486
SFQGPVLLGSSHGGVNLEDVAAETPEALLK, S24T
MVH=23.0266
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 124468
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=74.6637
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 83859
TATESFASDPLLRYRPLAVALDTK, V16I
MVH=48.3444
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 15821
TCSFDFGAVEDLSK, G3S
MVH=68.8247
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 87341
TTPLEAASSGAR, T11A
MVH=36.7688
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 56599
TVASPGVSVEEAQEQLDLGGVTLLR, T8S
MVH=66.9958
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 60201
TYGQVSGEALK, D2Y
MVH=45.0837
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 58585
VPVTQATR, L3V
MVH=33.3551
p-value=0.0012
sample: TCGA-AA-A01D-01A, spectrum: 101659
VQLPTESLQELLDLHR, T7S
MVH=46.5334
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 7388
VVLQPEALFSLYSK, F8L
MVH=46.8376
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 107457
WERPFEVKDTEEEEDFHVDQATTVK, V20A
MVH=57.4205
p-value=0.0001
sample: TCGA-AA-A01D-01A, spectrum: 63333
YVSLLYTNYEAGKDDYVK, I2V
MVH=28.8057
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 20642
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=30.5313
p-value=0.0003

m/z

Intensity(%)
sample: TCGA–AA–A01F–01A, spectrum: 42178
AAAPAPVSEAVSR, C12S
MVH=26.2412
p−value=0.0002
sample: TCGA-AA-A01F-01A, spectrum: 14224
AAPSVTLFPPSEELQANK, T2A
MVH=38.3153
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 69
AGVETTTPSK, K7T
MVH=49.7186
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 57598
ALSFNFGYAK, N3S
MVH=36.8069
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 89919
ASSSLLLNESEPTTNLQLR, D8N
MVH=56.9085
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 38333
AVEVATVVLQPTVLR, S12T
MVH=53.2559
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 27599
AYVVLLR, E1A
MVH=39.3243
p-value=0.0084
sample: TCGA-AA-A01F-01A, spectrum: 80406
DGYGFLNR, N1D
MVH=43.8062
p-value=0.0006
sample: TCGA-AA-A01F-01A, spectrum: 28522
DVPFLQQSQSSGPGQPAVWH, N11S
MVH=38.2296
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 15294
EAFEEAGVLLLQPR, R12Q
MVH=49.5864
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 35434
ELVDDSLNNVR, V7I
MVH=45.0837
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 81820
EQPGSPEWLQLDK, Q13K
MVH=45.0485
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 90945
FFGSLPDSWAR, S11R
MVH=38.2642
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 35275
FLDKLPQQTGDR, H12R
MVH=51.8811
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 22290
FLGQLLTAFPALR, A3G
MVH=42.8956
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 4747
FNKPVFLMLDQNTK, E11D
MVH=66.3027
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 48018
FQTATVTEK, I3T
MVH=28.0921
p-value=0.0007
sample: TCGA-AA-A01F-01A, spectrum: 32278
FRPHQDANSEKPR, P9S
MVH=39.1498
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 37362
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=51.1251
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 72424
FTVGDHSR, I3V
MVH=16.6685
p-value=0.0006
sample: TCGA–AA–A01F–01A, spectrum: 38540
FVSSSSSSGGYGGGGYGGVLTASDGLLAGNEK, A9G
MVH=74.6061
p–value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 83881
GFLSSLLDNVK, G5S
MVH=44.4610
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 97011
GLLDLLEER, V3I
MVH=43.2506
p-value=0.0038
sample: TCGA-AA-A01F-01A, spectrum: 20973
GQTGALLQNTVESLSK, D9N
MVH=62.5723
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 2185
GVAGSSVAVLCPYNR, G5S
MVH=54.4118
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 79808
GVALSNVVKH, I8V
MVH=41.8254
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 67101
KSVEEYANCHLAR, P2S
MVH=37.2936
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 51178
LAGALGPCLSLNVK, V9I
MVH=42.1704
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 88505
LDSTDFTSTLK, G8S
MVH=59.2753
p−value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 56541
LDVDKDGVFTEGELK, A3V
MVH=44.6572
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 14817
LFEEDPAVGALVLTGGDK, T1I
MVH=81.2769
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 25972
LFSQGLGGEQAK, Q12K
MVH=54.9006
p-value=0.0006
sample: TCGA-AA-A01F-01A, spectrum: 66573
LGGLQPSQDR, G7S
MVH=26.6014
p-value=0.0002
sample: TCGA-AA-A01F-01A, spectrum: 42135
LLHGQSSLK, H5Q
MVH=28.1275
p-value=0.0014
sample: TCGA-AA-A01F-01A, spectrum: 10419
LLNLLADLVER, R4L
MVH=59.9333
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 65183
LLPADALANCDLLL, V8A
MVH=61.4751
p–value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 7448
LLTQDEGPALVPGSR, G14S
MVH=37.5257
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 96375
LVTDYTLAEADAALQK, E11D
MVH=69.5510
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 67254
MGLSVER, M5V
MVH=34.0514
p-value=0.0022
sample: TCGA–AA–A01F–01A, spectrum: 2576
MQYAPNTQVELLPQGR, H16R
MVH=41.7921
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 14732
NPLLDLAAYDQEGR, R3L
MVH=37.9111
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 42846
NTNSVPETAPAALPETR, K17R
MVH=28.9600
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 98204
NTVLCNVVEKFLQADLAR, Q10K
MVH=36.7703
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 41189
PLAVALDTK, V2I
MVH=28.0954
p-value=0.0011

Intensity(%) vs. m/z

y5-NH3, y7-NH3, b4-H2O, y3-H2O, b5

m/z
Sample: TCGA-AA-A01F-01A, spectrum: 90890
SAVGELSEDSSNVVHLK, Q15H
MVH=36.1447
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 71870
SDPLCLLLQDVGGGSWAELGR, V6I
MVH=34.4573
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 30197
SDPVTLNVLYGPDVPTLPSK, G14V
MVH=52.1350
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 98013
SGGTLVGLVGLGSEMTTVPLLHAALR, N4T
MVH=44.2237
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 20997
SLSLLDSPGGLSGEK, V4I
MVH=57.0676
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 26301
SQNKEDYDGLKEEFR, A8D
MVH=87.2529
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 35036
SQNKEDYDGLKEEFRK, A8D
MVH=92.3060
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 9020
SSTTSTWELLDPR, Q12P
MVH=29.8703
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 67323
SVEEYANCHLAR, P1S
MVH=60.3251
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 45754
TLAQLNPESSLFLTASK, I14T
MVH=72.2743
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 31053
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=63.1678
p-value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 91598
VHSFPTLNFPASADR, K8N
MVH=49.6727
p-value=0.0001
sample: TCGA–AA–A01F–01A, spectrum: 90370
VPSFETAEGLGAELK, T12A
MVH=67.2127
p–value=0.0001
sample: TCGA-AA-A01F-01A, spectrum: 32645
VPVTQATR, L3V
MVH=44.5028
p-value=0.0012
sample: TCGA-AA-A01F-01A, spectrum: 91845
VVLQPEALFSLYSK, F8L
MVH=62.7759
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 51599
AAAAAAAAPAAAATAATTAATTAATAAAQ, P17A
MVH=42.9896
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 65256
AAAPAPVSEAVSR, C12S
MVH=51.0371
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 127918
AALEAVGGAVVLE, T9A
MVH=53.6538
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 42582
AAPSVTLPSSSEELQANK, T2A
MVH=54.3608
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 9968
AGVETTTPSK, K7T
MVH=54.1930
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 42026
APSQHLSSFDPCFYR, R5H
MVH=68.0845
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 59575
AQEGSLDEEAYLTEK, V4G
MVH=27.5459
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 14748
AWLSSQAAELER, V7A
MVH=52.2221
p-value=0.0001
sample: TCGA−AA−A01I−01A, spectrum: 105003
CDPGALVLPFSGALELK, Y1C
MVH=66.4185
p−value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 121809
CSGLLQVLFSPLEEEVK, A3G
MVH=45.4164
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 66205
DAGNEQDLGLQYK, N1D
MVH=42.7213
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 93283
DDDGTLHAACQVQPSATLDAQPR, A5T
MVH=42.1448
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 16848
DFYVVEPLAFEGTPEQK, I4V
MVH=57.0646
p–value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 117578
DGYGFLNR, N1D
MVH=45.3581
p-value=0.0006
sample: TCGA-AA-A01I-01A, spectrum: 38209
DLEAHVDSANK, I6V
MVH=45.0837
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 35053
DMAGAQAAAVALEEFLK, R18K
MVH=74.1060
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 4869
DTCVQSPPLSSFPR, C13R
MVH=54.8029
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 31027
DTEEEDFHVDQATTVK, V12A
MVH=58.6798
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 25515
EAPETDTSPSLWNVEFAK, D13N
MVH=41.5962
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 645
EASQGSSASSAPQSVK, H13Q
MVH=29.2716
p–value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 86618
EELGHLQNDLTSLENDK, M10L
MVH=44.0208
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 57779
ELVDDSLNNVR, V7I
MVH=50.7540
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 119214
EQPGSPEWLQLDK, Q13K
MVH=30.5209
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 53070
ESAEPGPVPEAPAGGPVHAVTVVTLLEK, R6P
MVH=28.7777
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 118886
EVAQQAVDADVHAVGVSTLAAGHK, I16V
MVH=28.3514
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 58553
FADVFAK, E7K
MVH=37.9046
p-value=0.0084
sample: TCGA-AA-A01I-01A, spectrum: 6785
FFGSLPDSWAR, S11R
MVH=36.4500
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 69022
FGLQAQLVTTDFQK, M7L
MVH=54.3695
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 69479
FNLSQESSYLATQYSLRPR, S2N
MVH=24.7891
p–value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 98424
FTVGDHSR, I3V
MVH=30.8166
p-value=0.0003
sample: TCGA–AA–A01I–01A, spectrum: 60800
FVSSSSSSGGYGGGYGGVLTASDGLLAGNEK A9G
MVH=76.0377
p–value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 6693
GFGTDEQALLDCLGSCSNK, R16C
MVH=60.3984
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 6912
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-A01I-01A, spectrum: 117267
GLSFDAAATSGGSASSEK, T2I
MVH=70.4618
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 43178
GQTGALLQNTVESLSK, D9N
MVH=59.3453
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 103312
HLDA2ALYGSEPELGEALKEDVGPGK, N10S
MVH=41.9709
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 3389
KAFSEYLGTDQSK, G5E
MVH=69.0814
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 94864
KKPSEEEAAAAAGGPPGGPQVNPLPVTDEVV, V10A
MVH=49.5293
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 52116
LADGGAGGTFQPYLDTLR, V1L
MVH=53.1690
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 126242
LDSTDFTSTLK, G8S
MVH=49.9366
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 34286
LFEEDPAVGALVLTGGDK, T1I
MVH=84.7385
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 107219
LGGLQPSQDR, G7S
MVH=35.0695
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 74267
LQELTPSSGDPGEHDPASTHK, P4L
MVH=60.7797
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 100132
LQQQHSEQPPLQPSPVTTR, M17T
MVH=58.8118
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 104939
LSDLQEQALDQALNHVR, Y14H
MVH=54.6887
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 22597
LSVATGALEAAQGSKPQCQTR, S16P
MVH=46.3295
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 69007
LSVFSTLDAPVAPSDK, V7I
MVH=46.7522
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 110388
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=48.4054
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 14454
MQYAPNTQVELLPQGR, H16R
MVH=52.0836
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 50095
MVDFAGMK, V7M
MVH=25.2412
p-value=0.0012
sample: TCGA-AA-A01I-01A, spectrum: 66091
NTNSVPETAPAALPETR, K17R
MVH=39.6115
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 30908
PVAEYWNSQK, D2V
MVH=28.2900
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 6523
QSGGSSQAGAVTVSDVQELMR, V10A
MVH=42.7663
p–value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 93005
RDDDGTLHAACQVQPSATLDAQPR-A6T
MVH=71.2561
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 84810
RQDLQSDGFSLETCK, K5Q
MVH=72.2422
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 56595
SPADPTDLGGQTSPR, I6T
MVH=68.6731
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 49301
SQNKEDYDGLKEEFR, A8D
MVH=63.2468
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 118270
TAASGVEASSRPLDHAQPPSSLVLDK, N9S
MVH=55.0372
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 118625
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=73.7074
p–value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 61337
TLDPFETMLK, S2L
MVH=34.5507
p−value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 85856
TLEGLQVEEPVYK, E14K
MVH=44.8531
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 99477
TPQEWAPHTAR, Q8H
MVH=36.5413
p-value=0.0002
sample: TCGA-AA-A01I-01A, spectrum: 56116
TSLSAPPNTSSTENPK, S9T
MVH=40.7674
p-value=0.0001
sample: TCGA−AA−A01I−01A, spectrum: 83111
TTPLEAASSGAR, T11A
MVH=40.6280
p−value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 53480
TVASPGVSVEAVEQLDLGGVTLLR, T8S
MVH=57.2634
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 70378
TVEDLDGLLQQL YR, H10Q
MVH=60.7245
p−value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 17440
VLFPGCTPPAYLLDGLVR, C11Y
MVH=42.2479
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 75919
VLLCGPVGPR, K10R
MVH=45.1880
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 59228
VLLDGVQNL, P9L
MVH=56.3425
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 68268
VPPVQVSPFLK, L9F
MVH=38.4737
p-value=0.0001
sample: TCGA-AA-A01I-01A, spectrum: 63405
VPVTQATR, L3V
MVH=41.1408
p-value=0.0012
sample: TCGA-AA-A01I-01A, spectrum: 90138
VVGACGVGK, R5C
MVH=32.3863
p-value=0.0014
sample: TCGA–AA–A01I–01A, spectrum: 7689
VVLQPEALFSLYSK, F8L
MVH=51.7375
p-value=0.0001
sample: TCGA–AA–A01I–01A, spectrum: 76219
VVLVTSAGAGLGR, G6S
MVH=65.1715
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 44508
AAPSVTLFPPSEELQANK, T2A
MVH=52.1102
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 10133
AGVETTTPSK, K7T
MVH=57.7760
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 138806
ASSSLLESEPTTNLQLR, D8N
MVH=64.6982
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 14888
AWLSSQAAELE, V7A
MVH=51.1678
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 99968
DDDGTLHAACQVQPSATLDAAQPR, A5T
MVH=46.5324
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 17021
DFVYVEPLAFEGTPEQK, I4V
MVH=53.3325
p–value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 127047
DGYGFLNR, N1D
MVH=44.9486
p-value=0.0006
sample: TCGA-AA-A01K-01A, spectrum: 30790
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=83.0611
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 31887
DTEEEDFHVDQATTVK, V12A
MVH=61.3348
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 109132
DVTVLQNTDGNNDNDAWAK, E14D
MVH=54.1518
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 45784
EALDVLDAVLK, G7D
MVH=54.9703
p-value=0.0003
sample: TCGA-AA-A01K-01A, spectrum: 128798
EQPGSPEWLQLDK, Q13K
MVH=26.2924
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 55513
ESALEPGPVPEAPAGGPVHAVTVVTLEK, R6P
MVH=42.7329
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 62027
FADVFAK, E7K
MVH=39.2553
p-value=0.0084
sample: TCGA-AA-A01K-01A, spectrum: 6783
FFGSLPDSWAR, S11R
MVH=35.7028
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 61045
FLDKLPQQTGDR, H12R
MVH=48.0255
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 61860
FLSLESQR, G6S
MVH=34.7124
p-value=0.0012
sample: TCGA-AA-A01K-01A, spectrum: 74013
FNLSQESSYLATQYSLRPR, S2N
MVH=28.3150
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 122514
FQLGNSGPNSTLK, S4G
MVH=18.1327
p-value=0.0002
sample: TCGA-AA-A01K-01A, spectrum: 129483
FQNEEEVFAWNNEVK, K2Q
MVH=55.8884
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 78469
FQATVTEK, I3T
MVH=30.6572
p-value=0.0014
sample: TCGA-AA-A01K-01A, spectrum: 105805
FTVGDHSR, I3V
MVH=40.9977
p-value=0.0003
sample: TCGA-AA-A01K-01A, spectrum: 74023
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=68.6428
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 118769
GKWERPFEVKDTEEEEDFHVDQATTVK, V22A
MVH=109.4332
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 6918
GLLDDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-A01K-01A, spectrum: 92887
GPVSVGVDAHHPSFFLYR, R10H
MVH=89.9936
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 44606
GQTGALLQNTVESLSK, D9N
MVH=53.8603
p–value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 23862
GVAGSSVAVLCPYNR, G5S
MVH=58.1675
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 101542
KKPSEEEAAAAAGPQVNPVTDEVV:V10A
MVH=50.5505
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 69785
KNPDSHYGELLEK, Q6H
MVH=35.5348
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 26095
LALLLMASQEPQR, T2A
MVH=54.5625
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 92453
LCLDAMHGVVPYVK, R2C
MVH=37.9772
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 125831
LCNNPAPQFGGK, T6A
MVH=54.3813
p–value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 35176
LFEEDPAVGALVLTGGDK, T1I
MVH=82.2121
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 46030
LFSLLSTALLR, V8A
MVH=59.8084
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 7833
LLDLFYPGDQQSVTFGLK, T17I
MVH=51.2139
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 17731
LLNLADLVER, R4L
MVH=55.4481
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 120631
LLSDLLPPSTGTFQEAQSR, S5L
MVH=41.1457
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 107464
LQQQHSEQPPLQPSPVTTR,M17T
MVH=50.2450
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 112412
LSDLQEALDQALNHVR, Y14H
MVH=52.0400
p−value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 52294
MVDFAGMK, V7M
MVH=30.7279
p-value=0.0006
sample: TCGA-AA-A01K-01A, spectrum: 70575
NTNSVPETAPAALPETR, K17R
MVH=37.5481
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 139279
QEPFLLSGGDDGALK, R1Q
MVH=21.0166
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 92496
QVTSTASTFKPLFSR, A2V
MVH=27.8871
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 116291
RGDLFYTSK, E2G
MVH=40.8105
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 27478
SALSGHLETLLGGLKK, V10L
MVH=77.1828
p−value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 139846
SAVGELSEDSSNVVHLLK, Q15H

MVH=59.5431
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 55146
SDPVTNLVLYGDVPTLSPSK, G14V
MVH=53.2809
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 129245
SEALPDLPTPSAPDLTEPK, A10T
MVH=43.9960
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 89019
SLNDLTAR, K8R
MVH=40.8238
p-value=0.0006
sample: TCGA-AA-A01K-01A, spectrum: 59994
SPADPTDLGGQTSPR, I6T
MVH=64.4645
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 128204
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=77.3907
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 91729
TLEGLQVEEEPVYK, E14K
MVH=48.0562
p-value=0.0001
sample: TCGA–AA–A01K–01A, spectrum: 88901
TTPLEAASSGAR, T11A
MVH=31.4938
p−value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 55932
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=49.5832
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 75044
TVEDLDGLLQQL YR, H10Q
MVH=59.6703
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 130131
TVEHGFPHQPSALGYSPSLHLLALGTR, R20H
MVH=64.3537
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 62736
VLLDGVQNLR, P9L
MVH=56.3425
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 67839
VPVTQATR, L3V
MVH=44.5028
p-value=0.0012
sample: TCGA-8A-A01K-01A, spectrum: 103529
VQLPTESLQELDLHR, T7S
MVH=27.0567
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 60020

VSYGLGEEHDEQEGR, D7E

MVH=32.0467

p-value=0.0001
sample: TCGA−AA−A01K−01A, spectrum: 7743
VVLOQPEALFSLYSK, F8L
MVH=56.7493
p−value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 82367
YVSLLYTNYEAGK, I2V
MVH=46.2028
p-value=0.0001
sample: TCGA-AA-A01K-01A, spectrum: 72917
YVSLLYTNYEAGKDDYVK, I2V
MVH=42.2519
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 5418
AAAAAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=42.8552
p-value=0.0001
sample: TCGA--AA--A01P--01A, spectrum: 135452
AAPSVTLPSSSEELQANK, T2A
MVH=52.1466
p−value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 43834
AGVETTTPSK, K7T
MVH=60.8672
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 121623
ALDRPYTSK, E3D
MVH=36.8597
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 105547
ANPQLGAYAPPPHVLGR, I14V
MVH=32.4102
p-value=0.0001
sample: TCGA–AA–A01P–01A, spectrum: 78597
ASSSLLLNESEPTTNLQLR, D8N
MVH=57.6775
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 12129
ATSSSSGSLSATGCLGR, R14C
MVH=51.9860
p−value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 107623
CDEPLNLVRR, S6N
MVH=37.2768
p-value=0.0001
sample: TCGA–AA–A01P–01A, spectrum: 40914
CSGLLQVLFSPLEEVEVK, A3G
MVH=57.2513
p-value=0.0001
sample: TCGA–AA–A01P–01A, spectrum: 108843
DFYVVEPLAFEGTPEQK, I4V
MVH=63.6788
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 47195
DGYGFLNR, N1D
MVH=40.1597
p-value=0.0006
sample: TCGA-AA-A01P-01A, spectrum: 108560
EKDLEDLFFK, Y9F
MVH=36.4257
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 114740
ELVDDSLNNVR, V7I
MVH=52.6904
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 59390
EQPGSPEWLQLDK, Q13K
MVH=32.1999
p-value=0.0001
sample: TCGA–AA–A01P–01A, spectrum: 145931
ESALEPGPVEAPAGGPVHAVTVTLLEK, R6P
MVH=24.4430
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 86669
EVTVMVLSPR, K1E
MVH=45.4347
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 50264
FFGSLPDSWAR, S11R
MVH=27.3976
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 27456
FGLQAQLVTTDFQK, M7L
MVH=54.3695
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 3596
FLSLESDR, G6S
MVH=33.5604
p-value=0.0012
sample: TCGA-AA-A01P-01A, spectrum: 60957
FNKPFVFLMLDQNTK, E11D
MVH=24.1114
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 21851
FTVGDHRS, I3V
MVH=46.5193
p-value=0.0003
sample: TCGA-AA-A01P-01A, spectrum: 89057
GFGTDEQALLDCLGSCSNK, R16C
MVH=58.0690
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 144877
GQTGALLQNTVESLSK, D9N
MVH=53.4752
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 115756
GVAGSSVAVLCPYNR, G5S
MVH=60.8495
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 15437
KKPSEEAAAAAGGPPGGPQVNLPVTDEVVTV10A
MVH=47.2949
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 78165
KLDSVFEEPLSK, R9P
MVH=36.0998
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 68197
LDSTDFTSTLK, G8S
MVH=46.6704
p-value=0.0001
sample: TCGA–AA–A01P–01A, spectrum: 127180
LFEEDPAVGALVLTGGDK, T1I
MVH=77.1711
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 61934
LLNLADLVER, R4L
MVH=44.7563
p-value=0.0002
sample: TCGA-AA-A01P-01A, spectrum: 140830
LQELTPSSGDPGEHDPASTHK, P4L
MVH=32.0656
p-value=0.0001
sample: TCGA–AA–A01P–01A, spectrum: 23533
LQQQHSEQPPLQPSPVTTR, M17T
MVH=49.3823
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 96780
LTPVSAQFQDLEGK, L8F
MVH=29.9553
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 142142
LWDTATGQCLSR, E5A
MVH=32.9663
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 106395
MQYAPNTQVELLPQGR, H16R
MVH=46.1031
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 127140
NPLLDLAAYDQEGR, R3L
MVH=43.2150
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 40574
NPSLLPLLLEAR, Q2P
MVH=31.8986
p-value=0.0001
sample: TCGA–AA–A01P–01A, spectrum: 55054
NSTLSEPGSGR, P4L
MVH=39.3140
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 123854
NTNSVPETAPAALPETR, K17R
MVH=39.2913
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 69845
QEPFLLSGGDDGALK, R1Q
MVH=23.2086
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 28142
QSAYCPYSHFPVGAAALTQEGR, K1Q
MVH=34.4099
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 79623
SAVGELSEDSSNVVHLLK, Q15H
MVH=64.1216
p-value=0.0001
sample: TCGA–AA–A01P–01A, spectrum: 6595
SDPVTLNVL YGPDVPTLSPSK, G14V
MVH=52.3556
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 59804
SEALPTDLPTPSAPDLTEPK, A10T
MVH=40.3500
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 20729
SPAADAKPAPK, T3A
MVH=34.0336
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 113471
SPADPTDLGGQTSPR, I6T
MVH=59.8825
p-value=0.0001
sample: TCGA–AA–A01P–01A, spectrum: 93410
STESLQTNVQR, A7T
MVH=49.5010
p–value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 113016
TSLSAPPNTSSTENPK, S9T
MVH=39.1472
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 140580
TTPLEAASSGAR, T11A
MVH=57.2560
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 37559
VFNNVLLQQTR, Q11R
MVH=49.3874
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 139501
VLSTTNAER, D6N
MVH=26.8358
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 29453
VPLASQGLPGSTVLLVVDKCDEPLNLLVR, S26N
MVH=66.1755
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 111834
VPVTQATR, L3V
MVH=42.7733
p-value=0.0012
sample: TCGA-AA-A01P-01A, spectrum: 29292
VQLPTESLQELLDLHR, T7S
MVH=73.5796
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 85473
VSEVLLSR, G8R
MVH=41.6414
p-value=0.0025
sample: TCGA-AA-A01P-01A, spectrum: 103599
VSYGLGEEEHDFQGR, D7E
MVH=31.5903
p-value=0.0003
sample: TCGA-AA-A01P-01A, spectrum: 51234
VVLQPEALFSLYSK, F8L
MVH=58.9975
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 133226
VWQTVSPVESR, G10S
MVH=41.1282
p-value=0.0001
sample: TCGA-AA-A01P-01A, spectrum: 26392
YVSLLYTNYEAGK, I2V
MVH=41.2036
p-value=0.0001
Sample: TCGA-AA-A01P-01A, spectrum: 15434
YVSLLYTNYEAGKDDYVK, I2V
MVH=73.5689
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 61064
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=48.7464
p-value=0.0001
sample: TCGA−AA−A01R−01A, spectrum: 75601
AAAPAPVSEAVSR, C12S
MVH=72.7810
p−value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 43315
AAPSVTLFPPSSEELQANK, T2A
MVH=52.6587
p–value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 18422
AGVETTTPSK, K7T
MVH=58.8009
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 18256
AGVETTTPSKQSNNK, K7T
MVH=49.4198
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 22126
ANPQLGAYAPPHPVLGR, I14V
MVH=29.0120
p−value=0.0002
sample: TCGA-AA-A01R-01A, spectrum: 18626
APPESCVSQGK, R6C
MVH=43.6830
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 42402
ATAECLQHPWLNS, R8Q
MVH=38.7613
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 79604
AVEVATVVLQPTVLR, S12T
MVH=51.5912
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 25408
DFYVVEPLAFEGTPEQK, I4V
MVH=42.3631
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 131572
DGYGFLNR, N1D
MVH=48.8163
p-value=0.0006
sample: TCGA-AA-A01R-01A, spectrum: 128590
DSRPSQAAGDNQGDEVK, A16V
MVH=63.9256
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 39499
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=90.8591
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 113064
DVDGLTSLNAGR, K12R
MVH=62.8531
p-value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 113858
DVTVLQNTDGNNNDWAK, E14D
MVH=63.7950
p−value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 53959
EALDVLDGLVK, G7D
MVH=54.9703
p-value=0.0003
sample: TCGA-AA-A01R-01A, spectrum: 96185
EALELDSLR, V2A
MVH=44.2028
p-value=0.0005
sample: TCGA-AA-A01R-01A, spectrum: 9721
EASQGSSASSAPQSVK, H13Q
MVH=46.3890
p-value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 67258
ELVDDSLNNVR, V7I
MVH=54.9703
p−value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 23178
EPSAPSLPTPAYQLSPLAGGHAPTPPTPAPR, S15L
MVH=24.9014
p-value=0.0001
sample: TCGA−AA−A01R−01A, spectrum: 133385
EQPGSPEWLQLDK, Q13K
MVH=41.7717
p−value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 15588
FFGSLPDSWAR, S11R
MVH=40.5045
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 67048
FLDKLPQQTGDR, H12R
MVH=50.5030
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 54283
FLGQLLTAFPALR, A3G
MVH=53.2707
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 77190
FLSGHTSELGFR, D11N
MVH=37.5786
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 79899
FNLSQESSYLATQYSLRPR, S2N
MVH=32.2741
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 32639
FPGPCDYNFASDCR, L4P
MVH=51.2461
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 110558
FTVGDHSR, I3V
MVH=42.4938
p-value=0.0003
sample: TCGA-AA-A01R-01A, spectrum: 79858
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G, MVH=58.1464
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 116238
GEAPCTVTSASPLEEATLSELK, V3A
MVH=43.2339
p-value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 26615
GLHSTLDASQTPDVVFASLLAAFSK, A5T
MVH=64.2122
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 15707
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-A01R-01A, spectrum: 130582
GLLVDTSR, I4V
MVH=33.7804
p-value=0.0012
sample: TCGA-AA-A01R-01A, spectrum: 52743
GQTGALLQNTVESLSK, D9N
MVH=70.0374
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 54242
GVLLMLFGGLPK, V10I
MVH=27.7659
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 91983
HMTAVVK, Y1H
MVH=33.7967
p-value=0.0044
sample: TCGA-AA-A01R-01A, spectrum: 74640
HNYEVAYR, F7Y
MVH=53.2515
p-value=0.0006
sample: TCGA-AA-A01R-01A, spectrum: 106278
KKPSEEEAAAAGGPPGGPQVNPLPVTDEVV V10A
MVH=20.9259
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 111897
KSVEEYANCHLAR, P2S
MVH=59.1584
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 41750
KVLLDGVQNLK, P10L
MVH=45.6989
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 12000
LALQPGTVGPQGR, V3I
MVH=53.9170
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 8110
LASDLLEWLQR, R10Q
MVH=63.4170
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 84718
LCTSVTESDVAR, E9D
MVH=52.2221
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 4395
LDSTDFTSTLK, G8S
MVH=59.7790
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 43926
LFEEDPAVGALVLTGGDK, T1I
MVH=74.5578
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 7981
LLGPNASPDGLLLLWTR, P13L
MVH=54.7019
p-value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 80501
LLSTCGLVQSLELQEKPDLAESPK, V11I
MVH=26.1750
p–value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 103475
LQQQHSEQPPLQPSPVTTR, M17T
MVH=53.4544
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 117390
LSDLQEALDQALNHVR, Y14H
MVH=39.7780
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 79421
LSVFSTLDAPVAPSDK, V7I
MVH=58.9518
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 99733
LTGSSVEMLQDVLDMKV, R2T
MVH=74.1987
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 7055
LTHVALDFWR, D3H
MVH=55.0187
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 123067
LVDPEQDMSLR, R6Q
MVH=55.9724
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 30908
LVVVGAGDVGK, G8D
MVH=67.7450
p-value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 3844
MGAQELLR, T1M
MVH=46.6637
p-value=0.0006
sample: TCGA-AA-A01R-01A, spectrum: 59405
MVDFAGMK, V7M
MVH=46.4054
p-value=0.0006
sample: TCGA-AA-A01R-01A, spectrum: 52857
NPLLDLASYDQGR, R3L
MVH=60.7245
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 36130
NSTLVFPLPLDLQGLGAK, M12T
MVH=56.7219
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 76402
NTNSVPETAPAALPETR, K17R
MVH=45.0411
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 69013
NTVLATWQPYSTSK, T11S
MVH=57.8862
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 49381
PVAEYWNSQK, D2V
MVH=54.6254
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 29285
QQHEGAQGTLDSGEPPQCR, A9T
MVH=42.0490
p-value=0.0001
sample: TCGA- AA- A01R- 01A, spectrum: 16461
RLEGLLEGLGLR, G7E
MVH=69.2013
p-value=0.0011
sample: TCGA-AA-A01R-01A, spectrum: 6986
SAVGELEDSSNVVHLLK, Q15H
MVH=64.9004
p-value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 62145
SDPVTLNVLYGDVPTLSPSK, G14V
MVH=55.6075
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 26269
SGGTLVLVLGSEMTTVPLLHAALR, N4T
MVH=35.0402
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 53847
SLDPGLKEDTLEFLLK, Q12E
MVH=54.8047
p-value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 263
SPAADAKPAPK, T3A
MVH=60.0660
p−value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 103324
SPPGAAAPAAAKPPPLSAK, S8P
MVH=28.1015
p-value=0.0003
sample: TCGA-AA-A01R-01A, spectrum: 58628
SQNKEDYDGLKEEFR, A8D
MVH=63.7301
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 66801
SQNKEDYDGLKEEFRK, A8D
MVH=57.2026
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 80521
SSGGPGAGLCLFPLDEVHAK, K16E
MVH=53.9298
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 112205
SVEEYANCHLAR, P1S
MVH=66.0660
p-value=0.0001
sample: TCGA–AA–A01R–01A, spectrum: 58799
SWGHVGTVLGSNK, R4H
MVH=34.0655
p−value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 132947
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=104.9084
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 24616
TCSFDTGAVEDLSK, G3S
MVH=69.5731
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 113905
TLNEADCATLPPALR, V10I
MVH=41.1864
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 130998
TLSGGLAVNGPR, P7A
MVH=62.1232
p−value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 93649
TPEFYNR, M1T
MVH=31.8562
p-value=0.0067
sample: TCGA-AA-A01R-01A, spectrum: 65513
TSLSAPPNTSSTENPK, S9T
MVH=46.8499
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 93421
TTPLEAASSGAR, T11A
MVH=54.9194
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 25879
VAALTGLPFVTAPNKFEALAAR, H22R
MVH=35.2740
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 86274
VLLCGPVGPR, K10R
MVH=55.3389
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 68768
VLLDGVQNLR, P9L
MVH=59.2865
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 93280
VMQVVDEK, I1V
MVH=49.8001
p-value=0.0019
sample: TCGA-AA-A01R-01A, spectrum: 6409
VPSFETAEGLGAELK, T12A
MVH=77.8336
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 64244
VPVTQATR, L3V
MVH=49.3666
p-value=0.0012
sample: TCGA-AA-A01R-01A, spectrum: 108444
VQLPTESLQELLDLHR, T7S
MVH=65.9051
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 120889
VSDLAAATAYK, N2S
MVH=55.3536
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 41542
VSTLAGLGLQGTDK, V4I
MVH=70.7830
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 23342
VTVAGLAGKDPVQCSHDVVLCPDASLEDAKK, R16H
MVH=104.6256
p−value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 8081
VVLQPEALFSLYSK, F8L
MVH=76.8180
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 49833
VWQTVSPVESR, G10S
MVH=49.7162
p-value=0.0001
sample: TCGA-AA-A01R-01A, spectrum: 82393
YLASGDCSK, R7C
MVH=37.8379
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 48746
AAAAAAPAATAATTAATAAQ, P17A
MVH=37.5058
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 40123
AAPSVTIFPPSSEELQANK, T2A
MVH=52.4798
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 103121
AARPPAASATPTAQPLPQPPAPR, T5P
MVH=45.8682
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 9297
AGVETTTPSK, K7T
MVH=59.0313
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 33078
ALEDVFDALEGK, M5V
MVH=64.9728
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 24043
AMQADLSEAAQLLSSDPSR, Q8E
MVH=53.5522
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 39389
APSQHLSSFDPCFYR, R5H
MVH=49.0909
p-value=0.0001
Sample: TCGA-AA-A01S-01A, spectrum: 65921
AVEVATVVLQPTVLR, S12T
MVH=45.0674
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 44166
CPAAPPPPAGGAANNHGAGSGAGGR, G1C
MVH=22.7021
p−value=0.0003
sample: TCGA-AA-A01S-01A, spectrum: 63017
DAGNEQDLGLQYK, N1D
MVH=42.7213
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 123415
DCGEAAQWLTSLK, T6A
MVH=50.7830
p–value=0.0001
sample: TCGA−AA−A01S−01A, spectrum: 64656
DDANNDPQWCEEQLLAHK, S10C
MVH=41.9597
p−value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 15928
DFYVVEPLAFEGTPEQK, I4V
MVH=56.9565
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 111533
DGYGFLNR, N1D
MVH=48.4897
p-value=0.0006
sample: TCGA-AA-A01S-01A, spectrum: 35677
DLEAHVDSANK, I6V
MVH=41.2452
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 29144
DTEEEDFHVDQATTVK, V12A
MVH=51.8204
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 56486
DVPGFLQSQSSGPGQPAVWHN, N11S
MVH=32.3707
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 96087
DVTVLQNTDGNNNDAYAK, E14D
MVH=40.9301
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 23952
EAPETDTSPSLWNVEFAK, D13N
MVH=37.3206
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 518
EASQGSSASSAPQSVK, H13Q
MVH=31.5044
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 82044
EELGHLQNDLTSLENDK, M10L
MVH=36.8273
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 13818
EPSAPSLPTPAYQSLPAGG#APTPPTPAPR, S15L
MVH=52.6128
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 113071
EQPGSPEWLQLDK, Q13K
MVH=30.5209
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 53619
EVGTSKELLET, I2V
MVH=32.9844
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 6365
FFGSLPDSWAR, S11R
MVH=39.3140
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 7183
FGQDLLSPLLSVR, K13R
MVH=31.1293
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 16174
FNKPFVFLMLDQNTK, E11D
MVH=59.0496
p-value=0.0001
sample: TCGA−AA−A01S−01A, spectrum: 92918
FTVGDHSR, I3V
MVH=32.2247
p−value=0.0003
sample: TCGA-AA-A01S-01A, spectrum: 66286
FVSSSSGSGYGGYGGVLTASDGLLAGNEK, A9G
MVH=72.0391
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 35686
GAQEKPQLSAAQSTQPQK, R3Q
MVH=41.7103
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 6494
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-A01S-01A, spectrum: 40538
GQTGALLQNTVESLSK, D9N
MVH=64.2610
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 89554
KKPSEEEAAAAGGPPGPQVNPLPVTDEVV_V10A
MVH=35.6909
p-value=0.0001
sample: TCGA- AA- A01S- 01A, spectrum: 120035
LDSTDFTSTLK, G8S
MVH=53.9249
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 81084
LDVDKDGFVTEGELK, A3V
MVH=50.7790
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 27084
LEGANVQEAQK, T4A
MVH=55.4896
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 32200
LFEEDPAVGLVTGGDK, T1I
MVH=82.2561
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 101332
LGGLQPSQDR, G7S
MVH=36.4514
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 25125
LLNLADLVER, R4L
MVH=59.4013
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 106107
LLSDLLPPSTGTFQEASR, S5L
MVH=39.2571
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 70755
LQELTPSSGPGEHDPASTHK, P4L
MVH=64.4634
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 94569
LQQQHSEQPPLQSPVTTR, M17T
MVH=41.0564
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 78547
LSNLENVK, T1I
MVH=39.1795
p-value=0.0012
sample: TCGA-AA-A01S-01A, spectrum: 13716
LTPVSAQFQDLEGK, L8F
MVH=34.2575
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 5724
LVTDYTLAEADAALQK, E11D
MVH=70.0546
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 61296
MVDFAGMK, V7M
MVH=25.2821
p-value=0.0006
sample: TCGA-AA-A01S-01A, spectrum: 103866
NLPSLAEGASDPPTVLSR, K7E
MVH=84.6791
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 32162
NPLLDLAAAYDQEGR, R3L
MVH=43.6565
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 18504
NSTLSEPGRSGR, P4L
MVH=35.7028
p–value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 62941
NTNSVPETAPAALPETR, K17R
MVH=41.1501
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 56203
NTVLATWQPYSTSK, T11S
MVH=46.6270
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 90822
NVVYPLYQLGGPQLR, R8Q
MVH=51.2040
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 80250
PSVAQPEDTVQFR, G2S
MVH=35.0093
p–value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 120967
QATVGNLINTERPGMLDFTGK, D6N
MVH=20.6353
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 60582
SDEAHPFR, G4A
MVH=38.3582
p-value=0.0003
sample: TCGA–AA–A01S–01A, spectrum: 49875
SDPVTNLNVL YGPDVPTLSPSK, G14V
MVH=45.4473
p−value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 113480
SEALPTDLPTPSAPDLTEPK, A10T
MVH=47.2019
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 53231
SLQEEQSRPTTAVSSPGGPAR, P10T
MVH=44.7451
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 116585
SPAADAKPAPK, T3A
MVH=35.2372
p-value=0.0004
sample: TCGA-AA-A01S-01A, spectrum: 53325
SPADPTDLGGQTSPR, I6T
MVH=63.0960
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 18138
SSSYSGEYGSGGGKR, G10S
MVH=24.3962
p-value=0.0002
sample: TCGA--AA--A01S--01A, spectrum: 23648
SSTTSTWELLDPR, Q12P
MVH=26.5976
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 44610
STESLQTVQR, A7T
MVH=58.2091
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 81316
TLEGLQVEEEPVYK, E14K
MVH=48.1908
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 52887
TSLSAPPNTSSTENPK, S9T
MVH=21.1725
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 78594
TTPLEAASSGAR, T11A
MVH=35.2458
p-value=0.0001
sample: TCGA–AA–A01S–01A, spectrum: 67194
TVEDLDGLLQQL YR, H10Q
MVH=62.7789
p–value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 39949
TVVQLEGDNKLVTAFK, T14A
MVH=48.8711
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 36981
VATLLATGGNR, M4I
MVH=43.4039
p-value=0.0001
sample: TCGA-AA-A01S-01A, spectrum: 64672
VFSVAELQAR, S9A
MVH=41.6154
p-value=0.0002
sample: TCGA-AA-A01S-01A, spectrum: 55953
VLLDGVQNLIR, P9L
MVH=59.4441
p-value=0.0001
sample: TCGA--AA--A01S--01A, spectrum: 77322
VLSTTNAER, D6N
MVH=28.6521
p-value=0.0003
sample: TCGA-AA-A01S-01A, spectrum: 60241
VPVTQATR, L3V
MVH=41.1408
p-value=0.0012
sample: TCGA-AA-A01S-01A, spectrum: 53361
VSYGLGEEHDEQEGR, D7E
MVH=48.2706
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 74129
AAAAAATAATTAATTAATAAQ, P17A
MVH=52.9089
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 55236
AAPSVTLFPPSSEELQANK, T2A
MVH=55.0252
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 115206
AFDQGADALYDHVNEGK, I13V
MVH=53.7743
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 9946
AGVETTTPSK, K7T
MVH=55.3940
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 46621
ALEDVFDALEKG, M5V
MVH=70.1622
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 118210
AVDVVLDCFLVK, A11V
MVH=49.1196
p-value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 123205
AVGEPMRPLAECCQLGLGLCDQVDLRR, P27A
MVH=21.3444
p-value=0.0009
sample: TCGA-AA-A01T-01A, spectrum: 80163
DAGNEQDLGLQYK, N1D
MVH=42.7213
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 27166
DFYVVEPLAFEGTPEQK, I4V
MVH=48.6266
p-value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 46465
DMAGAQAAVALNEEFLK, R18K
MVH=71.0982
p–value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 31533
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=44.3664
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 115200
DVTVLQNTDGNNNDAYWAKE, E14D
MVH=41.5962
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 56643
EALDVLDVLK, G7D
MVH=59.7899
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 90281
EALELDLR, V2A
MVH=38.7222
p-value=0.0005
sample: TCGA-AA-A01T-01A, spectrum: 36071
EAPETDTSPSLWNVEFAK, D13N
MVH=38.1898
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 9983
EASQGSSASSAPQSVK, H13Q
MVH=39.8740
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 99571
EELGHLQNDLTSLENDK, M10L
MVH=32.1504
p-value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 36937
EVVDGSPAAASTLSELTAEVNNFR, L23F
MVH=48.2523
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 16576
FFGSLPDSWAR, S11R
MVH=30.2691
p-value=0.0002
sample: TCGA–AA–A01T–01A, spectrum: 33010
FQLGNSGPNSTLK, S4G
MVH=42.4990
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 65172
FQPQSADFLDLTNPK, P6A
MVH=57.4399
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 52090
FTCTVLVAQK, P2T
MVH=51.3022
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 83371
FVSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=71.0844
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 50407
GAQEKPQLSAAQSTQPQK, R3Q
MVH=51.4039
p-value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 16379
GFGTDEQALLDCLGSCSNK, R16C
MVH=69.5344
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 65192
GQTGALLQNTVESLSK, D9N
MVH=72.1967
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 43579
GVAGSSVAVLCPYNR, G5S
MVH=54.0976
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 17261
GYPTLLLFGQGGK, R9Q
MVH=51.0700
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 107898
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=55.8577
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 108250
KKPSEEEAAAGGPPGQPQVNPLPVTDEVV, V10A
MVH=44.7760
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 4051
LDSTDFTSTLK, G8S
MVH=62.4346
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 98663
LDVDKDGTVTEGELK, A3V
MVH=43.3724
p-value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 45805
LFEEDPAVGALVLTGGDK, T1I
MVH=81.9968
p−value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 120984
LGGLQPSQDR, G7S
MVH=33.4848
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 7644
LLDTAFDLDFLK, V10I
MVH=39.0797
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 43488
LLTQDEGPALVPGSR, G14S
MVH=53.2370
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 42962
LSVATGALEAAQGSKPQCQTR, S16P
MVH=43.8002
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 73145
LTLQALTEK, A2T
MVH=54.8277
p-value=0.0005
sample: TCGA-AA-A01T-01A, spectrum: 24929
LTPVSAQFQDLEGK, L8F
MVH=52.6869
p-value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 54777
LVGLEEALSPGEAR, P4L
MVH=46.0327
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 35674
LVLSDEFSEALK, D2V
MVH=69.7415
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 15835
LVTDYTLAEADAALQK, E11D
MVH=75.0315
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 34393
MQYAPNTQVELLPQGR, H16R
MVH=58.1182
p-value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 42251
MVAVGLCR, H8R
MVH=32.1790
p–value=0.0006
sample: TCGA-AA-A01T-01A, spectrum: 136291
NEVLWHPTLNPLSPQGTVR+A3V
MVH=60.3146
p-value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 55722
NPLLDLAAYDQEGR, R3L
MVH=48.5136
p–value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 80166
NTNSVPETAPAALPETR, K17R
MVH=41.7389
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 82028
NTVLATWQPYSTSK, T11S
MVH=40.2198
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 82024
PVLLGNEP$\text{SLGVSQPR}$, T16R
MVH=33.5257
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 133246
QALSALEEAGAPAPGRSPATAPVPSSQPK, A23P
MVH=35.8536
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 124423
QLQEETPSGGPLTEALPPAR, P8S
MVH=44.8516
p-value=0.0001
sample: TCGA–AA–A01T–01A, spectrum: 90260
SAGLAPDCEASATAETTVSSVGTCEAAAK, G28A
MVH=27.2848
p−value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 75297
SDPVTNLNVLYGPDVPTLSPSK, G14V, MVH=73.1693, p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 70458
SPADPTDLGGQTPR, I6T
MVH=58.7409
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 30059
SSSYSGEYGSGGGK, G10S
MVH=65.9205
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 20440
SSSYSGEYGSGGGKR, G10S
MVH=48.1908
p-value=0.0002
sample: TCGA-AA-A01T-01A, spectrum: 45574
SSTTSTWELLDPR, Q12P
MVH=34.5969
p-value=0.0001
sample: TCGA--AA--A01T--01A, spectrum: 98887
TLEGLQVEEPVYK, E14K
MVH=53.2529
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 136588
TPFAAPSPFAELVLPPQQ, A1T
MVH=36.9678
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 69966
TSLSAPPNTSSTENPK, S9T
MVH=33.9435
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 55037
TVVQLEGDNKLVTAFK, T14A
MVH=48.8034
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 71579
VDDSSSEDKTEFLVK, T12I
MVH=33.4964
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 72895
VLTGTGNVNLQPNYPAAAR, I10V
MVH=53.1948
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 5884
VPSFETAEGGLGAELK, T12A
MVH=55.4517
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 68630
VPVTQATR, L3V
MVH=44.6448
p-value=0.0012
sample: TCGA-AA-A01T-01A, spectrum: 136447
VQVLAQQLSEMKE, D11E
MVH=61.7363
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 121676
VSDLAATAYK, N2S
MVH=49.8843
p-value=0.0001
sample: TCGA-AA-A01T-01A, spectrum: 12478
VSEVLLSR, G8R
MVH=31.0709
p-value=0.0025
sample: TCGA−AA−A01T−01A, spectrum: 43419
VSTLAGLGLQGTDK, V4I
MVH=45.9502
p−value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 80272
AAAPAPVSEAVSR, C12S
MVH=54.0766
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 39442
AAPSVTLFPPSSEELQANK, T2A
MVH=58.6969
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 150287
ACNVLQSSHLEDYPFDAEY, N16D
MVH=44.6905
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 140711
AFEPYPLELLELYSTK, V11L
MVH=55.8398
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 11538
AGVETTTPSK, K7T
MVH=57.3776
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 11310
AGVETTTPSKQSNNK, K7T
MVH=44.7583
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 15801

APVLRPGGTLGSAADSDAR, H21R

MVH=64.3563

p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 159718
ASSSLLLNESEPTTNLQLR, D8N
MVH=64.4516
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 84923
AVEVATVVLQPTVLR, S12T
MVH=38.0617
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 151640
CSGLLQVLFSPLEEEVK, A3G
MVH=42.6519
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 115435
DDDGTLHAACQVQPSATLDAAQPR, A5T
MVH=67.0576
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 19001
DFYVVEPLAFEGTPEQK, I4V
MVH=61.0881
p−value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 19913
DGTVLCELLNALYPK, E15K
MVH=40.3079
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 146899
DGYGFLNR, N1D
MVH=46.5577
p-value=0.0006
sample: TCGA-AA-A01V-01A, spectrum: 79848
DLEAHVDSANKNRDEALK, I6V
MVH=31.2768
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 149624
DLLDKQTWTDEGSVSEQMLR, R17Q
MVH=27.9715
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 35312
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V

MVH=70.1874
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 72396
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=40.8853
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 108830
EKLDSVLEFNLPSLLLR, S10N
MVH=56.3244
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 70006
ELVDDSLNNVR, V7I
MVH=49.1254
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 148754
EQPGSPEWLQLDK, Q13K
MVH=31.2747
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 63520
ESALEPGPVPEAPAGGPVHAVTVVTLLEK, R6P
MVH=32.9525
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 136564
EVSSSFQVLK, H8Q
MVH=38.5545
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 7394
FFGSLPDSWAR, S11R
MVH=38.7958
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 69783
FLDKLPQQTGDR, H12R
MVH=48.3335
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 85316
FNLSQESSYLATQYSLRPR, S2N
MVH=28.8633
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 106145
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=43.3668
p–value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 122431
FTVGDHSR, I3V
MVH=38.5489
p-value=0.0003
sample: TCGA-AA-A01V-01A, spectrum: 96515
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=77.2908
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 93958
FYLGGPTSVR, I9V
MVH=45.6760
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 7529
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA–AA–A01V–01A, spectrum: 51282
GQTGALLQNTVESLSK, D9N
MVH=66.0021
p−value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 26842
GVAGSSVAVLCPYNR, G5S
MVH=55.0333
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 26266
GVAGSSVAVLCPYNRK, G5S
MVH=39.3891
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 100613
HMTAVVK, Y1H
MVH=29.0708
p-value=0.0044
sample: TCGA–AA–A01V–01A, spectrum: 117159
KKPSEEAAAAGGPPGPGPQVNPLPVDEVVV10A
MVH=57.0892
p–value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 130163
LDSVLEFNLPDSLLLR, S8N
MVH=52.0836
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 40370
LFEEDPAVGALVLTGGDK, T1I
MVH=74.7132
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 59515
LHVLEVDHFK, Q2H
MVH=60.7220
p-value=0.0003
sample: TCGA-AA-A01V-01A, spectrum: 129384
LLDAETTAGAWPNVAAVSLTGR, A9G
MVH=47.4705
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 37703
LLTQDEGPALVPGR, G14S
MVH=50.2648
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 86265
LPPGDLVFDPDQRGDVVLPFQR, P6L
MVH=27.0194
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 91446
LQELTPSSGDPEHDPASTHK, P4L
MVH=77.0132
p–value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 124368
LQQQHSEQPPLQPSPVTTR, M17T
MVH=67.0945
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 129962
LSDLQEALDQALNHVR, Y14H
MVH=43.0940
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 16385
LTPVSAQFQDLEGK, L8F
MVH=37.7177
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 74447
LYDALDLSLLER, V7I
MVH=76.2131
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 83696
MKDVPGLQSQSGPGPAVWHR, N13S
MVH=107.9082
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 16331
MQYAPNTQVELLPQGR, H16R
MVH=59.8446
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 36317
MVAVGLCR, H8R
MVH=42.1076
p-value=0.0006
sample: TCGA-AA-A01V-01A, spectrum: 45704
NKSTESLQTNVQR, A9T
MVH=62.0639
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 23811
QQHEGAQGTLDGSQPPQCR, A9T
MVH=41.1623
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 107690
QSAACPYSHPFPVGAALLTQEGR, K1Q
MVH=28.7590
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 37619
QVGDFHQVLLR, A2V
MVH=34.2125
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 115084
RDDDGTLHAACQVQPSATLDAAGPR, A6T
MVH=95.7849
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 30917
SALSGHLETLLLGLLK, V10L
MVH=63.1790
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 130418
SDPCLLQDVGGSWAELGR, V6I
MVH=62.2550
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 63123
SDPVTLNLYGPDPVPTLSPSK, G14V
MVH=51.4867
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 19646
SGGTLVLVGLGSEMTTVPLLHAALR,N4T
MVH=32.7828
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 63957
SLDLDDWPLELLK, V9I
MVH=51.5420
p–value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 68694
SPADPTDLGGQTSPR, I6T
MVH=59.5314
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 59012
SQNKEDYDGLKEEFR, A8D
MVH=40.1050
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 69527
SQNKEDYDGLKEEFRK, A8D
MVH=86.1263
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 56946
STESLQTNVQR, A7T
MVH=55.0222
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 102204
TTPLEAASSGAR, T11A
MVH=48.8888
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 64001
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=70.2947
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 86458
TVEDLDGLLQQL YR, H10Q
MVH=60.7245
p-value=0.0001
sample: TCGA–AA–A01V–01A, spectrum: 116735
VCVALDECELDV, M12V
MVH=65.1335
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 5694
VLEVDTQGTVVCSLDR, G16R
MVH=57.5527
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 102033
VMQVVDEK, I1V
MVH=43.3144
p-value=0.0019
sample: TCGA-AA-A01V-01A, spectrum: 66725
VPVTQATR, L3V
MVH=44.3623
p-value=0.0012
sample: TCGA-AA-A01V-01A, spectrum: 119383
VQLPTESLQELLDLHR, T7S
MVH=38.9685
p-value=0.0001
sample: TCGA-AA-A01V-01A, spectrum: 8376
VVLQPEALFSLYSK, F8L
MVH=47.6035
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 39306
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=31.9288
p-value=0.0002
sample: TCGA–AA–A01X–01A, spectrum: 52425
AAAPAPVSEAVSR, C12S
MVH=66.8654
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 22656
AAPSVTLFPPSEELQANK, T2A
MVH=57.4684
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 8667
AGVETTTPSK, K7T
MVH=57.0148
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 111010
AQQNLSWEELTK, A11T
MVH=62.8426
p−value=0.0001
Sample: TCGA-AA-A01X-01A, spectrum: 111548
ASSSLLLLNESEPTTNLQLR, D8N
MVH=72.0320
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 48008
AVEVATVVLQPTVLR, S12T
MVH=59.0564
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 29730
AYVVLLR, E1A
MVH=49.9956
p-value=0.0084
sample: TCGA–AA–A01X–01A, spectrum: 64529
CLFASGSPFEPVK, G10E
MVH=56.2677
p−value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 34714
CPAAPPPPAGGAANNHGAGSGAGGR, G1C
MVH=27.7234
p-value=0.0001
sample: TCGA–AA–A01X–01A, spectrum: 78746
DDDGTLHAACQVQPSATLDAAQPR, A5T
MVH=60.6446
p–value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 7019
DFYVVEPLAFEGTPEQK, I4V
MVH=38.1562
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 101354
DGYGFLNR, N1D
MVH=44.3623
p-value=0.0006
sample: TCGA-AA-A01X-01A, spectrum: 120547
DSKEPFSSVELQAALSK, E3K
MVH=44.9158
p−value=0.0001
sample: TCGA–AA–A01X–01A, spectrum: 71236
EALELDSLR, V2A
MVH=42.7337
p–value=0.0005
sample: TCGA-AA-A01X-01A, spectrum: 14625
EAPETDTSPSLWNVEFAK, D13N
MVH=34.6264
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 27007
ECEPPSAGAAVSAR, T12S
MVH=33.0505
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 72224
EELGHQLNDLTSLENDK, M10L
MVH=40.5897
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 62210
EHTLHLEAELEK, S4L
MVH=33.7763
p-value=0.0002
sample: TCGA–AA–A01X–01A, spectrum: 45067
ELVDDSLNNVR, V7I
MVH=52.9082
p-value=0.0001
sample: TCGA–AA–A01X–01A, spectrum: 119752
EPSAPSLPTPAYQSLSLPAGGHAFTPPTPAPR, S15L
MVH=41.4903
p−value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 95216
EQPGSPEWLQLDK, Q13K
MVH=41.5554
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 45777
FADVFAK, E7K
MVH=48.3686
p-value=0.0084
sample: TCGA-AA-A01X-01A, spectrum: 112636
FFGSLPDSWAR, S11R
MVH=40.9925
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 36667
FLDKLPQQTGDR, H12R
MVH=69.3534
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 7291
FNKPFVFMLDQNTK, E11D
MVH=59.8900
p-value=0.0001
sample: TCGA–AA–A01X–01A, spectrum: 48236
FNLSQESSYLATQYSLRPR, S2N
MVH=29.8904
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 63848
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=56.6032
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 19487
FTCTLVaqK, P2T
MVH=51.3022
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 83240
FTVGDHSR, I3V
MVH=41.5009
p-value=0.0003
sample: TCGA-AA-A01X-01A, spectrum: 48202
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=53.1613
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 54397
FYLGGPTSVR, I9V
MVH=52.9789
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 100683
GCAGVLTNLNPK, T3A
MVH=38.7247
p-value=0.0001
sample: TCGA–AA–A01X–01A, spectrum: 120994
GFGTDEQALLDCLGSCSNK, R16C
MVH=60.8620
p−value=0.0001
sample: TCGA–AA–A01X–01A, spectrum: 112361
GGTLSTPQTGSENDALYEYL, G5S
MVH=41.3801
p−value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 121181
GLLDLLEER, V3I
MVH=50.2393
p-value=0.0038
sample: TCGA-AA-A01X-01A, spectrum: 92417
GLLVDTSR, I4V
MVH=35.2502
p-value=0.0012
sample: TCGA-AA-A01X-01A, spectrum: 12416
GVAGSSVAVLCPYNR, G5S
MVH=48.6987
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 79981
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=65.1043
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 117992
HASSGSFLSSANEHLK, P9S
MVH=48.3397
p-value=0.0001
sample: TCGA–AA–A01X–01A, spectrum: 39774
LADGGAGGTQFQPLTTLR, V1L
MVH=57.6097
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 113403
LEGLLEGLGLR, G6E
MVH=63.7749
p-value=0.0006
sample: TCGA-AA-A01X-01A, spectrum: 23142
LFEEDPAVGALVTGGDK, T11
MVH=84.1306
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 32819
LFSLLSTALLR, V8A
MVH=71.2336
p−value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 2669
LGNFTVK, I5T
MVH=37.4886
p-value=0.0022
sample: TCGA-AA-A01X-01A, spectrum: 15943
LLNLADLVER, R4L
MVH=60.9095
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 12294
LLTQDEGPALVPGSR, G14S
MVH=58.0806
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 85688
LQEQHLSSPQGVQLDR, I16R
MVH=63.1346
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 117060
LTQSSAFYSQR, T6A
MVH=59.7964
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 120506
LVTDYTLAEADAALQK, E11D
MVH=83.1009
p−value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 23054
NPLLDLAAAYDQEGR, R3L
MVH=67.5131
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 34919
NSLSETVR, M3L
MVH=37.0402
p-value=0.0006
sample: TCGA-AA-A01X-01A, spectrum: 9119
NSTLSEPGSGR, P4L
MVH=45.5035
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 78483
RDDGTLHAACQVQPSATLDAQPR, A6T
MVH=80.7653
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 92396
RGDLFYTSK, E2G
MVH=46.0537
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 112558
SAVGELSEDSSNVVHLKK, Q15H
MVH=30.7383
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 118663
SGGVERPFVLAR, M4V
MVH=55.2156
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 62109
SQPVSQPLTYESSPDEVR, G13S
MVH=71.3675
p-value=0.0001
sample: TCGA–AA–A01X–01A, spectrum: 17384
SSSYSGEYGSGGGK, G10S
MVH=59.4325
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 86591
TLNEADCATLPPALR, V10I
MVH=47.9849
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 68606
TTPLEAASSGAR, T11A
MVH=35.4191
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 43834
TYGQVSGEALK, D2Y
MVH=49.1254
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 46548
VLLDGVQLNR, P9L
MVH=53.5488
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 112012
VPSFETAEGLGAELK, T12A
MVH=60.5276
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 42271
VPVTQATR, L3V
MVH=43.1832
p-value=0.0012
sample: TCGA-AA-A01X-01A, spectrum: 74102
VQLPTESLQELLDLHR, T7S
MVH=27.3669
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 92288
VSDLAATAYK, N2S
MVH=59.1603
p-value=0.0001
sample: TCGA-AA-A01X-01A, spectrum: 15655
WLLCNPGLANTLVEK, D11N
MVH=83.5848
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 14276
AAAAAAAPAAAATAATTAATAAATQAQ, P17A
MVH=48.6822
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 74900
AAPSVTLFPSEELQANK, T2A
MVH=42.0269
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 28681
ACANPAAGSVLLPENLR, L13P
MVH=77.8266
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 5610
AGVETTTPSK, K7T
MVH=27.8164
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 32145
ALEDVFDLEGK, M5V
MVH=58.8872
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 87927
ALLQPLGLLR, T3I
MVH=38.4752
p-value=0.0011
sample: TCGA-AA-A01Z-01A, spectrum: 12963
AYVLLR, E1A
MVH=41.1372
p-value=0.0084
sample: TCGA-AA-A01Z-01A, spectrum: 78803
DGYGFLNR, N1D
MVH=42.2916
p-value=0.0006
sample: TCGA–AA–A01Z–01A, spectrum: 40384
DYCVLLEGSLALR, G3C
MVH=74.4667
p–value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 3547
FFGSLPDSWAR, S11R
MVH=27.0676
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 4493
FGQDLLSPLLSVR, K13R
MVH=43.1469
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 22658
FTVGDHSR, I3V
MVH=32.9982
p-value=0.0003
sample: TCGA-AA-A01Z-01A, spectrum: 92459
GQTGALLQNTVESLSK, D9N
MVH=51.7210
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 73755
GVAGSSVAVLCPYNR, G5S
MVH=51.7911
p-value=0.0001
sample: TCGA–AA–A01Z–01A, spectrum: 4523
LEGLLEGGLLR, G6E
MVH=43.9954
p-value=0.0012
sample: TCGA-AA-A01Z-01A, spectrum: 39895
LFEEDPAVGLVTLGGDK, T1I
MVH=64.7368
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 26259
LHVLVEPDHFK, Q2H
MVH=69.1396
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 10712
LLNLLADLVER, R4L
MVH=52.9781
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 19616
LSVFSTLDAPVAPSDK, V7I
MVH=41.0411
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 28177
MQYAPNTQVELLPQGR, H16R
MVH=56.0232
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 87075
NPLLDLAAYDQEGR, R3L
MVH=39.5427
p-value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 11403
SSSYSGEYGSGGGK, G10S
MVH=37.6704
p-value=0.0001
sample: TCGA–AA–A01Z–01A, spectrum: 32803
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=37.8362
p–value=0.0001
sample: TCGA-AA-A01Z-01A, spectrum: 42561
VPVTQATR, L3V
MVH=32.9553
p-value=0.0012
sample: TCGA-AA-A01Z-01A, spectrum: 93807
VVLQPEALFSLYSK, F8L
MVH=33.6579
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 51990
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=45.5249
p-value=0.0001
sample: TCGA–AA–A024–01A, spectrum: 38890
AAPSVTLFPPSSEELQANK, T2A
MVH=62.6113
p-value=0.0001
sample: TCGA−AA−A024−01A, spectrum: 95760
ACNVLQSSHLEDYPFDAEY, N16D
MVH=51.7791
p−value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 70841
APPRPGPVPEAAQPFLFTTR, P19T
MVH=59.8385
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 64927
AVEVATVVLQPTVLR, S12T
MVH=42.7742
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 44588
AYVLLR, E1A
MVH=40.9199
p-value=0.0084
sample: TCGA-AA-A024-01A, spectrum: 91766
CLAVYQAGAR, R1C
MVH=51.9117
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 56005
DAGNEQDLGLQYK, N1D
MVH=48.8137
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 75101
DDDGTLHAACQVPSATLDAAQPR, A5T
MVH=64.3487
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 19068
DFYVVEPLAFEGTPEQK, I4V
MVH=61.0881
p−value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 92813
DGYGFLNR, N1D
MVH=45.3581
p-value=0.0006
sample: TCGA-AA-A024-01A, spectrum: 74683
DVDGLTSLNAGR, K12R
MVH=62.8426
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 40177
EALDVLDALVK, G7D
MVH=47.7825
p-value=0.0001
sample: TCGA–AA–A024–01A, spectrum: 63303
ECALELDSLRL, V2A
MVH=32.7122
p−value=0.0005
sample: TCGA–AA–A024–01A, spectrum: 94480
EQPGSPEWLQLDK, Q13K
MVH=43.0652
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 47122
ESALEPGPVPEAPAGGPVHAVTVTLEK, R6P
MVH=31.4091
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 11029
FFGSLPDSWAR, S11R
MVH=40.9925
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 40468
FLGQLLTAFPALR, A3G
MVH=35.0099
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 19362
FNKPFVFLMLDQNTK, E11D
MVH=71.6666
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 23554
FPGPCDYNFASDCR, L4P
MVH=68.6564
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 11037
FVSSSSSSGYYGGYGGVLTASDGLLAGNEK, A9G
MVH=73.0181
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 68969
FYLGGPTSVR, I9V
MVH=42.1381
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 10905
GFGTDEQALLDCLGSCSNK, R16C
MVH=71.7488
p-value=0.0001
sample: TCGA–AA–A024–01A, spectrum: 76361
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=60.1213
p–value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 19729
HEPVGVCGLLPWNFPLVQGWK, M19V
MVH=48.5067
p-value=0.0001
sample: TCGA–AA–A024–01A, spectrum: 14276
KGCAGVLTNLNPK, T4A
MVH=46.5073
p–value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 65956
KPAAGLSAAPVPTTPAAGAPLMDFGNDFFVPPAPR, A14T
MVH=47.9044
p-value=0.0001
sample: TCGA–AA–A024–01A, spectrum: 69108
LDVDKDGFVTEGELK, A3V
MVH=43.3724
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 32714
LFEEDPAVGLVLTGGDK, T1I
MVH=82.0725
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 58788
LGLTPEGQSYLDQFR, V3I
MVH=47.6220
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 8373
LHVLVEPDHFK, Q2H
MVH=67.8796
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 19762
LLNLLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 30696
LLTQDEGPALVPGR, G14S
MVH=56.7511
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 70757
LPTEQWWLKL, K3T
MVH=51.3022
p-value=0.0002
sample: TCGA-AA-A024-01A, spectrum: 22842
LTVAPPLAEPGAGK, P1L
MVH=60.7498
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 15065
MAQWGNKPLC, V9I
MVH=37.9555
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 23572
MQYAPNTQVELLPQGR, H16R
MVH=60.4230
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 59209
NLSLSGHVGFDLPDKLVNK, Q16K
MVH=46.6754
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 55982
NTNSVPETAPAALPETR, K17R
MVH=49.1296
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 57788
NTVLATWQPYSTSK, T11S
MVH=49.8289
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 1337
NVSPVALPR, N3S
MVH=39.8083
p-value=0.0003
sample: TCGA-AA-A024-01A, spectrum: 74844
RDDDGTLHAACQVQPSATLDAAQPR, A6T
MVH=88.2114
p-value=0.0001
sample: TCGA–AA–A024–01A, spectrum: 53477
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=56.5148
p–value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 48545
SPADPTDLGGQTSPR, I6T
MVH=68.9928
p-value=0.0001
sample: TCGA−AA−A024−01A, spectrum: 41502
STESLQTNVQR, A7T
MVH=56.7842
p−value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 38061
TALALLDHPSEYAAR, R8H
MVH=36.9814
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 38566
TVVQLEGDNKLVTAFK, T14A
MVH=56.3736
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 42152
VSYGLGEEEHDEQGR, D7E
MVH=29.7732
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 63976
YVSLLYTNYEAGK, I2V
MVH=55.2739
p-value=0.0001
sample: TCGA-AA-A024-01A, spectrum: 58138
YVSLLYTNYEAGKDDYVK, I2V
MVH=39.2382
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 68627
AAAAAAAAAPAAAATAATTAATTAATTAATAAQ, P17A
MVH=38.6752
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 48465
AAPSVTLPSSSEELQANK, T2A
MVH=56.6091
p–value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 140092
ACNVLQSSHLEDYPDAEY, N16D
MVH=33.6731
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 11518
AGVETTTPSK, K7T
MVH=59.1995
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 110083
ALSFNFGYAK, N3S
MVH=34.2963
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 89656
APPRPGPVPEAAQPFLFTTR, P19T
MVH=63.4077
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 15471
APVLRPGGTLGLSEAADSDAR, H21R
MVH=67.0299
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 149243
ASSSLLLLNESEPTTNLQLR, D8N
MVH=48.2514
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 111827
AVDVLDCFLVK, A11V
MVH=56.5032
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 56901
AYVVLLR, E1A
MVH=39.3505
p-value=0.0084
sample: TCGA-AA-A029-01A, spectrum: 112130
CDPGALVLPFSGAELEK, Y1C
MVH=58.9218
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 18324
DFYVVEPLAFEGTPEQK, I4V
MVH=66.2351
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 137082
DGYGFLNR, N1D
MVH=43.3463
p-value=0.0006
sample: TCGA-AA-A029-01A, spectrum: 43681
DLEAHVDSANK, l6V
MVH=50.5395
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 39610
DMAGAQAAVAVALNEEFLK, R18K
MVH=82.5279
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 34527
DSRPSQAAGDNQGDEVKEQTFS GGTSQDTK, A16V
MVH=78.0992
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 35649
DTEEEDFHVDQATTVK, V12A
MVH=61.9302
p–value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 57862
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=42.4460
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 117684
DVTVLQNTDGNNNDAWAK, E14D
MVH=30.9540
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 679
EASQGSSASSAPQSVK, H13Q
MVH=24.4585
p–value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 99684
EELGHLQNDLTSLENDK, M10L
MVH=40.0801
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 66085
ELVDDSLNNVR, V7I
MVH=49.1254
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 138745
EQPGSPEWLQLDK, Q13K
MVH=36.5559
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 6897
FFGSLPDSWAR, S11R
MVH=38.7658
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 7888
FGQDLLSPLLSVR, K13R
MVH=54.5033
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 65883
FLDKLPQQTGDR, H12R
MVH=53.6016
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 79413
FVSSSSGSGGGGGGYGGVLTASDGLLAGNEK, A9G
MVH=69.2026
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 87611
FYLGPTSVR, I9V
MVH=49.2401
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 43709
GAQEKPQLSAAQSTQPQK, R3Q
MVH=47.6699
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 6973
GFGTDEQALLDCLGSCSNK, R16C
MVH=67.0565
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 16601
GLGTDEFTLYR, N10Y
MVH=50.7890
p-value=0.0001
Sample: TCGA-AA-A029-01A, spectrum: 7027

GLLDLLEER, V3I

MVH = 44.4068

p-value = 0.0038
sample: TCGA-AA-A029-01A, spectrum: 48604
GQGTGALLQNTVESLSK, D9N
MVH=68.1979
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 26058
GVAGSSVAVLCPYNR, G5S
MVH=55.4203
p−value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 94409
HMTAVVK, Y1H
MVH=36.0104
p-value=0.0044
sample: TCGA-AA-A029-01A, spectrum: 3450
KAFSEYLGTDQSK, G5E
MVH=61.2692
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 89195
KAPPRPGPVPEAAQPFLFTTR, P20T
MVH=62.5880
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 3152
LALQPGTVGPQGR, V3I
MVH=44.6004
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 141203
LASDLLEWLQR, R10Q
MVH=62.1428
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 147833
LDSTDFTSTLK, G8S
MVH=47.8873
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 33518
LEGANVQEAQK, T4A
MVH=54.8445
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 38679
LFEEDPAVGALVLTGGDK, T1I
MVH=74.5578
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 150810
LFVASNQEALHLVQLSGGSFK, G8E
MVH=35.6884
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 38173
LLDVDNVLDAMGK, I4V
MVH=70.4069
p−value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 26297
LLESGDLMSVSK, I12V
MVH=58.8481
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 129816
LLSDLPPSTGTFQEAQSR, S5L
MVH=46.6790
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 96163
LPAEPLTR, E3A
MVH=31.6526
p-value=0.0012
sample: TCGA–AA–A029–01A, spectrum: 148533
LPQGLPTEENMSNTCLK, A7T
MVH=40.6733
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 85343
LQELTPSSGDPGEHDPASTHK, P4L
MVH=65.3491
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 115966
LQQQHSEQPPLQPSPVTTR, M17T
MVH=46.6314
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 121219
LSDLQEALDQALNHVR, Y14H
MVH=36.4935
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 25483
LSVATGALEAAQGSKPQCQTR, S16P
MVH=45.8057
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 151450
LTAEFEEAQTSACLLQEELEK, R14L
MVH=60.9306
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 128043
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=44.8277
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 102283
LTGSSVEMLQDVLDMK, R2T
MVH=31.2788
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 49625
MGTPVLEALGDGEFVK, V9L
MVH=28.9649
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 15956
MQYAPNTQVELLPQGR, H16R
MVH=69.8254
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 56573
MVDFAGMK, V7M
MVH=29.2694
p-value=0.0025
sample: TCGA-AA-A029-01A, spectrum: 130631
NEVLWHPTLNPLLSPQGTVR, A3V
MVH=39.9894
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 69328
NLSLSGHVGFDSPDKLVNK, Q16K
MVH=29.9914
p-value=0.0002
sample: TCGA-AA-A029-01A, spectrum: 75928
NTNSVPETAPAALPETR, K17R
MVH=43.0542
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 59448
SDPVTLNVLYGPDVPTLPSK, G14V
MVH=41.9402
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 139191
SEALPTDLPTPSAPDLTEPK, A10T
MVH=50.7974
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 40092
SELPLDPLPLPTEEGNPLLK, V10L
MVH=45.8377
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 64891
SPADPTDLGGQTSPR, I6T
MVH=61.3114
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 106837
SPPGAAAPAAAPPPPLSAK, S8P
MVH=34.0100
p-value=0.0002
sample: TCGA–AA–A029–01A, spectrum: 137744
TAASGVEASSRPLDHAQPPSSLVLDK, N9S
MVH=52.3759
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 138109
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=60.6327
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 59475
TLDPFETMLK, S2L
MVH=25.4365
p-value=0.0011
sample: TCGA-AA-A029-01A, spectrum: 95825
TTPLEAASSGAR, T11A
MVH=30.3935
p-value=0.0002
sample: TCGA-AA-A029-01A, spectrum: 60491
TVASPGVSVEAAVEQLDLGGVTLLR, T8S
MVH=50.4130
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 80656
TVEDLDGGLQQLYR, H10Q
MVH=61.7247
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 94794
VLGTAGTEEGQK, I1V
MVH=48.5716
p-value=0.0001
sample: TCGA–AA–A029–01A, spectrum: 95587
VMQVVDEK, I1V
MVH=49.3803
p−value=0.0019
sample: TCGA–AA–A029–01A, spectrum: 73095
VPVTQATR, L3V
MVH=42.7514
p-value=0.0012
sample: TCGA–AA–A029–01A, spectrum: 130962
VQVLAQQLLSEMKG, D11E
MVH=71.1131
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 137322
VSQAELSSLQSVR, A1V
MVH=62.1339
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 64874
VSYGLGEEEHQGER, D7E
MVH=28.1876
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 148145
VVFPSEEVVEQK, G6E
MVH=19.2746
p-value=0.0001
sample: TCGA-AA-A029-01A, spectrum: 151486
VVLQPEALFSLYSK, F8L
MVH=53.8852
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 43123
AAAAAAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=48.1401
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 55477
AAAPAPVSEAVSR, C12S
MVH=63.3901
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 27766
AAPSVTTLPPSSEELQANK, T2A
MVH=55.5336
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 87603
AFDQGADALYDHVNEGK, I13V
MVH=57.4188
p-value=0.0001
sample: TCGA–AA–A02E–01A, spectrum: 8152
AGVETTTPSK, K7T
MVH=39.3973
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 41774
AYVVLLR, E1A
MVH=39.3072
p-value=0.0084
sample: TCGA–AA–A02E–01A, spectrum: 79828

DDDGTLHAACQVQPSATLDAQPR, A5T

MVH=49.6269

p−value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 102470
DGYGFLNR, N1D
MVH=47.8578
p-value=0.0006
sample: TCGA-AA-A02E-01A, spectrum: 79599
DLGLAQDSALSTK, T10I
MVH=68.2527
p-value=0.0001
sample: TCGA–AA–A02E–01A, spectrum: 87609
DVTVLQNTDGNNDAWK, E14D
MVH=58.2630
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 36881
EALDVLDAVLK, G7D
MVH=47.0134
p-value=0.0001
sample: TCGA–AA–A02E–01A, spectrum: 73785
EELGHLQNDLTSLENDK, M10L
MVH=45.6051
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 103877
EQPGSPEWLQLDK, Q13K
MVH=41.5554
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 47823
EVGTSDEKELLTSR, I2V
MVH=31.7929
p-value=0.0003
sample: TCGA-AA-A02E-01A, spectrum: 49237
FADVFAK, E7K
MVH=37.1433
p-value=0.0084
sample: TCGA-AA-A02E-01A, spectrum: 6817
FGQDLLSPLLQVR, K13R
MVH=54.7587
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 49152
FLSLESDR, G6S
MVH=39.5114
p-value=0.0012
sample: TCGA-AA-A02E-01A, spectrum: 13040
FNKPFVFLMLDQNTK, E11D
MVH=53.2591
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 62357
FQTATVTEK, I3T
MVH=30.7601
p-value=0.0021
sample: TCGA-AA-A02E-01A, spectrum: 84478
FTVGDHSR, I3V
MVH=40.6427
p-value=0.0006
sample: TCGA-AA-A02E-01A, spectrum: 51522
FVSSSSSSGYYGGGYGGVLASDGLLAGNEK, A9G
MVH=53.6017
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 6008
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-A02E-01A, spectrum: 35626
GQTGALLQNTVESLSK, D9N
MVH=66.8315
p-value=0.0001
sample: TCGA–AA–A02E–01A, spectrum: 81015
GYQQDAYDGKDYLANEDLR, R3Q
MVH=37.1066
p–value=0.0001
sample: TCGA–AA–A02E–01A, spectrum: 43379
LADGGGAGGTQPYLDTLR, V1L
MVH=54.6061
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 6816
LEGLLEGLGLR, G6E
MVH=57.1244
p-value=0.0012
sample: TCGA-AA-A02E-01A, spectrum: 27958
LFEEDPAVGALVLTGGDK, T1I
MVH=81.0988
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 92717
LGGLQPSQDR, G7S
MVH=44.8592
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 86701
LQEQHLSSPQGVQLDR, I16R
MVH=74.1175
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 78637
LQQQHSEQPPLQPSPVTTR, M17T
MVH=56.3516
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 58741
LSVFSTLDAPVAPSDK, V7I
MVH=52.7911
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 55179
LTGHGAEDSLADQAANK, R4H
MVH=64.8002
p-value=0.0001
sample: TCGA–AA–A02E–01A, spectrum: 10642
MQYAPNTQVELLPQGR, H16R
MVH=65.2234
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 41442
MVDFAGMK, V7M
MVH=36.3635
p-value=0.0006
sample: TCGA-AA-A02E-01A, spectrum: 95212
NLPSLAEGASDPPTVSR, K7E
MVH=58.3172
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 27861
NPLLDLAAYDQEGR, R3L
MVH=65.3603
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 56197
NTNSVPETAPAALPETR, K17R
MVH=43.4511
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 112990
SAVGELEDSEDSSNVVHLLK, Q15H
MVH=27.4064
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 43999
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=67.3072
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 47620
SPADPTDLGGQTSPR, I6T
MVH=75.4471
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 78476
SPPGAAAPAAAKPPPLSAK, S8P
MVH=40.4023
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 39151
STESLTQTVQR, A7T
MVH=53.6827
p-value=0.0001
Sample: TCGA-AA-A02E-01A, spectrum: 86077
SVEEYANCHLAR, P1S
MVH=44.1036
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 103034
TAASGVEASSRPLDHAQPPSSLVLDK, N9S
MVH=58.9586
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 43981
TLDPFETMLK, S2L
MVH=30.0059
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 45077
TVASPGVSVEAAVEQLDLGGVTLLR, T8S
MVH=44.9878
p-value=0.0001
sample: TCGA–AA–A02E–01A, spectrum: 60391
TVEDLDGLLQQL YR, H10Q
MVH=52.0247
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 41891
VLTGTVNVLQPNYPAAR, I10V
MVH=44.4010
p-value=0.0001
sample: TCGA–AA–A02E–01A, spectrum: 70268
VMQVVDEK, I1V
MVH=48.2033
p-value=0.0019
sample: TCGA-AA-A02E-01A, spectrum: 46063
VPVTQATR, L3V
MVH=45.5688
p-value=0.0012
sample: TCGA-AA-A02E-01A, spectrum: 98435
VQVLAQLLSEMK, D11E
MVH=70.3849
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 93406
VSDLAAATAYK, N2S
MVH=52.4712
p-value=0.0001
sample: TCGA-AA-A02E-01A, spectrum: 23016
VSRPESEQLR, N6S
MVH=48.0466
p-value=0.0002
sample: TCGA-AA-A02E-01A, spectrum: 114237
VVLQPEALFSYSK, F8L
MVH=59.7165
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 61421
AAAAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=50.6213
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 79419
AAAPAPVSEAVSR, C12S
MVH=51.3009
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 74296
AAGAELDSLLKPELLSALEK, P6L
MVH=51.0791
p-value=0.0001
sample: TCGA–AA–A02H–01A, spectrum: 50171
AAPSVTLPSSPSEQANK, T2A
MVH=50.3071
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 11342
AGVETTTPSK, K7T
MVH=58.2600
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 49436
APSQHLSSFDPCFYB, R5H
MVH=52.2695
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 147230
APWLEQERPEYWDQETR, G8R
MVH=60.8703
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 157980
ASSSLLLNESEPPTNLQLR, D8N
MVH=40.9961
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 59842
AYVLLR, E1A
MVH=38.8796
p-value=0.0084
sample: TCGA–AA–A02H–01A, spectrum: 160497
DCGEAAQWLTSFLK, T6A
MVH=71.5992
p−value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 103228
DFENSLNQVK, M6I
MVH=33.2122
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 18492
DFYVVEPLAFEGTPEQK, I4V
MVH=50.6643
p-value=0.0001
sample: TCGA–AA–A02H–01A, spectrum: 145286
DGYGFLNR, N1D
MVH=42.7733
p–value=0.0006
sample: TCGA-AA-A02H-01A, spectrum: 127945
EAGFPPGVVNLTTGYGP6TAGAALQHMDVDK, V27M
MVH=33.6241
p-value=0.0001
sample: TCGA–AA–A02H–01A, spectrum: 407
EASQGSSASSAPQSVK, H13Q
MVH=43.1224
p−value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 46153
ECEPPSAGAAVSAR, T12S
MVH=37.1125
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 105448
EELGHLQNDLTSLENDK, M10L
MVH=32.3166
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 153871
EEPVSSGPEEAAGK, V12A
MVH=33.2655
p-value=0.0001
sample: TCGA–AA–A02H–01A, spectrum: 69643
ELVDDSLNNVR, V7I
MVH=53.1193
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 16172
EPSAPSLPTPAYQSLPAGGHAPTPPTPAPR, S15L
MVH=27.9920
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 147028
EQPGSPEWLQLDK, Q13K
MVH=30.3210
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 62989
ESALEPGPVPVPAAPAGGPVHAVTVVTLLEK, R6P
MVH=32.9751
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 70176
FADVFAK, E7K
MVH=34.2241
p-value=0.0084
sample: TCGA-AA-A02H-01A, spectrum: 6575
FFGSLPDSWAR, S11R
MVH=37.1168
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 94992
FGLQQLVTEDFQK, M7L
MVH=48.0562
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 69351
FLDKLPQQTGDR, H12R
MVH=44.5180
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 83727
FNLSQESSYLATQYSLRPR, S2N
MVH=34.3288
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 157820
FNSVTELCAELPEQK, V11I
MVH=41.2833
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 90258
FQTATVTEK, I3T
MVH=27.2457
p-value=0.0007
sample: TCGA-AA-A02H-01A, spectrum: 72909
FVSSSSSGGYGGYGGVLTASDGLLAGNEK_A9G
MVH=67.0883
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 6612
GFGTDEQALLDCLGSCSNK, R16C
MVH=58.9051
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 6719
GLLDLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AA-A02H-01A, spectrum: 147705
GTDECALESVAVAATPLPK, I10V
MVH=31.5337
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 115603
GYQQDAYDGKDYLANEDLR, R3Q
MVH=62.6245
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 35002
KFSKEEPVSSGPEEAAGK, V16A
MVH=35.9464
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 26712
LAALALASSENSSTPEECEETSEKPK, M22T
MVH=58.2042
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 156608
LDSTDFTSTLKLK, G8S
MVH=49.9366
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 7579
LEGLLEGLGLR, G6E
MVH=59.8084
p-value=0.0006
sample: TCGA-AA-A02H-01A, spectrum: 39942
LFEEDPAVGALVLTGGDK, T1I
MVH=83.1747
p-value=0.0001
sample: TCGA–AA–A02H–01A, spectrum: 80996
LHVLVEPDHFK, Q2H
MVH=60.3090
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 7915
LLDLFYPGDQQSVTFGLK, T17I
MVH=40.6698
p-value=0.0001
sample: TCGA–AA–A02H–01A, spectrum: 160417
LLDTAFDLDFLK, V10I
MVH=72.7211
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 30852
LLNLLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 137002
LLSDLPPSTGFQEAQSR, S5L
MVH=35.2765
p−value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 19108
LQQELDDLLVDLDHQCQSACNLEK, R16C
MVH=57.7772
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 122751
LQQQHSEQPPLQPSPVTTR, M17T
MVH=53.9644
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 127898
LSDLQEALDQALNHVR, Y14H
MVH=44.9808
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 160121
LTAEFEEAQTSACLLQEELEK, R14L
MVH=74.1703
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 135206
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=48.9182
p-value=0.0001
sample: TCGA–AA–A02H–01A, spectrum: 15992
MQYAPNTQVELLPQGR, H16R
MVH=45.8528
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 134734
NLPSLAEGSADPPTVSR, K7E
MVH=55.8550
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 72995
NLSLSGHVGFDLDPDKLVNK, Q16K
MVH=33.3260
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 51159
NPGAVNACHLSCSALLQDNLADAVACAK, T1N
MVH=43.2344
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 80332
NTNSVPETAPAALPETR, K17R
MVH=47.9394
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 24268
QQHEGAQGTLDSEPPQCR, A9T
MVH=29.8999
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 7347
RLEGLLEGLGLR, G7E
MVH=65.7634
p-value=0.0004
sample: TCGA-AA-A02H-01A, spectrum: 62970
SALVHLLNYQDDAELATHALPELTK, R18H
MVH=75.0886
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 62434
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=56.5617
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 147695
SEALPTDLPTPSAPDLTEPK, A10T
MVH=57.1935
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 41387
SELPLDPLPLPTEEGNPLLK, V10L
MVH=56.5055
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 19431
SGGTLVLVGLGSEMTTVPLLHAALR, N4T
MVH=34.2922
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 68270
SLQEEQSRPTTAVVSPGPAR, P10T
MVH=39.5861
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 68396
SPADPTDLGGQTSPR, I6T
MVH=60.5276
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 112937
SPPGAAAPAAAKPPPLSAK, S8P
MVH=28.4642
p-value=0.0004
sample: TCGA-AA-A02H-01A, spectrum: 58624
SQNKEDYDGLKEEFR, A8D
MVH=67.3916
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 69049
SQNKEDYDGLKEEFRK, A8D
MVH=80.9568
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 125500
TGENVEDAFLGAAP, E11G
MVH=61.9181
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 121967
TPQEWAPHTAR, Q8H
MVH=32.5683
p-value=0.0008
sample: TCGA-AA-A02H-01A, spectrum: 101660
TTPLEAASSGAR, T11A
MVH=35.2458
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 85288
TVEDLDGLLQQL YR, H10Q
MVH=57.8862
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 160175
VALLQFGGPGEQQVAFPLR, S19R
MVH=66.2685
p-value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 118618
VGDPADFGTFLSAVLDAKF12L
MVH=66.6593
p-value=0.0001
sample: TCGA–AA–A02H–01A, spectrum: 71092
VLLDGVQNLR, P9L
MVH=59.4441
p–value=0.0001
sample: TCGA-AA-A02H-01A, spectrum: 66595
VPVTQATR, L3V
MVH=38.1197
p-value=0.0012
sample: TCGA–AA–A02H–01A, spectrum: 118219
VQLPTESLQELLDLHR, T7S
MVH=33.9499
p−value=0.0001
sample: TCGA–AA–A02H–01A, spectrum: 68311
VSYGLGEEEHQEG, D7E
MVH=25.2961
p–value=0.0002
sample: TCGA-AA-A02H-01A, spectrum: 7787
VVLQPEALFSLYSK, F8L
MVH=45.8159
p−value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 41595
AAAAAAAPAAATAATTAATTAATAAQ, P17A
MVH=30.0411
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 54700
AAAPAPVSEAVSR, C12S
MVH=30.5468
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 34144
AAPSVTLFPPSSEELQANK, T2A
MVH=40.6936
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 6596
AGVETTTPSK, K7T
MVH=43.5237
p–value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 28092
ALEDVFDALEGK, M5V
MVH=61.6720
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 109535
ASSSLLLNESEPTTNLQLR, D8N
MVH=53.3880
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 89335
CDPGALVLPFSGLKELK, Y1C
MVH=28.8310
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 104326
CSGLLQVLFSPLEEEVK, A3G
MVH=42.4974
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 11908
DFYVVEPLAFEGTPEQK, I4V
MVH=39.8638
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 100411
DGYGFLNR, N1D
MVH=40.5540
p-value=0.0006
sample: TCGA-AA-A02J-01A, spectrum: 2332
DTCVQSPLSSFPR, C13R
MVH=39.8538
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 78439
DVDGLTLSNLNAGR, K12R
MVH=35.5995
p-value=0.0001
sample: TCGA−AA−A02J−01A, spectrum: 35768
EALDVLDAVLK, G7D
MVH=57.6542
p−value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 73171
EELGHLQNDLTSLENDK, M10L
MVH=32.1757
p–value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 48029
ELVDDSLNNVR, V7I
MVH=43.8173
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 9880
EPSAPSLPTPAYQSLPAGGHAPTPPTPAPR, S15L
MVH=31.9588
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 101732
EQPGSPEWQLDK, Q13K
MVH=20.9048
p-value=0.0002
sample: TCGA-AA-A02J-01A, spectrum: 4718
FGQDLLSPILLSVR, K13R
MVH=46.6134
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 50883
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=66.9587
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 3976
GFGTDEQALLDCLGSCSNK, R16C
MVH=57.4765
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 34750
GQTGALLQNTVESLSK, D9N
MVH=27.8652
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 59773
GVAALTSDPAVQALVDMAVLDK, T18M
MVH=41.6295
p-value=0.0001
sample: TCGA--AA--A02J--01A, spectrum: 17791
GVAGSSVAVLCPYNR, G5S
MVH=33.5584
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 91701
KSVEEYANCHLAR, P2S
MVH=34.1141
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 42443
LADGGAGGTFQPYLDTLR, V1L
MVH=46.9173
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 108385
LDSTDFTSTLK, G8S
MVH=57.2310
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 27118
LFEEDPAVGA LVLGDK, T11
MVH=72.8371
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 91079
LGGLQPSQDR, G7S
MVH=33.8833
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 20804  
LLNLADLVER, R4L  
MVH=54.7605  
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 95535
LLSDLPPSTGTFQEAQSR, S5L
MVH=52.2049
p–value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 62370
LQELTPSSGDGEHDPASTHK, P4L
MVH=38.2544
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 111444
LTLVPVYTSPQLDSCPLLQQNK, A4V
MVH=44.1298
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 59466
LTPDDEAFLSANAGALLSQFEK, A3P
MVH=66.0220
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 93410
NLPSLAEQGASDPPTVASR, K7E
MVH=73.5363
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 27179
NPLLDLAAYDQEGR, R3L
MVH=44.8531
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 55418
NTNSVPETAPAALPETR, K17R
MVH=23.4276
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 100054
QLTVGVPR, K8R
MVH=27.4258
p-value=0.0012
sample: TCGA-AA-A02J-01A, spectrum: 110485
SAVGELEDSSNVVHLK, Q15H
MVH=28.4438
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 43037
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=42.2131
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 28207
SELPLDPLPLPTEEGNPLLK, V10L
MVH=55.1048
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 46934
SPADPTDLGGQTSPR, I6T
MVH=31.0065
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 84843
SVEEYANCHLAR, P1S
MVH=36.0540
p-value=0.0001
sample: TCGA–AA–A02J–01A, spectrum: 59327
TVEDLDGLLQQL YR, H10Q
MVH=57.0889
p–value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 56979
VLLDGVQNLR, P9L
MVH=47.3808
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 8954
VLLNDGGYYDPK, E12K
MVH=46.3772
p-value=0.0001
sample: TCGA-AA-A02J-01A, spectrum: 45732
VPVTQATR, L3V
MVH=25.2316
p-value=0.0049
sample: TCGA–AA–A02O–01A, spectrum: 45040
AAAAAAAAAAAPAAAAATAATTAATTAATTAATAAQ, P17A
MVH=41.1460
p–value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 95551
AAAPAPVSEAVSR, C12S
MVH=51.3124
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 38411
AAPSVTLFPPSSEELQANK, T2A
MVH=54.0366
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 113160
AELGVLEGDEAASPELMK, K2E
MVH=42.3401
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 66867
AFDQGADALYDHVNEGK, I13V
MVH=32.7820
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 8155
AGVETTTPSK, K7T
MVH=57.9303
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 21335
ANPQLGAYAPPHVLGR, I14V
MVH=30.8356
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 100592
APSPLYSVFSEEPFGVLVHR, R20H
MVH=57.6209
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 37552
APSQHLSSFDPCFYR, R5H
MVH=36.0790
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 77686
CPSPPMNTNLLSVGGQHQGVFGLPR, I7T
MVH=55.9283
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 85860
CSGLLQVLFSPLEEEVK, A3G
MVH=49.0550
p–value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 93037
DCGEAAQWLTSFLK, T6A
MVH=60.5922
p−value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 59468
DDDGTLHAACQVQPSATLDAAQPR, A5T
MVH=40.1772
p–value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 14648
DFYVVEPLAFEGTPEQK, I4V
MVH=54.6088
p−value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 81598
DGYGFLNR, N1D
MVH=49.8947
p–value=0.0006
sample: TCGA–AA–A02O–01A, spectrum: 37843
DSMFGGLTKV, A7T
MVH=44.8163
p–value=0.0001
sample: TCGA--AA--A02O--01A, spectrum: 28176
DSRPSQAAGDNQGDEVKEQTFSGGTSQDK, A16V
MVH=85.8326
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 39452
EALDVLDAVLK, G7D
MVH=56.6259
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 100400
EATSVPHLYALGDVVEGRPELTPTALMAGR, I24T
MVH=73.0251
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 95190
ECPCVHNNDLYSSSAK, G14S
MVH=25.2989
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 83282
EQPGSPEWLQLDK, Q13K
MVH=34.3981
p−value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 5249
FFGSLPDSWAR, S11R
MVH=46.4161
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 5828
FGQDLLSPLLsVR, K13R
MVH=46.8284
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 12857
FGQGSGPLVLDEVR, D12E
MVH=49.7889
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 96457
FLDKLPQQTGDR, H12R
MVH=45.7551
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 39751
FLGQLLTAFPALR, A3G
MVH=47.7644
p–value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 14933
FNKPFVFLMLDQNTK, E11D
MVH=64.3524
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 20741
FQLGNSGPNSTLK, S4G
MVH=43.0646
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 105645
FYLGGPTSVR, I9V
MVH=47.9836
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 5076
GFGTDEQALLDCLGSCSNK, R16C
MVH=68.5652
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 31217
GLDVTAYSLGSSDR, E3D
MVH=54.8685
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 81305
GLSFDAAATSGGSASSEK, T2I
MVH=64.4936
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 38377
GQTGALLQNTVESLSK, D9N
MVH=68.1979
p–value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 30438
GVAGSSVAVLCPYNR, G5S
MVH=44.9689
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 60863
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=57.0620
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 77159
HLAVLNGAMVSTPHYSPLLLEK, V9M
MVH=61.5158
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 72713
HVGDLGNVTAAK, D11A
MVH=32.9131
p-value=0.0002
sample: TCGA-AA-A02O-01A, spectrum: 68754
KFFGSLPDSWAR, S12R
MVH=45.6306
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 27656
KFSKEEPVSSGPEEAAGK, V16A
MVH=42.4945
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 45707
LADGGAGGTFQPYLDTLR, V1L
MVH=53.0072
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 5879
LEGLLEGLGLR, G6E
MVH=63.0108
p-value=0.0006
sample: TCGA-AA-A02O-01A, spectrum: 32427
LFEEDPAVGA[L/LGDK, T1I
MVH=80.5250
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 1601
LHGHLYTPGQELTNDC, E17K
MVH=63.8838
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 25051
LLNLADLVER, R4L
MVH=56.4843
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 65522
LQQQHSEQPPLQPSPVTTR, M17T
MVH=21.0313
p−value=0.0002
sample: TCGA-AA-A02O-01A, spectrum: 108233
LTQ AQLFDYSELPNFPR, G10S
MVH=43.0740
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 4486
LVTDTLAEADAALQK, E11D
MVH=60.1891
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 20357
LVVVGADGVGK, G7D
MVH=45.5810
p-value=0.0005
sample: TCGA-AA-A02O-01A, spectrum: 10559
MAQWGNKPLC, V9I
MVH=37.2229
p-value=0.0003
sample: TCGA-AA-A02O-01A, spectrum: 12154
MQYAPNTQVELLPQGR, H16R
MVH=69.4157
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 99435
NTLSNLAMRPGLEGYALPR, T4S
MVH=37.4835
p–value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 96385
NTNSVPETAPAALPETR, K17R
MVH=36.3988
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 4895
QSGGSSQAGAVTVSDVQELMR, V10A
MVH=37.6769
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 30282
QVGDFHQVLLR, A2V
MVH=37.9524
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 59227
RDDDGTLHAACQVQPSATLDAAQPR, A6T
MVH=74.7188
p−value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 5779
RWLLLCNPNGLANTLVEK, D12N
MVH=53.4927
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 91913
SAVGELEDSSNVVHLLK, Q15H
MVH=31.8275
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 46415
SDPVTLNLYGPDVPTLSPSK, G14V
MVH=47.5476
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 33363
SELPLDPLPLPTEEGNPLLK, V10L
MVH=59.1951
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 15292
SGGTLVLVGLGSEMTTVPLLHAALRN4T
MVH=41.1638
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 65560
SVEEYANCHLAR, P1S
MVH=31.8022
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 82779
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=80.0713
p−value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 14034
TCSFDFTGAVEDLSK, G3S
MVH=70.5122
p−value=0.0001
sample: TCGA-AA-A020-01A, spectrum: 114646
TGSLQLLFK, C8F
MVH=32.6032
p-value=0.0002
sample: TCGA-AA-A02O-01A, spectrum: 100674
TVEDLDGLLQQL YR, H10Q
MVH=53.2529
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 94563
VPVTQATR, L3V
MVH=27.4122
p-value=0.0012
sample: TCGA-AA-A02O-01A, spectrum: 30259
VYGDLHYTPAK, H7Y
MVH=51.6590
p-value=0.0001
sample: TCGA–AA–A02O–01A, spectrum: 24714
WLLLCNPGLANTLVEK, D11N
MVH=76.0343
p-value=0.0001
sample: TCGA-AA-A02O-01A, spectrum: 98772
YVSLLYTNYEAGKDDYVK, I2V
MVH=26.1912
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 56304
AAAAAAAAAPAAATAATTAATAATTAATAAQ, P17A
MVH=39.4417
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 36916
AAPSVTLFPPSSEELQANK, T2A
MVH=58.2196
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 10799
AGVETTTPSK, K7T
MVH=60.6183
p−value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 63559
ALFMDCGLHAR, T4M
MVH=41.1097
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 18138
ALPLALALHELGAGR, V7A
MVH=77.8336
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 77287
APSPLYSVEFSEEPFGVLVHR, R20H
MVH=61.9978
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 143576
ASSSLLLNESEPTTNLQLR, D8N
MVH=52.4052
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 75682
AVEVATVVLQPTVLR, S12T
MVH=36.0124
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 136336
CSGLLQVLFSPLEEEVK, A3G
MVH=52.5543
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 103849
DDDGTLHAACQVQPSATLDAAQPR, A5T
MVH=58.3530
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 17411
DFYVVEPLAFEGTPEQK, I4V
MVH=64.1779
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 131895
DGYGFLNR, N1D
MVH=43.6055
p-value=0.0006
sample: TCGA-AA-A02R-01A, spectrum: 102717
DLSTNYVSYK, A8V
MVH=49.1254
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 33178
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=70.2479
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 47025
DTLVLLCKPEPELNAALPSVNPAK, A20V
MVH=20.2579
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 65103
DVPGFLQSQSSGPQPAVWHR, N11S
MVH=31.4759
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 48016
EALDVLAVLK, G7D
MVH=45.0342
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 708
EASQGSSASSAPQSVK, H13Q
MVH=35.1723
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 95455
EELGHLQNDLTSLENDK, M10L
MVH=38.4375
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 47712
ELAPYDENWFYMR, T12M
MVH=31.2747
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 63136
ELVDDLNNVR, V7I
MVH=49.1254
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 15340
EPSAPSLPTPAYQSLPAGGHA\text{PT}PAPR, S15L
MVH=42.5309
p−value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 133474
EQPGSPEWLQLDK, Q13K
MVH=21.7996
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 57648
ESALEPGPVEAPAGGPVHAVTVTLLEK, R6P
MVH=33.8351
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 6500
FFGSLPDSWAR, S11R
MVH=26.3696
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 76009
FNLSQESSYLATQYSLRPR, S2N
MVH=25.5100
p-value=0.0002
sample: TCGA-AA-A02R-01A, spectrum: 81262
FQTATVTEK, I3T
MVH=28.5386
p-value=0.0009
sample: TCGA-AA-A02R-01A, spectrum: 18564
FSLDALLTNVLPFEK, I10V
MVH=55.1905
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 110098
FTVGDHSR, I3V
MVH=40.5928
p-value=0.0003
sample: TCGA-AA-A02R-01A, spectrum: 83995
FYLGGPTSVR, I9V
MVH=41.0564
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 6576
GFGTDEQALLDCLGSCSNK, R16C
MVH=67.3350
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 46682
GQTGALLQNTVESLSK, D9N
MVH=64.3641
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 25307
GVAGSSVAVLCPYNR, G5S
MVH=50.6251
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 90449
HMTAVVK, Y1H
MVH=32.6822
p-value=0.0044
sample: TCGA-AA-A02R-01A, spectrum: 71010
HNYEVAYR, F7Y
MVH=40.6565
p-value=0.0006
sample: TCGA–AA–A02R–01A, spectrum: 18412
KFSLDALLTNVLPFEK, I11V
MVH=77.4070
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 105229
KKPSEEEAAAAAGGPPGPGPQVNPLPVTDEVV V10A
MVH=61.2064
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 120825
KSVEEYANCHLAR, P2S
MVH=64.1831
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 56545
LADGGAGGTFQPYLDTLR, V1L
MVH=44.5178
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 18049
LALSPNAQLLALASGSSLHLYNTR, V9I
MVH=42.0818
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 7501
LEGLLEGLGLR, G6E
MVH=57.2310
p-value=0.0006
sample: TCGA-AA-A02R-01A, spectrum: 37224
LFEEDPAVGALVLTGGDK, T1I
MVH=82.1438
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 48343
LFSLLSTALLR, V8A
MVH=59.8084
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 105656
LGRPGLGSSGLAGAWLK, K3R
MVH=58.5941
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 28955
LLNLLADLVER, R4L
MVH=53.6736
p–value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 44718
LSQELDFVSHHVR, R3Q
MVH=34.2620
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 145741
LTAEFEAQTSACLLQEELEK, R14L
MVH=82.6882
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 98006
LTGSSVEMLQDVLDMK, R2T
MVH=61.9913
p–value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 87022
LTQAQLFDYSELPNFPR, G10S
MVH=42.6184
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 56846
MQQNLQELEEQLEEEESTR, A18T
MVH=64.2606
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 15137
MQYAPNTQVELLPQGR, H16R
MVH=75.7241
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 23901
MVAVGLCR, H8R
MVH=37.0649
p−value=0.0012
sample: TCGA–AA–A02R–01A, spectrum: 125679
NEVLWHPTLNPLSPQGTVR, A3V
MVH=56.8995
p–value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 37171
NPLLDLAAYDQEGR, R3L
MVH=44.8531
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 18537
NSTLVFPLPLDLQGLLGAK, M12T
MVH=43.2074
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 72738
NTNSVPETAPAALPETR, K17R
MVH=43.0542
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 43565
PVAEYWNSQK, D2V
MVH=33.1870
p–value=0.0001
sample: TCGA−AA−A02R−01A, spectrum: 62823
QQHEGAQGALDSGEPPPLCR, Q17L
MVH=47.8627
p−value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 34931
QVGDFHQVLLR, A2V
MVH=41.3213
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 103514
RDDGTLHAACQVQPSATLDAAQPR, A6T
MVH=89.0835
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 7228
RLEGLLEGLGLR, G7E
MVH=67.2215
p-value=0.0006
sample: TCGA-AA-A02R-01A, spectrum: 29115
SALSGHLETLLLGLLK, V10L
MVH=77.0123
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 144552
SAVGELSEDSSNVHLLK, Q15H
MVH=64.1216
p–value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 57163
SDPVTNLVLYGPDVPTLSPSK, G14V
MVH=34.9303
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 48028
SFQGPVLLGSSHGGVNLEDVAAETPEALLK, S24T
MVH=24.4300
p–value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 18362
SGGTLVGLGSEMTTVPLLHAALRN4T
MVH=33.9477
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 62001
SPADPTDLGGQTSP, I6T
MVH=63.0960
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 102447
SPPGAAAPAAAKPPPLSAK, S8P
MVH=32.1205
p-value=0.0004
sample: TCGA–AA–A02R–01A, spectrum: 21716
SSSYSGEYGSGGGK, G10S
MVH=63.0392
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 21583
SSSYSGEYGSGGGKR, G10S
MVH=24.5387
p-value=0.0002
sample: TCGA–AA–A02R–01A, spectrum: 111729
SVEEYANCHLAR, P1S
MVH=61.6720
p-value=0.0001
sample: TCGA–AA–A02R–01A, spectrum: 94705
TLEGLQVEEPVYK, E14K
MVH=56.3230
p–value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 91892
TTPLEAASSGAR, T11A
MVH=48.4902
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 77410
TVEDLDGLLQQL YR, H10Q
MVH=59.6703
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 14151
VAPQNDSTGTQLPPMHQQR, S20R
MVH=28.6766
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 104902
VCVALDECELDR, M12V
MVH=40.6582
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 60241
VPVTQATR, L3V
MVH=35.7887
p-value=0.0012
sample: TCGA-AA-A02R-01A, spectrum: 107537
VQLPTESLQELLDLHR, T7S
MVH=68.7043
p-value=0.0001
sample: TCGA-AA-A02R-01A, spectrum: 145768
VVLQPEALFSLYSK, F8L
MVH=47.4412
p-value=0.0001
sample: TCGA–AA–A03F–01A, spectrum: 65597
AAAAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=43.9497
p–value=0.0001
sample: TCGA–AA–A03F–01A, spectrum: 84216
AAAPAPVSEAVSR, C12S
MVH=67.9998
p−value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 42696
AAPSVTLPFSSEELQANK, T2A
MVH=43.3923
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 130280
AFDQGADALYDHVNEGK, I13V
MVH=37.4129
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 12698
AGVETTTPSK, K7T
MVH=54.1497
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 44746
ALEDVFDALEGK, M5V
MVH=64.9728
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 161474
ASSSLLNSEEPTTNLQLR, D8N
MVH=57.0120
p-value=0.0001
sample: TCGA–AA–A03F–01A, spectrum: 17859
AWLSSQAAELER, V7A
MVH=60.3682
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 20212
DFYVVEPLAFEGTPEQK, I4V
MVH=50.1004
p-value=0.0001
sample: TCGA–AA–A03F–01A, spectrum: 149732
DGYGFLNR, N1D
MVH=42.7733
p-value=0.0006
sample: TCGA-AA-A03F-01A, spectrum: 146806
DSRPSQAAGDNQGDEVK, A16V
MVH=16.6371
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 38836
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=107.3632
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 65003
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=30.1413
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 841
EASQGSSASSAPQSVK, H13Q
MVH=49.6276
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 73729
ELVDDSLNNVR, V7I
MVH=48.3676
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 151378
EQPGSPEWLQLDK, Q13K
MVH=31.2747
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 77416
EVQDGLAPWMFK, R9W
MVH=29.1446
p-value=0.0002
sample: TCGA-AA-A03F-01A, spectrum: 7485
FFGSLPDSWAR, S11R
MVH=37.8705
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 73384
FLDKLPQQTGDR, H12R
MVH=56.7926
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 20818
FNKPFVFLMLDQNTK, E11D
MVH=47.9341
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 157601
FNLSTDQR, R7Q
MVH=26.4955
p-value=0.0006
sample: TCGA-AA-A03F-01A, spectrum: 161378
FNSVTELCAELPEQK, V11I
MVH=43.6595
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 65855
FQPQSADFLDLTNPK, P6A
MVH=43.2500
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 95204
FQTATVTEK, I3T
MVH=30.2011
p-value=0.0005
sample: TCGA-AA-A03F-01A, spectrum: 126712
FTVGDHSR, I3V
MVH=40.5431
p-value=0.0003
sample: TCGA-AA-A03F-01A, spectrum: 77212
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=59.0913
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 98355
FYLGGPTSVR, I9V
MVH=36.4257
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 7501
GFGTDEQALLDCLGSCSNK, R16C
MVH=47.9010
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 7607
GLLDLLEER, V3I
MVH=40.9251
p-value=0.0038
sample: TCGA-AA-A03F-01A, spectrum: 54696
GQTGALLQNTVESLSK, D9N
MVH=67.9881
p-value=0.0001
sample: TCGA–AA–A03F–01A, spectrum: 29374
GVAGSSVAVLCPYNR, G5S
MVH=50.0621
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 70784
KADLLNR, V5I
MVH=35.0625
p-value=0.0088
sample: TCGA-AA-A03F-01A, spectrum: 111252
KKPSEEEAAAAAGGPPGGPQVNPLPVTDEVV_V10A
MVH=41.3053
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 160099
LDSTDFTSTL, G8S
MVH=45.0323
p-value=0.0001
sample: TCGA–AA–A03F–01A, spectrum: 43506
LFEEDPAVGA\text{LVLTGGDK}, T1I
MVH=80.9820
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 8865
LLDLFYPGDQSQSVTFLK, T17I
MVH=48.9706
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 33437
LLNLADLVER, R4L
MVH=54.4199
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 161445
LPPGDLVFDPDQR, P6L
MVH=35.7031
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 28497
LQAAYNLVK, R2Q
MVH=35.8432
p-value=0.0005
sample: TCGA-AA-A03F-01A, spectrum: 95953
LQELTPSSGDGEPDEHPASTEHK, P4L
MVH=66.4747
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 118637
LQQQHSEQPPLQPSPVTTR, M17T
MVH=39.2444
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 6823
LVTDYTLAEADAALQK, E11D
MVH=61.9302
p-value=0.0001
Sample: TCGA-AA-A03F-01A, spectrum: 17562
MQYAPNTQVELLPQGR, H16R
MVH=42.3711
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 140400
NLPSLAEQQGASDPPTVASR, K7E
MVH=67.9548
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 85195
NTNSVPETAPAALPETR, K17R
MVH=40.1954
p-value=0.0001
sample: TCGA–AA–A03F–01A, spectrum: 162542
SAVGELSEDSSNVVHLLK, Q15H
MVH=51.2559
p–value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 44905
SELPLDPLPLPTEEGNPLLK, V10L
MVH=49.2696
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 21248
SGGTLVVLVGLGSEMTTVPLLHAALRN4T
MVH=33.1547
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 72329
SPADPTDLGGQTSPR, I6T
MVH=65.1525
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 25311
SSSYSGEYGSGGGK, G10S
MVH=37.1091
p-value=0.0001
sample: TCGA–AA–A03F–01A, spectrum: 25132
SSSYSGEYGSGGGKR, G10S
MVH=16.7144
p–value=0.0006
sample: TCGA-AA-A03F-01A, spectrum: 110538
TLEGLQVEEEPVYK, E14K
MVH=44.8531
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 107389
TTPLEAASSGAR, T11A
MVH=38.2598
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 90196
TVEDLDGLLQQL YR, H10Q
MVH=62.7789
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 42736
TVVQUEGDKLVTAFK, T14A
MVH=51.3927
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 105992
VLSTTNAER, D6N
MVH=27.1740
p-value=0.0003
sample: TCGA-AA-A03F-01A, spectrum: 161993
VPSFETAEGLAGELK, T12A
MVH=71.5261
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 70509
VPVTQATR, L3V
MVH=39.2648
p−value=0.0012
sample: TCGA-AA-A03F-01A, spectrum: 33091
WLLLCNPGLANTLVEK, D11N
MVH=85.2622
p-value=0.0001
sample: TCGA-AA-A03F-01A, spectrum: 75948
YVSLLYTNYEAGKDDYVK, I2V
MVH=31.7019
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 40137
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=42.5511
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 53597
AAAPAPVSEAVSR, C12S
MVH=56.5947
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 22874
AAPSVTLFPPSEELQANK, T2A
MVH=54.0518
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 3575
AFSEYLGTDSK, G4E
MVH=61.4524
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 577
AGVETTTPSK, K7T
MVH=55.0120
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 73465
ALSFNFGYAK, N3S
MVH=40.0012
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 115827
AQQNLSWEELTK, A11T
MVH=56.7570
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 74958
AVDVLDCFLVK, A11V
MVH=69.0752
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 7169
DFYVVEPLAFEGTPEQK, I4V
MVH=41.5124
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 96486
DGYGFLNR, N1D
MVH=45.4814
p-value=0.0006
sample: TCGA–AA–A03J–01A, spectrum: 125852
DSKEPFSSVELQAALSK, E3K
MVH=54.7437
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 19186
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=99.3652
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 39788
DVPGFLQQSQSSGPGQPAVWH, N11S
MVH=34.2896
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 14904
EAPETDTSPSLWNVEFAK, D13N
MVH=53.7286
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 639
EASQGSSASSAPQSVK, H13Q
MVH=54.2838
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 73164
EELGLQNDLTSLENKD, M10L
MVH=39.1299
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 46267
ELVDDSLNNVR, V7I
MVH=54.8445
p-value=0.0001
sample: TCGA–AA–A03J–01A, spectrum: 107290
EQPGSPEWLQLDK, Q13K
MVH=35.1721
p−value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 115781
FEEGENSLLHLK, A4G
MVH=57.6320
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 117523
FFGSLPDSWAR, S11R
MVH=27.1168
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 48894
FGLQAQLVTTDFQK, M7L
MVH=64.5486
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 46135
FLDKLPQQTGDR, H12R
MVH=59.3529
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 7449
FNKPFVFLMLDQNTK, E11D
MVH=53.2918
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 49276
FNLSQESSYLATQYSLRPR, S2N
MVH=25.7444
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 60978
FQTATVTEK, I3T
MVH=32.9574
p-value=0.0007
sample: TCGA-AA-A03J-01A, spectrum: 85192
FTVGDHSR, I3V
MVH=38.3452
p-value=0.0003
sample: TCGA-AA-A03J-01A, spectrum: 49282
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=69.6945
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 55503
FYLGGPTSVR, I9V
MVH=52.9323
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 126488
GLLDLLEER, V3I
MVH=49.2025
p-value=0.0038
sample: TCGA-AA-A03J-01A, spectrum: 23316
GQTGALLQNTVESLSK, D9N
MVH=55.9239
p-value=0.0001
sample: TCGA–AA–A03J–01A, spectrum: 123278
HASSGSFLSSANEHLK, P9S
MVH=60.0344
p-value=0.0001
sample: TCGA–AA–A03J–01A, spectrum: 81564
KKPSEEAAAAAGPPGGPQVNPLPVTDEVV, V10A
MVH=51.5561
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 124538
KPTDSASSSSNCVTDLHSLV, G5S
MVH=62.7700
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 72256
LDVDKDGFVTEGELK, A3V
MVH=52.4200
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 14917
LFEEDPAVGA[LVLTGGDK, T1I
MVH=92.3375
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 21317
LGLHSTLLDEK, A6T
MVH=43.7890
p-value=0.0002
sample: TCGA-AA-A03J-01A, spectrum: 7747
LLNLADLVER, R4L
MVH=56.3304
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 78771
LQQQHSEQPPLQPSPVTTR, M17T
MVH=42.9708
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 83440
LSDLQEALDQALNHVR, Y14H
MVH=41.9483
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 3848
LSVATGAEAAQGSKPQCQTR, S16P
MVH=47.2295
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 39147
LTLQALTEK, A2T
MVH=52.5211
p-value=0.0005
sample: TCGA-AA-A03J-01A, spectrum: 124842
LTPVSAQFQDLEGK, L8F
MVH=59.3047
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 23425
NPLLDLAAYDQEGR, R3L
MVH=67.8063
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 9415
NSTLSEPGSGR, P4L
MVH=41.2452
p-value=0.0001
sample: TCGA–AA–A03J–01A, spectrum: 54421
NTNSVPETAPAALPETR, K17R
MVH=51.9140
p–value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 53978
QQPNPGSELCYK, N7S
MVH=26.6906
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 95277
RGDLFYTSK, E2G
MVH=44.8252
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 117489
SAVGELSEDSSNVVHLLK, Q15H
MVH=30.2278
p-value=0.0001
sample: TCGA–AA–A03J–01A, spectrum: 100026
SDPVTLNVLYGPDVPTLSK, G14V
MVH=48.7902
p−value=0.0001
sample: TCGA–AA–A03J–01A, spectrum: 37782
SQNKEDYDGLKEEFR, A8D
MVH=75.8847
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 45885
SQNKEDYDGLKEEFRK, A8D
MVH=96.3636
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 94200
STESLQTNVQR, A7T
MVH=59.5380
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 69543
TTPLEAASSGAR, T11A
MVH=46.3183
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 45025
TYGQVSGEALK, D2Y
MVH=42.3570
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 68107
VLSTTNAER, D6N
MVH=35.9993
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 116886
VPSFETAEGLGAELK, T12A
MVH=63.9623
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 51696
VPVTQATR, L3V
MVH=49.1024
p-value=0.0012
sample: TCGA-AA-A03J-01A, spectrum: 75107
VQLPTESLQELLDLHR, T7S
MVH=25.2824
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 113757
YFHNQEEFVR, L9V
MVH=43.6071
p-value=0.0001
sample: TCGA-AA-A03J-01A, spectrum: 46917
YGLLVGGAVSHR, A9V
MVH=57.9239
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 25416
AAAAAAAPAAAAATATATAATTAATAAAQ, P17A
MVH=37.1455
p–value=0.0003
sample: TCGA–AF–2691–01A, spectrum: 17053
AAPSVTLPSSSEELQANK, T2A
MVH=33.9839
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 2875
AFSEYLGTDQSK, G4E
MVH=54.7958
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 331
AGVETTTPSK, K7T
MVH=55.5765
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 150
AGVETTTPSKQSNNK, K7T
MVH=15.1071
p–value=0.0003
sample: TCGA–AF–2691–01A, spectrum: 12352
ALEDVFDALEGK, M5V
MVH=55.5759
p−value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 16204
APSQHLSSFDPCFYR, R5H
MVH=45.4545
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 101191
ASSSLNLNESEGPTNLQLLR, D8N
MVH=54.2087
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 23930
AYVLLR, E1A
MVH=41.6690
p−value=0.0084
sample: TCGA–AF–2691–01A, spectrum: 90396
DGYGFLNR, N1D
MVH=43.9760
p-value=0.0006
sample: TCGA–AF–2691–01A, spectrum: 22411
DTEEEDFHVDQATTVK, V12A
MVH=32.1729
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 38355
ELVDDSLNNVR, V7I
MVH=42.8821
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 92341
EQPGSPEWLQLDK, Q13K
MVH=44.6233
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 27204
ESALEPGPVPEAPAGGPVHAVTVTLLKEK, R6P
MVH=22.6113
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 102276
FFGSLPDSWAR, S11R
MVH=52.9082
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 94499
FGQDLLSPLLSVR, K13R
MVH=53.1298
p–value=0.0001
sample: TCGA-AF-2691-01A, spectrum: 38157
FLDKLPQQTGDR, H12R
MVH=55.5799
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 41877
FNLSQESSYLATQYSLRPR, S2N
MVH=32.4339
p−value=0.0001
sample: TCGA-AF-2691-01A, spectrum: 79453
FTVGDHSR, I3V
MVH=43.5982
p-value=0.0003
sample: TCGA-AF-2691-01A, spectrum: 50058
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=48.3108
p-value=0.0001
sample: TCGA-AF-2691-01A, spectrum: 111039
GFGTDEQALLDCLGSCSNK, R16C
MVH=65.8727
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 17164
GQTGALLQNTVESLSK, D9N
MVH=48.7806
p−value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 63726
KFFGSLPDSWAR, $\$12R
MVH=31.8773
p-value=0.0001
sample: TCGA-AF-2691-01A, spectrum: 20906
KFSKEEPVSSGPEEAAGK, V16A
MVH=49.7443
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 99902
KLSEKLDSTDFTSTLK, G13S
MVH=41.7634
p−value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 9717
KVLLDGVQNLR, P10L
MVH=43.6284
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 94610
LASDLLEWLQR, R10Q
MVH=60.3718
p−value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 99629
LDSTDFTSTLK, G8S
MVH=51.2206
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 17354
LFEEDPAVGALVTGGDK, T1I
MVH=75.8172
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 112324
LLDLFYPGDQSQVTFGLK, T17I
MVH=61.1642
p–value=0.0001
sample: TCGA-AF-2691-01A, spectrum: 67550
LQQQHSEQPPLQPSPVTTR, M17T
MVH=50.7927
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 106806
LTQSSAFYSQR, T6A
MVH=54.9703
p–value=0.0001
sample: TCGA-AF-2691-01A, spectrum: 110544
LVTDYTLAEADAALQK, E11D
MVH=73.5796
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 17287
NPLLDLAAYDQEGR, R3L
MVH=55.1354
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 47155
NTNSVPETAPAALPETR, K17R
MVH=22.9774
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 80947
RGDLFYTSK, E2G
MVH=38.6963
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 26742
SDPVTLNLYGPDVPTLSPSK, G14V
MVH=48.2996
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 60216
SLNDLTAR, K8R
MVH=43.1666
p–value=0.0006
sample: TCGA-AF-2691-01A, spectrum: 37862
SQNKEDYDGLKEEFRK, A8D
MVH=62.9563
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 91879
TAASGVEASSRPLDHAQPPSSLVLDEXEYK, N9S
MVH=97.3554
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 99994
TPAGGFASALER, R2P
MVH=52.2133
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 59485
VLGQAASDNSGPEDAKR, A1V
MVH=26.6051
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 39991
VLLDGVQNLR, P9L
MVH=55.8403
p–value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 101671
VPSFETAEGLGAEK, T12A
MVH=61.6907
p-value=0.0001
sample: TCGA-AF-2691-01A, spectrum: 35459
VPVTQATR, L3V
MVH=39.4116
p-value=0.0012
sample: TCGA–AF–2691–01A, spectrum: 80848
VSDLAAATAYK, N2S
MVH=52.4712
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 9539
VYGDLLYTPAK, H7Y
MVH=43.3685
p-value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 54069
YQAVTDTLEEK, A6D
MVH=62.4346
p−value=0.0001
sample: TCGA–AF–2691–01A, spectrum: 40640
YVSLLYTNYEAGKDDYVK, I2V
MVH=32.5654
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 48483
AAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=65.4466
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 61610
AAAPAPVSEAVSR, C12S
MVH=58.9396
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 39770
AAPSVTLFPPSEELQANK, T2A
MVH=59.5444
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 9211
AGVETTPSK, K7T
MVH=56.1064
p−value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 123406
ASSSLLLNESEPTTNLQLR, D8N
MVH=66.7475
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 91206
AVDVLDCFLVK, A11V
MVH=56.5032
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 91595
CDPGALVLPFSGALELK, Y1C
MVH=65.2714
p-value=0.0001
sample: TCGA--AF--2692--01A, spectrum: 15724
DFYVVEPLAFEGTPEQK, I4V
MVH=51.6562
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 112940
DGYGFLNR, N1D
MVH=41.2878
p–value=0.0006
sample: TCGA–AF–2692–01A, spectrum: 33606
DMAGAQAAVALNEEFLK, R18K
MVH=72.9470
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 28708
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=107.3734
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 47876
DVPGFLQSQSQSSGPGQPAVWHR, N11S
MVH=34.3058
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 96377
DVTVLQNTDGNNDAWAK, E14D
MVH=71.3626
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 41563
EALDVLDAVLK, G7D
MVH=59.9622
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 81072
EELGLQNDLTSLENDK, M10L
MVH=40.5737
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 23580
ELTVSNNDLNEAGVHVLCQGLK, R15H
MVH=36.3237
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 114536
EQPGSPEWLQLDK, Q13K
MVH=41.1892
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 41362
ESALEPGPVPEAPAGGPVHAVTAVNLLEK, R6P
MVH=36.8388
p−value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 54906
FADVFAK, E7K
MVH=43.0132
p–value=0.0084
sample: TCGA–AF–2692–01A, spectrum: 6202
FFGSLPDSWAR, S11R
MVH=40.2968
p−value=0.0001
sample: TCGA-AF-2692-01A, spectrum: 54125
FLDKLPQQQTGDR, H12R
MVH=67.6387
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 41967
FLGQLLTAFLPALR, A3G
MVH=44.7310
p−value=0.0001
sample: TCGA-AF-2692-01A, spectrum: 34397
FLPLPMVQLLDR, V6M
MVH=57.7997
p-value=0.0001
sample: TCGA-AF-2692-01A, spectrum: 62940
FLSGHTSELGNFR, D11N
MVH=47.7968
p-value=0.0001
sample: TCGA−AF−2692−01A, spectrum: 54813
FLSLESDR, G6S
MVH=39.5114
p−value=0.0012
sample: TCGA–AF–2692–01A, spectrum: 7397
FNKPFVFLMLDQNTK, E11D
MVH=63.1834
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 48623
FQPQSADFLDLTNPK, P6A
MVH=74.9530
p−value=0.0001
sample: TCGA-AF-2692-01A, spectrum: 92971
FTVGDHSR, I3V
MVH=42.1632
p-value=0.0006
sample: TCGA-AF-2692-01A, spectrum: 6242
GFGTDEQALLDCLGSCSNK, R16C
MVH=64.3889
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 124192
GGTLSTPQTGSENDALEYELR, G5S
MVH=67.7415
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 6383
GLLDDLLEER, V3I
MVH=47.3709
p-value=0.0038
sample: TCGA–AF–2692–01A, spectrum: 40184
GQTGALLQNTVESLSK, D9N
MVH=66.0021
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 49152
GRPVPNMLPDELAPTYSLDTR, M7V
MVH=52.3581
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 76313
HMTAVVK, Y1H
MVH=29.6848
p-value=0.0044
sample: TCGA–AF–2692–01A, spectrum: 89708
KFFGSLPDSWAR, $S_{12R}$
MVH=58.1557
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 89303
KKPSEEEAAAAAGGPPGGPQVNPLPVTDEVV V10A
MVH=64.4277
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 72693
LCLDAMHGVGVPYVK, R2C
MVH=43.9152
p-value=0.0001
sample: TCGA-AF-2692-01A, spectrum: 80112
LDVDKDGTVTEGELK, A3V
MVH=52.7340
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 7179
LEGLLEGLGLR, G6E
MVH=67.7450
p-value=0.0006
sample: TCGA–AF–2692–01A, spectrum: 32806
LFEEDPAVGALVLTGGDK, T1I
MVH=82.6574
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 19985
LFSPTETER, S2F
MVH=31.4170
p–value=0.0006
sample: TCGA–AF–2692–01A, spectrum: 6907
LKEVFPMAALMPGAEK, T7M
MVH=56.8684
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 69529
LQELTPSSGDPGEHDPASTHK, P4L
MVH=59.7891
p−value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 95343
LQEQHLSSPQGVQLDR, I16R
MVH=63.4840
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 114028
LREPLTAQQLEMTTER, T12M
MVH=49.0489
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 11818
MAQWGNKPLC, V9I
MVH=44.1134
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 121545
MGAQELLR, T1M
MVH=45.8371
p-value=0.0006
sample: TCGA–AF–2692–01A, spectrum: 13553
MQYAPNTQVELLPQGR, H16R
MVH=72.9457
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 20565
MVAVGLCR, H8R
MVH=33.9961
p–value=0.0006
sample: TCGA–AF–2692–01A, spectrum: 99257
NEVLWHPTLNPLSPQGTVR, A3V
MVH=42.9644
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 104859
NLPSLAEQGASDPPTVASR, K7E
MVH=80.6767
p−value=0.0001
sample: TCGA-AF-2692-01A, spectrum: 16843
NSTLVFPLPLDLQGLLGAK, M12T
MVH=50.8589
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 62384
NTNSVPETAPAALPETR, K17R
MVH=56.9322
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 87611
RDDDGTLHAACQVQPSATLDAQPR, A6T
MVH=81.7523
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 6927
RLEGLLEGLGLR, G7E
MVH=61.7997
p−value=0.0032
sample: TCGA–AF–2692–01A, spectrum: 124338
SAVGELSEDSSNVHLLK, Q15H
MVH=44.8458
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 49357
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=53.8847
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 115068
SEALPTDLPTPSAPDLTEPK, A10T
MVH=40.1552
p-value=0.0001
sample: TCGA-AF-2692-01A, spectrum: 73281
SGTPQLSLPFAAR, R7S
MVH=24.9913
p-value=0.0003
sample: TCGA–AF–2692–01A, spectrum: 50432
SLDLDDWPLELLK, V9I
MVH=47.1423
p−value=0.0001
sample: TCGA-AF-2692-01A, spectrum: 86560
SPPGAAAPAAAKPPPLSAK, S8P
MVH=45.5791
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 18471
SSSYSGEYGSGGGK, G10S
MVH=52.9635
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 114009
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=92.3790
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 31470
TALALLDHPSEYAAR, R8H
MVH=42.9137
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 15122
TCSFDFTGAVEDLSK, G3S
MVH=64.6275
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 49330
TLDPFETMLK, S2L
MVH=26.1810
p–value=0.0002
sample: TCGA–AF–2692–01A, spectrum: 50477
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=51.0658
p−value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 66731
TVEDLDGLLQQL YR, H10Q
MVH=64.9011
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 32053
TVVQLEGDNKLVTAFK, T14A
MVH=67.3245
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 53191
TYGQVSGEALK, D2Y
MVH=56.8519
p-value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 63886
VFSVAELQAR, S9A
MVH=52.0268
p–value=0.0002
sample: TCGA–AF–2692–01A, spectrum: 62885
VLLCGPVGPR, K10R
MVH=35.1494
p–value=0.0002
sample: TCGA–AF–2692–01A, spectrum: 77532
VMQVVDEK, I1V
MVH=43.3144
p–value=0.0019
sample: TCGA-AF-2692-01A, spectrum: 51678
VPVTQATR, L3V
MVH=34.8150
p-value=0.0012
sample: TCGA–AF–2692–01A, spectrum: 91522
VQLPTESLQELLDLHR, T7S
MVH=47.9862
p–value=0.0001
sample: TCGA–AF–2692–01A, spectrum: 56255
YVSLLYTNYEAGKDDYVK, I2V
MVH=36.2130
p–value=0.0001
sample: TCGA-AF-3400-01A, spectrum: 31797
AAAAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=60.1011
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 23597
AAPSVTTLFPPSSEELQANK, T2A
MVH=50.6343
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 9158
AGVETTTPSK, K7T
MVH=65.0864
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 9021
AGVETTTPSKQSNNK, K7T
MVH=49.2336
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 22391
APSQHLSSFDPCFYR, R5H
MVH=48.4555
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 7075
DFYVVEPLAFEGTPEQK, I4V
MVH=52.0860
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 102504
DGYGFLNR, N1D
MVH=43.2774
p-value=0.0006
sample: TCGA–AF–3400–01A, spectrum: 29168
DTEEEDFHVDQATTVK, V12A
MVH=74.6398
p−value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 87225
DVTVLQNTDGNNDAWAK, E14D
MVH=71.8960
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 46270
ELVDDSLNNVR, V7I
MVH=57.1244
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 104323
EQPGSPEWQLLDK, Q13K
MVH=41.1892
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 33376
ESALEPGPVPEAPAGGPVHAVTVVTLLEK, R6P
MVH=29.1828
p−value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 113512
FFGSLPDSWAR, S11R
MVH=35.0065
p−value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 114367
FGQDLLSPLLSVR, K13R
MVH=55.9704
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 84068
FTVGDHSR, I3V
MVH=44.5440
p–value=0.0003
sample: TCGA–AF–3400–01A, spectrum: 41050
GDYPLEAVCMQHLLAR, R9C
MVH=47.8774
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 122334
GLLDDLLEER, V3I
MVH=44.4041
p−value=0.0038
sample: TCGA–AF–3400–01A, spectrum: 101447
GLLVDTSR, I4V
MVH=36.6078
p−value=0.0012
sample: TCGA–AF–3400–01A, spectrum: 32240
GQTGALLQNTVESLSK, D9N
MVH=72.6838
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 12943
GVAGSSVAVLCPYNR, G5S
MVH=50.4401
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 85327
KSVEEYANCHLAR, P2S
MVH=77.6431
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 13018
KVLLDGVQNLR, P10L
MVH=51.3000
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 111155
LDSTDFTSTLK, G8S
MVH=46.4161
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 15101
LFEEDPAVGLVLTGGDK, T1I
MVH=78.7155
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 16474
LLNLADLVER, R4L
MVH=56.1962
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 89485
LLSDLLPPSTGTFQEASR, S5L
MVH=43.7842
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 82465
LNEAVVAVQALLADPK, I5V
MVH=54.0231
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 4717
MQYAPNTQVELLPQGR, H16R
MVH=57.2995
p–value=0.0001
sample: TCGA-AF-3400-01A, spectrum: 23704
NPLLDLAYDGEGR, R3L
MVH=53.4528
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 54718
NTNSVPETAPAALPETR, K17R
MVH=46.9232
p−value=0.0001
Sample: TCGA–AF–3400–01A, spectrum: 40739
QGTLTEYCTMLMSLPTK, G9S
MVH=52.0529
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 113456
SAVGELSEDSSNVVHLKK, Q15H
MVH=49.8988
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 69561
SLNDLTAR, K8R
MVH=43.0975
p-value=0.0006
sample: TCGA–AF–3400–01A, spectrum: 37930
SQNKEDYDGLKEEFR, A8D
MVH=53.5568
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 45942
SQNKEDYDGLKEEFRK, A8D
MVH=88.3386
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 17953
SSSYSGEYGSGGGK, G10S
MVH=56.5107
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 93325
SVEEYANCHLAR, P1S
MVH=61.6720
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 41608
TPVLFDVYELK, I7V
MVH=62.8460
p−value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 78399
VDVDAATLAR, A1V
MVH=70.2780
p–value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 39233
VLLDGVQNL, P9L
MVH=67.6182
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 57600
VLLDGVQNLRAEDLVGK, P9L
MVH=46.8947
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 43308
VPVTQATR, L3V
MVH = 46.0061
p–value = 0.0012
sample: TCGA–AF–3400–01A, spectrum: 93038
VSDLAATAYK, N2S
MVH=54.6254
p–value=0.0001
sample: TCGA-AF-3400-01A, spectrum: 20688
VWQTVSPVESR, G10S
MVH=40.5045
p-value=0.0001
sample: TCGA-AF-3400-01A, spectrum: 62654
YQAVTDTLEEK, A6D
MVH=58.6405
p-value=0.0001
sample: TCGA–AF–3400–01A, spectrum: 48414
YVSSLTYNYEAGKDDYVK, I2V
MVH=30.0729
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 58493
AAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=41.9597
p–value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 37378
AAPSVTLPSSSEELQANK, T2A
MVH=54.5828
p-value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 11064
AGVETTTPSK, K7T
MVH=55.3918
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 88510
ALDSNSLENDLSAPGREGDFNPESR, H21D
MVH=37.9581
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 120577
APPAPGPASGCGEVDELFDVK, S12C
MVH=70.1714
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 80763
APSPLYSEFSEPFGVLVHR, R20H
MVH=58.8056
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 151391
ASSSLLLNSEEPTTNLQLR, D8N
MVH=57.0120
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 48833
AVPTWANVQQVVDPPGSLASVESPGTPK, S7N
MVH=31.6386
p–value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 49128
DFNHLDVELSLLGK, N6D
MVH=35.3975
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 17761
DFYVVEPLAFEGTPEQK, I4V
MVH=47.6612
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 57030
DGEVLSEATQQQHEVL, V5I
MVH=54.0551
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 138890
DGYYFLNR, N1D
MVH=42.7733
p-value=0.0006
sample: TCGA–AF–3913–01A, spectrum: 35094
DTEEEDFHVDQATTVK, V12A
MVH=55.1107
p−value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 68183
DVPGLQQSQSSGPGQPAVWH, N11S
MVH=29.6353
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 80062
DYCVLLEGSGLALR, G3C
MVH=78.8510
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 132572
EAGFPPGVVNLTLGYGPTAGAALAQHMDVDK, V27M
MVH=21.3830
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 784
EASQGSSASSAPQSVK, H13Q
MVH=33.4082
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 100021

EELGHLQNDLTSLENDK, M10L

MVH=44.5278

p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 87321
EHTLHLEAELEK, S4L
MVH=34.9373
p−value=0.0002
sample: TCGA–AF–3913–01A, spectrum: 66340
ELVDDSLNNVR, V7I
MVH=54.9703
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 117374
EPGYTPPGAGNQNPPGMHPVTGPK, Y18H
MVH=35.0318
p-value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 59925
ESALEPGPVPEAPAGGPVHAVTVTVLLEK, R6P
MVH=29.7900
p-value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 150708
FEEGENSLHLK, A4G
MVH=42.4887
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 6680
FFGSLPDSWAR, S11R
MVH=33.9047
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 7709
FGQDLLSPLLSVR, K13R
MVH=51.8332
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 66075
FLDKLPQQTGDR, H12R
MVH=49.3648
p−value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 50025
FLGQLLTAFPALR, A3G
MVH=33.8104
p−value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 115108
FTVGDHSR, I3V
MVH=46.1513
p-value=0.0003
sample: TCGA–AF–3913–01A, spectrum: 119747
FVGVLPQYHSSVNLAGSSAPVSTANSTEDAR, S14L
MVH=42.3798
p−value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 69275
FVSSSSSSGGYGGYYGGVLASDGLLAGNEK, A9G
MVH=71.1492
p–value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 88048
FYLGPGPTSVR, I9V
MVH=48.2574
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 6722
GFGTDEQALLDCLGSCSNK, R16C
MVH=68.5680
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 6808
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA–AF–3913–01A, spectrum: 57569
GLLSSLDHNSLR, T9N
MVH=42.2601
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 48344
GQTGALLQNTVESLSK, D9N
MVH=57.5761
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 109429
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=52.9593
p−value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 95025
HMTAVVK, Y1H
MVH=32.7040
p-value=0.0044
sample: TCGA–AF–3913–01A, spectrum: 63666
KADLLNR, V51
MVH=36.0485
p–value=0.0044
sample: TCGA–AF–3913–01A, spectrum: 109677
KKPSEEEAAAAAGGPPGPGPQVNPLPVTDEVV V10A
MVH=37.0769
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 25222
LAALALASSENSSTPEECEETSEKPK, M22T
MVH=43.7309
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 150035
LDSTDFTSTLK, G8S
MVH=46.6704
p−value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 38050
LFEEDPAVGALVLTGGDK, T1I
MVH=70.1442
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 29136
LLNLADLVER, R4L
MVH=54.2213
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 121721
LLPADALANCDLLLR, V8A
MVH=36.5608
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 131078
LLSDLPPSTGTFQEAQSR, S5L
MVH=38.8513
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 150709
LPQGLPTEENMSNTCLK, A7T
MVH=37.0685
p–value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 85865
LQELTPSSGDPGEHDPASTHK, P4L
MVH=54.2495
p-value=0.0003
sample: TCGA–AF–3913–01A, spectrum: 116851
LQQQHSEQPPLQPSPVTTR, M17T
MVH=55.1339
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 122015
LSDLQEALDQALNHVR, Y14H
MVH=56.6415
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 24883
LSVATGALEAAQGSKPQCQTR, S16P
MVH=42.9588
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 75151
LTGHGAEDSLADQAANK, R4H
MVH=43.8191
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 149458
MGAQELLR, T1M
MVH=46.6637
p–value=0.0006
sample: TCGA–AF–3913–01A, spectrum: 78283
MKDVPGLQQSSGPGQPAVWHR, N13S
MVH=82.2777
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 15547
MQYAPNTQVELLPQGR, H16R
MVH=60.6518
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 56705
MVDFAGMK, V7M
MVH=30.1634
p–value=0.0006
sample: TCGA–AF–3913–01A, spectrum: 128667
NLPSLAEGASDPPTVAVR, K7E
MVH=64.8559
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 38054
NPLLDLAAYDQEGR, R3L
MVH=50.1006
p-value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 139220
NYLTMDELHR, R9H
MVH=43.0757
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 6942
QLAQAYEVLSDAK, S3A
MVH=37.2199
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 152365
SAVGELSEDSSNVVHLLK, Q15H
MVH=48.9328
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 59436
SDPVTLNLYGPDVPTLSPSK, G14V
MVH=49.2362
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 75146
SGTVATLQGTPDHGDPR, S2G
MVH=34.2074
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 139508
SQEVVETMCVPAAATSNVHTVK, M21T
MVH=34.2401
p−value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 87668
SSPVEFECLNDK, E11D
MVH=48.4485
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 99549
TDTESELDFLSR, L9F
MVH=62.8531
p−value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 96520
TTPLEAASSGAR, T11A
MVH=46.3772
p-value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 80861
TVEDLDGLQQQLYR, H10Q
MVH=67.8063
p-value=0.0001
sample: TCGA−AF−3913−01A, spectrum: 37396
TVVQLEGDNKLVTAFK, T14A
MVH=42.3451
p−value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 65001
TYGQVSGEALK, D2Y
MVH=51.2206
p−value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 105177
VLGTAGTEEGQK, I1V
MVH=31.5673
p-value=0.0001
sample: TCGA-AF-3913-01A, spectrum: 63384
VPVTQATR, L3V
MVH=36.5093
p-value=0.0012
sample: TCGA–AF–3913–01A, spectrum: 111965
VQLPTESLQELLDLHR, T7S
MVH=32.1929
p–value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 7954
VVLQPEALFSLYSK, F8L
MVH=43.5364
p−value=0.0001
sample: TCGA–AF–3913–01A, spectrum: 45562
VWQTVSPVESR, G10S
MVH=41.1282
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 77723
AAAPAPVSEAVSR, C12S
MVH=40.8144
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 49088
AAPSVTLPFSSEELQANK, T2A
MVH=21.7101
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 11330
AGVETTTPSK, K7T
MVH=25.6936
p-value=0.0007
sample: TCGA-AG-3574-01A, spectrum: 83280
APSPLYSEFSEEPEFKLVHR, R20H
MVH=85.2860
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 16349
AWLSSQAAELER, V7A
MVH=68.4053
p-value=0.0001
sample: TCGA–AG–3574–01A, spectrum: 148680
CSGLLQVLFSPLEEEVK, A3G
MVH=40.3544
p–value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 148513
DCGEAAQWLTSFLK, T6A
MVH=62.4747
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 112319
DDDGTLHAACQVQPSATLDAQPR, A5T
MVH=70.9518
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 18692
DFYVVEPLAFEGTPEQK, I4V
MVH=63.6788
p-value=0.0001
sample: TCGA–AG–3574–01A, spectrum: 143796
DGYGFLNR, N1D
MVH=41.3881
p-value=0.0006
sample: TCGA-AG-3574-01A, spectrum: 54774
DLTTGYDSSQPNKK, V2I
MVH=40.5274
p-value=0.0001
sample: TCGA–AG–3574–01A, spectrum: 34583
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=64.9988
p−value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 50815
EALDVLDVAVLK, G7D
MVH=50.7540
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 83069
EATSVPHLYALGDVVEGRPELTPTALMAGR, I24T
MVH=54.6295
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 145758
EQPGSPEWLQLDK, Q13K
MVH=26.4787
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 61370
ESALEPGPVEAPAGGPVHAVTVTTLLEK, R6P
MVH=44.3652
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 7240
FFGSLPDSWAR, S11R
MVH=32.7271
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 67774
FLDKLPQQTGDR, H12R
MVH=43.1139
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 51127
FLGQLLTAFPALR, A3G
MVH=37.2065
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 79444
FLSGHTSEELGNFR, D11N
MVH=41.0765
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 103260
FSVPVQHFCGPNSTPLQVR, Q20R
MVH=46.0571
p-value=0.0001
sample: TCGA–AG–3574–01A, spectrum: 119712
FTVGDHSR, I3V
MVH=35.8705
p-value=0.0003
sample: TCGA-AG-3574-01A, spectrum: 71809
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK_A9G
MVH=76.1643
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 90854
FYLGGPTSVR, I9V
MVH=43.5179
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 44423
GAQEKPQLSAAQSTQPQK, R3Q
MVH=48.7510
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 145918
GEGHENAAVQGAGAAALGPPVQPQDANALEPPLNR, G35R
MVH=66.2804
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 7121
GFGTDEQALLDCLGSCSNK, R16C
MVH=55.8686
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 7359
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AG-3574-01A, spectrum: 98023
HMTAVVK, Y1H
MVH=25.6416
p-value=0.0044
sample: TCGA-AG-3574-01A, spectrum: 60253
LADGGAGGTFQPYLDTLR, V1L
MVH=54.6805
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 39365
LFEEDPAVGLVLTGGDK, T1I
MVH=83.2222
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 30190
LLNLLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 136433
LLSDLPPSTGTFQEASQSR, S5L
MVH=47.0255
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 50048
LMGLPEDEQMG LLR, E7D
MVH=31.9608
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 121571
LQQQHSEQPPLQPSPVTTR, M17T
MVH=53.4148
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 6384
LSTEVDLTNVDLSTVDKDQSLAPK, G6D
MVH=26.4879
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 58652
LTLQALTEK, A2T
MVH=44.5841
p-value=0.0005
sample: TCGA-AG-3574-01A, spectrum: 16135
LTPVSAQFQDLEGK, L8F
MVH=21.2016
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 155142
MGAQELLR, T1M
MVH=49.0579
p-value=0.0006
sample: TCGA-AG-3574-01A, spectrum: 16126
MQYAPNTQVELLPQGR, H16R
MVH=63.4690
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 78579
NTNSVPETAPAALPETR, K17R
MVH=30.4691
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 28201
QATVGNLINTERPGMLDFTGK, D6N
MVH=21.5861
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 111955
RDDDGTLHAACQVQPSATLDAQPR, A6T
MVH=96.4867
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 111702
RYEVPLETPR, H10R
MVH=35.7099
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 60978
SDPVTLNVL YGPDVPTLSPSK, G14V
MVH=43.1541
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 146283
SEALPTRLPSARPDLTEPK, A10T
MVH=46.5986
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 60192
SLSLLDSPGLLSGEK, V4I
MVH=51.6369
p-value=0.0001
sample: TCGA–AG–3574–01A, spectrum: 46507
SQNKEDYDGLKEEFR, A8D
MVH=71.5824
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 67462
SQNKEDYDGLKEEFRK, A8D
MVH = 92.4447
p-value = 0.0001
sample: TCGA-AG-3574-01A, spectrum: 54946
STESLQTNVQR, A7T
MVH=49.3603
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 59615
SVMDDTQLAGLNCLR, A5T
MVH=43.7228
p-value=0.0001
sample: TCGA–AG–3574–01A, spectrum: 66015
TSLSAPPNTSSTENPK, S9T
MVH=35.3999
p–value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 66468
TYGQVSGEALK, D2Y
MVH=48.8353
p-value=0.0001
sample: TCGA--AG--3574--01A, spectrum: 137588
VPLASQGLGPGSTVLLVVDKCDEPLNLLVR, S26N
MVH=78.6039
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 64626
VPVTQATR, L3V
MVH=45.9301
p-value=0.0012
sample: TCGA-AG-3574-01A, spectrum: 8158
VVLQPEALFSLYSK, F8L
MVH=47.9351
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 91812
YVSLYYNYEAGK, I2V
MVH=53.5602
p-value=0.0001
sample: TCGA-AG-3574-01A, spectrum: 70402
YVSLLYTNYEAGKDDYVK, I2V
MVH=71.3133
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 78720
AAAAAAAAAPAAAATAATTAATTAATAAAQ, P17A
MVH=40.1753
p-value=0.0002
sample: TCGA-AG-3580-01A, spectrum: 85326
AAAPAPVSEAVSR, C12S
MVH=48.4294
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 58588
AAPSVTLPSSSEELQANK, T2A
MVH=51.8902
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 18852
AGVETTTPSK, K7T
MVH=45.2697
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 49004
ALEDVFDLEGK, M5V
MVH=64.9728
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 57313
APSQHLSSFDPCFYR, B5H
MVH=58.9799
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 134056
AVDVVLDCFLVK, A11V
MVH=64.9728
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 7069
CSGLLQVLFSPLEEPVEVK, A3G
MVH=51.2827
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 120461
DEPLHALYDNVEK, V2E
MVH=38.2081
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 37714
DFYVVEPLAFEGTPEQK, I4V
MVH=49.4069
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 151248
DGYGFLNR, N1D

MVH=43.2774
p-value=0.0006
sample: TCGA-AG-3580-01A, spectrum: 31748
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=105.2499
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 12242
DTCVQSPLSSFPR, C13R
MVH=44.1582
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 78191
DVPGFLQSQSSGPGQPAVWHR, N11S
MVH=25.8443
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 130159
DVTVLQNTDGNNNDAWAK, E14D
MVH=52.9716
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 60149
EALDVLDVLK, G7D
MVH=54.7308
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 36962
EAPETDTSPSLWNVEFAK, D13N
MVH=52.3211
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 110673
EELGHLQNDLTSLENDK, M10L
MVH=28.2858
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 86782
EHTLHLEAELEK, S4L
MVH=34.6526
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 75644
ELVDDSLNNVR, V7I
MVH=43.8173
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 153207
EQPGSPEWLQLDK, Q13K
MVH=26.4787
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 69966
ESALEPGPVEAPAGGPGVHAVTVTLLEK, R6P
MVH=30.3622
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 3535
FEEGENSLHNLK, A4G
MVH=41.9309
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 14394
FFGSLPDSWAR, S11R
MVH=34.2856
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 86286
FLDKLPQQTGDR, H12R
MVH=52.8695
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 60541
FLGQLLTAFPALR, A3G
MVH=52.6116
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 154414
FLQENVFVAANHNASPLSLK, G14A
MVH=30.5288
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 26884
FNKPFVFLMLDQNTK, E11D
MVH=68.9077
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 101177
FNLSQESSYLATQYSLRPR, S2N
MVH=30.4635
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 35025
FPGPCDYNFASDCR, L4P
MVH=40.0915
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 68669
FQPQSADFLDLTNPK, P6A
MVH=45.3743
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 126383
FTVGDHSR, I3V
MVH=34.1752
p-value=0.0003
sample: TCGA-AG-3580-01A, spectrum: 90357
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=61.0955
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 25602
GFGTDEQALLDCLGSCSNK, R16C
MVH=59.8553
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 68713
GQTGALLQNTVESLSK, D9N
MVH=66.2349
p-value=0.0001
sample: TCGA–AG–3580–01A, spectrum: 21943
HASSGSFLSSANEHLK, P9S
MVH=50.1584
p–value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 133548
LAAAGLDVTSPEPLPTNHPFLTLK, L20F
MVH=45.9780
p-value=0.0001
sample: TCGA–AG–3580–01A, spectrum: 121250
LAGALGPCLSLNVK, V9I
MVH=57.0440
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 2779
LDSTDFTSTLK, G8S
MVH=49.9366
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 47819
LFEEDPAVGLVLTGGDK, T1I
MVH=79.2035
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 27341
LLNLLADLVER, R4L
MVH=49.1714
p-value=0.0001
Sample: TCGA-AG-3580-01A, spectrum: 37890
LLSLFPLSCQK, L5F
MVH=39.0482
p-value=0.0001
sample: TCGA–AG–3580–01A, spectrum: 106934
LPAEPLTR, E3A
MVH=31.6267
p−value=0.0012
sample: TCGA-AG-3580-01A, spectrum: 96120
LQELTPSSGDPEHDPASTHK, P4L
MVH=31.2645
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 155737
NEVLWHPTNLPLSPQGTVR, A3V
MVH=58.8507
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 58933
NPLLLDLAAYDQEGR, R3L
MVH=57.5657
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 86295
NTNSVPETAPAALPETR, K17R
MVH=46.1025
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 91283
NTVELFKFEEGENSLLHLK, A11G
MVH=53.9152
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 88563
NTVLATWQPSTSK, T11S
MVH=48.0562
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 127203
QLTVGVPR, K8R
MVH=27.1624
p-value=0.0006
sample: TCGA-AG-3580-01A, spectrum: 5281
SAVGELSEDSSNVVHLK, Q15H
MVH=25.3357
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 49146
SELPLDPLPLPTEEGNPLLK, V10L
MVH=55.6674
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 15980
SGGTLVVLGSEMVTIPPLLHAALRN4T
MVH=41.1954
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 81044
SLDLDDWPLELLK, V9I
MVH=48.0475
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 68694
SLSLLDSPGLLSGEK, V4I
MVH=42.6791
p-value=0.0001
sample: TCGA–AG–3580–01A, spectrum: 74308
SPADPTDLGGQTSPR, I6T
MVH=56.9878
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 30189
SSSYSGEYGSGGGKR, G10S
MVH=41.4510
p-value=0.0002
sample: TCGA–AG–3580–01A, spectrum: 63520
STESLQTNVQR, A7T
MVH=51.1028
p–value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 152608
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=61.5876
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 73795
TSLSAPPNTSSTENPK, S9T
MVH=33.4298
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 134660
VGDPADFGTFLSAVLDAK, F12L
MVH=67.7377
p-value=0.0001
sample: TCGA-AG-3580-01A, spectrum: 72440
VPVTQATR, L3V
MVH=46.2425
p-value=0.0012
sample: TCGA-AG-3580-01A, spectrum: 134230
VQLPTESLQELDLHR, T7S
MVH=30.0307
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 60381
AAAAAAAAAAPAAAATAATTAATTAATTAATAAQ, P17A
MVH=47.6898
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 77143
AAAPAPVSEAVSR, C12S
MVH=47.7436
p-value=0.0001
sample: TCGA–AG–3584–01A, spectrum: 119208
AALQVLDDLEK, V3I
MVH=51.1028
p–value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 38974
AAPSVTLPSSSEELQANK, T2A
MVH=45.3059
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 11543
AGVETTTPSK, K7T
MVH=59.9155
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 40743
ALEDVFDALEGK, M5V
MVH=61.6720
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 91233
APPRPGPVPEAAQPFETTR, P19T
MVH=59.4692
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 111902
AVDVVLDCFLVK, A11V
MVH=58.8872
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 112180
CDPGALVLPFSGAELEK, Y1C
MVH=41.0233
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 78200
DAGNEQDLGLQYK, N1D
MVH=46.2324
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 108586
DDDGTLHAACQVQPSATLDAAQPR, A5T
MVH=41.4971
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 18461
DFYVVEPLAFEGTPEQK, I4V
MVH=33.9786
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 29936
DLGDLLEATGFDR, E10G
MVH=56.1569
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 108038
DVDGLTSLNAGR, K12R
MVH=50.5872
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 51233
EALDVLDVLK, G7D
MVH=52.9082
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 818
EASQGSSASSAPQSVK, H13Q
MVH=36.0727
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 100816
EELGHQLQNDLTSLENKD, M10L
MVH=26.5677
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 127899
EQPGSPEWLQLDK, Q13K
MVH=28.5292
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 61806
ESALEPGPVPEAPAGGPVHAVTVTTLLEK, R6P
MVH=18.5132
p-value=0.0003
sample: TCGA-AG-3584-01A, spectrum: 6919
FFGSLPDSWAR, S11R
MVH=39.3049
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 67642
FLDKLPQQTGDR, H12R
MVH=45.9616
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 18948
FNKPFVFLMLDQNTK, E11D
MVH=70.3397
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 147418
FNSVTELCAELPEQK, V11I
MVH=28.6631
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 6992
GFGTDEQALLDCLGSCSNK, R16C
MVH=73.8196
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 6994
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA–AG–3584–01A, spectrum: 49972
GQTGALLQNTVESLSK, D9N
MVH=62.5079
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 60702
LADGGAGGTFQPYLDTLR, V1L
MVH=41.3848
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 34162
LEGANVQEAQK, T4A
MVH=54.9703
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 39544
LFEEDPAVGAQTLGGDK, T1I
MVH=81.2788
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 70705
LGLTPEGQSYLDQFR, V3I
MVH=49.7418
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 7620
LKEVFPMAALMPGAEK, T7M
MVH=46.5840
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 26471
LLTQDEGPALVPGSR, G14S
MVH=45.2919
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 97304
LPAEPLTR, E3A
MVH=35.1713
p-value=0.0012
sample: TCGA-AG-3584-01A, spectrum: 87162
LQELTPSSGDGEHDPASTHK, P4L
MVH=68.9379
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 107155
LQQQHSEQPPLQPSPVTTR, M17T
MVH=47.6361
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 6742
LSELLPAEVEAEVK, E7A
MVH=26.3387
p-value=0.0003
sample: TCGA-AG-3584-01A, spectrum: 14335
MAQWGNKPLC, V9I
MVH=40.1483
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 16129
MQYAPNTQVELLPQGR, H16R
MVH=64.4069
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 25161
MVAVGLCR, H8R
MVH=39.9122
p-value=0.0006
sample: TCGA-AG-3584-01A, spectrum: 39535
NPLLDLAAYDQEGR, R3L
MVH=51.7881
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 139323
QLAQAYEVLSDAK, S3A
MVH=25.0905
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 100664
QVTASTFVKPLFSR, A2V
MVH=32.5903
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 61280
SDPVTLNVL YGPDVPTLSPSK, G14V
MVH=43.1541
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 22839
SSSYSGEYGSGGGK, G10S
MVH=59.2033
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 22702
SSSYSGEYGSGGGKR, G10S
MVH=39.5788
p-value=0.0002
sample: TCGA-AG-3584-01A, spectrum: 55828
STESLQTNVQR, A7T
MVH=48.9309
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 61376
TLDPFETMLK, S2L
MVH=29.7505
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 135543
TLSGGLAVNGPR, P7A
MVH=49.9422
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 97008
TTPLEAASSGAR, T11A
MVH=31.0776
p-value=0.0002
sample: TCGA–AG–3584–01A, spectrum: 82567
TVEDLDG LLQQL YR, H10Q
MVH=62.7789
p−value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 38820
TVVQLEGDNKLVTAFAK, T14A
MVH=43.0940
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 14976
VLLNDGGYYDPK, E12K
MVH=49.9422
p-value=0.0001
sample: TCGA–AG–3584–01A, spectrum: 58966
VLTGTGNVNVLPNYPAAR, I10V
MVH=44.2050
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 96801
VMQVVD, I1V
MVH=34.5372
p-value=0.0019
sample: TCGA-AG-3584-01A, spectrum: 148115
VPSFETAEGGLGAELK, T12A
MVH=51.1859
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 64825
VPVTQATR, L3V
MVH=36.9039
p-value=0.0012
sample: TCGA-AG-3584-01A, spectrum: 129145
VVDLLNQATLLTNDSK, A9T
MVH=53.3733
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 30096
WLLLCNPGLANTLVEK, D11N
MVH=80.2429
p-value=0.0001
sample: TCGA-AG-3584-01A, spectrum: 116585
YPVDTLPTSK, I3V
MVH=41.1354
p-value=0.0002
sample: TCGA-AG-3593-01A, spectrum: 63700
AAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=47.3395
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 82369
AAAPAPVSEAVSR, C12S
MVH=45.7097
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 41599
AAPSVTLFPPSEELQANK, T2A
MVH=49.5839
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 12527
AGVETTTPSK, K7T
$MVH = 56.5437$
$p$-value = 0.0001
sample: TCGA-AG-3593-01A, spectrum: 43256
ALEDVFDALEGK, M5V
MVH=62.7843
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 164863
ASSSLLNESEPTTNLQLR, D8N
MVH=58.2630
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 122732
AVDVVLDCFLVK, A11V
MVH=56.5032
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 17636
AWLSSQAELEER, V7A
MVH=46.9516
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 20104
DFYVVEPLAFEGTPEQK, I4V
MVH=58.2709
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 139986
DGYGFLNR, N1D
MVH=38.7115
p-value=0.0006
sample: TCGA-AG-3593-01A, spectrum: 37271
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=87.0921
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 63088
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=21.3194
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 54292
EALDVLDAVLK, G7D
MVH=42.3570
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 797
EASQGSSASSAPQSVK, H13Q
MVH=22.2677
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 30309
ELTVSNNDLNEAGVHVLCQGLK, R15H
MVH=24.4580
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 153532
EQPGSPEWQLDK, Q13K
MVH=34.6930
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 65360
ESALEPGPVPEAPAGGPVHAVTVVTLEK, R6P
MVH=22.8194
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 72743
FADVFAK, E7K
MVH=34.6981
p-value=0.0084
sample: TCGA−AG−3593−01A, spectrum: 7497
FFGSLPDSWAR, S11R
MVH=37.1168
p−value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 8653
FGQDLLSPLLSVR, K13R
MVH=50.4397
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 71777
FLDKLPQQTGDR, H12R
MVH=48.5933
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 126305
FTVGDHSR, I3V
MVH=33.7547
p-value=0.0003
sample: TCGA-AG-3593-01A, spectrum: 75648
FVSSSSSGGYGGGYGGVTASDGLLAGNEK, A9G
MVH=54.0567
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 7558
GFGTDEQALLDCLGSCSNK, R16C
MVH=53.6137
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 7644
GLLDDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AG-3593-01A, spectrum: 52935
GQTGALLQNTVESLSK, D9N
MVH=57.2666
p-value=0.0001
sample: TCGA–AG–3593–01A, spectrum: 28413
GVAGSSVAVLCPYNR, G5S
MVH=51.2238
p−value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 5320
HLTSYGETCPGLEQYALK, Q1H
MVH=54.4548
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 4458
HLTSYGETCPGLEQYALKK, Q1H
MVH=43.6581
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 64074
LADGGGAGGTFQPYLDTLR, V1L
MVH=51.3321
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 3324
LALQPGTVGPQGR, V3I
MVH=56.0629
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 163308
LDSTDFTSTLK, G8S
MVH=46.6704
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 41984
LFEEDPAVGALVLTGGDK, T1I
MVH=83.2258
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 75215
LGLTPEGQSYLDQFR, V3I
MVH=44.5977
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 32597
LLNLLADLVER, R4L
MVH=56.2209
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 27535
LQAAYNLVK, R2Q
MVH=34.4443
p-value=0.0002
sample: TCGA-AG-3593-01A, spectrum: 94437
LQELTPSSGDPEHDPASTHK, P4L
MVH=37.6484
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 109957
LQHLVNELTHDLLTK, E5V
MVH=96.7611
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 117346
LQQQHSEQPPLQPSPVTTR, M17T
MVH=43.8593
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 141424
LTGSSAQEAASGVALGEAPDHSYESLR, E9A
MVH=38.6874
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 62338
LTLQALTEK, A2T
MVH=44.2028
p-value=0.0005
sample: TCGA-AG-3593-01A, spectrum: 90398
LVVVGASGVGK, G7S
MVH=24.8655
p-value=0.0004
sample: TCGA-AG-3593-01A, spectrum: 133428
NEVLWHPTLNPLSPQGTVR, A3V
MVH=42.0201
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 140855
NLPSLAEQGASDPPTVASR, K7E
MVH=67.9330
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 41998
NPLLDLAAYDQEGR, R3L
MVH=53.4528
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 58774
NSLSETVR, M3L
MVH=32.0452
p-value=0.0006
sample: TCGA–AG–3593–01A, spectrum: 83452
NTNSVPETAPAALPETR, K17R
MVH=41.9507
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 151136
QLTVGVPR, K8R
MVH=24.3092
p-value=0.0018
sample: TCGA-AG-3593-01A, spectrum: 25457
QQHEGAQGTLDGGEPPQCR, A9T
MVH=31.4307
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 165889
SAVGELSEDSSNVVHLLK, Q15H
MVH=56.0758
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 64778
SDPVTLNLYGPDVPTLSK, G14V
MVH=49.4924
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 54271
SFQGPVLLGSSHHGVNLEDVAAETPEALLK, S24T
MVH=33.9761
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 70736
SPADPTDLGGQTSPR, I6T
MVH=54.1544
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 117293
SPPGAAAPAAAKPPPPLSAK, S8P
MVH=36.8395
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 60887
SQNKEDYDGLKEEFR, A8D
MVH=36.0848
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 24423
SSSYSGEYGSGGGK, G10S
MVH=38.8005
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 24301
SSSYSGEYGSGGGKR, G10S
MVH=27.3073
p-value=0.0002
sample: TCGA–AG–3593–01A, spectrum: 128133
SVEEYANCHLAR, P1S
MVH=43.8982
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 108816
TLEGLQVEEFPYK, E14K
MVH=49.9387
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 105690
TTPLEAASSGAR, T11A
MVH=34.6306
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 65957
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=53.5828
p-value=0.0001
sample: TCGA–AG–3593–01A, spectrum: 88801
TVEDLDGLLQQL YR, H10Q
MVH=62.7789
p–value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 71363
VAALNSEEESDPPTYK, T3A
MVH=41.5610
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 73607
VLLDGVQNLR, P9L
MVH=59.4441
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 68862
VPVTQATR, L3V
MVH=39.0125
p-value=0.0012
sample: TCGA-AG-3593-01A, spectrum: 122984
VQLPTESLQELDLHR, T7S
MVH=31.6897
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 167087
VVLQPEALFSLYSK, F8L
MVH=57.0440
p-value=0.0001
sample: TCGA-AG-3593-01A, spectrum: 74345
YVSLLYNYEAGKDDYVK, I2V
MVH=28.4687
p-value=0.0001
sample: TCGA−AG−3594−01A, spectrum: 58163
AAAAAAAPAAATAATTAATTAATAAAQ, P17A
MVH=39.5762
p−value=0.0002
sample: TCGA-AG-3594-01A, spectrum: 75073
AAAPAPVSEAVSR, C12S
MVH=51.9598
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 38134
AAPSVTLFPPSSEELQANK, T2A
MVH=51.0185
p-value=0.0001
sample: TCGA–AG–3594–01A, spectrum: 11710
AGVETTTPSK, K7T
MVH=59.6070
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 40104
ALEDVFDALEGK, M5V
MVH=58.7783
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 149111
ASSSLLLNESEPTTNLQLR, D8N
MVH=43.4373
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 18651
DFYVVEPLAFEGTPEQK, I4V
MVH=40.5432
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 137092
DGYGFLNR, N1D
MVH=43.8062
p-value=0.0006
sample: TCGA-AG-3594-01A, spectrum: 39785
DMAGAQQAAVALNEEFLK, R18K
MVH=54.1518
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 34488
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=98.5374
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 35641
DTEEEDFHVDQATTVK, V12A
MVH=49.5671
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 57609
DVPGLQQSQSSGPGQPAVWHR, N11S
MVH=32.9526
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 117488
DVTVLQNTDGNNNDAWAK, E14D
MVH=55.9438
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 50441
EALDVLDVAVLK, G7D
MVH=55.5004
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 690
EASQGSSASSAPQSVK, H13Q
MVH=39.4765
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 76437
EHLPDEFLKDEQNK, S3L
MVH=28.8929
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 138677
EQPGSPEWLQLDK, Q13K
MVH=29.4215
p-value=0.0001
sample: TCGA–AG–3594–01A, spectrum: 111245
ESQKEDLVFLFWAPESAPLK, K3Q
MVH=62.2365
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 7030
FFGSLPDSWAR, S11R
MVH=35.2545
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 7978
FGQDLLSPLLSVR, K13R
MVH=52.5457
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 65518
FLDKLPQQTGDR, H12R
MVH=41.8081
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 84820
FQTATVTEK, I3T
MVH=29.5205
p-value=0.0005
sample: TCGA–AG–3594–01A, spectrum: 19738
FSLDALLTNVLPFEK, I10V
MVH=39.3048
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 114061
FTVGDHSR, I3V
MVH=36.5120
p-value=0.0006
sample: TCGA-AG-3594-01A, spectrum: 58746
FVSSSSGGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=51.2758
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 87803
FYLGGPTSVR, I9V
MVH=48.2574
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 7079
GFGTDEQALLDCLGSCSNK, R16C
MVH=56.3932
p-value=0.0001
sample: TCGA–AG–3594–01A, spectrum: 17021
GFSLVADTPELQR, V4I
MVH=54.7446
p−value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 7126
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AG-3594-01A, spectrum: 49104
GQTGALLQNTVESLSK, D9N
MVH=70.0374
p-value=0.0001
sample: TCGA–AG–3594–01A, spectrum: 26461
GVAGSSVAVLCYPNR, G5S
MVH=56.0654
p−value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 108969
KKPSEEAAAAAGGPPGGPQVNPLPVTDEVV, V10A
MVH=60.8059
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 33468
LEGANVQEAQK, T4A
MVH=61.6593
p-value=0.0001
sample: TCGA−AG−3594−01A, spectrum: 38932
LFEEDPAVGLLVTGGDK, T1I
MVH=80.3876
p−value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 68633
LGLTPEGQSYLDQFR, V3I
MVH=44.7784
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 129569
LLSDLPPSTGTFQEAQSR, S5L
MVH=49.9111
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 106141
LQQQHSEQPPLQSPVTTR, M17T
MVH=41.4678
p-value=0.0001
sample: TCGA–AG–3594–01A, spectrum: 151264
LTAEFEAAQTSACLLQEELEK, R14L
MVH=61.4391
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 56916
LTLQALTEK, A2T
MVH=54.4976
p-value=0.0005
sample: TCGA-AG-3594-01A, spectrum: 57573
LYEPVVLVPVGR, K11R
MVH=40.5045
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 24988
MVAVGLCR, H8R
MVH=38.5986
p-value=0.0006
sample: TCGA-AG-3594-01A, spectrum: 38868
NPLLDLAYDQEGR, R3L
MVH=56.8885
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 6796
QSGGSSQAGAVTVSDVQELMR, V10A
MVH=31.5001
p-value=0.0001
sample: TCGA–AG–3594–01A, spectrum: 118068
QTWTDEGSVSEQMLR, R12Q
MVH=48.9419
p–value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 30351
SALSGHLETLLLGLLK, V10L
MVH=49.8748
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 150131
SAVGELEDSSNVVHLLK, Q15H
MVH=35.6395
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 64508
SPADPTDLGGQTSPR, I6T
MVH=56.9878
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 22661
SSSYSGEYGSGGGK, G10S
MVH=58.9975
p-value=0.0001
sample: TCGA–AG–3594–01A, spectrum: 22573
SSSYSGEYGSGGGKR, G10S
MVH=51.4236
p-value=0.0002
sample: TCGA-AG-3594-01A, spectrum: 117400
TLNEADCATLPPALR, V10I
MVH=30.0084
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 136324
TLSGGLAVNGPR, P7A
MVH=58.2173
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 95449
TTPLEAASSGAR, T11A
MVH=40.1752
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 60154
TVASPGVSVVEAQLDLGVTLLR, T8S
MVH=40.1245
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 80741
TVEDLDGLLQQL YR, H10Q
MVH=59.3382
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 94394
VLGTAGTEEGQK, I1V
MVH=48.8926
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 62635
VPVTQATR, L3V
MVH=41.6287
p-value=0.0012
sample: TCGA-AG-3594-01A, spectrum: 111220
VQLPTESLQELLDLHR, T7S
MVH=42.3929
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 151325
VVLQPEALFSLYSK, F8L
MVH=41.6175
p-value=0.0001
sample: TCGA-AG-3594-01A, spectrum: 29921
WLLLLCNPGLANTLVEK, D11N
MVH=71.8078
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 31255
AAAAAATAAATTAATTAATAAQA, P17A
MVH=36.4883
p-value=0.0002
sample: TCGA-AG-4007-01A, spectrum: 17329
AAPSVTLFPPSSEELQANK, T2A
MVH=37.2182
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 6503
AGVETTTPSK, K7T
MVH=26.3925
p-value=0.0002
sample: TCGA-AG-4007-01A, spectrum: 90951
ASSSLLLNESEPTTNLQLR, D8N
MVH=42.9756
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 38403
AVEVATVVLQPTVLR, S12T
MVH=33.4946
p-value=0.0002
sample: TCGA–AG–4007–01A, spectrum: 83088
DGYGFLNR, N1D
MVH=42.9114
p–value=0.0006
sample: TCGA-AG-4007-01A, spectrum: 18676
EALDVLDVLK, G7D
MVH=47.8977
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 50645
EHTLHLEAELEK, S4L
MVH=35.9438
p-value=0.0002
sample: TCGA-AG-4007-01A, spectrum: 43090
ELVDDSLNNVR, V7I
MVH=50.5395
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 84523
EQPGSPEWLQLDK, Q13K
MVH=45.1318
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 25606
ESALEPGPVPEAPAGGPVHAVTVTLLEK, R6P
MVH=25.8965
p-value=0.0001
sample: TCGA–AG–4007–01A, spectrum: 36640
FADVFAK, E7K
MVH=48.0010
p–value=0.0084
sample: TCGA-AG-4007-01A, spectrum: 91882
FFGSLPDSWAR, S11R
MVH=39.7688
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 92624
FGQDLLSPLLSVR, K13R
MVH=63.9745
p-value=0.0001
sample: TCGA–AG–4007–01A, spectrum: 72524
FLQENVFVAANHNASPLSLK, G14A
MVH=30.2387
p−value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 45875
FVSSSSSSGYYGGYGGVLTASDGLLAGNEK, A9G
MVH=44.0353
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 98546
GFGTDEQALLDCLGSCSNK, R16C
MVH=49.0158
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 98755
GLLDLLEER, V3I
MVH=48.8505
p-value=0.0038
sample: TCGA-AG-4007-01A, spectrum: 24696
GQTGALLQNTVESLSK, D9N
MVH=49.5474
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 40745
KADLLNR, V5I
MVH=42.9246
p-value=0.0044
sample: TCGA-AG-4007-01A, spectrum: 59533
KFFGSLPDSWAR, S12R
MVH=38.1097
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 88556
KGCAGVLTLLNRPK, T4A
MVH=33.2422
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 11020
LALLLMASQEPQR, T2A
MVH=31.6924
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 89860
LDSTDFSTSLK, G8S
MVH=54.9687
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 58291
LDVDKDGFVTEGELK, A3V
MVH=29.5019
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 21783
LFDTYGGAQR, V6G
MVH=30.1632
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 17833
LFEEDPAVGLVLTGGDK, T1I
MVH=66.8000
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 52836
LFQAEAQDLFR, E3Q
MVH=69.3062
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 22834
LHVLVEPDHFK, Q2H
MVH=62.1439
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 18992
LLNLLADLVER, R4L
MVH=59.2726
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 11900
LLNLLADLVERDR, R4L
MVH=36.0640
p-value=0.0004
sample: TCGA-AG-4007-01A, spectrum: 85223
LLNLPGYLQK, S2L
MVH=36.7175
p-value=0.0003
sample: TCGA-AG-4007-01A, spectrum: 72690
LLSDLLPPSTGTFQEAQSR, S5L
MVH=47.7374
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 62965
LNQPQPNFTK, D7N
MVH=41.8493
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 8186
MVAVGLCR, H8R
MVH=34.5794
p-value=0.0006
sample: TCGA-AG-4007-01A, spectrum: 17784
NPLLDLAAYDQEGR, R3L
MVH=57.0889
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 80185
NPSLLPLLLEAR, Q2P
MVH=48.8879
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 42940
NTNSVPETAPAALPETR, K17R
MVH=47.4139
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 91837
SAVGELSEDSSNVVHLLK, Q15H
MVH=39.1882
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 32213
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=40.9393
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 99696
SGGTLLVGGLGSEMVTTLPLLHAALR, N4T
MVH=33.5552
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 66740
SGLLPLLVR, K9R
MVH=36.3887
p-value=0.0010
sample: TCGA-AG-4007-01A, spectrum: 99404
TLACVCALLVWHPAGPGEK, S4C
MVH=37.1764
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 82640
TLSGGLAVNGPR, P7A
MVH=52.3935
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 56058
TTPLEAASSGAR, T11A
MVH=27.7947
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 32915
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=33.4991
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 17279
TVVQLEGDNKLVTAFK, T14A
MVH=66.7074
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 95142
VAQLLKEPR, K9R
MVH=29.3701
p-value=0.0005
sample: TCGA–AG–4007–01A, spectrum: 65241
VCVALDECELDVR, M12V
MVH=64.5064
p–value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 91358
VPSFETAEGGLGAELK, T12A
MVH=46.9336
p-value=0.0001
sample: TCGA-AG-4007-01A, spectrum: 33796
VPVTQATR, L3V
MVH=38.3446
p-value=0.0012
sample: TCGA-AG-4007-01A, spectrum: 86449
VVLQPEALFSLYSK, F8L
MVH=74.6491
p-value=0.0001
sample: TCGA−AG−A002−01A, spectrum: 6432
AAAAAAAAPAAAATAATTAATTAATAAAQ, P17A
MVH=62.4214
p−value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 127669
AAAPAPVSEAVSR, C12S
MVH=49.3690
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 142449
AAPSVTLFPPSSEELQANK, T2A
MVH=57.1900
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 44820
AGVETTTPSK, K7T
MVH=50.4177
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 133506
ALEDVFDLEGK, M5V
MVH=51.0410
p-value=0.0001
sample: TCGA–AG–A002–01A, spectrum: 58285
ALSSVSSPQSPGDLR, A5V
MVH=41.4061
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 60730
APWLEQERPEYWDQETR, G8R
MVH=67.0563
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 62396
ASLEAALADAEQHGEALK, R13H
MVH=75.5351
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 89766
ASSSLLLNESEPPTNLQLR, D8N
MVH=56.0394
p-value=0.0001
sample: TCGA–AG–A002–01A, spectrum: 99921
AWLSSQAAELER, V7A
MVH=54.9060
p−value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 25701
DDDGTLHAACQVQPSATLDAAQPR, A5T
MVH=38.7831
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 155352
DFNHLDVELSLLGK, N6D
MVH=72.1465
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 112845
DFYVVEPLAFEGTPEQK, I4V
MVH=49.4069
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 58784
DGYGFLNR, N1D
MVH=41.3486
p-value=0.0006
sample: TCGA-AG-A002-01A, spectrum: 123074
DLGDLLLEATGFDR, E10G
MVH=59.3157
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 24442
DLSTNYVYSEQK, A8V
MVH=46.5440
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 100897
DSKEPFSSVELQAALSK, E3K
MVH=41.1973
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 76645
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=88.6140
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 87248
DTEEEDFHVDQATTVK, V12A
MVH=29.8579
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 25190
DVDGLTSLNAGR, K12R
MVH=46.3772
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 37594
DVTVLQNTDGNNDWAWK, E14D
MVH=55.7414
p-value=0.0001
sample: TCGA–AG–A002–01A, spectrum: 155610
EALDVLDALVK, G7D
MVH=51.2796
p-value=0.0001
sample: TCGA–AG–A002–01A, spectrum: 33675
EASQGSSASSAPQSVK, H13Q
MVH=31.9294
p−value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 122401
ELAPYDDNWFYTR, E7D
MVH=42.4990
p-value=0.0001
sample: TCGA–AG–A002–01A, spectrum: 118876
ELVDDSLNNVR, V7I
MVH=47.7825
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 60560
EQPGSPEWLQLDK, Q13K
MVH=27.4563
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 13251
FLDKLPQQTGDR, H12R
MVH=33.6843
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 102661
FLGQLLTAFPALR, A3G
MVH=52.6116
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 78716
FTQNEFNLESK, R3Q
MVH=45.0323
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 17247
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK_A9G
MVH=61.0249
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 26241
FYLGGPTSVR, I9V
MVH=38.3082
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 101420
GFGTDEQALLDCLGSCSNK, R16C
MVH=64.9587
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 90637
GGTLSTPQTGSENDALYEYL, G5S
MVH=24.0567
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 91057
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AG-A002-01A, spectrum: 154272
GQTGALLQNTVESLSK, D9N
MVH=56.7980
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 119972
GVAGSSVAVLCPYNR, G5S
MVH=46.5291
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 15648
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=60.6824
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 130016
KVLLDGVQNLRR, P10L
MVH=59.1714
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 27669
LAGALGPCLSLNVK, V9I
MVH=40.5458
p-value=0.0001
Sample: TCGA-AG-A002-01A, spectrum: 126448
LCNNPAPQFGGK, T6A
MVH=21.2520
p-value=0.0002
sample: TCGA-AG-A002-01A, spectrum: 78730
LDSTDFTSTLK, G8S
MVH=47.8873
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 132495
LFEEDPAVGALVLGGDK, T1I
MVH=84.1696
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 151541
LGLQSLCNR, R7C
MVH=36.8320
p-value=0.0002
sample: TCGA-AG-A002-01A, spectrum: 97444
LHGHLYTPGQELTNDC, E17K
MVH=70.8779
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 41726
LLDTAFDLDFLK, V10I
MVH=64.9089
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 63151
LLNLLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 108032
LLNNTDNLVR, E6D
MVH=45.6760
p-value=0.0002
sample: TCGA-AG-A002-01A, spectrum: 40261
LLSDLPPSTGTFQEAQSR, S5L
MVH=47.5870
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 39930
LPDQLVLLYMK, D9Y
MVH=30.6527
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 149463
LQELTPSSGDPGEHDPASTHK, P4L
MVH=37.4928
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 24284
LQQQHSEQPPLQPSPVTTR, M17T
MVH=39.2444
p-value=0.0001
sample: TCGA–AG–A002–01A, spectrum: 109808
MQYAPNTQVELLPQGR, H16R
MVH=28.8399
p−value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 59510
NLPSLAEQGASDPPTVASR, K7E
MVH=58.1158
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 143335
NPLLDLAAYDQEGR, R3L
MVH=46.3148
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 139578
NTNSVPETAPAALPETR, K17R
MVH=39.1324
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 15459
NTVLATWQPYSTSK, T11S
MVH=46.7799
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 70134
QLAQAYEVLSDAK, S3A
MVH=29.4450
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 106084
QLTVGVPR, K8R
MVH=26.4723
p-value=0.0012
sample: TCGA-AG-A002-01A, spectrum: 27639
QVTSTASTFVKPLFSR, A2V
MVH=27.9703
p-value=0.0002
sample: TCGA-AG-A002-01A, spectrum: 81057
SAVGELSEDSSNVVHLLK, Q15H
MVH=58.5129
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 61009
SEALPTDLPTPSAPDLTEPK, A10T
MVH=49.9032
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 144464
SELPLDPLPLPTEEGNPLLK, V10L
MVH=56.0130
p-value=0.0001
sample: TCGA–AG–A002–01A, spectrum: 6909
SLSLLDSPGLLSGEK, V4I
MVH=41.2965
p–value=0.0001
sample: TCGA–AG–A002–01A, spectrum: 117529
SPADPTDLGGQTSPR, I6T
MVH=60.0630
p–value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 106564
STESLQTNVQR, A7T
MVH=51.1028
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 52365
TLQDLLALNPLYR, R3Q
MVH=38.2081
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 116974
TSLSAPPNTSSTENPK, S9T
MVH=44.9926
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 1996
TTPLEAASSGAR, T11A
MVH=28.0874
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 142530
TVVQLEGDNKLVTAFK, T14A
MVH=39.8435
p-value=0.0001
sample: TCGA–AG–A002–01A, spectrum: 99955
VLEVDQGTVC SLDR, G16R
MVH=50.1378
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 919
VLGTAGTEEGQK, I1V
MVH=43.0367
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 15210
VLLDGVQNLR, P9L
MVH=61.3970
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 685
VLSTTNAER, D6N
MVH=41.7105
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 80509
VPSFETAEGLGAELK, T12A
MVH=46.1214
p-value=0.0001
sample: TCGA-AG-A002-01A, spectrum: 125682
VPVTQATR, L3V
MVH=36.5269
p-value=0.0012
sample: TCGA-AG-A002-01A, spectrum: 41816
VSADLGAEAGLQQLLGALR, P2S
MVH=80.9859
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 58262
AAAAAATAATTAAGAAAT, P17A
MVH=37.8577
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 44093
AAPSVTLFPPSSEELQANK, T2A
MVH=50.9478
p-value=0.0001
sample: TCGA–AG–A008–01A, spectrum: 36017
AHDGGLYALSWPDSTR, H17R
MVH=55.9232
p–value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 82217
APPRPGPVPEAAQPFLFTTR, P19T
MVH=49.5472
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 43538
APSQHLSSFDPCFYR, R5H
MVH=71.3476
p-value=0.0001
sample: TCGA−AG−A008−01A, spectrum: 57079
AYVVLRR, E1A
MVH=41.8711
p−value=0.0084
sample: TCGA-AG-A008-01A, spectrum: 6139
CSGLLQVLFSPLEEEVK, A3G
MVH=32.4580
p-value=0.0001
sample: TCGA–AG–A008–01A, spectrum: 20479
DFYVVEPLAFEGTPEQK, I4V
MVH=41.2839
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 102465
DGYGFLNR, N1D
MVH=48.8163
p-value=0.0006
sample: TCGA-AG-A008-01A, spectrum: 78106
DSGTCHSCPPNTLLK, T10P
MVH=35.2189
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 24294
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=74.8458
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 9515
DTCVQSPPLLSSFPR, C13R
MVH=43.5845
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 86965
DVDGLTSLNAGR, K12R
MVH=54.3730
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 57874
DVPGFLQSQSSGPGQPAVWH, N11S
MVH=29.1175
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 45645
EALDVLDVLK, G7D
MVH=56.9545
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 62272
ECPCVHNNDLYSSSAK, G14S
MVH=31.8265
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 72947
EELGHQLQNDLTSLENDK, M10L
MVH=37.7936
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 63954
EHTLHLEAELEK, S4L
MVH=31.2709
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 28239
ELTVSNNDLEAGVHVLCQGLK, R15H
MVH=26.5950
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 49080
ELVDDSLNNVR, V7I
MVH=47.7825
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 104213
EQPGSPEWLQLDK, Q13K
MVH=37.5272
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 52820
ESALEPGPVEAPAGGPVHAVTVVTLEK, R6P
MVH=42.6945
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 11441
FFGSLPDSWAR, S11R
MVH=40.2968
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 12278
FGQDLLSPLLSVR, K13R
MVH=42.0824
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 63489
FLDKLPQQTGDR, H12R
MVH=49.5197
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 45943
FLGQLLTAFPALR, A3G
MVH=46.5235
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 71319
FLSGHTSELGNFR, D11N
MVH=41.7538
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 20755
FNKPFVFLMLDQNTK, E11D
MVH=68.0965
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 21345
FSLDALLTNVLPFEK, I10V
MVH=39.1395
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 81106
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=52.3391
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 66704
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=57.8403
p-value=0.0003
sample: TCGA-AG-A008-01A, spectrum: 71790
FYLLGGPTSVR, I9V
MVH=39.5773
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 11330
GFGTDEQALLDCLGSCSNK, R16C
MVH=53.0726
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 11579
GLLDLLEER, V3I
MVH=44.7346
p-value=0.0038
sample: TCGA−AG−A008−01A, spectrum: 67314
GQELGGGQDPVQLLSGFPR, E2Q
MVH=45.8850
p−value=0.0001
sample: TCGA–AG–A008–01A, spectrum: 44636
GQTGALLQNTVESLSK, D9N
MVH=64.2490
p−value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 35022
GVAGSSVAVLCPYNR, G5S
MVH=54.5322
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 16477
HASSGSFLSSANEHLK, P9S
MVH=44.3080
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 81840
KAPPRPGPVPEAAQPFLFTTR, P20T
MVH=50.7386
p-value=0.0002
sample: TCGA-AG-A008-01A, spectrum: 97534
KFFGSLPDSWAR, $S_{12R}$
MVH=50.4391
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 12809
KFSLDALLTNVLPFEK, I11V
MVH=49.5093
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 81297

KKPSEEEAAAAAGGPPGPQVNPLPVTDEVV\textsubscript{V10A}

MVH=52.5318

p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 74872
KPAAGLSAAPVPTTPAAGAPLMDFGNDVFPPAPR, A14T
MVH=38.2324
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 81352
LCLDAMHGVVGPYVK, R2C
MVH=36.1676
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 37038
LFEEDPAVGALVLTGGDK, T1I
MVH=71.0227
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 8062
LHGHLYTPGQELTNDCCK, E17K
MVH=46.1982
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 12489
LLDLFYPGDQQSVTFGLK, T17I
MVH=36.3574
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 21187
LLNLADLVER, R4L
MVH=53.3980
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 105485
LLSDLPPSTGTQEAQSR, S5L
MVH=31.0554
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 34894
LLTQDEGPALVPGSR, G14S
MVH=44.0474
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 77845
LPAEPLTR, E3A
MVH=33.6381
p-value=0.0012
sample: TCGA-AG-A008-01A, spectrum: 108659
LPAPTHTPATAPVPAR, R6H
MVH=52.5061
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 69626
LQELTPSSGDPGEHDPASTHK, P4L
MVH=26.5543
p-value=0.0003
sample: TCGA-AG-A008-01A, spectrum: 19832
LQPEDMFVYDLNEK, C9Y
MVH=35.2626
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 94105
LQQQHSEQPPLQPSPVTTR, M17T
MVH=51.2330
p-value=0.0001
sample: TCGA–AG–A008–01A, spectrum: 82306
LRPEMEGPSFTLFAPSNK, E19K
MVH=55.9049
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 66299
LSVFSTLDAPVAPSDK, V7I
MVH=46.7226
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 18002
MQYAPNTQVELLPQGR, H16R
MVH=61.1890
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 33731
MVAVGLCR, H8R
MVH=40.1201
p-value=0.0006
sample: TCGA-AG-A008-01A, spectrum: 66792
NLSLSGHVGFDSPDKLNK, Q16K
MVH=38.9603
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 63477
NTNSVPETAPAALPETR, K17R
MVH=45.1726
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 33725
PVAEYWNSQK, D2V
MVH=32.9493
p-value=0.0001
sample: TCGA–AG–A008–01A, spectrum: 23792
QQHEGAQGTLDSGEPPQCR, A9T
MVH=45.8823
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 89229
QVTSTASTFVKPLFSR, A2V
MVH=28.7922
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 59386
SDPVTLNVL YGPDVPTLSPSK, G14V
MVH=41.9402
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 111853
SEALPTDLPTPSAPDLTEPK, A10T
MVH=45.4200
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 17091
SGGVERPFVLAR, M4V
MVH=55.3124
p-value=0.0001
sample: TCGA–AG–A008–01A, spectrum: 60123
SLDLDDWPLELLK, V9I
MVH=46.1650
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 51868
SLSLLDSPGLLSGEK, V4I
MVH=48.2641
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 19755
TCSFDFTGAEDLSK, G3S
MVH=63.8616
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 67538
TVEDLDQLQQL YR, H10Q
MVH=49.9387
p-value=0.0001
sample: TCGA–AG–A008–01A, spectrum: 65085
VLLDGVQNLR, P9L
MVH=60.3902
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 101139
VSDLAATAYK, N2S
MVH=59.1603
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 47844
VSYGLGEEHDEQEGRD7E
MVH=26.6983
p-value=0.0001
sample: TCGA-AG-A008-01A, spectrum: 65683
YVSLLYTNYEAGKDDYVK, I2V
MVH=29.6376
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 34346
AAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=43.8495
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 45056
AAAPAPVSEAVSR, C12S
MVH=33.4524
p-value=0.0002
sample: TCGA-AG-A00C-01A, spectrum: 19818
AAPSVTLPSPSSEELQANK, T2A
MVH=49.8236
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 491
AGVETTTPSK, K7T
MVH=52.5231
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 50864
ALDRPYTSK, E3D
MVH=29.3305
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 18897
APSQHLSSFDPCFYR, R5H
MVH=57.9757
p-value=0.0001
sample: TCGA–AG–A00C–01A, spectrum: 25692
AYVLLR, E1A
MVH=43.3637
p-value=0.0084
sample: TCGA-AG-A00C-01A, spectrum: 51834
CALTGDEVKK, Y1C
MVH=21.2019
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 70765
CDPGALVLPFSGAELK, Y1C
MVH=38.9688
p-value=0.0001
sample: TCGA–AG–A00C–01A, spectrum: 7006
DFYVVEPLAFEGTPEQK, I4V
MVH=45.8421
p-value=0.0001
sample: TCGA–AG–A00C–01A, spectrum: 85911
DGYGFLNR, N1D
MVH=40.9453
p–value=0.0006
sample: TCGA-AG-A00C-01A, spectrum: 24460
DTEEEDFHVDQATTVK, V12A
MVH=38.0638
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 33950
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=41.7660
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 561
EASQGSSASSAPQSVK, H13Q
MVH=36.0167
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 57500
EKLDSVLEFNLPSLLLR, S10N
MVH=39.6961
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 39345
ELVDDSLNNVR, V7I
MVH=46.7663
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 46654
ENVATTDLTESTTVGSSV, T16S
MVH=44.7765
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 87461
EQPGSPEWLQLDK, Q13K
MVH=34.8929
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 39208
FLDKLPQQTGDR, H12R
MVH=33.6817
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 68565
FLLNQPALK, H2L
MVH=50.3828
p-value=0.0002
sample: TCGA-AG-A00C-01A, spectrum: 46734
FYLGGPTSVR, I9V
MVH=46.1710
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 99668
GFGTDEQALLDCLGSCSNK, R16C
MVH=38.1208
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 99904
GLLDLLEER, V3I
MVH=40.1881
p-value=0.0038
sample: TCGA–AG–A00C–01A, spectrum: 27004
GQTGALLQNTVESLSK, D9N
MVH=68.9832
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 46389
KENVATTDLESTTVGSSV, T17S
MVH=27.5856
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 34750
LADGGGAGGTQPYLDTLR, V1L
MVH=44.6282
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 89458
LASDLLEWLQR, R10Q
MVH=62.2100
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 92294
LDSTDFTSTLK, G8S
MVH=44.7854
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 70855
LDSVLEFNLPSLLLR, S8N
MVH=32.7033
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 95017
LEGLLEGLGLR, G6E
MVH=66.6580
p-value=0.0006
sample: TCGA-AG-A00C-01A, spectrum: 20174
LFEEDPAVGALVLTGGDK, T1I
MVH=80.1767
p-value=0.0001
Sample: TCGA-AG-A00C-01A, spectrum: 21371
LLNLLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 13453
LLNLLADLVERDR, R4L
MVH=36.2472
p-value=0.0003
sample: TCGA-AG-A00C-01A, spectrum: 32667
LSLVPVCR, R7C
MVH=39.9883
p-value=0.0012
sample: TCGA-AG-A00C-01A, spectrum: 25840
LTLQALTEK, A2T
MVH=43.4683
p-value=0.0009
sample: TCGA-AG-A00C-01A, spectrum: 99226
LVTDYLAEADAALQK, E11D
MVH=48.7594
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 20060
NPLLDLAAYDQEGR, R3L
MVH=49.9387
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 33609
NTVLATWQPYSTSK, T11S
MVH=50.0744
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 27135
QALTLLNELK, V2A
MVH=27.9223
p-value=0.0003
sample: TCGA-AG-A00C-01A, spectrum: 55576
QVTSTASTFVKPLFSR, A2V
MVH=26.9258
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 94930
RLEGLEGLGLR, G7E
MVH=67.7337
p-value=0.0006
sample: TCGA-AG-A00C-01A, spectrum: 35390
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=53.4908
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 44854
SPADPTDLGGQTSPR, I6T
MVH=37.0204
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 37797
STESLQTNVQR, A7T
MVH=50.5573
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 72656
SVEEYANCHLAR, P1S
MVH=47.1182
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 87047
TAASGVEASSRPLDHAQPPSSLVLDESEVYK, N9S
MVH=90.6450
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 85390
TLSGGLAVNGPR, P7A
MVH=52.2221
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 59537
TTPLEAASSGAR, T11A
MVH=35.4779
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 34279
VEHWGLDKPLLK, Q8K
MVH=67.8995
p-value=0.0001
sample: TCGA-AG-A00C-01A, spectrum: 93783
VPSFETAEGLGAELK, T12A
MVH=50.0430
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 66731
AAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=45.1269
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 73133
AAAPAPVSEAVSR, C12S
MVH=71.9372
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 46711
AAPSVTLFPPSEELQANK, T2A
MVH=55.8720
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 146305
AETSLGLPSPSELSTEVK, G9S
MVH=25.8539
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 11011
AGVETTTPSK, K7T
MVH=58.4914
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 38376
ALEDVFDLEGEK, M5V
MVH=58.7783
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 145689
ASSSLLLLNESEPTTNLQLR, D8N
MVH=53.3880
p-value=0.0001
sample: TCGA–AG–A00Y–01A, spectrum: 104493
DDDGTLHAACQVPSATLDAQPR, A5T
MVH=52.5964
p–value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 17778
DFYVVEPLAFEGTPEQK, I4V
MVH=53.3325
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 133521
DGYGFLNR, N1D
MVH=44.3623
p-value=0.0006
sample: TCGA-AG-A00Y-01A, spectrum: 38138
DMAGAQAAAVALEEEFLK, R18K
MVH=71.1443
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 56155
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=41.3760
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 48198
EALDVLDAVLK, G7D
MVH=49.3971
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 719
EASQGSSASSAPQSVK, H13Q
MVH=42.8816
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 135168
EQPGSPEWLQLDK, Q13K
MVH=35.6467
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 64855
FADVFAK, E7K
MVH=37.5369
p-value=0.0084
sample: TCGA-AG-A00Y-01A, spectrum: 7636
FGQDLLSPLLSVR, K13R
MVH=48.1013
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 64068
FLDKLPQQTGDR, H12R
MVH=44.0344
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 86370
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=50.7016
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 110972
FTVGDHSR, I3V
MVH=45.2115
p-value=0.0003
sample: TCGA-AG-A00Y-01A, spectrum: 67353
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK-A9G
MVH=58.9950
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 85369
FYLGGPTSVR, I9V
MVH=52.8393
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 146607
GGTLSTPQTGEYHLVDAYEYLR, G5S
MVH=35.7340
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 6750
GLLDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AG-A00Y-01A, spectrum: 122019
GLLVDTSR, I4V
MVH=35.2490
p-value=0.0012
sample: TCGA–AG–A00Y–01A, spectrum: 46968
GQTGALLQNTVESLSK, D9N
MVH=67.9881
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 98165
GSPMELSLPLTLSK, A11T
MVH=55.9898
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 135781
GTDECALESVAVAATPLPK, I10V
MVH=65.0586
p-value=0.0001
sample: TCGA–AG–A00Y–01A, spectrum: 25235
GVAGSSVAVLCPYNR, G5S
MVH=50.6269
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 15964
GVGAVPGAVLEPVAPAPSVR, R16P
MVH=47.9962
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 91557
HMTAVVK, Y1H
MVH=29.3363
p-value=0.0044
sample: TCGA-AG-A00Y-01A, spectrum: 24981
LAALALASSENSSTPEECEETSEKPK, M22T
MVH=38.9777
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 86556
LCLDAMHGVVGYVK, R2C
MVH=45.1427
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 144292
LDSTDFTSTLK, G8S
MVH=49.9366
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 37263
LFEEDPAVGALVLTGGDK, T1I
MVH=81.5169
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 35039
LLTQDEGPALVPGSR, G14S
MVH=37.7949
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 145000
LPQGLPTEENMSNTCLK, A7T
MVH=45.4954
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 24447
LQAAYNLVK, R2Q
MVH=31.1799
p-value=0.0006
sample: TCGA-AG-A00Y-01A, spectrum: 83168
LQELTPSSGDPEHDPASTHK, P4L
MVH=72.6093
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 113427
LQEQLSSPQGVQLDR, I16R
MVH=70.2526
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 17165
LQPEDMFVYDLNEK, C9Y
MVH=26.5102
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 103116
LQQQHSEQPPLQPSPVTTR, M17T
MVH=46.9460
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 23981
LVVVGAGDVGGK, G8D
MVH=51.2796
p-value=0.0001
sample: TCGA–AG–A00Y–01A, spectrum: 15456
MQYAPNTQVELLPQGR, H16R
MVH=69.6573
p−value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 54885
MVDFAGMK, V7M
MVH=30.4896
p-value=0.0031
sample: TCGA-AG-A00Y-01A, spectrum: 124103
NLPSLAEGASDPPTVASR, K7E
MVH=68.3475
p-value=0.0001
sample: TCGA–AG–A00Y–01A, spectrum: 37199
NPLDLAAYDQEGR, R3L
MVH=55.4013
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 73970
NTNSVPETAPAALPETR, K17R
MVH=43.9839
p-value=0.0001
sample: TCGA–AG–A00Y–01A, spectrum: 25977
QATVGNLINTERPGMLDFTGK, D6N
MVH=16.3106
p-value=0.0002
sample: TCGA-AG-A00Y-01A, spectrum: 22486
QQHEGAQGTLDGPPQCR, A9T
MVH=37.0880
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 146786
SAVGELSEDSSNVVHLLK, Q15H
MVH=45.2009
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 72831
SGTVATLQGTPDHGDPR, S2G
MVH=36.9149
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 63033
SLQEEQSRPTAVSSPGGPAR, P10T
MVH=32.6117
p-value=0.0001
sample: TCGA–AG–A00Y–01A, spectrum: 63122
SPADPTDLLLLQTR, I6T
MVH=59.7753
p-value=0.0001
sample: TCGA–AG–A00Y–01A, spectrum: 103035
SPPGAAAPAAAKKPPPLSAK, S8P
MVH=28.0141
p–value=0.0005
sample: TCGA-AG-A00Y-01A, spectrum: 21531
SSSYSGEYGSGGGK, G10S
MVH=65.2641
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 21417
SSSYSGEYGGGGKR, G10S
MVH=30.8826
p-value=0.0002
sample: TCGA–AG–A00Y–01A, spectrum: 52418
STESLQTNVQR, A7T
MVH=58.2935
p–value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 269
TAASGVEASSR, N9S
MVH=42.9024
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 134289
TAASGVEASSRPLDHAQPSSLVLKDN9S
MVH=63.0800
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 57688
TLDPFETMLK, S2L
MVH=33.8527
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 95859
TLEGLQVEEPVYK, E14K
MVH=55.4013
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 42600
TQPATATTAAEK, A9T
MVH=31.9961
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 92915
TTPLEAASSGAR, T11A
MVH=39.0483
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 78401
TVEDLDGLLQQL YR, H10Q
MVH=62.7789
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 63066
TYGQVSGEALK, D2Y
MVH=46.5440
p-value=0.0001
Sample: TCGA-AG-A00Y-01A, spectrum: 91934
VLGTAGTEEGQK, I1V
MVH=46.9954
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 91664
VLSTTNAER, D6N
MVH=21.7601
p-value=0.0004
sample: TCGA-AG-A00Y-01A, spectrum: 55315
VLTGTGNVNVILQPNYPAAAR, I10V
MVH=31.8850
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 61312
VPVTQATR, L3V
MVH=40.1862
p-value=0.0012
sample: TCGA-AG-A00Y-01A, spectrum: 108141
VQLPTESLQELLDLHR, T7S
MVH=26.4706
p-value=0.0002
sample: TCGA-AG-A00Y-01A, spectrum: 127504
VQVLAAQLLSEMK, D11E
MVH=57.4224
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 63108
VSYGLGEEEHDQEGRD7E
MVH=41.5429
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 7814
VVLQPEALFSL YSK, F8L
MVH=36.3351
p-value=0.0001
sample: TCGA-AG-A00Y-01A, spectrum: 86190
YVSLLYTNYEAGK, I2V
MVH=34.9344
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 54203
AAPSVTLFPPSEELQANK, T2A
MVH=54.3995
p-value=0.0001
sample: TCGA–AG–A011–01A, spectrum: 18843
AGVETTTPSK, K7T
MVH=58.7246
p–value=0.0001
sample: TCGA–AG–A011–01A, spectrum: 18711
AGVETTPSKQSNNK, K7T
MVH=34.3858
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 47019
ALEDVFDALEGK, M5V
MVH=64.1342
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 82937
APSPLYSVFSEEHPFGVLVHR, R20H
MVH=55.5199
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 53517
APSQHLSSFDPFYR, R5H
MVH=53.5732
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 5223
AQQNLSWEELTK, A11T
MVH=59.5418
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 5881
ASSSLLLNESEPTTNLQLR, D8N
MVH=71.1443
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 23726
AWLSSQAAELER, V7A
MVH=65.7364
p-value=0.0001
sample: TCGA–AG–A011–01A, spectrum: 26200
DFYVVEPLAFEGTPEQK, I4V
MVH=66.2178
p–value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 129515
DGYGFLNR, N1D
MVH=45.5688
p-value=0.0006
sample: TCGA-AG-A011-01A, spectrum: 41307
DSRPSQAAGDNNQGDEVKEQTFSGGTSQDTK, A16V
MVH=75.5080
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 42401
DTEEEDFHVDQATTVK, V12A
MVH=46.8962
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 113067
DVTVLQNTDGNNDAWAK, E14D
MVH=68.9320
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 9754
EASQGSSASSAPQSVK, H13Q
MVH=40.0455
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 97930
EELGHLQNDLTSLENDK, M10L
MVH=38.0693
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 79073
EHLPDEFLKDEQNK, S3L
MVH=37.8345
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 69583
ELVDDSLNNVR, V7I
MVH=57.6542
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 70544
ENVATTDLESTTVGSSV, T16S
MVH=70.0013
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 23812
EPSAPSLPTPAYQSLPAGGHAPTPPTAPR, S15L
MVH=23.6226
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 131323
EQPGSPEWLQDLK, Q13K
MVH=48.0475
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 65081
ESALEPGPVEAPAGGPVHAVTVTLLLEK, R6P
MVH=48.1301
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 16135
FFGSLPDSWAR, S11R
MVH=46.5440
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 17110
FGQDLLSPLLSVR, K13R
MVH=59.9073
p-value=0.0001
sample: TCGA–AG–A011–01A, spectrum: 69422
FLDKLPQQTGDR, H12R
MVH=62.7029
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 79346
FLSGHTSELGNFR, D11N
MVH=36.6247
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 27259
FSLDALLTNLVPFEK, I10V
MVH=52.0859
p-value=0.0001

Intensity(%) vs m/z
sample: TCGA-AG-A011-01A, spectrum: 89270
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=44.9703
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 109814
FTVGDHSR, I3V
MVH=39.2287
p-value=0.0003
sample: TCGA–AG–A011–01A, spectrum: 88357
FYLGGPTSVR, I9V
MVH=47.2857
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 16003
GFGTDEQALLDCLGSCSNK, R16C
MVH=55.7790
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 122075
GKWERPFEVKDTEEEEEDFHVDQATTVK, V22A
MVH=70.2523
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 16242
GLLDLLEER, V3I
MVH=45.0763
p-value=0.0038
sample: TCGA-AG-A011-01A, spectrum: 54771
GQTGALLQNTVESLSK, D9N
MVH=75.9960
p-value=0.0001
sample: TCGA–AG–A011–01A, spectrum: 27123
KFSLDALLTNVLPFEK, I11V
MVH=53.7502
p–value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 106317
KKPSEEEEAAAGGPPGGPQVNPLPVTDEVVE V10A
MVH=41.6924
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 5251
KLDSVFEEPLSK, R9P
MVH=57.3363
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 119403
KSVEEYANCHLAR, P2S
MVH=67.2862
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 63914
LADGGGAGGTQPYLDTLR, V1L
MVH=65.8019
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 4272
LDSTDFTSTLK, G8S
MVH=57.2310
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 45935
LFEEDPAVGLVLTGGDK, T1I
MVH=82.5772
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 14994
LPPGDLVFDPDQR, P6L
MVH=46.6366
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 15384
LSTEVDLTNVDLSTVDKDQSLAPK, G6D
MVH=36.2380
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 81471
LSVFSTLDAPVAPSDK, V7I
MVH=56.0232
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 23502
MQYAPNTQVELLPQGR, H16R
MVH=62.3269
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 68065
NCNFTVEK, R2C
MVH=46.7961
p-value=0.0006
sample: TCGA-AG-A011-01A, spectrum: 95790
QADPYLSEGLHPR, L4P
MVH=39.6546
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 30434
QQHEGAQGTLDSGEPPQCR, A9T
MVH=36.7865
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 104445
RDDDGTLHAACQVQPSATLDAQPR-A6T
MVH=66.1389
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 17011
RLEGLEGLGLR, G7E
MVH=62.8118
p-value=0.0004
sample: TCGA-AG-A011-01A, spectrum: 65086
SALVHLLNYQDDAELATHALPELTK, R18H
MVH=48.4062
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 7034
SAVGELSEDSSNVVHLLK, Q15H
MVH=70.4304
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 131905
SEALPTDLPTPSAPDLTEPK, A10T

MVH=52.1929
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 47175
SELPLDPLPLPTEEGNPLLK, V10L
MVH=60.6976
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 27073
SGGTLVVLVGLGSEMTTVPLLHAALR-N4T
MVH=36.3936
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 60798
SQNKEDYDGLKEEFR, A8D
MVH=69.5540
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 133449
SSFGLQVLENHFGGER, S3F
MVH=44.7215
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 29429
SSSYSGEYSGGGK, G10S
MVH=70.4952
p-value=0.0001
sample: TCGA–AG–A011–01A, spectrum: 29335
SSSYSGEYGSGGGKR, G10S
MVH=41.6369
p-value=0.0002
sample: TCGA-AG-A011-01A, spectrum: 58950
STESLQTNVQR, A7T
MVH=58.9031
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 111438
SVEEYANCHLAR, P1S
MVH=54.6622
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum 130882
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=67.0196
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 54224
TVVQLEGDNKLVTAFK, T14A
MVH=45.9004
p-value=0.0001
sample: TCGA–AG–A011–01A, spectrum: 92923
VLSTTNAER, D6N
MVH=49.6363
p−value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 6400
VPSFETAEGGLGAELK, T12A
MVH=77.6437
p-value=0.0001
sample: TCGA-AG-A011-01A, spectrum: 75792
VPVTQATR, L3V
MVH=46.2425
p-value=0.0012
sample: TCGA-AG-A011-01A, spectrum: 122361
WERPFEVKDTEEDFHVDQATTVK, V20A
MVH=73.2126
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 35505
AAPSVTFLPPSSEELQANK, T2A
MVH=56.7504
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 10028
AGVETTTPSK, K7T
MVH=62.2317
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 9822
AGVETTTPSKQSNNK, K7T
MVH=44.8020
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 82088
ALSFNFGYAK, N3S
MVH=42.9855
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 50030
ASGVQLEAK, A4V
MVH=45.5994
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 125516
ASSSLLNESEPTTNLQLR, D8N
MVH=61.9541
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 24509
ATAAECLQHPWLNS, R8Q
MVH=36.7912
p-value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 55238
AVEVATVVLQPTVLR, S12T
MVH=49.3564
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 5469
AWLSSQAAELER, V7A
MVH=66.9450
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 92676
CDPGALVLPFSGAELK, Y1C
MVH=53.9714
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 7818
DFYVVEPLAFEGTPEQK, I4V
MVH=59.4176
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 114322
DGYGFLNR, N1D
MVH=46.9290
p-value=0.0006
sample: TCGA-AG-A014-01A, spectrum: 27203
DMAGAQAAVALNEEFLK, R18K
MVH=90.2008
p-value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 120430
DSRPSQAAGDNQGDEVK, A16V
MVH=50.9901
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 96916
DVDGLTSLNAGR, K12R
MVH=66.9450
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 44696
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=41.0810
p-value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 27471
EALDVLDAVLK, G7D
MVH=60.8553
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 695
EASQGSSASSAPQSVK, H13Q
MVH=52.0411
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 81799
EELGLQLQNLTSLENKD, M10L
MVH=38.8541
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 52090
ELVDDSLNNVR, V7I
MVH=64.4442
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 134214
EPSAPSLPTPAYQSLPAGHHAPTPPTPAPR, S15L
MVH=28.7193
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 116227
EQPGSPEWLQLDK, Q13K
MVH=34.4851
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 37175
ESALEPGPVPEAPAGGPVHAVTVTLLEK, R6P
MVH=24.8354
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 126656
FFGSLPDSWAR, S11R
MVH=52.6904
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 127597
FGQDLLSPLLSVR, K13R
MVH=57.0008
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 51939
FLDKLPQQTGDR, H12R
MVH=46.3566
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 52712
FLSGHTSELGNFR, D11N
MVH=34.8887
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 8214
FNKPFVFLMLDQNTK, E11D
MVH=60.6272
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 94337
FTVGDHSR, I3V
MVH=40.4020
p-value=0.0003
sample: TCGA-AG-A014-01A, spectrum: 55514
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=57.8509
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 62419
FYLGGPTSVR, I9V
MVH=55.0480
p-value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 135557
GFGTDEQALLDCLGSCSNK, R16C
MVH=66.8459
p–value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 126403
GGTLSTPQTGSENDALYEYL, G5S
MVH=29.5136
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 135783
GLLDLLEER, V3I
MVH=45.4297
p-value=0.0038
sample: TCGA-AG-A014-01A, spectrum: 113178
GLLVDTSR, I4V
MVH=40.7313
p-value=0.0012
sample: TCGA-AG-A014-01A, spectrum: 114056
GLSFDAATSGGSASEK, T2I
MVH=82.5076
p-value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 116902
GTDECALESVAVAATPLPK, I10V
MVH=39.2649
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 5939
GVGGAVPGAVLEPVAPAPSVR, R16P
MVH=48.0361
p-value=0.0001

m/z

Intensity(%)
sample: TCGA–AG–A014–01A, spectrum: 76419
HMTAVVK, Y1H
MVH=34.5030
p-value=0.0044
sample: TCGA-AG-A014-01A, spectrum: 58762
KADLLNR, V5I
MVH=40.4767
p-value=0.0044
sample: TCGA-AG-A014-01A, spectrum: 90554
KKPSEEAAAAGGPPGQVNPLPVTDEVV, V10A
MVH=25.8936
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 124948
KLDSVFEEPLSK, R9P
MVH=53.1193
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 124036
LDSTDFTSTLK, G8S
MVH=51.2796
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 26330
LFEEDPAVGA^LTGGDK, T1I
MVH=83.4429
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 23693
LGLHSTLLDEK, A6T
MVH=53.7739
p-value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 73466
LGRPGLGGSSGLAGAWLK, K3R
MVH=48.6330
p–value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 10789
LLHGQSSLK, H5Q
MVH=51.0463
p-value=0.0005
sample: TCGA-AG-A014-01A, spectrum: 18260
LLNLADLVER, R4L
MVH=61.2124
p-value=0.0001
sample: TCGA--AG--A014--01A, spectrum: 100033
LLSDLPPSTGTFQEAQSR, S5L
MVH=48.7841
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 78285
LQELTPSSGDPEHDPASTHK, P4L
MVH=58.9339
p-value=0.0002
sample: TCGA-AG-A014-01A, spectrum: 43961
LTLQALTEK, A2T
MVH=52.9525
p-value=0.0005
sample: TCGA-AG-A014-01A, spectrum: 132710
LVSESSDLLPK, V8I
MVH=72.8811
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 32108
LVVVGASGVGK, G7S
MVH=68.1303
p-value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 3375
MAQWGKPLC, V9I
MVH=44.8638
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 54128
MKDVPGFLQUQSSSGPGQPAVWHR, N13S
MVH=71.4397
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 5305
MQYAPNTQVELLPQGR, H16R
MVH=66.1733
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 12518
MVAVGLCR, H8R
MVH=35.4137
p-value=0.0006
sample: TCGA-AG-A014-01A, spectrum: 16307
NPEQEPLPLVFR, L11F
MVH=53.8518
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 61257
NTNSVPETAPAALPETR, K17R
MVH=53.9667
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 73968
QSA-CPYSHF-PGVGLL-TQER, K1Q
MVH=44.6931
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 46438
SDPVTLNVL YGPDVPTLSPSK, G14V
MVH=51.8154
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 27335
SLDPGLKEDTLEFLK, Q12E
MVH=43.0868
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 87493
SPPGAAAPAAAKPPPLSAK, S8P
MVH=34.3386
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 19978
SSYSGEYGSGGGK, G10S
MVH=66.7935
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 81019
TLEGLQVEEEPVYK, E14K
MVH=64.9011
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 77924
TTPLEAASSGAR, T11A
MVH=48.0058
p-value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 37682
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=41.4665
p–value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 56743
TVEDLDGLLQQL YR, H10Q
MVH=58.8420
p–value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 60112
TYGQVSGEALK, D2Y
MVH=32.5624
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 126021
VPSFETAEGLGAELK, T12A
MVH=60.5276
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 58334
VPVTQATR, L3V
MVH=46.2425
p-value=0.0012
sample: TCGA-AG-A014-01A, spectrum: 83877
VQLPTESLQELLDLHR, T7S
MVH=41.9830
p-value=0.0001
sample: TCGA--AG--A014--01A, spectrum: 100982
VQVLAALQLLSMK, D11E
MVH=55.2739
p-value=0.0001
sample: TCGA-AG-A014-01A, spectrum: 104221
VSDLAATAYK, N2S
MVH=59.1603
p-value=0.0001
sample: TCGA–AG–A014–01A, spectrum: 118513
YTALPLVGVQFQSQCK, H14Q
MVH=78.1936
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 61070
AAAAAAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=47.5004
p−value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 77551
AAAPAPVSEAVSR, C12S
MVH=67.8043
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 50717
AAPSVTLPSSSEELQANK, T2A
MVH=44.4235
p–value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 11886
AGVETTPSK, K7T
MVH=49.0940
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 72753
AQLNVGNVLPVGMPEGTLVCCLEEKPGDR, I5V
MVH=25.6160
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 151137
ASSSLLLNESEPTTNLQLR, D8N
MVH=56.3615
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 114668
AVDVVLDCFLVK, A11V
MVH=58.8872
p–value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 71396
AVEVATVLQPTVLR, S12T
MVH=41.2643
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 92772
CLFASGSPFEPVK, G10E
MVH=44.1582
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 78585
DAGNEQDLGLQYK, N1D
MVH=43.8379
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 19163
DFYVVEPLAFEGTPEQK, I4V
MVH=45.5684
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 139665
DGYGFLNR, N1D
MVH=43.8062
p-value=0.0006
sample: TCGA-AG-A015-01A, spectrum: 41377
DMAGAQAAVALNEEFLK, R18K
MVH=63.9394
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 36094
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=74.2444
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 37202
DTEEEDFHVDQATTVK, V12A
MVH=47.5655
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 793
EASQGSSASSAPQSVK, H13Q
MVH=32.9757
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 77152
ECPCVHNNDLYSSSAK, G14S
MVH=25.3721
p-value=0.0002
sample: TCGA-AG-A015-01A, spectrum: 68553
ELVDDSLNNVR, V7I
MVH=47.7825
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 141329
EQPGSPEWLQLDK, Q13K
MVH=32.9836
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 51850
ESALEPGPVPEAPAGGPVHAVTVVTLEK, R6P
MVH=23.4517
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 69161
FADVFAK, E7K
MVH=35.0011
p-value=0.0084
sample: TCGA-AG-A015-01A, spectrum: 7019
FFGSLPDSWAR, S11R
MVH=31.7870
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 68307
FLDKLPPQQTGD, H12R
MVH=52.2218
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 19643
FNKPFVFLMLDQNTK, E11D
MVH=60.1397
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 82112
FNLSQESSYLATQYSLLPR, S2N
MVH=29.9018
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 15055
FQLGNSGPNSTLK, S4G
MVH=35.6467
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 87982
FQTATVTEK, I3T
MVH=26.7558
p-value=0.0073
sample: TCGA-AG-A015-01A, spectrum: 152458
FQYLLCVPYSYDPTK, L8P
MVH=41.2835
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 92012
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=49.9598
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 117284
FTVGDHSR, I3V
MVH=42.7547
p-value=0.0003
sample: TCGA-AG-A015-01A, spectrum: 71725
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=56.9694
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 91017
FYLGPGPSVR, I9V
MVH=40.3499
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 59010
GALQFVTHYQQSSTQR, H11Q
MVH=44.8564
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 6981
GFGTDEQALLDCLGSCSNK, R16C
MVH=57.8287
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 7107
GLLDDLEER, V3I
MVH=38.2672
p-value=0.0057
sample: TCGA-AG-A015-01A, spectrum: 129591
GLSFDAATSGGSASSEK, T2I
MVH=57.8029
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 50747
GQTGALLQNTVESLSK, D9N
MVH=70.3572
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 27665
GVAGSSVAVLCPYNR, G5S
MVH=52.5728
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 65799
KADLLNR, V5I
MVH=30.8266
p-value=0.0044
sample: TCGA-AG-A015-01A, spectrum: 77550
KNPDSHYGELLEK, Q6H
MVH=56.5502
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 92258
LCLDAMHGVVGPYVK, R2C
MVH=31.6222
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 40520
LFEEDPAVGVGTLOGDK, T1I
MVH=77.4932
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 47367
LHGHL YTGPQELTNDC, E17K
MVH=51.3599
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 114098
LLDAETTAGAWPNVAAVSLTGR, A9G
MVH=27.9350
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 153511
LLDTAFDLDFLK, V10I
MVH=58.2198
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 31353
LLNLADLVER, R4L
MVH=61.1708
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 27468
LLTQDEGPALVPGSR, G14S
MVH=43.1200
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 109793
LQQQHSEQPPLQSPVTTR, M17
MVH = 48.5914
p-value = 0.0001
sample: TCGA-AG-A015-01A, spectrum: 26917
LSVATGALEAAQGSKPQCQTR, S16P
MVH=39.7175
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 6389
LVTDYTLAEADAALQK, E11D
MVH=58.8229
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 16638
MQYAPNTQVELLPQGR, H16R
MVH=45.8528
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 123741
NEVLWHPTLNPLSPQGTVR, A3V
MVH=31.0048
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 130623
NLPSLAEGASDPPTVASR, K7E
MVH=78.8007
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 40743
NPGAVNACHLSCSALLQDNLADAVACAK, T1N
MVH=24.5269
p–value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 62020
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=46.5129
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 41839
SELPLDPLPLPTEEGNPLLK, V10L
MVH=57.8050
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 20045
SGGTLVLVGLGSEMTTVPLLHAALRN4T
MVH=32.2349
p–value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 67244
SLQEEQSRPTTAHVSGPGR, P10T
MVH=37.9003
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 145621
SPAADAKPAPK, T3A
MVH=54.9518
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 67315
SPADPTDLGGQTSPR, I6T
MVH=68.6731
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 109673
SPPGAAAPAAAKPPPLSAK, S8P
MVH=34.0859
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 56309
STESLQTNVQR, A7T
MVH=51.7102
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 119042
SVEEYANCHLAR, P1S
MVH=31.2585
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 99270
TTPLEAASSGAR, T11A
MVH=36.0954
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 63112
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=38.4410
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 83392
TVEDLDGLLQQL YR, H10Q
MVH=65.1266
p-value=0.0001
sample: TCGA-AG-A015-01A, spectrum: 65461
VPVTQATR, L3V
MVH=39.4116
p-value=0.0012
sample: TCGA-AG-A015-01A, spectrum: 139980
VSQAELSSLQSVR, A1V
MVH=56.0402
p-value=0.0001
sample: TCGA–AG–A015–01A, spectrum: 67286
VSYGLGEEEHDEGQR, D7E
MVH=29.1904
p–value=0.0002
sample: TCGA-AG-A015-01A, spectrum: 60665
YHQAASDSYLQLLK, E11Q
MVH=49.6985
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 30937
AAAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=37.1331
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 41146
AAAPAPVSEAVSR, C12S
MVH=36.7936
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 23600
AAPSVTLFPPSSEELQANK, T2A
MVH=43.6798
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 5598
AGVETTTPSK, K7T
MVH=19.4599
p-value=0.0002
sample: TCGA-AG-A016-01A, spectrum: 15003
APSQHLSSFDPCFYR, R5H
MVH=37.8398
p-value=0.0001
sample: TCGA–AG–A016–01A, spectrum: 57867
AVDVLDCFLVK, A11V
MVH=63.0077
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 2794
AWLSSQAAELE, V7A
MVH=57.0542
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 65370
CDPGALVLPFSGALELK, Y1C
$MVH=50.9588$
$p$-value$=0.0001$
sample: TCGA-AG-A016-01A, spectrum: 63126
DEPLHALYDNVEK, V2E
MVH=44.4441
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 79913
DGYGFLNR, N1D
MVH=42.3481
p-value=0.0006
sample: TCGA-AG-A016-01A, spectrum: 20985
DTEEEDFHVDQATTVK, V12A
MVH=50.9188
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 61644
DVDGLTSLNAGR, K12R
MVH=59.5418
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 25229
EALDVLDADVKL, G7D
MVH=54.8445
p-value=0.0001
sample: TCGA–AG–A016–01A, spectrum: 35529
ELVDDSLNNVR, V7I
MVH=51.7052
p–value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 81266
EQPGSPEWLQLDK, Q13K
MVH=25.4049
p-value=0.0003
sample: TCGA-AG-A016-01A, spectrum: 2874
EVGETLLYYSCR, G10S
MVH=29.5611
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 74938
EVSSSFQVLK, H8Q
MVH=27.0015
p-value=0.0001
sample: TCGA–AG–A016–01A, spectrum: 87794
FFGSLPDSWAR, S11R
MVH=23.9829
p−value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 88558
FGQDLLSPLLSVR, K13R
MVH=58.0868
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 38072
FNLSQESSYLATQYSLRPR, S2N
MVH=31.6524
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 66433
FTVGDHSR, I3V
MVH=39.1078
p-value=0.0003
sample: TCGA-AG-A016-01A, spectrum: 31546
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=41.1781
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 42768
FYLGGPTSVR, I9V
MVH=41.0149
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 93677
GFGTDEQALLDCLGSCSNK, R16C
MVH=52.7953
p-value=0.0003
sample: TCGA-AG-A016-01A, spectrum: 79766
GLSFDAATSGGSASSEK, T2I
MVH=64.1962
p-value=0.0001
sample: TCGA–AG–A016–01A, spectrum: 15898
GQTGALLQNTVESLSK, D9N
MVH=57.2060
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 63626
KKPSEEEAAAAAGGGPPGGPQVNLPVTDEVV, V10A
MVH=40.5459
p-value=0.0001
sample: TCGA–AG–A016–01A, spectrum: 41206
KNPDSHYGELLEK, Q6H
MVH=40.4124
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 73570
LCNNPAPQFGGK, T6A
MVH=33.0118
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 47682
LCTSVTESDVAR, E9D
MVH=43.9899
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 55559
LDVDKDGFVTEGELK, A3V
MVH=31.4521
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 9854
LFEEDPAVGALVLTGGDK, T1I
MVH=75.9719
p-value=0.0001
sample: TCGA–AG–A016–01A, spectrum: 8132
LLTQDEGPALVPGSR, G14S
MVH=42.6061
p−value=0.0001
sample: TCGA–AG–A016–01A, spectrum: 60965
LQQQHSEQPPLQPSPVTTR, M17T
MVH=57.2870
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 37724
LSVFSTLDAPVAPSDK, V7I
MVH=44.2252
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 74987
NLPSLAEQGASDPPTVASR, K7E
MVH=51.9580
p-value=0.0001
sample: TCGA–AG–A016–01A, spectrum: 15985
NPLDLAAYDQEGR, R3L
MVH=53.9736
p−value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 27284
NSLSETVR, M3L
MVH=37.4083
p-value=0.0006
sample: TCGA-AG-A016-01A, spectrum: 11126
SALSGHLETLLLGLLK, V10L
MVH=72.9618
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 24132
SLSLLDSPGLLSGEK, V4I
MVH=53.2370
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 34524
SPADPTDLGGQTSPR, I6T
MVH=45.3864
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 15489
TVVQLEGDNKLVTAFK, T14A
MVH=41.5897
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 30180
VLLDGVQNLR, P9L
MVH=61.7390
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 87280
VPSFETAEGLAGELK, T12A
MVH=49.7418
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 33111
VPVTQATR, L3V
MVH=23.1364
p-value=0.0012
sample: TCGA-AG-A016-01A, spectrum: 86130
VVFPSEEVVEQK, G6E
MVH=35.6288
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 83145
VVLQPEALFSLYSK, F8L
MVH=47.0427
p-value=0.0001
sample: TCGA-AG-A016-01A, spectrum: 37241
YVSSLTYNYEAGKDDYVK, I2V
MVH=22.3239
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 93090
AAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=37.1358
p-value=0.0004
sample: TCGA-AG-A01J-01A, spectrum: 69878
AAPSVLFLPSSSEELQANK, T2A
MVH=53.0691
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 176246
ACNVLQSSHLEDYPFDAEY, N16D
MVH=29.3333
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 12865
AGVETTTPSK, K7T
MVH=58.8699
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 12626
AGVETTTPSKQSNNK, K7T
MVH=31.3253
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 98681
ALDRPYTSK, E3D
MVH=35.3735
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 90873
ALFMDCGLHAR, T4M
MVH=47.7915
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 18883
ASSSLLLNESEPTTNLQLR, D8N
MVH=62.7406
p-value=0.0001
sample: TCGA–AG–A01J–01A, spectrum: 116446
AVEVATVVLQPTVLR, S12T
MVH=33.1574
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 30836
AWLSSQAAELER, V7A
MVH=55.8333
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 101380
DAGNEQDLGLQYK, N1D
MVH=40.6978
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 136187
DDDGTLHAACQVQPSATLDAAQPR, A5T
MVH=52.3075
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 45783
DFYVVEPLAFEGTPEQK, I4V
MVH=47.0204
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 172221
DGYGFLNR, N1D
MVH=40.9630
p-value=0.0006
sample: TCGA-AG-A01J-01A, spectrum: 92648
DVPGFLQSQSSGPGQPAVWR, N11S
MVH=26.6460
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 71242
EALDVLDAVLK, G7D
MVH=50.5395
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 90090
ELVDDSLNNVR, V7I
MVH=54.9703
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 30934
EPSAPSLPTPAYQSLPAGGHAPTPPTPAPR, S15L
MVH=33.6527
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 83120
ESALEPGPVPEAPAGGPVHAVTVTLLEK, R6P
MVH=63.1883
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 20226
FFGSLPDSWAR, S11R
MVH=39.0482
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 101318
FLDKLPQQTGDR, H12R
MVH=44.1719
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 113552
FLSGHTSELGNFR, D11N
MVH=38.4490
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 33851
FNKPFVFLMLDQNTK, E11D
MVH=59.3159
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 41310
FQLGNSGPNSTLK, S4G
MVH=42.1230
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 34453
FSLDALLTNVLPEK, I10V
MVH=32.1518
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 143929
FTVGDHSR, I3V
MVH=41.6279
p-value=0.0003
sample: TCGA–AG–A01J–01A, spectrum: 105363
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=55.6052
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 125479
FYLGGPTSVR, I9V
MVH=43.5219
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 3493
GCAGVLTLNRPK, T3A
MVH=38.1985
p-value=0.0001
sample: TCGA–AG–A01J–01A, spectrum: 19992
GFGTDEQALLDCLGSCSNK, R16C
MVH=48.4173
p−value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 19851
GGTLSTPQTGSENDALYEYL, G5S
MVH=54.7509
p-value=0.0001
sample: TCGA–AG–A01J–01A, spectrum: 81892
GQTGALLQNTVESLSK, D9N
MVH=67.9881
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 137781
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=57.9178
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 21936
KFSLDALLTNVLPFEK, I11V
MVH=44.5316
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 93742
LADGGGAGGTFQPYLDTLR, V1L
MVH=45.0351
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 45099
LALLLMASQEPQR, T2A
MVH=51.4610
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 28328
LALQPGTVGPQGR, V3I
MVH=51.5654
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 57641
LFEEDPAVGLALVTGGDK, T1I
MVH=74.7132
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 21643
LGFAGLVQEMSFGTTK, I10M
MVH=68.9609
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 78918
LHVLVEPDHFK, Q2H
MVH=60.0769
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 34313
LLNLLADLVER, R4L
MVH=54.9419
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 176160
LLSDLLPPSTGTFQEAQSR, S5L
MVH=42.6641
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 54782
LLTQDEGPALVPGSR, G14S
MVH=42.1110
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 111297
LQELTPSSGDPGEHDPASTHK, P4L
MVH=57.1798
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 138683
LQHLVNELTHDLLTK, E5V
MVH=89.4672
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 164583
LSDLQEAALDQALNHVR, Y14H
MVH=53.8024
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 91867
LTEFCHGFLEGK, R7G
MVH=62.5224
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 30674
LTPVSAQFQDLEGK, L8F
MVH=33.0798
p-value=0.0001
sample: TCGA–AG–A01J–01A, spectrum: 30670
MQYAPNTQVELLPQGR, H16R
MVH=47.8446
p−value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 53186
MVAVGLCR, H8R
MVH=45.2651
p-value=0.0006
sample: TCGA-AG-A01J-01A, spectrum: 70058
NPLLDLAAYDQEGR, R3L
MVH=43.6121
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 4250
NVSPVALPR, N3S
MVH=50.8168
p-value=0.0002
sample: TCGA-AG-A01J-01A, spectrum: 139530
QSAVPYSHFPVGAALLTQEGR, K1Q
MVH=33.8969
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 135816
RDDGTLHAACQVQPSATLDAQPR, A6T
MVH=78.4565
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 21233
RLEGLLEGLGLR, G7E
MVH=42.0453
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 34489
SALSGHLETLLLGLLK, V10L
MVH=77.9944
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 7749
SAVGELSEDSSNVVHLLK, Q15H
MVH=65.1459
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 43652
SCCDYALHVDVTHWNDSVK, I11V
MVH=61.8031
p-value=0.0001
sample: TCGA–AG–A01J–01A, spectrum: 93853
SFDMYSGDVMHLVK, A1S
MVH=40.1996
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 21905
SGGTLVVLGLGSEMTTVPLLHAALR7-N4T
MVH=40.3927
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 95385
SLDLDDWPLELLK, V9I
MVH=55.9704
p-value=0.0001
Sample: TCGA-AG-A01J-01A, spectrum: 34057
SLSAFLVPMPTPGLTLGK, G1S
MVH=38.4716
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 88568
SPADPTDLGGQTSPR, I6T
MVH=54.9384
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 77785
SQNKEDYDGLKEEFRK, A8D
MVH=71.9404
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 37825
SSSYSGEGYGGGK, G10S
MVH=57.5302
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 37711
SSSYSGEYGSGGKR, G10S
MVH=49.1345
p-value=0.0002
sample: TCGA-AG-A01J-01A, spectrum: 173795
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=81.7234
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 94679
TLDPFETMLK, S2L
MVH=36.6568
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 125996
TLEGLQVEEEPVYK, E14K
MVH=56.4215
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 95443
TVASPGVSVEAVEQLDLGGVTLLR, T8S
MVH=35.0104
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 69205
TVVQLEGDNKLVTAFK, T14A
MVH=43.4726
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 27575
VAQLLKEPR, K9R
MVH=45.2549
p-value=0.0004
sample: TCGA-AG-A01J-01A, spectrum: 137638
VCVALDECELDVR, M12V
MVH=54.2197
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 7127
VPSFETAEGLGAELK, T12A
MVH=55.9724
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 86480
VPVTQATR, L3V
MVH=40.5057
p-value=0.0012
sample: TCGA-AG-A01J-01A, spectrum: 76832
VSYGLGEEEHDQEGR, D7E
MVH=27.0170
p-value=0.0001
sample: TCGA-AG-A01J-01A, spectrum: 104121
YVSLLYTNYEAGKDDYVK, I2V
MVH=38.8793
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 53767
AAAAAAAAAPAAAAATAATTAATTAATTAATAAQ, P17A
MVH=33.7379
p-value=0.0013
sample: TCGA-AG-A01L-01A, spectrum: 57002
AAAPAPVSEAVSR, C12S
MVH=51.1645
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 32698
AAPSVTLPSSSEELQANK, T2A
MVH=51.6805
p-value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 101447
ACNVLQSSHLEDYPFDAEY, N16D
MVH=37.4256
p–value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 35519
AGVETTTPSK, K7T
MVH=25.9116
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 26770
ALEDVFDAGLEGK, M5V
MVH=61.6720
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 32248
APSQHLSSFDPCFYR, R5H
MVH=54.8080
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 52673
AYVLLR, E1A
MVH=38.9442
p-value=0.0084
sample: TCGA-AG-A01L-01A, spectrum: 78885
DDDGTLHAACQVQPSATLDAAQPR, A5T
MVH=44.8063
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 34076
DFNHLDVELSLLGK, N6D
MVH=49.1982
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 11866
DFYVVEPLAFEGTPEQK, I4V
MVH=54.6088
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 101534
DGDSLMVLPTLPEEEAK, V5L
MVH=24.4680
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 91688
DGYGFLNR, N1D
MVH=46.9290
p-value=0.0006
sample: TCGA–AG–A01L–01A, spectrum: 22645
DTEEEDFHVDQATTVK, V12A
MVH=54.7654
p−value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 78429
DVDGLTSLNAGR, K12R
MVH=60.3682
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 53472
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=29.5772
p-value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 67108
EELGHLQNDLTSLENDK, M10L
MVH=33.2265
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 93325
EQPGSPEWLQLDK, Q13K
MVH=27.4200
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 41141
FFGSLPDSWAR, S11R
MVH=45.0342
p-value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 41895
FGQDLLSPLLSVR, K13R
MVH=44.1415
p–value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 57874
FLDKLPQQTGDR, H12R
MVH=51.3043
p–value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 68025
FNLSQESSYLATQYSLRPR, S2N
MVH=26.7105
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 9405
FPGPCDYNFASDCR, L4P
MVH=53.2529
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 61057
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=71.0563
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 66035
FYLGGPTSVR, I9V
MVH=47.8245
p-value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 41033
GFGTDEQALLDCLGSCSNK, R16C
MVH=41.2218
p–value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 33291
GQTGALLQNTVESLSK, D9N
MVH=67.2281
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 23831
GVAGSSVAVLCPYNR, G5S
MVH=40.5994
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 34429
GVGTNEDALLELLTTR, A2V
MVH=58.6740
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 7890
HASSGSFLSSANEHLK, P9S
MVH=29.0625
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 87350 KFFGSLPDSWAR, S12R
MVH=46.9712
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 73671
KKPSEEAEAAAAGGPPGGPQVNPLPVTDEVV V10A
MVH=46.6151
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 47322
LADGGAGGTFQPYLDTLR, V1L
MVH=56.3932
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 64173
LCTSVTESDVAR, E9D
MVH=30.8348
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 25934
LFEEDPAVGALVTGGDK, T1I
MVH=75.8727
p-value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 12591
LLNLLADLVER, R4L
MVH=43.7021
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 78753
LQEENLVVTPR, I8V
MVH=55.2105
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 63944
LQELTPSSGDGEHDPASTHK, P4L
MVH=69.0448
p-value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 83958
LQQQHSEQPPLQPSPVTTR, M17T
MVH=35.5196
p-value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 55032
LYDALDLSLLER, V7I
MVH=72.7211
p–value=0.0001
sample: TCGA–AG–A01L–01A, spectrum: 9471
MQYAPNTQVELLPQGR, H16R
MVH=68.1972
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 22444
MVAVGLCR, H8R
MVH=42.9535
p-value=0.0006
sample: TCGA–AG–A01L–01A, spectrum: 57824
NTNSVPETAPAALPETR, K17R
MVH=38.9089
p–value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 53205
NTVLATWQPYSTSK, T11S
MVH=53.9844
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 22518
PVAEYWNNSQK, D2V
MVH=37.7481
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 13974
QLEKQGESALTSQPR, E6G
MVH=15.9708
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 26899
SELPLDPLPLPTEEGNPLLK, V10L
MVH=46.8962
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 54401
SFDMYSGDVMHLVK, A1S
MVH=40.9993
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 42347
SGGTLVGLGSEMTPVPLLHAALRN4T
MVH=34.3157
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 77590
SPPGAAAPAAAAPPLSAK, S8P
MVH=33.9025
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 61595
SSGGPGAGLCLFPLDEVHAK, K16E
MVH=54.0444
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 66364
TLEGLQVEEEPVK, E14K
MVH=55.4013
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 85493
TLNEADCATLPPALR, V10I
MVH=39.1680
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 32843
TVVQLEGDNKLVTAFK, T14A
MVH=47.4625
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 88603
VQLPTESLQELLDLHR, T7S
MVH=26.4798
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 102263
VQVLAAQLLSEMK, D11E
MVH=56.3682
p-value=0.0001
sample: TCGA-AG-A01L-01A, spectrum: 12198
WLLLCNPGALNTLVEK, D11N
MVH=83.1376
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 67597
AAAAAATAATTAATAAQ, P17A
MVH=56.1805
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 72973
AAAPAPVSEAVSR, C12S
MVH=62.2049
p-value=0.0001
sample: TCGA–AG–A01N–01A, spectrum: 50184
AAPSVTLPSPSEELQANK, T2A
MVH=47.9056
p–value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 22071
AFSEYLGTDSK, G4E
MVH=57.4370
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 105333
AGDLGVDLTSK, P1A
MVH=62.7307
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 18977
AGVETTTPSK, K7T
MVH=51.7439
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 14300
ASSSLLLNESEPTTNLQLR, D8N
MVH=63.2270
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 23573
AWLSSQAAELER, V7A
MVH=62.8531
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 120535
DGYGFLNR, N1D
MVH=47.6805
p-value=0.0006
sample: TCGA-AG-A01N-01A, spectrum: 42551
DMAGAQAAVALNEEFLK, R18K
MVH=61.8763
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 105935
DVTVLQNTDGNNDAWAK, E14D
MVH=69.6834
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 82915
EALELDSL, V2A
MVH=32.3265
p-value=0.0005
sample: TCGA-AG-A01N-01A, spectrum: 122197
EQPGSPEWLQLDK, Q13K
MVH=32.4524
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 74561
FADVFAK, E7K
MVH=34.2247
p-value=0.0084
sample: TCGA-AG-A01N-01A, spectrum: 15398
FFGSLPDSWAR, S11R
MVH=34.2856
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 76837
FVSSSSGGYYGGYGGVLTASDGLLAGNEK, A9G.
MVH=45.1205
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 90889
FYLGPGPTSVR, I9V
MVH=45.2266
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 24778
GFGTDEQALLDCLGSCSNK, R16C
MVH=60.3832
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 15554
GLLDLLEER, V3I
MVH=40.9251
p-value=0.0038
sample: TCGA-AG-A01N-01A, spectrum: 59235
GQTGALLQNTVESLSK, D9N
MVH=68.7469
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 12219
KAFSEYLGTDQSK, G5E
MVH=55.5837
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 4877
KLDSVFEELSK, R9P
MVH=62.6967
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 119559
LCNNPAPQFGGK, T6A
MVH=38.1373
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 4027
LDSTDFTSTLKLK, G8S
MVH=49.1254
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 122049
LDSVFEELSK, R8P
MVH=40.9925
p-value=0.0001
sample: TCGA–AG–A01N–01A, spectrum: 41872
LFEEDPAVGALVLTGGDK, T1I
MVH=74.1987
p−value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 110895
LGGLQPSQDR, G7S
MVH=39.3763
p-value=0.0001
sample: TCGA–AG–A01N–01A, spectrum: 38793
LLESGDLSMSSVK, I12V
MVH=38.2121
p−value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 26063
LLNLLADLVER, R4L
MVH=47.2282
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 39846
LLTQDEGPALVPGR, G14S
MVH=46.6896
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 4679
LPQGLPTEENMSNTCLK, A7T
MVH=50.3256
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 84423
LSVFSTLDAPVAPSDK, V7I
MVH=47.2790
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 23406
LTPVSAQFQDLEGK, L8F
MVH=43.6121
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 31517
LTVAPPLAEPGAGK, P1L
MVH=48.4313
p-value=0.0001
sample: TCGA–AG–A01N–01A, spectrum: 32095
MQYAPNTQVELLPQGR, H16R
MVH=66.8310
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 57260
MVDFAGMK, V7M
MVH=38.4002
p-value=0.0006
sample: TCGA-AG-A01N-01A, spectrum: 45407
NSLSETVR, M3L
MVH=37.5311
p-value=0.0006
sample: TCGA-AG-A01N-01A, spectrum: 19452
NSTLSEPGSGR, P4L
MVH=44.3998
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 73721
NTNSVPETAPAALPETR, K17R
MVH=38.7641
p-value=0.0001
sample: TCGA–AG–A01N–01A, spectrum: 46986
PVAEYWNSQK, D2V
MVH=44.5223
p–value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 76646
QGTLTEYCASTLMSLPTK, G9S
MVH=36.0476
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 114238
QLQETPSGGPLTEALPPAR, P8S
MVH=33.5132
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 120230
QLTVGPR, K8R
MVH=37.0516
p-value=0.0006
sample: TCGA–AG–A01N–01A, spectrum: 6423
SAVGELSEDSSNVVHLLK, Q15H
MVH=48.9328
p–value=0.0001
sample: TCGA–AG–A01N–01A, spectrum: 68742
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=56.6891
p–value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 120640
SGFEPASFK, L8F
MVH=32.3939
p-value=0.0002
sample: TCGA-AG-A01N-01A, spectrum: 64073
SPADPTDLGGQTSPR, I6T
MVH=63.1766
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 97092
SPPGAAAPAAAKPPPLSAK, S8P
MVH=38.0141
p-value=0.0001
sample: TCGA–AG–A01N–01A, spectrum: 28014
SSSYSGEYGSGGGK, G10S
MVH=40.5572
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 51474
SVVSDVPEELDFLVPK, A3V
MVH=31.3404
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 4309
TAASGVEASSRPLDHAQPPSSLVLDK, N9S
MVH=53.1951
p-value=0.0002
sample: TCGA-AG-A01N-01A, spectrum: 85118
TLAQLNPESSLFLTASK, I14 T
MVH=86.7988
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 68898
TLDPFETMLK, S2L
MVH=26.9347
p-value=0.0002
sample: TCGA–AG–A01N–01A, spectrum: 91231
TLEGLQVEEEPVYK, E14K
MVH=37.7191
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 119985
TLSGGLAVNGPR, P7A
MVH=51.0700
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 63641
TSLSAPPNTSSTENPK, S9T
MVH=37.8505
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 88522
TTPLEAASSGAR, T11A
MVH=35.2458
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 83296
VFSVAELQAR, S9A
MVH=47.2857
p-value=0.0002
sample: TCGA-AG-A01N-01A, spectrum: 79152
VLSTTNAER, D6N
MVH=25.9045
p-value=0.0003
sample: TCGA-AG-A01N-01A, spectrum: 66432
VLTGTVNVLQPNYPAAAR, I10V
MVH=48.2516
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 62410
VPVTQATR, L3V
MVH=48.6039
p-value=0.0012
sample: TCGA-AG-A01N-01A, spectrum: 111609
VSDLAATAYK, N2S
MVH=55.7832
p-value=0.0001
sample: TCGA--AG--A01N--01A, spectrum: 16269
VVLQPEALFSLYSK, F8L
MVH=59.2033
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 39797
VYGDLLYTPAK, H7Y
MVH=54.9703
p-value=0.0001
sample: TCGA-AG-A01N-01A, spectrum: 25783
WLLLCNPGLANTLVEK, D11N
MVH=76.0343
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 57244
AAAAAATAATTAATTAATAAQ, P17A
MVH=24.4684
p-value=0.0003
sample: TCGA-AG-A01W-01A, spectrum: 62275
AAAPAPVSEAVSR, C12S
MVH=45.5844
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 40210
AAPSVTLFPPSEELQANK, T2A
MVH=60.1039
p-value=0.0001
sample: TCGA–AG–A01W–01A, spectrum: 9084
AGVETTTPSK, K7T
MVH=53.9793
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 39461
APSQHLSSFDPCFYR, b5H
MVH=62.3406
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 123867
ASSSLLESEPTTLQLRL, D8N
MVH=54.8592
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 15629
DFYVVEPLAFEGTPEQK, I4V
MVH=58.2709
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 113630
DGYGFLNR, N1D
MVH=40.5540
p-value=0.0006
sample: TCGA-AG-A01W-01A, spectrum: 27945
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=86.6475
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 29012
DTEEEDFHVDQATTVK, V12A
MVH=56.8952
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 56816
DVPGFLQQSQSSGPGQPAVWHN, N11S
MVH=36.0287
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 41744
EALDVLDAVLK, G7D
MVH=57.1244
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 636
EASQGSSASSAPQSVK, H13Q
MVH=20.1302
p-value=0.0002
sample: TCGA-AG-A01W-01A, spectrum: 36168
ECEPPSAGAAVSAR, T12S
MVH=20.6782
p-value=0.0007
sample: TCGA-AG-A01W-01A, spectrum: 82607
EELGHLQNDLTSLENDK, M10L
MVH=38.0305
p-value=0.0001
sample: TCGA--AG--A01W--01A, spectrum: 54840
ELVDDSLNNVR, V7I
MVH=43.8173
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 115286
EQPGSPEWLQLDK, Q13K
MVH=32.2317
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 50382
ESALEPGPVPEAPAGGPVHAVTVTLLLEK, R6P
MVH=26.9695
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 6400
FFGSLPDSWAR, S11R
MVH=38.7958
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 54623
FLDKLPQQTGDR, H12R
MVH=38.0948
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 21966
FPGPCDYNFASDCR, L4P
MVH = 51.4034
p-value = 0.0001
sample: TCGA-AG-A01W-01A, spectrum: 73903
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=48.4460
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 94402
FTVGDHSR, I3V
MVH=38.2563
p-value=0.0003
sample: TCGA-AG-A01W-01A, spectrum: 57909
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=64.5069
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 72988
FYLGPGPTSVR, I9V
MVH=41.0564
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 6310
GFGTDEQALLDCLGSCSNK, R16C
MVH=50.2019
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 106190
GKWERPFEVKDTEEEDFHVDQATTVK, V22A
MVH=90.2454
p-value=0.0001
sample: TCGA–AG–A01W–01A, spectrum: 40612
GQTGALLQNTVESLSK, D9N
MVH=53.8603
p–value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 90418
GYQQDAYDGKDYLALNEDLR, R3Q
MVH=40.6413
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 122640
LDSTDFTSTLK, G8S
MVH=42.6061
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 81637
LDVDKDGFVTEGELK, A3V
MVH=53.4476
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 32157
LFEEDPAVGALVLTGGDK, T1I
MVH=79.6251
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 37387
LHGHL YTPGQELTNDC, E17K
MVH=43.6581
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 24825
LLNLADLVER, R4L
MVH=56.7939
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 107927
LLSDLLPPSTGTFQEAQSR, S5L
MVH=36.4849
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 100779
LSDLQEALDQALNHVR, Y14H
MVH=54.3151
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 13426
LTPVSAQFQDLEGK, L8F
MVH=39.9972
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 12690
LTVAPPLAEPGAGK, P1L
MVH=39.1088
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 5774
LVTDYTLAEADAALQK, E11D
MVH=64.4518
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 63095
NTNSVPETAPAALPETR, K17R
MVH=44.1401
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 29945
QVGDFHQVLLR, A2V
MVH=33.3088
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 24969
SALSGHLETLLLGLLK, V10L
MVH=69.5711
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 124892
SAVGELSEDSSNVVHLKLK, Q15H
MVH=27.1694
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 101174
SDPLCLLLQDVGGSGWAELGR, V6I
MVH=35.0971
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 49964
SDPVTLNVLYGPDVPTLSPSK, G14V
MVH=43.1541
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 33246
SELPLDPLPLPTEEGNPLLK, V10L
MVH=44.7134
p-value=0.0001
sample: TCGA−AG−A01W−01A, spectrum: 53689
SPADPTDLGGQTSPR, I6T
MVH=58.3528
p−value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 46448
SQNKEDYDGLKEEFR, A8D
MVH=40.9226
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 54354
SQNKEDYDGLKEEFRK, A8D
MVH=75.7542
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 17952
SSYSGEYSGGGK, G10S
MVH=61.2526
p-value=0.0001
sample: TCGA–AG–A01W–01A, spectrum: 17830
SSSYSGEYGSGGGKR, G10S
MVH=46.2594
p–value=0.0002
sample: TCGA-AG-A01W-01A, spectrum: 114681
TAASGVEASSRPLDHAQPPSSLVLDKESEVYK, N9S
MVH=51.4051
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 81869
TLEGLQVEEEPVYK, E14K
MVH=55.2059
p-value=0.0001
sample: TCGA–AG–A01W–01A, spectrum: 125632
TLTLEVEPLDTLENVK, S9L
MVH=55.4899
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 79133
TTPLEAASSGAR, T11A
MVH=40.8328
p-value=0.0001
sample: TCGA–AG–A01W–01A, spectrum: 50800
TVASPGVSVEEAVEQLDLGGVTLLR, T8S
MVH=57.6017
p-value=0.0001
sample: TCGA–AG–A01W–01A, spectrum: 67524
TVEDLDGLLQQLYR, H10Q
MVH=65.1266
p−value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 40091
TVVQLEGDNKLVTAFK, T14A
MVH=32.8532
p-value=0.0002
sample: TCGA-AG-A01W-01A, spectrum: 86264
VLGTAGTEEGQK, I1V
MVH = 39.6019
p-value = 0.0001
sample: TCGA-AG-A01W-01A, spectrum: 72481
VLLCGPVGPR, K10R
MVH=45.4347
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 60395
VPVTQATR, L3V
MVH=34.8150
p-value=0.0012
sample: TCGA-AG-A01W-01A, spectrum: 92620
VQLPTESLQELLDLHR, T7S
MVH=44.2394
p-value=0.0001
sample: TCGA−AG−A01W−01A, spectrum: 2812
VSEVLLSR, G8R
MVH=34.8670
p−value=0.0025
sample: TCGA-AG-A01W-01A, spectrum: 53658
VSYGGLGEEEHDQEGR, D7E
MVH=34.8053
p-value=0.0001
sample: TCGA-AG-A01W-01A, spectrum: 7283
VVLQPEALFSLYSK, F8L
MVH=51.8409
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 42003
AAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=33.2813
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 32913
AAPSVTLFPPSSEELQANK, T2A
MVH=60.7936
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 9577
AGVETTTPSK, K7T
MVH=63.1147
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 9366
AGVETTTPSKQSNNK, K7T
MVH=43.6400
p-value=0.0001
sample: TCGA–AG–A01Y–01A, spectrum: 118279
ASSSLLENESEPTTNQLR, D8N
MVH=53.9758
p–value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 51489
AVEVATVVLQPTVLR, S12T
MVH=54.0757
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 83864
DDDGLHAACQVQPSATLDAAQPR, A5T
MVH=46.0833
p-value=0.0001
sample: TCGA–AG–A01Y–01A, spectrum: 7396
DFYVVEPLAFEGTPEQK, I4V
MVH=39.9941
p−value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 20059
DSRPSQAAGDNQGDDEVKEQTFSGGTSQDTK, A16V
MVH=76.6678
p-value=0.0001
sample: TCGA–AG–A01Y–01A, spectrum: 48595
ELVDDSLNNVR, V7I
MVH=43.6043
p-value=0.0001
sample: TCGA–AG–A01Y–01A, spectrum: 109628
EQPGSPEWLQLDK, Q13K
MVH=26.9212
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 34666
esalepgpvpeapagpgpvhavtvvtllek, R6P
MVH=47.8665
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 119367
FFGSLPDSWAR, S11R
MVH=30.8186
p-value=0.0003
sample: TCGA-AG-A01Y-01A, spectrum: 48417
FLDKLPQQTGDR, H12R
MVH=36.9802
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 7793
FNKPFVFLMLDQNTK, E11D
MVH=67.5215
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 68234
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=49.1723
p-value=0.0001
sample: TCGA–AG–A01Y–01A, spectrum: 88937
FTVGDHSR, I3V
MVH=44.7313
p-value=0.0003
sample: TCGA-AG-A01Y-01A, spectrum: 51779
FVSSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=42.9102
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 58638
FYLGGPTSVR, I9V
MVH=51.0849
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 71973
HMTAVVK, Y1H
MVH=35.2282
p-value=0.0044
sample: TCGA-AG-A01Y-01A, spectrum: 85480
KKPSEEEAAAAAGGPPGGPQVNPLPVTDEVV10A
MVH=51.2788
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 56753
KNPDSHYGELLEK, Q6H
MVH=45.1461
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 76053
LDVDKDGFVTEGELK, A3V
MVH=48.7152
p-value=0.0001
sample: TCGA–AG–A01Y–01A, spectrum: 24506
LFEEDPAVGALVLTGGDK, T11
MVH=59.8563
p–value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 112143
LLDTAFDLDFLK, V10I
MVH=81.9081
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 17022
LLNLADLVER, R4L
MVH=59.0754
p-value=0.0001

m/z
Intensity(%)
sample: TCGA-AG-A01Y-01A, spectrum: 87419
LSDLQEALDQALNHVR, Y14H
MVH=57.1589
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 3329
MAQWGNNKPLC, V9I
MVH=47.2594
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 50485
MKDVPGFLQQSQSSGPGQPAVWHR, N13S
MVH=75.2121
p-value=0.0001
sample: TCGA–AG–A01Y–01A, spectrum: 126321
MQYAPNTQVELLPQGR, H16R
MVH=65.3815
p–value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 11915
MVAVGLCR, H8R
MVH=46.1577
p-value=0.0006
sample: TCGA-AG-A01Y-01A, spectrum: 31269
MVDFAGMK, V7M
MVH=43.8060
p-value=0.0006
sample: TCGA–AG–A01Y–01A, spectrum: 57527
NTNSVPETAPAALPETR, K17R
MVH=46.4782
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 14228
QATVGNLINTERPGMLDFTGK, D6N
MVH=25.6994
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 13051
QVGDFHQVLLR, A2V
MVH=34.0277
p-value=0.0002
sample: TCGA-AG-A01Y-01A, spectrum: 111797
RWLLLCPGGLANTLVEK, D12N
MVH=62.3401
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 25594
SFQGPVLLGSSHGGVNLEDVAAETPEALLK, S24T
MVH=22.0882
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 129365
SGGLVLVGLGSEMTTVPLLHAALR, N4T
MVH=31.6838
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 108613
SQEVETMCPVAAATSNVHTVK, M21T
MVH=38.0144
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 39574
SQNKEDYDGLKEEFR, A8D
MVH=72.4401
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 48175
SQNKEDYDGLKEEFRK, A8D
MVH=77.8098
p-value=0.0001
sample: TCGA–AG–A01Y–01A, spectrum: 6643
TCSFDFTGAVEDLSK, G3S
MVH=55.8398
p−value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 57767
TKAEAEQAALAAANQESNLAR, A1T
MVH=58.4458
p-value=0.0001
sample: TCGA–AG–A01Y–01A, spectrum: 43286
TLDPFETMLK, S2L
MVH=34.6557
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 107241
TLSGGLAVNGPR, P7A
MVH=61.1417
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 73285
TTPLEAASSGAR, T11A
MVH=59.7917
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 41058
VEHWGLDKPLLK, Q8K
MVH=66.0574
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 3910
VLLNDGGYYDPK, E12K
MVH=62.7220
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 80476
VLSTTNAER, D6N
MVH=27.3564
p-value=0.0006
sample: TCGA-AG-A01Y-01A, spectrum: 45672
VPVTQATR, L3V
MVH=34.3620
p-value=0.0012
sample: TCGA-AG-A01Y-01A, spectrum: 87409
VQLPTESLQELLDLHR, T7S
MVH=30.6071
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 16693
WLLLCNPGALNTLVEK, D11N
MVH=72.8029
p-value=0.0001
sample: TCGA-AG-A01Y-01A, spectrum: 50651
YVSLLYTNYEAGKDDYVK, I2V
MVH=37.6101
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 40644
AAAAAAAPAAAATAATTAATTAATAAQAQ, P17A
MVH=51.1328
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 52292
AAAPAPVSEAVSR, C12S
MVH=24.2031
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 32741
AAPSVTLFPPSSEELQANK, T2A
MVH=55.6369
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 7706
AGVETTTPSK, K7T
MVH=46.8142
p-value=0.0001
sample: TCGA–AG–A020–01A, spectrum: 27322
ALEDVFDALEGK, M5V
MVH=52.8919
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 32015
APSQHLSSFDPCFYR, R5H
MVH=55.2128
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 56606
AQLNVGNVLPVGMPEGTLVCCLEEKPGDR, I5V
MVH=33.9986
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 10542
AWLSSQAEELER, V7A
MVH=57.0542
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 46216
AYVVLLR, E1A
MVH=38.8796
p-value=0.0084
sample: TCGA-AG-A020-01A, spectrum: 96411
DGYGFLNR, N1D
MVH=44.9486
p-value=0.0006
sample: TCGA-AG-A020-01A, spectrum: 81575
DVDGLTSLNAGR, K12R
MVH=56.8852
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 47385
DVPGFLQQSQSSGPGQPAVWHR, N11S
MVH=43.5560
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 82474
DVTVLQNTDGNNDAWAK, E14D
MVH=54.4270
p-value=0.0001
sample: TCGA–AG–A020–01A, spectrum: 41641
EADLTEELEENLR, T8I
MVH=48.3294
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 68696
EELGHQLQNDLTSLENDK, M10L
MVH=36.6702
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 60436
EHTLHLEAELEK, S4L
MVH=32.3323
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 45331
ELVDDSLNNVR, V7I
MVH=35.1264
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 98191
EQPGSPEWLQLDK, Q13K
MVH=34.3981
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 5120
FFGSLPDSWAR, S11R
MVH=41.8754
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 34740
FLGQLLTAFPALR, A3G
MVH=62.8460
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 92172
FLQENVFVAANHNASPLSLK, G14A
MVH=34.8624
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 13207
FNKPFVFLMLDQNTK, E11D
MVH=50.9899
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 4903
GFGTDEQALLDCLGSCSNK, R16C
MVH=71.1720
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 33291
GQTGALLQNTVESLSK, D9N
MVH=66.5877
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 85845
HVGSSETNLLQHLEACGR, K8N
MVH=42.2563
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 1283
KAFSEYLGTDQSK, G5E
MVH=37.3829
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 84682
KFFGSLPDSWAR, S12R
MVH=47.4899
p-value=0.0001
sample: TCGA–AG–A020–01A, spectrum: 76150
KKPSEEEAAAGGPPGGPQVNPLPVTDEVV V10A
MVH=56.3175
p−value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 24078
KVLLDGQQLR, P10L
MVH=43.0620
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 41263
LADGGAGGTFQPYLDTLR, V1L
MVH=52.7374
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 103850
LDSTDFTSTLK, G8S
MVH=54.9216
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 26416
LFEEDPAVGLVLGDK, T1I
MVH=73.4771
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 38584
LHVLVEPDHFK, Q2H
MVH=53.5190
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 107677
LLDTAFDLDFLK, V10I
MVH=76.2131
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 46609
LLETMTEVVR, N4T
MVH=56.3425
p-value=0.0001
sample: TCGA–AG–A020–01A, spectrum: 20516
LLNLLADLVER, R4L
MVH=54.0323
p-value=0.0001
sample: TCGA–AG–A020–01A, spectrum: 92427
LLSDLLPPSTGTFQEAQSR, S5L
MVH=44.3864
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 12306
LQPEDMFVYDLNEK, C9Y
MVH=40.5625
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 86103
LSDLQEALDQALNHVR, Y14H
MVH=57.4956
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 38212
LVQNCGLGTLR, W7G
MVH=56.4498
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 4301
LVTDYTLAEADAALQK, E11D
MVH=79.0055
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 10235
MQYAPNTQVELLPQGR, H16R
MVH=51.0284
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 93095
NEVLWHPTLNLPLSPQGTVR, A3V
MVH=43.5589
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 26377
NPLLHLAYDQEGR, R3L
MVH=49.9323
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 46847
NTVLATWQPYSTSK, T11S
MVH=56.8885
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 17672
QATVGNLINTERPGMLDFTGK, D6N
MVH=16.6652
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 5744
RLEGLEGLGLR, G7E
MVH=63.3955
p-value=0.0014
sample: TCGA-AG-A020-01A, spectrum: 42012
SDPVTLYNVLYGDVPTLSK, G14V
MVH=48.9765
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 9184
SGGVERPFVLAR, M4V
MVH=50.8840
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 41248
SLSLLDSPGLLSGEK, V4I
MVH=51.5544
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 37968
SQNKEDYDGLKEEFR, A8D
MVH=71.2339
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 45072
SQNKEDYDGLKEEFRK, A8D
MVH=46.9938
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 36293
STESLQTNVQR, A7T
MVH=37.5077
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 73325
TSELPPLK, A2S
MVH=30.7089
p-value=0.0012
sample: TCGA–AG–A020–01A, spectrum: 56763
TVEDLDGLLQQLYR, H10Q
MVH=65.1266
p−value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 60635
VLLCGPVGPR, K10R
MVH=39.6834
p-value=0.0002
sample: TCGA-AG-A020-01A, spectrum: 46625
VLLDGVQNLR, P9L
MVH=59.4441
p-value=0.0001
sample: TCGA-AG-A020-01A, spectrum: 51223
VPVTQATR, L3V
MVH=22.4646
p-value=0.0012
sample: TCGA-AG-A020-01A, spectrum: 78206
VQLPTESLQELLDLHR, T7S
MVH=27.2287
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 42590
AAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=45.6329
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 24990
AAPSVTLFPPSEELQANK, T2A
MVH=55.1485
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 9796
AGVETTTPSK, K7T
MVH=62.4905
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 55578
ALDRPYTSK, E3D
MVH=40.1968
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 131809
APFAAPLPFAELVLPPQQ, S7L
MVH=17.8455
p-value=0.0002
sample: TCGA-AG-A02N-01A, spectrum: 104987
ASPLLALGQTLAR, V5L
MVH=58.0882
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 120754
ASSSLLLNESEPTTNLQLR, D8N
MVH=48.4472
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 7779
DFYVVEPLAFEGTPEQK, I4V
MVH=56.7395
p-value=0.0001
sample: TCGA–AG–A02N–01A, spectrum: 110058
DGYGLNR, N1D
MVH=46.2273
p-value=0.0006
sample: TCGA-AG-A02N-01A, spectrum: 129915
DSKEPFSSVELQAALSK, E3K
MVH=56.7740
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 115672
DSRPSQAAGDNQGDEVK, A16V
MVH=60.8573
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 20487
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=81.5812
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 92889
DVDGLTSLNAGR, K12R
MVH=62.8531
p-value=0.0001
sample: TCGA–AG–A02N–01A, spectrum: 42148
DVPGLQQSQSSGPGQPAVWH, N11S
MVH=42.1463
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 35294
EALDVLDAVLK, G7D
MVH=54.0323
p-value=0.0003
sample: TCGA-AG-A02N-01A, spectrum: 652
EASQGSSASSAPQSVK, H13Q
MVH=48.2944
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 116293
EEPVSSGPEEAAGK, V12A
MVH=47.1497
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 5521
EPSAPSLPTPAYQSLPAGGHAPTPPTPAPR, S15L
MVH=23.4436
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 111844
EQPGSPEWLQLDK, Q13K
MVH=32.4524
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 121912
FFGSLPDSWAR, S11R
MVH=42.3570
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 122745
FGQDLLSPLLSVR, K13R
MVH=52.1157
p-value=0.0001
sample: TCGA–AG–A02N–01A, spectrum: 48816
FLDKLPQQTGDR, H12R
MVH=52.1164
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 95873
FLQENVFVAANHNASPLSLK, G14A
MVH=26.0224
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 52427
FNLSQESSYLATQYSLRPR, S2N
MVH=26.6269
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 60363
FSVPVQHFCGGNPSTPLQVR, Q20R
MVH=44.0133
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 90204
FTVGDHSR, I3V
MVH=42.3887
p-value=0.0003
sample: TCGA-AG-A02N-01A, spectrum: 52367
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=50.9665
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 59308
FYLGPGTTSVR, I9V
MVH=52.2546
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 130631
GLLDLLEER, V3I
MVH=46.1704
p-value=0.0038
sample: TCGA-AG-A02N-01A, spectrum: 25004
GQTGALLQNTVESLSK, D9N
MVH=74.2790
p-value=0.0001
sample: TCGA–AG–A02N–01A, spectrum: 78208
KKPSEEEAAAGGPPGGPQVNPLPVTDEVV, V10A
MVH=43.6578
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 119304
LDSTDFTSTLK, G8S
MVH=58.6185
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 25207
LFEEDPAVGLVTGGDK, T1I
MVH=77.2508
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 114362
LLDTAFLDLDFK, V10I
MVH=72.7211
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 17560
LLNLLADLVER, R4L
MVH=59.6797
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 32400
LTLQALTEK, A2T
MVH=48.4127
p-value=0.0005
sample: TCGA-AG-A02N-01A, spectrum: 128876
LTPVSAQFQDLEGK, L8F
MVH=56.3230
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 36705
LVTDQETGSSK, R5Q
MVH=70.2113
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 5252
MQYAPNTQVELLPQGR, H16R
MVH=54.0588
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 25132
NPLLDLAAYDQEGR, R3L
MVH=67.8063
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 58083
NTNSVPETAPAALPETR, K17R
MVH=54.5147
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 41743
NTVLATWQPYSTSK, T11S
MVH=55.1354
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 103555
SEALPTDLPTPSAPDLTEPK, A10T
MVH=49.7941
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 34041
SLSLLDSPGLLSGEK, V4I
MVH=50.1136
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 83664
SPPGAAAPAAAKPPPLSAK, S8P
MVH=36.0755
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 19039
SSSYSGEYGSGGGK, G10S
MVH=58.9032
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 111415
TAASGVEASSRPLDHAPPSLYLDKESEVYK, N9S
MVH=80.6598
p-value=0.0001
sample: TCGA–AG–A02N–01A, spectrum: 47299
TSLSAPPNTSSTENPK, S9T
MVH=44.7545
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 24437
TVVQLEGDNKLVTAFK, T14A
MVH=50.9614
p-value=0.0001
sample: TCGA–AG–A02N–01A, spectrum: 121252
VPSFETAEGLGAELK, T12A
MVH=69.8881
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 55090
VPVTQATR, L3V
MVH=47.5588
p-value=0.0012
sample: TCGA-AG-A02N-01A, spectrum: 100000
VSDLAAATAYK, N2S
MVH=52.4712
p-value=0.0001
sample: TCGA-AG-A02N-01A, spectrum: 51231
YVSLLYTNYEAGKDDYVK, I2V
MVH=33.2443
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 28767
AAAAAAAAAPAAAAATAATTAATTAATAAQ, P17A
MVH=48.8522
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 21574
AAPSVTLFPPSEELQANK, T2A
MVH=51.6048
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 3392
ASSSLLLNESEPTTNLQLR, D8N
MVH=54.8617
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 90556
DGYGFLNR, N1D
MVH=46.9290
p-value=0.0006
sample: TCGA-AG-A02X-01A, spectrum: 35142
DVPGFLQSQSSGPGQPAVWHR, N11S
MVH=30.8982
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 47394
EHTLHLEAELEK, S4L
MVH=34.5275
p-value=0.0002
sample: TCGA-AG-A02X-01A, spectrum: 92237
EQPGSPEWLQLDK, Q13K
MVH=25.0905
p-value=0.0002
sample: TCGA-AG-A02X-01A, spectrum: 30213
ESALEPGPVEAPAGGPVHAVTVVTLEK, R6P
MVH=27.8505
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 4530
FFGSLPDSWAR, S11R
MVH=30.6004
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 50052
FGLQAGLVTDFQK, M7L
MVH=45.0738
p-value=0.0001
sample: TCGA−AG−A02X−01A, spectrum: 4916 FGQDLLSPLLSVR, K13R
MVH=44.8887
p−value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 39419
FLDKLPQQTGDR, H12R
MVH=44.2268
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 10676
FNKPFVFLMLDQNTK, E11D
MVH=61.7535
p-value=0.0001
sample: TCGA–AG–A02X–01A, spectrum: 50538
FNLSQESSYLATQYSLRPR, S2N
MVH=23.3515
p–value=0.0003
sample: TCGA-AG-A02X-01A, spectrum: 70168
FVSEDDRNSFLK, T11S
MVH=27.4200
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 42980
FVSSSSSGGYGGGYGGVLTASDGLLAGNEK, A9G
MVH=49.3622
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 84557
GKWERPFEVKDTEEEDFHVDQATEVK, V22A
MVH=87.0041
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 22206
GQTGALLQNTVESLSK, D9N
MVH=69.3809
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 70834
GVAGSSVAVLCPYNR, G5S
MVH=44.3977
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 79280
KFFGSLPDSWAR, S12R
MVH=51.2128
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 64491
KKPSEEEAAAAGGPPGPQVNLPVTDEVV V10A
MVH=53.5683
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 38569
KNPDSHYGELLEK, Q6H
MVH=50.7487
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 14789
KVLLDGVQNLR, P10L
MVH=52.2727
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 100826
LASDLLEWLQR, R10Q
MVH=58.9384
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 97540
LDSTDFTSTLK, G8S
MVH=45.0837
p-value=0.0001
sample: TCGA--AG--A02X--01A, spectrum: 16934
LFEEDPAVGALVLTGGDK, T11
MVH=75.6672
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 100953
LKQFQYFYVASTLQDLLR, A10S
MVH=55.7394
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 74099
LLNLADLVER, R4L
MVH=55.2092
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum 73974
LLNLADLVERDR, R4L
MVH=38.8073
p-value=0.0001
sample: TCGA–AG–A02X–01A, spectrum: 75926
LQQQHSEQPPLQPSPVTTR, M17T
MVH=34.4186
p–value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 80471
LSDLQEA LDQLNHVR, Y14H
MVH=56.8688
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 27879
LTLQALTEK, A2T
MVH=50.1725
p-value=0.0005
sample: TCGA-AG-A02X-01A, spectrum: 8112
MQYAPNTQVELLPQGR, H16R
MVH=51.8204
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 16888
NPLLDLAAYDQEGR, R3L
MVH=60.7245
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 39376
NTNSVPETAPAALPETR, K17R
MVH=33.9679
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 97030
NVSPVALPR, N3S
MVH=40.2386
p-value=0.0003
sample: TCGA-AG-A02X-01A, spectrum: 74266
SALSGHLETLLLGLLK, V10L
MVH=77.7679
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 17769
SELPLDPLPLPTEEGNPLLK, V10L
MVH=50.5822
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 24831
STESLQTVQR, A7T
MVH=42.1814
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 36781
TPVLFDVYELK, I7V
MVH=56.7842
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 43913
TVEDLDGLLQQL YR, H10Q
MVH=63.6746
p-value=0.0006
sample: TCGA-AG-A02X-01A, spectrum: 31855
TYGQVSGEALK, D2Y
MVH=49.2671
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 78188
WERPFEVKDTEEEDFHVDQATTVK, V20A
MVH=81.5592
p-value=0.0001
sample: TCGA-AG-A02X-01A, spectrum: 41851
YVSLLYTYNEAGKDDYVK, I2V
MVH=26.2766
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 50557
AAAAAAAPAAAAATAATTAATTAATAAAQ, P17A
MVH=43.3306
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 64582
AAAPAPVSEAVSR, C12S
MVH=66.3503
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 41539
AAPSVTLPSSSEELQANK, T2A
MVH=51.9578
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 106960
AARPPAASATPTAQPLQPAPR, T5P
MVH=59.4565
p-value=0.0001
sample: TCGA–AG–A032–01A, spectrum: 9084
AGVETTTPSK, K7T
MVH=53.5620
p–value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 31826
AHDGGGLYALSWPDSTR, H17R
MVH=40.0944
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 77033
APPRPGPVPEAAQPFLFTTR, P19T
MVH=61.1350
p-value=0.0001
sample: TCGA–AG–A032–01A, spectrum: 125755
ASSSLLLNESEPTTNLQLR, D8N
MVH=51.0206
p–value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 48884
AYVVLLR, E1A
MVH=45.4507
p-value=0.0084
sample: TCGA-AG-A032-01A, spectrum: 91846
DDDGTLLAACQVQPSATLDAAQPR, A5T
MVH=41.4971
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 115450
DGYGFLNR, N1D
MVH=42.0068
p-value=0.0006
sample: TCGA-AG-A032-01A, spectrum: 14314
DSKEPFSSVELQAALSK, E3K
MVH=52.3968
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 28880
DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK, A16V
MVH=98.4613
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 29879
DTEEEDFHVDQATTVK, V12A
MVH=31.8553
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 58933
DVPGFLQQSQSSGPGQPAVWHN11S
MVH=33.3945
p-value=0.0001

Intensity(%)
sample: TCGA-AG-A032-01A, spectrum: 99858
DVTVLQNTDGNNNDNWAK, E14D
MVH=67.0423
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 42906
EALDVLDAVLK, G7D
MVH=49.1254
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 74399
EHTLHLEAELEK, S4L
MVH=34.7998
p-value=0.0002
sample: TCGA-AG-A032-01A, spectrum: 23559
ELTVSNNDLEAGVHVLCQGLK, R15H
MVH=24.7084
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 56876
ELVDDSLNNVR, V7I
MVH=47.7825
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 13475
EPSAPSLPTPAYQSLPAGGHAPTPPTPAPR, S15L
MVH=50.4497
p-value=0.0001
sample: TCGA–AG–A032–01A, spectrum: 116969
EQPGSPEWLQLDK, Q13K
MVH=25.7008
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 5874
FFGSLPDSWAR, S11R
MVH=34.0237
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 76889
FGLQAQLVTTDFQK, M7L
MVH=61.9215
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 56631
FLDKLPQQTGDR, H12R
MVH=36.8344
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 66038
FLSGHTSELGNFR, D11N
MVH=43.3964
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 68665
FNLSQESSYLATQYSLRPR, S2N
MVH=33.5976
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 96751
FTVGDHSR, I3V
MVH=28.1894
p-value=0.0003
sample: TCGA-AG-A032-01A, spectrum: 68731
FVSSSSSGGYGGYGGVLTASDGLLAGNEK, A9G
MVH=58.0276
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 75082
FYLGGPTSVR, I9V
MVH=48.6920
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 108249
GKWERPFEVKDTTEEDFHVDQATTVK, V22A
MVH=92.8289
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 6007
GLLDDLLEER, V3I
MVH=44.4068
p-value=0.0038
sample: TCGA-AG-A032-01A, spectrum: 41594
GQTGALLQNTVESLSK, D9N
MVH=60.7285
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 22034
GVAGSSVAVLCPYNR, G5S
MVH=47.2841
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 76512
KAPPRPGPVPEAAQPFLLTTR, P20T
MVH=61.7666
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 93174
KKPSEEAAAAAGPPGPPQVNPLPVTDEVV:V10A
MVH=42.4612
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 64510
KNPDSHYGELLEK, Q6H
MVH=53.2957
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 81375
KNPLPPSAGVVDKK, V8A
MVH=51.6710
p-value=0.0001
sample: TCGA–AG–A032–01A, spectrum: 16063
LALSPNAQLLALASGSSLHYNTR, V9I
MVH=47.3112
p–value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 124494
LDSTDFTSTLK, G8S
MVH=45.0323
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 27901
LEGANVQEAQK, T4A
MVH=51.2796
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 32866
LFEEDPAVGALVLTGGDK, T1I
MVH=77.1711
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 16424
LLNLADLVER, R4L
MVH=50.2256
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 109868
LLSDLLPPSTGTFQEASQR, S5L
MVH=54.9867
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 103180
LSDLQEALDQALNHVR, Y14H
MVH=44.1639
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 15556
LYTLVTYVPVNTFK, T11N
MVH=62.9680
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 13297
MQYAPNTQVELLPQGR, H16R
MVH=52.8174
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 95313
NEDEDSPNKLYTLVTVYVPVNTFK, T20N
MVH=28.1391
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 107772
NLPSLAEQGASDPPTVASR, K7E
MVH=77.6069
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 65395
NTNSVPETAPAALPETR, K17R
MVH=43.0542
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 91544
RDDDGTLHAACQVQPSATLDAAQPR, A6T
MVH=61.6459
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 105813
RGDLFYTSK, E2G
MVH=37.9574
p-value=0.0001
sample: TCGA–AG–A032–01A, spectrum: 6635
RLEGLEGLGLR, G7E
MVH=45.6992
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 16381
SGGTLVVLGLGSEMTTVPDLLHAALR, N4T
MVH=37.8852
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 81521
SLNDLTAR, K8R
MVH=37.6594
p-value=0.0006
sample: TCGA-AG-A032-01A, spectrum: 55650
SLQEEQSRPTTAVSSPGGPAR, P10T
MVH=41.5741
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 50707
SLSLLDSPGLLSGEK, V4I
MVH=42.3932
p-value=0.0001
sample: TCGA–AG–A032–01A, spectrum: 55754
SPADPTDLGGQTSPR, I6T
MVH=63.0960
p–value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 90466
SPPGAAAPAAAKPPPLSAK, S8P
MVH=34.4764
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 69116
SSGGPGAGLCLFPLDEVHAK, K16E
MVH=31.8868
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 116118
TAASGVEASSRPLDHAQPPSSLVLDK, N9S
MVH=51.3048
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 116490
TAASGVEASSRPLDHAQPPSSLVLDESEVYK, N9S
MVH=81.3225
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 78472
TATESFASDPLLRYRPLAVALDTK, V16I
MVH=40.1278
p-value=0.0001
sample: TCGA–AG–A032–01A, spectrum: 69974
TVEDLDGLLQQYL, H10Q
MVH=62.7789
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 32149
TVVQLEGDNKLVTAFK, T14A
MVH=58.4310
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 53966
VPVTQATR, L3V
MVH=34.8150
p-value=0.0012
sample: TCGA-AG-A032-01A, spectrum: 95420
VQLPTESLQELLDLHR, T7S
MVH=30.7699
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 7058
VVLQPEALFSLYSK, F8L
MVH=57.0440
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 98594
YPVDTLPTSK, I3V
MVH=39.6834
p-value=0.0001
sample: TCGA-AG-A032-01A, spectrum: 58921
YVSLLYTNYEAGKDDYVK, I2V
MVH=29.9337
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 28927
AAAAAAAAAAPAAAATAATTAATTAATAAQ, P17A
MVH=41.5493
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 49013
AAAPAPVSEAVSR, C12S
MVH=50.2353
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 29082
AAPSVTLPSSSEELQANK, T2A
MVH=60.4910
p-value=0.0001

m/z

Intensity(%)
sample: TCGA–AG–A036–01A, spectrum: 8206
AGVETTTPSK, K7T
MVH=62.1209
p-value=0.0001
sample: TCGA–AG–A036–01A, spectrum: 103140
ASSSLLLNESEPTTNLQLR, D8N
MVH=51.7817
p–value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 75965
AVDVVLDCFLVK, A11V
MVH=61.6720
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 6745
AVPPNNSNAEDDLPTVELQGLVPR, V22L
MVH=28.3381
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 76139
CDPGALVPFSGAELELK, Y1C
MVH=64.9562
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 6701
DFYVVEPLAFEGTPEQK, I4V
MVH=42.1843
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 93837
DGYGFLNR, N1D
MVH=42.2916
p-value=0.0006
sample: TCGA-AG-A036-01A, spectrum: 37929
DLLQDPSLLGGTLSAYK, V3L
MVH=67.2065
p-value=0.0001
sample: TCGA–AG–A036–01A, spectrum: 26572
DTEEEDFHVDQATTVK, V12A
MVH=67.1985
p–value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 30393
EALDVLDAVLK, G7D
MVH=57.2812
p-value=0.0001
sample: TCGA−AG−A036−01A, spectrum: 66993
EELGHLQNDLTSLENDK, M10L
MVH=29.9813
p−value=0.0001
sample: TCGA–AG–A036–01A, spectrum: 50804
ENVATTDTLESTTVGSSV, T16S
MVH=71.1443
p−value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 95486
EQPGSPEWLQKLDK, Q13K
MVH=36.7726
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 42044
FLDKLPQQTGDR, H12R
MVH=52.4029
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 84362
FTVGDHSR, I3V
MVH=37.1010
p-value=0.0003
sample: TCGA-AG-A036-01A, spectrum: 50845
FYLGGPTSVR, I9V
MVH=41.1613
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 111935
GFGTDEQALLDCLGSCSNK, R16C
MVH=60.6646
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 92959
GLLVDTSR, I4V
MVH=35.5707
p-value=0.0012
sample: TCGA–AG–A036–01A, spectrum: 88836
GTDECALESVAVAATPLPK, I10V
MVH=60.4826
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 30127
GVETLANDVVSLAAK, T14A
MVH=73.9952
p-value=0.0001
sample: TCGA–AG–A036–01A, spectrum: 50501
KENVATTDLESTTVGSSV, T17S
MVH=62.7434
p–value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 74284
KKPSEEAAAAGGPPPPQVNPLPVTDEVV, V10A
MVH=41.1077
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 66414
LCASGAGATADTALEELKEK, P10A
MVH=32.8421
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 101842
LDSTDFTSTLK, G8S
MVH=51.2206
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 66149
LDVDKDGFVTEGELK, A3V
MVH=52.0366
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 21630
LFEEDPAVGALVLTGGDK, T1I
MVH=87.0980
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 30623
LFSLLSTALLR, V8A
MVH=39.8941
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 14901
LLNLADLVER, R4L
MVH=59.6594
p-value=0.0001
sample: TCGA–AG–A036–01A, spectrum: 4544
MQYAPNTQVELLPQGR, H16R
MVH=58.9518
p-value=0.0001
sample: TCGA–AG–A036–01A, spectrum: 10536
MVAVGLCR, H8R
MVH=34.3603
p-value=0.0006
sample: TCGA-AG-A036-01A, spectrum: 45205
NLSLSGHVGFDSDLPDKLVNK, Q16K
MVH=35.5044
p-value=0.0001
sample: TCGA–AG–A036–01A, spectrum: 21572
NPLLDLAYDQEGR, R3L
MVH=61.0914
p–value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 49796
NTNSVPETAPAALPETR, K17R
MVH=52.5853
p-value=0.0001
Sample: TCGA-AG-A036-01A, spectrum: 104112
SAVGELSEDSSNVVHLKK, Q15H
MVH=35.3531
p-value=0.0001
sample: TCGA–AG–A036–01A, spectrum: 95954
SEALPTDLPTPSAPDLTEPK, A10T
MVH=43.9231
p–value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 52544
SGTPQSLPFAAR, R7S
MVH=33.3407
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 71500
SPPGAAAPAAAKPPPLSAK, S8P
MVH=34.2240
p-value=0.0002
sample: TCGA-AG-A036-01A, spectrum: 53134
TLAQLNPESSLFLTASK, I14T
MVH=70.1923
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 66350
TLEGLQVEEEPVYK, E14K
MVH=52.4846
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 63725
TTPLEAASSGAR, T11A
MVH=59.5418
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 101709
VALSSQTEVALAR, E6Q
MVH=60.0819
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 39387
VPVTQATR, L3V
MVH=45.4814
p-value=0.0012
sample: TCGA-AG-A036-01A, spectrum: 42815
YGLLVGGAVSHR, A9V
MVH=63.7261
p-value=0.0001
sample: TCGA-AG-A036-01A, spectrum: 44126
YVSLLYTNYEAGKDDYVK, I2V
MVH=32.1887
p-value=0.0001