QAGSVGGFQWCGEPK 57.02200@C11,144.10207@K15,144.10207@Q1, 3+
m= 1894.9245, matched intensity=69.1%, largest gap=1, sum gaps=1, gap at F8=0
H20120525_JQ_CPTAC2_Compref4_protfxn05, scan:21325

QAIDDDCNQTGQMTAGFLDWPQGTFASQVMLEGDK 57.02200@C7,144.10207@K35,144.10207@Q1, 3+
m= 4161.8967, matched intensity=87.1%, largest gap=2, sum gaps=5, gap at M30=0
H20130119_PM_CompRef_BC1_proteome_fxn15, scan:41222

QATSDVQESTQESATVEK 144.10207@K18,144.10207@Q1, 3+
m= 2225.0903, matched intensity=81.2%, largest gap=0, sum gaps=0, gap at T15=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f06, scan:9211

QDIQSDGFSIETCK 57.02200@C13,144.10207@K14,144.10207@Q1, 2+
m= 1914.9242, matched intensity=84.9%, largest gap=0, sum gaps=0, gap at Q4=0
H20120525_JQ_CPTAC2_Compref4_protfxn16, scan:18374

QDSDALPSPELLPQDQDKPFLR 144.10207@K18,144.10207@Q1,79.96633@S8, 3+
m= 2876.4201, matched intensity=65.1%, largest gap=2, sum gaps=6, gap at Q16=1
CPTAC_CompREF_00_iTRAQ_NiNTA_03b_26Mar12_Lynx_12-02-29, scan:23168

QEEDNTQSDDILEESDQPTQESK 144.10207@K23,144.10207@Q1, 3+
m= 2952.3200, matched intensity=82.3%, largest gap=0, sum gaps=0, gap at E21=0
CompRef_P5-91_P6-74_P5-100_P6-108_W_BI_20131004_fA, scan:14085

QEELEAALQRAK 144.10207@K12,144.10207@Q1, 3+
m= 1672.9352, matched intensity=72.1%, largest gap=0, sum gaps=0, gap at A11=0
CompRef_P32_P33_iTRAQ_18_121206, scan:6497

QEVWLANGAAESWGLR 144.10207@Q1, 2+
m= 1929.9819, matched intensity=68.4%, largest gap=1, sum gaps=3, gap at W13=1
H20130119_PM_CompRef_BC1_proteome_fxn18, scan:32049

QGAACNVLFINSVDMESLTGPQAISK 57.02200@C5,144.10207@K26,144.10207@Q1, 3+
m= 3037.5462, matched intensity=87.2%, largest gap=1, sum gaps=1, gap at I10=0
CompRef_2A_P5-29_P5-61_P6-34_P6-38_W_BI_20130502_H-JQ_f22, scan:34758


QITLHALSLVGEK 144.10207@K13,144.10207@Q1, 3+
m= 1696.0127, matched intensity=72.2%, largest gap=0, sum gaps=0, gap at T3=0
H20120605_JQ_CPTAC2_Compref4_protfxn24, scan:23541
Intensity
m/z
0
500000
1000000
1500000
2000000
200
300
400
500
600
700
800
900
1000
Q I T L H A L S L V G E K
b1
y1
y5+2
b2o
b5+2
b2
y2o
b6+2
y2
b7+2
b3o
y3
b3
b8*+2
b8o+2
b8+2
b9+2
b9o+2
[M+H]+3
y4
b4*
b4o
b4
y5
b5
y6
b7i
y7
y8

QIVGYVIGTQQATPGPANSGR 144.10207@Q1, 3+
m= 2257.1937, matched intensity=72.8%, largest gap=1, sum gaps=1, gap at V6=0
G20120208_PM_CompRef1_SCX_proteome_fxn03, scan:20085


QLLNLWISDTISSTEPPSK 144.10207@K19,144.10207@Q1, 3+
m= 2416.3093, matched intensity=81.4%, largest gap=0, sum gaps=0, gap at I11=0
H20120525_JQ_CPTAC2_Compref4_protfxn04, scan:35586
Q L L N L W I S D T I S S T E P P S K
Intensity
1600000
1400000
1200000
1000000
800000
600000
400000
200000
0
m/z
200
400
600
800
1000
1200
y3+2
b1
y4+2
y1
y2o
y2
b2
y6+2
y6o
y3
b3
b7+2
y4o
b8+2
y4
b4
b10o+2
b10+2
y5o
y5
y5
b5
y6
y7
b6
y8
b7
b8
b9
b10o
b10

QLQEETPSGGPLTEALPPARK 144.10207@K21,144.10207@Q1, 3+
m= 2506.3635, matched intensity=86.6%, largest gap=2, sum gaps=3, gap at S8=1
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f01, scan:18537

QQHEGAQGTLDSGEPPQCR 57.02200@C18,144.10207@Q1, 3+
m= 2238.0211, matched intensity=87.6%, largest gap=1, sum gaps=1, gap at T9=0
CPTAC_CompRef_00_iTRAQ_18_2Feb12_Cougar_11-10-11, scan:2057

QQPNPGSELCYK 57.02200@C10,144.10207@K12,144.10207@Q1, 2+
m= 1707.8499, matched intensity=51.2%, largest gap=0, sum gaps=0, gap at S7=0
CPTAC_CompRef_00_iTRAQ_01_2Feb12_Cougar_11-10-09, scan:5306

QQQAAVSNK 144.10207@K9,144.10207@Q1, 2+
m= 1260.7030, matched intensity=70.8%, largest gap=0, sum gaps=0, gap at N8=0
H20130119_PM_CompRef_BC1_proteome_fxn10, scan:2872

QQQDYWLMDVR 144.10207@Q1, 2+
m= 1624.7790, matched intensity=68.1%, largest gap=0, sum gaps=0, gap at M8=0
CPTAC_CompRef_test_X_iTRAQ_22_10Jan13_Lynx_12-11-08, scan:8506

QRAQEALLQLSQALSLMETVK 144.10207@K21,144.10207@Q1, 3+
m= 2644.4826, matched intensity=89.3%, largest gap=2, sum gaps=2, gap at A13=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f10, scan:40361

QSAAELDLVLQR 144.10207@Q1, 2+
m= 1485.8273, matched intensity=56.8%, largest gap=0, sum gaps=0, gap at S2=0
H20120525_JQ_CPTAC2_Compref4_protfxn01, scan:23441

QSPGLANELLKEYLVTLAK 144.10207@K11,144.10207@K19,144.10207@Q1, 3+
m= 2518.4736, matched intensity=83.8%, largest gap=2, sum gaps=3, gap at L5=2
H20120525_JQ_CPTAC2_Compref4_protfxn06, scan:36071

QSSQDDELK 144.10207@K9,144.10207@Q1, 2+
m= 1336.6714, matched intensity=83.0%, largest gap=0, sum gaps=0, gap at D6=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f04, scan:4608


QSSQDDELKSSMLK 144.10207@K9,144.10207@K14,144.10207@Q1, 3+
m= 2027.0571, matched intensity=85.0%, largest gap=0, sum gaps=0, gap at D6=0
H20120525_JQ_CPTAC2_Compref4_protfxn15, scan:13294

QTFIDNTDSVVK 144.10207@K12,144.10207@Q1, 2+
m= 1653.8818, matched intensity=84.6%, largest gap=0, sum gaps=0, gap at V10=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f21, scan:17737

QVTSSGVSYGGTVSLQDAVTR 144.10207@Q1, 3+
m= 2255.1515, matched intensity=60.9%, largest gap=1, sum gaps=1, gap at Y9=0
TCGA_CompRef_W_PNNL_B2S7_f18, scan:7147

QVVECVGNQMGVGK 57.02200@C5,144.10207@K14,144.10207@Q1, 3+
m= 1791.9221, matched intensity=64.9%, largest gap=0, sum gaps=0, gap at C5=0
H20120525_JQ_CPTAC2_Compref4_protfxn04, scan:17466

QYAPNTQVEILPQGR 144.10207@Q1, 2+
m= 1856.9867, matched intensity=84.7%, largest gap=0, sum gaps=0, gap at R15=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f05, scan:20554

RDDDGTLHAACQVQPSATLDAAQPR 57.02200@C11,144.10207@R1, 3+
m= 2836.3649, matched intensity=79.2%, largest gap=2, sum gaps=4, gap at T6=1
cptac_p5p6_w_pool_jhu_05172013_f1, scan:6284


RDDKIDKPSLLTMMK 144.10207@K4,144.10207@K7,144.10207@K15,144.10207@R1, 3+
m= 2366.3513, matched intensity=91.2%, largest gap=1, sum gaps=1, gap at D6=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f16, scan:18832

REEMEQLFHDDQGSVTR 144.10207@R1, 3+
m= 2220.0351, matched intensity=55.0%, largest gap=2, sum gaps=5, gap at S14=2
cptac_p32p33_global_itraq4_trypticpep_fraction_02, scan:6266

REPITLQDPAAK 144.10207@K12,144.10207@R1, 3+
m= 1625.9345, matched intensity=59.5%, largest gap=1, sum gaps=1, gap at A10=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f19, scan:12542

REVGTSDKEILTSR 144.10207@K8,144.10207@R1, 3+
m= 1878.0414, matched intensity=84.5%, largest gap=2, sum gaps=2, gap at V3=0
CPTAC_CompRef_test_X_iTRAQ_06_7Jan13_Lynx_12-11-07, scan:1701

RGTDECAIESVAVAATPIPK 57.02200@C6,144.10207@K20,144.10207@R1, 3+
m= 2372.2619, matched intensity=94.4%, largest gap=1, sum gaps=2, gap at V11=0
H20130119_PM_CompRef_BC1_proteome_fxn02, scan:24037

RLAAETGEGEGEPLSR 144.10207@R1, 3+
m= 1814.9244, matched intensity=75.7%, largest gap=2, sum gaps=2, gap at A4=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f09, scan:10329

RLEGILEGLGLR 144.10207@R1, 3+
m= 1468.8848, matched intensity=69.4%, largest gap=1, sum gaps=1, gap at E7=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f11, scan:29269

RLLNLPGYLQK 144.10207@K11,144.10207@R1, 3+
m= 1601.9861, matched intensity=66.1%, largest gap=0, sum gaps=0, gap at L3=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f08, scan:23569

RLMDEAMILK 144.10207@K10,144.10207@R1, 3+
m= 1506.8506, matched intensity=77.6%, largest gap=0, sum gaps=0, gap at M7=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f09, scan:21350

RNTNSVPETAPAAIPETR 144.10207@R1, 3+
m= 2067.0831, matched intensity=72.2%, largest gap=1, sum gaps=3, gap at R18=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f18, scan:10793

RPEGACGDGQSSK 57.02200@C6,144.10207@K13,144.10207@R1, 3+
m= 1635.7884, matched intensity=50.2%, largest gap=1, sum gaps=2, gap at K13=0
H20120525_JQ_CPTAC2_Compref4_protfxn05, scan:3268

RPEGPGAQAPR 144.10207@R1, 3+
m= 1278.6915, matched intensity=58.7%, largest gap=1, sum gaps=1, gap at R11=0
cptac_p5p6_w_itraq4_jhu_04292013_f12, scan:2271

RPQVTLLDPSEK 144.10207@K12,144.10207@R1, 3+
m= 1669.9607, matched intensity=69.2%, largest gap=1, sum gaps=1, gap at S10=0
cptac_p5p6_w_itraq4_jhu_04292013_f10, scan:6902

RQDIQSDGFSIETCK 57.02200@C14,144.10207@K15,144.10207@R1, 3+
m= 2071.0253, matched intensity=75.6%, largest gap=0, sum gaps=0, gap at Q5=0
cptac_p32p33_global_itraq4_trypticpep_fraction_06, scan:5681

RQDYQEILDSPIK 144.10207@K13,144.10207@R1,79.96633@S10, 3+
m= 1971.9911, matched intensity=64.5%, largest gap=1, sum gaps=1, gap at R1=1
CPTAC_CompREF_00_iTRAQ_NiNTA_05b_26Mar12_Lynx_12-02-31, scan:14416

RREPITLQDPAAK 144.10207@K13,144.10207@R1, 3+
m= 1782.0356, matched intensity=81.1%, largest gap=1, sum gaps=1, gap at A11=0
CompRef_2A_P5-29_P5-61_P6-34_P6-38_W_BI_20130502_H-JQ_f21, scan:8502


RTSDPALCPLIVSAAADSAVR 57.02200@C8,144.10207@R1, 3+
m= 2313.2238, matched intensity=67.8%, largest gap=2, sum gaps=4, gap at P9=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f12, scan:25934

RYEEEEEEEEEDEEEMEEEK 144.10207@K19,144.10207@R1, 3+
m= 2806.1378, matched intensity=64.0%, largest gap=2, sum gaps=2, gap at K19=0
CompRef_2A_P5-29_P5-61_P6-34_P6-38_W_BI_20130502_H-JQ_fA, scan:10885

RYNDLLASAK 144.10207@K10,144.10207@R1, 3+
m= 1437.8184, matched intensity=80.0%, largest gap=0, sum gaps=0, gap at R1=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f07, scan:12683

SAAEIVQEIENIEK 144.10207@K14,144.10207@S1, 3+
m= 1860.0084, matched intensity=84.8%, largest gap=0, sum gaps=0, gap at Q7=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f24, scan:32360

SAASCAPISLPAAASR 57.02200@C5,144.10207@S1, 3+
m= 1672.8694, matched intensity=59.4%, largest gap=0, sum gaps=0, gap at A6=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f09, scan:19382

SADFEGLYQE 144.10207@S1, 2+
m= 1301.5898, matched intensity=62.1%, largest gap=0, sum gaps=0, gap at D3=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f13, scan:21600

SAEVIAQSR 144.10207@S1, 2+
m= 1103.6057, matched intensity=58.5%, largest gap=0, sum gaps=0, gap at S8=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f16, scan:6261

SAGLAPDCEASATAETTVSSVGTCEAAAK 57.02200@C8,57.02200@C24,144.10207@K29,144.10207@S1, 3+
m= 3099.4591, matched intensity=78.0%, largest gap=1, sum gaps=3, gap at A28=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_P_BI_20130510_H-JQ_f06, scan:19325

SAPEVTAPGAPAYCVLMEQLTSVSEELDVR 57.02200@C14,144.10207@S1, 3+
m= 3362.6501, matched intensity=79.1%, largest gap=2, sum gaps=6, gap at C14=1
TCGA_CompRef_W_PNNL_B2S7_f17, scan:15835


SCEESADAPVDQNSVVIPAAAK 57.02200@C2,144.10207@K22,144.10207@S1, 3+
m= 2545.2579, matched intensity=81.4%, largest gap=0, sum gaps=0, gap at C2=0
CPTAC_CompRef_test_X_iTRAQ_02_10Jan13_Lynx_12-11-07, scan:4499
S C E E S A D A P V D Q N S V V I P A A A K
Intensity
m/z
0
5000
10000
15000
20000
25000
30000
35000
40000
200
400
600
800
1000
1200
1400
b1
y1
y5+2
y2
b2
y3
b7+2
b8+2
y4
b3
b9o+2
b9+2
y5o
y5
b4
y6
b5
b6o
y7
b14+2
b7o
b7
y8
b8o
b8
y9
b9
y10
b10
b11
b12


SDEEGQAPR 144.10207@S1, 2+
m= 1131.5278, matched intensity=68.0%, largest gap=0, sum gaps=0, gap at P8=0
H20120605_JQ_CPTAC2_Compref4_protfxnA, scan:2915
Intensity
m/z
0
50000
100000
150000
200000
250000
200
300
400
500
600
700
800
900
1000
S D E E G Q A P R
[M+H]+2
[M+H-iTRAQ]+1
[M+H-NH3]+2
[M+H-H2O]+2
b1
y2*
y2
b2
b3
y5
b4
y6
b5
y7
b6
b7
y8

SDINVTVLIGCK 57.02200@C11,144.10207@K12,144.10207@S1, 3+
m= 1605.9009, matched intensity=84.1%, largest gap=0, sum gaps=0, gap at C11=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f15, scan:26448

SDQSCEIMLNHLATAR 57.02200@C5,144.10207@S1, 3+
m= 1988.9535, matched intensity=50.6%, largest gap=0, sum gaps=0, gap at S1=0
CompRef_P5-91_P6-74_P5-100_P6-108_W_BI_20131004_f07, scan:20682

SDSELNNEVAAR 144.10207@S1, 2+
m= 1447.7025, matched intensity=85.9%, largest gap=0, sum gaps=0, gap at N7=0
cptac_p5p6_w_pool_jhu_05172013_f6, scan:2819

SDSELNNEVAARK 144.10207@K13,144.10207@S1, 3+
m= 1719.8995, matched intensity=81.8%, largest gap=1, sum gaps=1, gap at N7=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f12, scan:7611

 
SDVSENLCTPQQSR 57.02200@C8,144.10207@S1, 2+
m= 1763.8236, matched intensity=87.7%, largest gap=0, sum gaps=0, gap at V3=0
H20130119_PM_CompRef_BC1_proteome_fxn14, scan:10369

SEALPTDLPTPSAPDLTEPK 144.10207@K20,144.10207@S1, 3+
m= 2366.2461, matched intensity=68.5%, largest gap=1, sum gaps=4, gap at T10=1
TCGA_CompRef_W_PNNL_B1S7_f14, scan:7494

SEANDQGPPREDGVTR 144.10207@S1, 3+
m= 1870.8891, matched intensity=92.7%, largest gap=0, sum gaps=0, gap at R10=0
A120511_CotterR_TS_fraction4, scan:1540

SEDYEQAAAHIHR 144.10207@S1, 3+
m= 1669.7930, matched intensity=68.7%, largest gap=0, sum gaps=0, gap at I11=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f14, scan:8905

SEESSHCSTEK 57.02200@C7,144.10207@K11,144.10207@S1, 2+
m= 1567.7033, matched intensity=84.8%, largest gap=0, sum gaps=0, gap at C7=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f04, scan:2543

SEIPLQEQNYPAVD 144.10207@S1, 2+
m= 1745.8594, matched intensity=55.7%, largest gap=1, sum gaps=1, gap at P11=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f14, scan:24205

SELLLLACVHNYQPCVQR 57.02200@C8,57.02200@C15,144.10207@S1, 3+
m= 2343.1960, matched intensity=66.8%, largest gap=2, sum gaps=2, gap at E2=0
CPTAC_CompRef_test_X_iTRAQ_02_10Jan13_Lynx_12-11-07, scan:9521
S E L L L L A C V H N Y Q P C V Q R
Intensity
m/z
0
10000
20000
30000
40000
50000
200
400
600
800
1000
1200
1400
1600
b1
y2
b5i
y5i+2
b2
b6+2
b4i
b3
b4
y9*+2
y9+2
b10+2
y5+3
y10*+2
y5
b11+2
b5
y6*
[M+H]+3
y6
b6
y13+2
b7
y7
b8*
y8
[M+H-iTRAQ]+2
y9
y10
y11
y12

SELSGNFEQVIVGMMMPTVLYDVQELR 144.10207@S1, 3+
m= 3228.5991, matched intensity=74.7%, largest gap=2, sum gaps=3, gap at M16=0
CPTAC_CompRef_00_iTRAQ_15_2Feb12_Cougar_11-10-09, scan:16452

SFGVLAPGK 144.10207@K9,144.10207@S1, 2+
m= 1162.6954, matched intensity=73.5%, largest gap=0, sum gaps=0, gap at L5=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f14, scan:17765

SFQGPVLIGSSHGGVNIEDVAAETPEAIIK 144.10207@K30,144.10207@S1, 3+
m= 3322.7653, matched intensity=84.5%, largest gap=1, sum gaps=4, gap at T24=0
cptac_p32p33_global_itraq4_trypticpep_fraction_01, scan:13052

SFSQGPIGGANR 144.10207@S1, 2+
m= 1333.6861, matched intensity=71.1%, largest gap=0, sum gaps=0, gap at S3=0
CPTAC_CompRef_test_iTRAQ_12_PD_7Jan13_Lynx_12-11-08, scan:2234

SFTFVQAGQDLEENMDEDISEK 144.10207@K22,144.10207@S1, 3+
m= 2819.3051, matched intensity=81.3%, largest gap=0, sum gaps=0, gap at F2=0
CPTAC_CompRef_test_iTRAQ_13_PD_7Jan13_Lynx_12-11-08, scan:11395

SGAHVVVTGPPNAGK 144.10207@K15,144.10207@S1, 3+
m= 1677.9406, matched intensity=89.2%, largest gap=2, sum gaps=3, gap at A3=2
TCGA_CompRef_W_PNNL_B2S7_f09, scan:2530

SGGKDVSAQATGK 144.10207@K4,144.10207@K13,144.10207@S1, 2+
m= 1636.9110, matched intensity=84.2%, largest gap=1, sum gaps=1, gap at S1=0
cptac_p32p33_global_itraq4_trypticpep_fraction_22, scan:1535

SGMSLTQDMLNGELK 144.10207@K15,144.10207@S1, 2+
m= 1910.9685, matched intensity=57.5%, largest gap=0, sum gaps=0, gap at G2=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f06, scan:27518

SGTPQLSLPFAAR 144.10207@S1, 2+
m= 1487.8218, matched intensity=77.8%, largest gap=1, sum gaps=1, gap at S7=0
H20120525_JQ_CPTAC2_Compref4_protfxn03, scan:26822

SHAVGPQEIQER 144.10207@S1, 3+
m= 1493.7708, matched intensity=57.0%, largest gap=1, sum gaps=1, gap at Q10=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f11, scan:5682

SHIAEGPADLEDPLNPK 144.10207@K17,144.10207@S1, 3+

m= 2090.0888, matched intensity=69.6%, largest gap=0, sum gaps=0, gap at L14=0

CompRef_2A_P5-29_P5-61_P6-34_P6-38_W_BI_20130502_H-JQ_f15, scan:19602

SHIYFWTLDGGSLSK 144.10207@K15,144.10207@S1, 3+
m= 1998.0455, matched intensity=76.1%, largest gap=0, sum gaps=0, gap at D9=0
CompRef_P5-91_P6-74_P5-100_P6-108_W_BI_20131004_f03, scan:28040

SIAASVDVSAPK 144.10207@K12,144.10207@S1, 2+
m= 1431.8177, matched intensity=85.6%, largest gap=0, sum gaps=0, gap at A3=0
cptac_p5p6_w_itraq4_jhu_04292013_f7, scan:6730

SIAIGSQPLLTVGTTHISK 144.10207@K19,144.10207@S1, 3+
m= 2210.2878, matched intensity=80.6%, largest gap=0, sum gaps=0, gap at L9=0
CompRef_2A_P5-29_P5-61_P6-34_P6-38_W_BI_20130502_H-JQ_f01, scan:26473

SIDPGLKEDTLEFLIK 144.10207@K7,144.10207@K16,144.10207@S1, 3+
m= 2249.2884, matched intensity=83.1%, largest gap=0, sum gaps=0, gap at E12=0
cptac_p5p6_w_itraq4_jhu_04292013_f22, scan:16297

SIPPEGLVQSELMR 144.10207@S1, 3+
m= 1698.9096, matched intensity=57.5%, largest gap=0, sum gaps=0, gap at V8=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f06, scan:27124

SIPQPHQLLGR 144.10207@S1,79.96633@S1, 3+
m= 1324.6653, matched intensity=57.3%, largest gap=0, sum gaps=0, gap at L8=0
H20120518_JQ_CPTAC2_COMPREF4_IMAC_09, scan:16344

SISELSDQDKQEK 144.10207@K10,144.10207@K13,144.10207@S1, 3+
m= 1938.0271, matched intensity=73.4%, largest gap=1, sum gaps=1, gap at D9=0
H20120525_JQ_CPTAC2_Compref4_protfxn10, scan:10190

SISTPYSCAMHLSEWYCR 57.02200@C8,57.02200@C17,144.10207@S1, 3+
m= 2391.0579, matched intensity=83.2%, largest gap=0, sum gaps=0, gap at S1=0
cptac_p32p33_global_itraq4_trypticpep_fraction_18, scan:10756

SKVEETTEHFVTK 144.10207@K2,144.10207@K13,144.10207@S1, 3+
m= 1966.0737, matched intensity=88.7%, largest gap=1, sum gaps=1, gap at F10=0
H20120525_JQ_CPTAC2_Compref4_protfxn19, scan:12320

SKVPVLDEGLTSVETYIPAIR 144.10207@K2,144.10207@S1, 3+
m= 2574.4513, matched intensity=80.2%, largest gap=2, sum gaps=3, gap at I17=0
cptac_p5p6_w_itraq4_jhu_04292013_f11, scan:16736

SLAVLQLYINK 144.10207@K11,144.10207@S1, 3+
m= 1548.9483, matched intensity=66.6%, largest gap=0, sum gaps=0, gap at V4=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f10, scan:31151

SLDLDDWPIELIK 144.10207@K13,144.10207@S1, 3+
m= 1844.0175, matched intensity=70.8%, largest gap=0, sum gaps=0, gap at I9=0
CompRef_2A_P5-29_P5-61_P6-34_P6-38_W_BI_20130502_H-JQ_f14, scan:40700

SLDNKGDTDGEDQVCVSK 57.02200@C15,144.10207@K5,144.10207@K18,144.10207@S1, 3+
m= 2398.1653, matched intensity=92.6%, largest gap=1, sum gaps=2, gap at K18=0
H20120525_JQ_CPTAC2_Compref4_protfxn08, scan:11469

SLDVLGWEER 144.10207@S1, 2+
m= 1346.6952, matched intensity=81.4%, largest gap=0, sum gaps=0, gap at V4=0
H20130119_PM_CompRef_BC1_proteome_fxn06, scan:29332

SLETEILESLR 144.10207@S1, 2+
m= 1432.7895, matched intensity=76.7%, largest gap=0, sum gaps=0, gap at R11=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f05, scan:32781

SLGNIIMVCR 57.02200@C9,144.10207@S1, 2+
m= 1305.7024, matched intensity=60.6%, largest gap=0, sum gaps=0, gap at I5=0
CompRef_P5-91_P6-74_P5-100_P6-108_W_BI_20131004_f24, scan:24117

SLKEESIEAVK 144.10207@K3,144.10207@K11,144.10207@S1, 2+
m= 1663.9722, matched intensity=84.8%, largest gap=0, sum gaps=0, gap at I7=0
H20120525_JQ_CPTAC2_Compref4_protfxn16, scan:13863

SLPEETVDFMVQHTSFK 144.10207@K17,144.10207@S1, 3+
m= 2282.1497, matched intensity=70.8%, largest gap=1, sum gaps=1, gap at M10=0
cptac_p32p33_global_itraq4_trypticpep_fraction_07, scan:12876

SLQAEPWFFGAIR 144.10207@S1, 3+
m= 1664.8797, matched intensity=68.1%, largest gap=0, sum gaps=0, gap at R13=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f07, scan:35660

SLQEEQSRPTTAVSSPGGPAR 144.10207@S1, 3+
m= 2298.1686, matched intensity=87.0%, largest gap=1, sum gaps=3, gap at T10=0
CPTAC_CompRef_test_iTRAQ_19_PD_10Jan13_Lynx_12-11-08, scan:1592

SLQSPQEQIILAPSLAK 144.10207@K17,144.10207@S1, 3+
m= 2110.2242, matched intensity=71.3%, largest gap=1, sum gaps=1, gap at Q3=0
CompRef_P5-25_P5-19_P6-85_P6-58_W_BI_20130717_f14, scan:28272

SLQTISSWFK 144.10207@K10,144.10207@S1, 3+
m= 1483.8279, matched intensity=76.7%, largest gap=0, sum gaps=0, gap at S6=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f09, scan:29836

SLTEEMALGEPAAAAAALLGGEEI 144.10207@S1, 3+
m= 2457.2431, matched intensity=69.3%, largest gap=2, sum gaps=4, gap at G9=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f10, scan:40947

SLVQESLSTNSSDLVAPSPDAFR 144.10207@S1,79.96633@S18, 3+
m= 2643.2551, matched intensity=72.6%, largest gap=1, sum gaps=4, gap at E5=0
CPTAC_CompREF_00_iTRAQ_NiNTA_09b_26Mar12_Lynx_12-02-31, scan:19335

SMQDVVEDFKNKYEDEINR 144.10207@K10,144.10207@K12,144.10207@S1, 3+
m= 2790.3860, matched intensity=88.2%, largest gap=0, sum gaps=0, gap at R19=0
TCGA_CompRef_W_PNNL_B2S7_f23, scan:11285

SNFLVVCYLHDVK 57.02200@C7,144.10207@K13,144.10207@S1, 3+
m= 1881.0068, matched intensity=79.1%, largest gap=0, sum gaps=0, gap at V6=0
cptac_p32p33_global_itraq4_trypticpep_fraction_17, scan:10583

SPADPTDLGGQTSPR 144.10207@S1, 2+
m= 1641.8080, matched intensity=79.6%, largest gap=0, sum gaps=0, gap at T6=0
cptac_p5p6_w_pool_jhu_05172013_f16, scan:5147

SPAINLMGFNVEEMCEAHAWIQR 57.02200@C15,144.10207@S1, 3+
m= 2846.3430, matched intensity=68.3%, largest gap=0, sum gaps=0, gap at C15=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f02, scan:34308


SPAPGMALGSGR 144.10207@S1, 2+
m= 1243.6465, matched intensity=79.0%, largest gap=0, sum gaps=0, gap at P2=0
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f02, scan:10696
Intensity
m/z
0
200000
400000
600000
800000
1000000
1200000
1400000
200
400
600
800
1000
S P A P G M A L G S G R
y2*
b2
b1
y1
y3*
y3
y4*
y4
b3
y5*
y5
y6*
b5
y6
[M+H-NH3]+2
[M+H]+2
b6
y7
y8
b7
y9*
y9
y10
b10*
b10
y10
b11
[M+H-iTRAQ]+1

 
SPAPGMALGSGRR 144.10207@S1, 3+
m= 1399.7476, matched intensity=63.8%, largest gap=2, sum gaps=2, gap at P2=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f07, scan:8005

SPLYSVEFSEEPFGVIVHR 144.10207@S1, 3+
m= 2335.1970, matched intensity=79.9%, largest gap=0, sum gaps=0, gap at H18=0
CPTAC_CompRef_test_iTRAQ_14_PD_7Jan13_Lynx_12-11-08, scan:11246

SPPGAAAPAAAKPPPLSAK 144.10207@K12,144.10207@K19,144.10207@S1, 3+
m= 2130.2527, matched intensity=58.3%, largest gap=1, sum gaps=3, gap at P8=1
CompRef_P5-65_P6-20_P5-71_P6-62_W_BI_20131120_f06, scan:13895

SQDKDVSEGETSDGVR 144.10207@K4,144.10207@S1, 3+
m= 1995.9589, matched intensity=60.9%, largest gap=2, sum gaps=4, gap at S7=0
cptac_p5p6_w_pool_jhu_05172013_f4, scan:2256

SQNKEDYDGLK 144.10207@K4,144.10207@K11,144.10207@S1, 2+
m= 1727.9056, matched intensity=87.5%, largest gap=0, sum gaps=0, gap at D8=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f12, scan:6536

SQNKEDYDGLKEEFRK 144.10207@K4,144.10207@K11,144.10207@K16,144.10207@S1, 3+
m= 2561.3573, matched intensity=87.6%, largest gap=1, sum gaps=2, gap at D8=1
cptac_p5p6_w_itraq4_jhu_04292013_f4, scan:5181

SQPAASTLESESVQR 144.10207@S1, 2+
m= 1732.8713, matched intensity=75.5%, largest gap=0, sum gaps=0, gap at E11=0
CPTAC_CompRef_00_iTRAQ_20_2Feb12_Cougar_11-10-11, scan:4235

SRLELELQIR 144.10207@S1, 3+

m= 1399.8269, matched intensity=82.3%, largest gap=0, sum gaps=0, gap at I9=0

H20120525_JQ_CPTAC2_Compref4_protfxn10, scan:21813

SSAEVIAQSR 144.10207@S1, 2+
m= 1190.6377, matched intensity=77.4%, largest gap=0, sum gaps=0, gap at S9=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f15, scan:6108

SSEEAGFPGDPHEDKQ 144.10207@K15,144.10207@S1, 3+
m= 2016.9269, matched intensity=55.9%, largest gap=1, sum gaps=2, gap at S2=1
cptac_p5p6_w_itraq4_jhu_04292013_f6, scan:3774


SSFYSLTSSNVSK 144.10207@K13,144.10207@S1, 2+
m= 1693.8767, matched intensity=66.8%, largest gap=0, sum gaps=0, gap at V11=0
TCGA_CompRef_W_PNNL_B2S7_f04, scan:7049
S S F Y S L T S S N V S K
Intensity
25000
20000
15000
10000
5000
0
200
400
600
800
1000
1200
1400
m/z
b1o
b1
y1
b2o
b2
y2o
y2
b3*
b3
b3o
y3o
b3
y3
y4*
y4
b4
y5
b5*
b5o
b5
y6*
y6
b6o
b6
y7o
y7
y8
y9
y10

SSGIWENGGGPTPATPESFSK 144.10207@K21,144.10207@S1, 3+
m= 2393.1743, matched intensity=66.9%, largest gap=1, sum gaps=2, gap at G9=0
H20130119_PM_CompRef_BC1_proteome_fxn05, scan:24521

SSHSQLDLFDDVGTFASGPPK 144.10207@K21,144.10207@S1, 3+
m= 2492.2427, matched intensity=85.3%, largest gap=2, sum gaps=2, gap at H3=2
cptac_p32p33_global_itraq4_trypticpep_fraction_22, scan:11184

SSKPSDMSVQVCGYISK 57.02200@C12,144.10207@K3,144.10207@K17,144.10207@S1, 3+
m= 2304.1825, matched intensity=87.0%, largest gap=2, sum gaps=3, gap at S1=0
CompRef_2B_P5-29_P5-61_P6-34_P6-38_W_BI_20130503_H-JQ_f10, scan:17519

SSLVIPSISK 144.10207@K10,144.10207@S1, 3+
m= 1317.8112, matched intensity=63.6%, largest gap=0, sum gaps=0, gap at I5=0
CompRef_2A_P5-29_P5-61_P6-34_P6-38_W_BI_20130502_H-JQ_f17, scan:22034